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(54) ESOPHAGEAL CANCER DETECTION KIT OR DEVICE, AND DETECTION METHOD

(57) It is intended to provide a kit or a device for the detection of esophageal cancer and a method for detecting esophageal cancer. The present invention provides a kit or a device for the detection of esophageal cancer, comprising nucleic acid(s) capable of specifically binding to miRNA(s) in a sample of a subject, and a method for detecting esophageal 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 esophageal cancer, comprising a nucleic acid capable of specifically binding to a particular miRNA, which is used for examining the presence or absence of esophageal cancer in a subject, and a method for detecting esophageal cancer, comprising measuring an expression level of the miRNA using the nucleic acid.

Background Art

[0002] The esophagus is a tubular organ that conveys food from the mouth to the stomach, and is positioned between the trachea and the backbone. The wall of the esophagus is divided into 4 layers: mucosa, submucosa, proper muscular layer, and outer membrane from inside toward outside. These layers have their respective functions of conveying food from the mouth to the stomach (Non-Patent Literature 1). According to the 2012 statistics of cancer type in Japan disclosed by the Center for Cancer Control and Information Services, National Cancer Center, the number of esophageal cancer deaths climbed to 11,592 people, and esophageal cancer is the 10th leading cause of cancer type-specific mortality. Japanese men have 5.6 times higher risk of mortality due to esophageal cancer than women, and smoking and alcohol intake are reported risk factors for esophageal cancer (Non-Patent Literature 1). Also, it is estimated that one out of 125 American men and one out of 435 American women experience esophageal cancer. The estimated number of individuals affected by esophageal cancer in 2014 climbed to 18,170 people, among which approximately 15,450 people reportedly died (Non-Patent Literature 1).

[0003] The progressed stages of esophageal cancer are defined in Non-Patent Literature 2 and classified into stage 0 (Tis/N0/M0), stage IA (T1/N0/M0), stage IB (T2/N0/M0), stage IIA (T3/N0/M0), stage IIB (T1 to T2/N1/M0s), stage IIIA (T4a/N0/M0, T3/N1/M0, and T1 to T2/N2/M0), stage IIIB (T3/N2/M0), stage IIIC (T4a/N1 to N2/M0, T4b/M0, and N3/M0), and stage IV (M1) according to tumor size (Tis, T1 to T3, and T4a to T4b), lymph node metastasis (N1 to N3), distant metastasis (M0 to M1), etc.

[0004] The 5-year relative survival rate of esophageal cancer largely depends on the stages of cancer progression and is reportedly 39% for tumors limited to esophageal tissues, 21% for tumors limited to esophageal and adjacent tissues, and 4% for tumors that have metastasized distantly (Non-Patent Literature 1). Thus, the early detection of esophageal cancer leads to drastic improvement in the survival rate. Therefore, the provision of an approach that permits the early detection is strongly desired.

[0005] The method for treating esophageal cancer is determined in view of the stages of cancer progression and general conditions and mainly includes endoscopic therapy, surgery, radiotherapy, and anticancer agents. Esophageal cancer that has progressed to some extent is treated by multimodality therapy which combines these treatment methods to exert synergistic effects by exploiting their respective features (Non-Patent Literature 1). Early esophageal cancer at stage 0, 1, or the like may be adaptable to endoscopic therapy or photo dynamic therapy, which places less burden on patients (Non-Patent Literature 1).

[0006] According to Non-Patent Literature 1, initial diagnostic tests of esophageal cancer are X-ray esophagography and endoscopy. In addition, CT scan, MRI scan, endosonography, ultrasonography, or the like is performed in order to examine the degree of cancer spread. When there are findings on suspected esophageal cancer by these initial tests, pathological examination which involves inserting a needle into a lesion and collecting cells or tissues to be examined under a microscope is carried out as a secondary test. For example, CEA and SCC are known as tumor markers in blood for the detection of esophageal cancer (Non-Patent Literature 3).

[0007] As shown in Patent Literature 1, there is a report, albeit at a research stage, on the detection of esophageal 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 esophageal cancer by measuring miRNAs such as miR-663a, miR-92a-3p, and miR-575 in serum.

Citation List

Patent Literature

[0009] Patent Literature 1: Published U.S. Patent Application No. 2014/031246

Non-Patent Literature

[0010]

Non-Patent Literature 1: American Cancer Society, "Esophagus Cancer", 2014, p. 2 to 8, 19 to 20, and 29 to 41
Non-Patent Literature 2: Sobin, L. et al., "TNM Classification of Malignant Tumours, the 7th edition, Japanese version", 2009, p. 63 to 68
Non-Patent Literature 3: Terada, T. et al., 2013, International Journal of Clinical and Experimental Medicine, Vol. 6 (3), p. 219-26

Summary of Invention

Technical Problem

[0011] An object of the present invention is to find a novel tumor marker for esophageal cancer and to provide a method that can effectively detect esophageal cancer using a nucleic acid capable of specifically binding to the marker.

[0012] As described in Non-Patent Literature 1, general tests of esophageal cancer are X-ray esophagography and endoscopy. However, ordinary medical checkup places emphasis on stomach cancer screening and often insufficiently observes the esophagus. Although these tests are now popularized, the number of esophageal cancer deaths in Japan is still increasing. Thus, such diagnostic imaging cannot always serve as a deterrent against esophageal cancer. In addition, CT scan or MRI scan is capable of detecting esophageal cancer with high performance, but requires a special apparatus and high examination costs. Therefore, these tests are not suitable for widely used as primary tests for esophageal cancer.

[0013] For example, CEA and SCC are known as tumor markers in blood for the detection of esophageal cancer (Non-Patent Literature 3). These markers, however, present problems associated with accuracy in such a way that the markers also elevate in cancers other than esophageal cancer. Therefore, their usefulness has not yet been established. If use of these markers causes false diagnosis of other cancers as esophageal cancer, this wastes appropriate therapeutic opportunity or places unnecessary economical and physical burdens on patients due to the application of wrong medicine. Hence, the esophageal cancer guidebook provided by the American Cancer Society makes no mention about these markers (Non-Patent Literature 1).

[0014] As described below, there is a report, albeit at a research stage, on the determination of esophageal cancer using the expression levels of microRNAs (miRNAs) in biological samples including blood, none of which, however, have yet to be brought into the practical use.

[0015] Patent Literature 1 discloses a method for detecting esophageal cancer by measuring miRNAs such as miR-663a, miR-92a-3p, and miR-575 in serum. Specifically, this literature shows a list of miRNAs that vary in serum in 16 esophageal cancer patients compared with 12 healthy subjects, and the presence or absence of esophageal cancer is determined by measuring the expression levels of these miRNAs. This detection method, however, includes few Examples or statements regarding specific detection performance such as accuracy, sensitivity, or specificity for determining esophageal cancer, and is thus industrially less practical. hsa-miR-345, which was only one miRNA validated therein, had AUC of 0.814 and is difficult to use alone for determining esophageal cancer according to the description.

[0016] As mentioned above, the existing tumor markers exhibit low performance in the detection of esophageal 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 carrying out needless extra examination due to the false detection of healthy subjects as being esophageal cancer patients, or might waste therapeutic opportunity because of overlooking esophageal cancer patients. In addition, the measurement of dozens of miRNAs increases examination costs and is therefore difficult to use in large-scale screening such as medical checkup. Furthermore, the collection of esophageal tissues for measuring the tumor markers is highly invasive to patients and is not favorable. Hence, there is a demand for a highly accurate esophageal cancer marker that is detectable from blood, which can be collected with limited invasiveness, and is capable of correctly identifying an esophageal cancer patient as an esophageal cancer patient and a healthy subject as a healthy subject. Particularly, the early detection and treatment of esophageal cancer can drastically improve survival rates. In addition, endoscopic therapy or photo dynamic therapy which places less burden on patients can be applied as a therapeutic choice. Therefore, a highly sensitive esophageal cancer marker capable of detecting esophageal cancer even at an early progressed stage is desired.

Solution to Problem

[0017] 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 esophageal cancer from blood and

finding that esophageal cancer can be significantly detected by using nucleic acids capable of specifically binding to any of these markers.

<Summary of Invention>

[0018] The present invention has the following features:

(1) A kit for the detection of esophageal cancer, comprising nucleic acid(s) capable of specifically binding to at least one polynucleotide selected from the group consisting of the following esophageal cancer markers: miR-204-3p, miR-1247-3p, miR-6875-5p, miR-6857-5p, miR-6726-5p, miR-3188, miR-8069, miR-4257, miR-1343-3p, miR-7108-5p, miR-6825-5p, miR-7641, miR-3185, miR-4746-3p, miR-6791-5p, miR-6893-5p, miR-4433b-3p, miR-3135b, miR-6781-5p, miR-1908-5p, miR-4792, miR-7845-5p, miR-4417, miR-3184-5p, miR-1225-5p, miR-1231, miR-1225-3p, miR-150-3p, miR-4433-3p, miR-6125, miR-4513, miR-6787-5p, miR-6784-5p, miR-615-5p, miR-6765-3p, miR-5572, miR-6842-5p, miR-8063, miR-6780b-5p, miR-187-5p, miR-128-1-5p, miR-6729-5p, miR-6741-5p, miR-6757-5p, miR-7110-5p, miR-7975, miR-1233-5p, miR-6845-5p, miR-3937, miR-4467, miR-7109-5p, miR-6088, miR-6782-5p, miR-5195-3p, miR-4454, miR-6724-5p, miR-8072, miR-4516, miR-6756-5p, miR-4665-3p, miR-6826-5p, miR-6820-5p, miR-6887-5p, miR-3679-5p, miR-7847-3p, miR-6721-5p, miR-3622a-5p, miR-939-5p, miR-602, miR-7977, miR-6749-5p, miR-1914-3p, miR-4651, miR-4695-5p, miR-6848-5p, miR-1228-3p, miR-642b-3p, miR-6746-5p, miR-3620-5p, miR-3131, miR-6732-5p, miR-7113-3p, miR-23a-3p, miR-3154, miR-4723-5p, miR-3663-3p, miR-4734, miR-6816-5p, miR-4442, miR-4476, miR-423-5p, miR-1249, miR-6515-3p, miR-887-3p, miR-4741, miR-6766-3p, miR-4673, miR-6779-5p, miR-4706, miR-1268b, miR-4632-5p, miR-3197, miR-6798-5p, miR-711, miR-6840-3p, miR-6763-5p, miR-6727-5p, miR-371a-5p, miR-6824-5p, miR-4648, miR-1227-5p, miR-564, miR-3679-3p, miR-2861, miR-6737-5p, miR-4725-3p, miR-6716-5p, miR-4675, miR-1915-3p, miR-671-5p, miR-3656, miR-6722-3p, miR-4707-5p, miR-4449, miR-1202, miR-4649-5p, miR-744-5p, miR-642a-3p, miR-451a, miR-6870-5p, miR-4443, miR-6808-5p, miR-4728-5p, miR-937-5p, miR-135a-3p, miR-663b, miR-1343-5p, miR-6822-5p, miR-6803-5p, miR-6805-3p, miR-128-2-5p, miR-4640-5p, miR-1469, miR-92a-2-5p, miR-3940-5p, miR-4281, miR-1260b, miR-4758-5p, miR-1915-5p, miR-5001-5p, miR-4286, miR-6126, miR-6789-5p, miR-4459, miR-1268a, miR-6752-5p, miR-6131, miR-6800-5p, miR-4532, miR-6872-3p, miR-718, miR-6769a-5p, miR-4707-3p, miR-6765-5p, miR-4739, miR-4525, miR-4270, miR-4534, miR-6785-5p, miR-6850-5p, miR-4697-5p, miR-1260a, miR-4486, miR-6880-5p, miR-6802-5p, miR-6861-5p, miR-92b-5p, miR-1238-5p, miR-6851-5p, miR-7704, miR-149-3p, miR-4689, miR-4688, miR-125a-3p, miR-23b-3p, miR-614, miR-1913, miR-16-5p, miR-6717-5p, miR-3648, miR-3162-5p, miR-1909-3p, miR-8073, miR-6769b-5p, miR-6836-3p, miR-4484, miR-6819-5p and miR-6794-5p.

(2) The kit according to (1), wherein miR-204-3p is hsa-miR-204-3p, miR-1247-3p is hsa-miR-1247-3p, miR-6875-5p is hsa-miR-6875-5p, miR-6857-5p is hsa-miR-6857-5p, miR-6726-5p is hsa-miR-6726-5p, miR-3188 is hsa-miR-3188, miR-8069 is hsa-miR-8069, miR-4257 is hsa-miR-4257, miR-1343-3p is hsa-miR-1343-3p, miR-7108-5p is hsa-miR-7108-5p, miR-6825-5p is hsa-miR-6825-5p, miR-7641 is hsa-miR-7641, miR-3185 is hsa-miR-3185, miR-4746-3p is hsa-miR-4746-3p, miR-6791-5p is hsa-miR-6791-5p, miR-6893-5p is hsa-miR-6893-5p, miR-4433b-3p is hsa-miR-4433b-3p, miR-3135b is hsa-miR-3135b, miR-6781-5p is hsa-miR-6781-5p, miR-1908-5p is hsa-miR-1908-5p, miR-4792 is hsa-miR-4792, miR-7845-5p is hsa-miR-7845-5p, miR-4417 is hsa-miR-4417, miR-3184-5p is hsa-miR-3184-5p, miR-1225-5p is hsa-miR-1225-5p, miR-1231 is hsa-miR-1231, miR-1225-3p is hsa-miR-1225-3p, miR-150-3p is hsa-miR-150-3p, miR-4433-3p is hsa-miR-4433-3p, miR-6125 is hsa-miR-6125, miR-4513 is hsa-miR-4513, miR-6787-5p is hsa-miR-6787-5p, miR-6784-5p is hsa-miR-6784-5p, miR-615-5p is hsa-miR-615-5p, miR-6765-3p is hsa-miR-6765-3p, miR-5572 is hsa-miR-5572, miR-6842-5p is hsa-miR-6842-5p, miR-8063 is hsa-miR-8063, miR-6780b-5p is hsa-miR-6780b-5p, miR-187-5p is hsa-miR-187-5p, miR-128-1-5p is hsa-miR-128-1-5p, miR-6729-5p is hsa-miR-6729-5p, miR-6741-5p is hsa-miR-6741-5p, miR-6757-5p is hsa-miR-6757-5p, miR-7110-5p is hsa-miR-7110-5p, miR-7975 is hsa-miR-7975, miR-1233-5p is hsa-miR-1233-5p, miR-6845-5p is hsa-miR-6845-5p, miR-3937 is hsa-miR-3937, miR-4467 is hsa-miR-4467, miR-7109-5p is hsa-miR-7109-5p, miR-6088 is hsa-miR-6088, miR-6782-5p is hsa-miR-6782-5p, miR-5195-3p is hsa-miR-5195-3p, miR-4454 is hsa-miR-4454, miR-6724-5p is hsa-miR-6724-5p, miR-8072 is hsa-miR-8072, miR-4516 is hsa-miR-4516, miR-6756-5p is hsa-miR-6756-5p, miR-4665-3p is hsa-miR-4665-3p, miR-6826-5p is hsa-miR-6826-5p, miR-6820-5p is hsa-miR-6820-5p, miR-6887-5p is hsa-miR-6887-5p, miR-3679-5p is hsa-miR-3679-5p, miR-7847-3p is hsa-miR-7847-3p, miR-6721-5p is hsa-miR-6721-5p, miR-3622a-5p is hsa-miR-3622a-5p, miR-939-5p is hsa-miR-939-5p, miR-602 is hsa-miR-602, miR-7977 is hsa-miR-7977, miR-6749-5p is hsa-miR-6749-5p, miR-1914-3p is hsa-miR-1914-3p, miR-4651 is hsa-miR-4651, miR-4695-5p is hsa-miR-4695-5p, miR-6848-5p is hsa-miR-6848-5p, miR-1228-3p is hsa-miR-1228-3p, miR-642b-3p is hsa-miR-642b-3p, miR-6746-5p is hsa-miR-6746-5p, miR-3620-5p is hsa-miR-3620-5p, miR-3131 is hsa-miR-3131, miR-6732-5p is hsa-miR-6732-5p, miR-7113-3p is hsa-miR-7113-3p, miR-23a-3p is hsa-miR-23a-3p, miR-3154 is hsa-miR-3154, miR-4723-5p is hsa-miR-4723-5p, miR-3663-3p is hsa-miR-3663-3p, miR-4734 is hsa-miR-4734, miR-6816-5p is hsa-miR-6816-5p, miR-4442 is hsa-miR-4442, miR-4476 is

hsa-miR-4476, miR-423-5p is hsa-miR-423-5p, miR-1249 is hsa-miR-1249, miR-6515-3p is hsa-miR-6515-3p, miR-887-3p is hsa-miR-887-3p, miR-4741 is hsa-miR-4741, miR-6766-3p is hsa-miR-6766-3p, miR-4673 is hsa-miR-4673, miR-6779-5p is hsa-miR-6779-5p, miR-4706 is hsa-miR-4706, miR-1268b is hsa-miR-1268b, miR-4632-5p is hsa-miR-4632-5p, miR-3197 is hsa-miR-3197, miR-6798-5p is hsa-miR-6798-5p, miR-711 is hsa-miR-711, miR-6840-3p is hsa-miR-6840-3p, miR-6763-5p is hsa-miR-6763-5p, miR-6727-5p is hsa-miR-6727-5p, miR-371a-5p is hsa-miR-371a-5p, miR-6824-5p is hsa-miR-6824-5p, miR-4648 is hsa-miR-4648, miR-1227-5p is hsa-miR-1227-5p, miR-564 is hsa-miR-564, miR-3679-3p is hsa-miR-3679-3p, miR-2861 is hsa-miR-2861, miR-6737-5p is hsa-miR-6737-5p, miR-4725-3p is hsa-miR-4725-3p, miR-6716-5p is hsa-miR-6716-5p, miR-4675 is hsa-miR-4675, miR-1915-3p is hsa-miR-1915-3p, miR-671-5p is hsa-miR-671-5p, miR-3656 is hsa-miR-3656, miR-6722-3p is hsa-miR-6722-3p, miR-4707-5p is hsa-miR-4707-5p, miR-4449 is hsa-miR-4449, miR-1202 is hsa-miR-1202, miR-4649-5p is hsa-miR-4649-5p, miR-744-5p is hsa-miR-744-5p, miR-642a-3p is hsa-miR-642a-3p, miR-451a is hsa-miR-451a, miR-6870-5p is hsa-miR-6870-5p, miR-4443 is hsa-miR-4443, miR-6808-5p is hsa-miR-6808-5p, miR-4728-5p is hsa-miR-4728-5p, miR-937-5p is hsa-miR-937-5p, miR-135a-3p is hsa-miR-135a-3p, miR-663b is hsa-miR-663b, miR-1343-5p is hsa-miR-1343-5p, miR-6822-5p is hsa-miR-6822-5p, miR-6803-5p is hsa-miR-6803-5p, miR-6805-3p is hsa-miR-6805-3p, miR-128-2-5p is hsa-miR-128-2-5p, miR-4640-5p is hsa-miR-4640-5p, miR-1469 is hsa-miR-1469, miR-92a-2-5p is hsa-miR-92a-2-5p, miR-3940-5p is hsa-miR-3940-5p, miR-4281 is hsa-miR-4281, miR-1260b is hsa-miR-1260b, miR-4758-5p is hsa-miR-4758-5p, miR-1915-5p is hsa-miR-1915-5p, miR-5001-5p is hsa-miR-5001-5p, miR-4286 is hsa-miR-4286, miR-6126 is hsa-miR-6126, miR-6789-5p is hsa-miR-6789-5p, miR-4459 is hsa-miR-4459, miR-1268a is hsa-miR-1268a, miR-6752-5p is hsa-miR-6752-5p, miR-6131 is hsa-miR-6131, miR-6800-5p is hsa-miR-6800-5p, miR-4532 is hsa-miR-4532, miR-6872-3p is hsa-miR-6872-3p, miR-718 is hsa-miR-718, miR-6769a-5p is hsa-miR-6769a-5p, miR-4707-3p is hsa-miR-4707-3p, miR-6765-5p is hsa-miR-6765-5p, miR-4739 is hsa-miR-4739, miR-4525 is hsa-miR-4525, miR-4270 is hsa-miR-4270, miR-4534 is hsa-miR-4534, miR-6785-5p is hsa-miR-6785-5p, miR-6850-5p is hsa-miR-6850-5p, miR-4697-5p is hsa-miR-4697-5p, miR-1260a is hsa-miR-1260a, miR-4486 is hsa-miR-4486, miR-6880-5p is hsa-miR-6880-5p, miR-6802-5p is hsa-miR-6802-5p, miR-6861-5p is hsa-miR-6861-5p, miR-92b-5p is hsa-miR-92b-5p, miR-1238-5p is hsa-miR-1238-5p, miR-6851-5p is hsa-miR-6851-5p, miR-7704 is hsa-miR-7704, miR-149-3p is hsa-miR-149-3p, miR-4689 is hsa-miR-4689, miR-4688 is hsa-miR-4688, miR-125a-3p is hsa-miR-125a-3p, miR-23b-3p is hsa-miR-23b-3p, miR-614 is hsa-miR-614, miR-1913 is hsa-miR-1913, miR-16-5p is hsa-miR-16-5p, miR-6717-5p is hsa-miR-6717-5p, miR-3648 is hsa-miR-3648, miR-3162-5p is hsa-miR-3162-5p, miR-1909-3p is hsa-miR-1909-3p, miR-8073 is hsa-miR-8073, miR-6769b-5p is hsa-miR-6769b-5p, miR-6836-3p is hsa-miR-6836-3p, miR-4484 is hsa-miR-4484, miR-6819-5p is hsa-miR-6819-5p, and miR-6794-5p is hsa-miR-6794-5p.

(3) The kit according to (1) or (2), wherein the nucleic acid(s) is/are 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 115, 117 to 189, and 666 to 675 or a nucleotide sequence 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 115, 117 to 189, and 666 to 675,
(c) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 1 to 115, 117 to 189, and 666 to 675 or a nucleotide sequence 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 115, 117 to 189, and 666 to 675 or a nucleotide sequence 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 polynucleotide(s) selected from other esophageal cancer markers miR-575 and miR-24-3p.

(5) The kit according to (4), wherein miR-575 is hsa-miR-575, and miR-24-3p is hsa-miR-24-3p.

(6) The kit according to (4) or (5), wherein the nucleic acid(s) is/are polynucleotide(s) 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: 116 and 676 or a nucleotide sequence 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: 116 and 676,

(h) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 116 and 676 or a nucleotide sequence 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: 116 and 676 or a nucleotide sequence 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 of (1) to (6), wherein the kit further comprises a nucleic acid capable of specifically binding to at least one polynucleotide selected from the group consisting of the following other esophageal cancer markers: miR-675-5p, miR-486-3p, miR-6777-5p, miR-4497, miR-296-3p, miR-6738-5p, miR-4731-5p, miR-6889-5p, miR-6786-5p, miR-92a-3p, miR-4294, miR-4763-3p, miR-6076, miR-663a, miR-760, miR-4667-5p, miR-6090, miR-4730, miR-7106-5p, miR-3196, miR-5698, miR-6087, miR-4665-5p, miR-8059 and miR-6879-5p.

(8) The kit according to (7), wherein miR-675-5p is hsa-miR-675-5p, miR-486-3p is hsa-miR-486-3p, miR-6777-5p is hsa-miR-6777-5p, miR-4497 is hsa-miR-4497, miR-296-3p is hsa-miR-296-3p, miR-6738-5p is hsa-miR-6738-5p, miR-4731-5p is hsa-miR-4731-5p, miR-6889-5p is hsa-miR-6889-5p, miR-6786-5p is hsa-miR-6786-5p, miR-92a-3p is hsa-miR-92a-3p, miR-4294 is hsa-miR-4294, miR-4763-3p is hsa-miR-4763-3p, miR-6076 is hsa-miR-6076, miR-663a is hsa-miR-663a, miR-760 is hsa-miR-760, miR-4667-5p is hsa-miR-4667-5p, miR-6090 is hsa-miR-6090, miR-4730 is hsa-miR-4730, miR-7106-5p is hsa-miR-7106-5p, miR-3196 is hsa-miR-3196, miR-5698 is hsa-miR-5698, miR-6087 is hsa-miR-6087, miR-4665-5p is hsa-miR-4665-5p, miR-8059 is hsa-miR-8059, and miR-6879-5p is hsa-miR-6879-5p.

(9) The kit according to (7) or (8), wherein the nucleic acid(s) is/are polynucleotide(s) 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: 190 to 214 or a nucleotide sequence 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: 190 to 214,

(m) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 190 to 214 or a nucleotide sequence 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: 190 to 214 or a nucleotide sequence 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 of (1) to (9), wherein the kit comprises at least two nucleic acids capable of specifically binding to at least two polynucleotides, respectively, selected from all of the esophageal cancer markers according to (1) or (2).

(11) A device for the detection of esophageal cancer, comprising nucleic acid(s) capable of specifically binding to at least one polynucleotide selected from the group consisting of the following esophageal cancer markers: miR-204-3p, miR-1247-3p, miR-6875-5p, miR-6857-5p, miR-6726-5p, miR-3188, miR-8069, miR-4257, miR-1343-3p, miR-7108-5p, miR-6825-5p, miR-7641, miR-3185, miR-4746-3p, miR-6791-5p, miR-6893-5p, miR-4433b-3p, miR-3135b, miR-6781-5p, miR-1908-5p, miR-4792, miR-7845-5p, miR-4417, miR-3184-5p, miR-1225-5p, miR-1231, miR-1225-3p, miR-150-3p, miR-4433-3p, miR-6125, miR-4513, miR-6787-5p, miR-6784-5p, miR-615-5p, miR-6765-3p, miR-5572, miR-6842-5p, miR-8063, miR-6780b-5p, miR-187-5p, miR-128-1-5p, miR-6729-5p, miR-6741-5p, miR-6757-5p, miR-7110-5p, miR-7975, miR-1233-5p, miR-6845-5p, miR-3937, miR-4467, miR-7109-5p, miR-6088, miR-6782-5p, miR-5195-3p, miR-4454, miR-6724-5p, miR-8072, miR-4516, miR-6756-5p, miR-4665-3p, miR-6826-5p, miR-6820-5p, miR-6887-5p, miR-3679-5p, miR-7847-3p, miR-6721-5p, miR-3622a-5p, miR-939-5p, miR-602, miR-7977, miR-6749-5p, miR-1914-3p, miR-4651, miR-4695-5p, miR-6848-5p, miR-1228-3p, miR-642b-3p, miR-6746-5p, miR-3620-5p, miR-3131, miR-6732-5p, miR-7113-3p, miR-23a-3p, miR-3154, miR-4723-5p, miR-3663-3p, miR-4734, miR-6816-5p, miR-4442, miR-4476, miR-423-5p, miR-1249, miR-6515-3p, miR-887-3p, miR-4741, miR-6766-3p, miR-4673, miR-6779-5p, miR-4706, miR-1268b, miR-4632-5p, miR-3197, miR-6798-5p, miR-711, miR-6840-3p, miR-6763-5p, miR-6727-5p, miR-371a-5p, miR-6824-5p, miR-4648, miR-1227-5p, miR-564, miR-3679-3p, miR-2861, miR-6737-5p, miR-4725-3p, miR-6716-5p, miR-4675, miR-1915-3p, miR-671-5p, miR-3656, miR-6722-3p, miR-4707-5p, miR-4449, miR-1202, miR-4649-5p, miR-744-5p, miR-642a-3p, miR-451a, miR-

6870-5p, miR-4443, miR-6808-5p, miR-4728-5p, miR-937-5p, miR-135a-3p, miR-663b, miR-1343-5p, miR-6822-5p, miR-6803-5p, miR-6805-3p, miR-128-2-5p, miR-4640-5p, miR-1469, miR-92a-2-5p, miR-3940-5p, miR-4281, miR-1260b, miR-4758-5p, miR-1915-5p, miR-5001-5p, miR-4286, miR-6126, miR-6789-5p, miR-4459, miR-1268a, miR-6752-5p, miR-6131, miR-6800-5p, miR-4532, miR-6872-3p, miR-718, miR-6769a-5p, miR-4707-3p, miR-6765-5p, miR-4739, miR-4525, miR-4270, miR-4534, miR-6785-5p, miR-6850-5p, miR-4697-5p, miR-1260a, miR-4486, miR-6880-5p, miR-6802-5p, miR-6861-5p, miR-92b-5p, miR-1238-5p, miR-6851-5p, miR-7704, miR-149-3p, miR-4689, miR-4688, miR-125a-3p, miR-23b-3p, miR-614, miR-1913, miR-16-5p, miR-6717-5p, miR-3648, miR-3162-5p, miR-1909-3p, miR-8073, miR-6769b-5p, miR-6836-3p, miR-4484, miR-6819-5p and miR-6794-5p.

(12) The device according to (11), wherein miR-204-3p is hsa-miR-204-3p, miR-1247-3p is hsa-miR-1247-3p, miR-6875-5p is hsa-miR-6875-5p, miR-6857-5p is hsa-miR-6857-5p, miR-6726-5p is hsa-miR-6726-5p, miR-3188 is hsa-miR-3188, miR-8069 is hsa-miR-8069, miR-4257 is hsa-miR-4257, miR-1343-3p is hsa-miR-1343-3p, miR-7108-5p is hsa-miR-7108-5p, miR-6825-5p is hsa-miR-6825-5p, miR-7641 is hsa-miR-7641, miR-3185 is hsa-miR-3185, miR-4746-3p is hsa-miR-4746-3p, miR-6791-5p is hsa-miR-6791-5p, miR-6893-5p is hsa-miR-6893-5p, miR-4433b-3p is hsa-miR-4433b-3p, miR-3135b is hsa-miR-3135b, miR-6781-5p is hsa-miR-6781-5p, miR-1908-5p is hsa-miR-1908-5p, miR-4792 is hsa-miR-4792, miR-7845-5p is hsa-miR-7845-5p, miR-4417 is hsa-miR-4417, miR-3184-5p is hsa-miR-3184-5p, miR-1225-5p is hsa-miR-1225-5p, miR-1231 is hsa-miR-1231, miR-1225-3p is hsa-miR-1225-3p, miR-150-3p is hsa-miR-150-3p, miR-4433-3p is hsa-miR-4433-3p, miR-6125 is hsa-miR-6125, miR-4513 is hsa-miR-4513, miR-6787-5p is hsa-miR-6787-5p, miR-6784-5p is hsa-miR-6784-5p, miR-615-5p is hsa-miR-615-5p, miR-6765-3p is hsa-miR-6765-3p, miR-5572 is hsa-miR-5572, miR-6842-5p is hsa-miR-6842-5p, miR-8063 is hsa-miR-8063, miR-6780b-5p is hsa-miR-6780b-5p, miR-187-5p is hsa-miR-187-5p, miR-128-1-5p is hsa-miR-128-1-5p, miR-6729-5p is hsa-miR-6729-5p, miR-6741-5p is hsa-miR-6741-5p, miR-6757-5p is hsa-miR-6757-5p, miR-7110-5p is hsa-miR-7110-5p, miR-7975 is hsa-miR-7975, miR-1233-5p is hsa-miR-1233-5p, miR-6845-5p is hsa-miR-6845-5p, miR-3937 is hsa-miR-3937, miR-4467 is hsa-miR-4467, miR-7109-5p is hsa-miR-7109-5p, miR-6088 is hsa-miR-6088, miR-6782-5p is hsa-miR-6782-5p, miR-5195-3p is hsa-miR-5195-3p, miR-4454 is hsa-miR-4454, miR-6724-5p is hsa-miR-6724-5p, miR-8072 is hsa-miR-8072, miR-4516 is hsa-miR-4516, miR-6756-5p is hsa-miR-6756-5p, miR-4665-3p is hsa-miR-4665-3p, miR-6826-5p is hsa-miR-6826-5p, miR-6820-5p is hsa-miR-6820-5p, miR-6887-5p is hsa-miR-6887-5p, miR-3679-5p is hsa-miR-3679-5p, miR-7847-3p is hsa-miR-7847-3p, miR-6721-5p is hsa-miR-6721-5p, miR-3622a-5p is hsa-miR-3622a-5p, miR-939-5p is hsa-miR-939-5p, miR-602 is hsa-miR-602, miR-7977 is hsa-miR-7977, miR-6749-5p is hsa-miR-6749-5p, miR-1914-3p is hsa-miR-1914-3p, miR-4651 is hsa-miR-4651, miR-4695-5p is hsa-miR-4695-5p, miR-6848-5p is hsa-miR-6848-5p, miR-1228-3p is hsa-miR-1228-3p, miR-642b-3p is hsa-miR-642b-3p, miR-6746-5p is hsa-miR-6746-5p, miR-3620-5p is hsa-miR-3620-5p, miR-3131 is hsa-miR-3131, miR-6732-5p is hsa-miR-6732-5p, miR-7113-3p is hsa-miR-7113-3p, miR-23a-3p is hsa-miR-23a-3p, miR-3154 is hsa-miR-3154, miR-4723-5p is hsa-miR-4723-5p, miR-3663-3p is hsa-miR-3663-3p, miR-4734 is hsa-miR-4734, miR-6816-5p is hsa-miR-6816-5p, miR-4442 is hsa-miR-4442, miR-4476 is hsa-miR-4476, miR-423-5p is hsa-miR-423-5p, miR-1249 is hsa-miR-1249, miR-6515-3p is hsa-miR-6515-3p, miR-887-3p is hsa-miR-887-3p, miR-4741 is hsa-miR-4741, miR-6766-3p is hsa-miR-6766-3p, miR-4673 is hsa-miR-4673, miR-6779-5p is hsa-miR-6779-5p, miR-4706 is hsa-miR-4706, miR-1268b is hsa-miR-1268b, miR-4632-5p is hsa-miR-4632-5p, miR-3197 is hsa-miR-3197, miR-6798-5p is hsa-miR-6798-5p, miR-711 is hsa-miR-711, miR-6840-3p is hsa-miR-6840-3p, miR-6763-5p is hsa-miR-6763-5p, miR-6727-5p is hsa-miR-6727-5p, miR-371a-5p is hsa-miR-371a-5p, miR-6824-5p is hsa-miR-6824-5p, miR-4648 is hsa-miR-4648, miR-1227-5p is hsa-miR-1227-5p, miR-564 is hsa-miR-564, miR-3679-3p is hsa-miR-3679-3p, miR-2861 is hsa-miR-2861, miR-6737-5p is hsa-miR-6737-5p, miR-4725-3p is hsa-miR-4725-3p, miR-6716-5p is hsa-miR-6716-5p, miR-4675 is hsa-miR-4675, miR-1915-3p is hsa-miR-1915-3p, miR-671-5p is hsa-miR-671-5p, miR-3656 is hsa-miR-3656, miR-6722-3p is hsa-miR-6722-3p, miR-4707-5p is hsa-miR-4707-5p, miR-4449 is hsa-miR-4449, miR-1202 is hsa-miR-1202, miR-4649-5p is hsa-miR-4649-5p, miR-744-5p is hsa-miR-744-5p, miR-642a-3p is hsa-miR-642a-3p, miR-451a is hsa-miR-451a, miR-6870-5p is hsa-miR-6870-5p, miR-4443 is hsa-miR-4443, miR-6808-5p is hsa-miR-6808-5p, miR-4728-5p is hsa-miR-4728-5p, miR-937-5p is hsa-miR-937-5p, miR-135a-3p is hsa-miR-135a-3p, miR-663b is hsa-miR-663b, miR-1343-5p is hsa-miR-1343-5p, miR-6822-5p is hsa-miR-6822-5p, miR-6803-5p is hsa-miR-6803-5p, miR-6805-3p is hsa-miR-6805-3p, miR-128-2-5p is hsa-miR-128-2-5p, miR-4640-5p is hsa-miR-4640-5p, miR-1469 is hsa-miR-1469, miR-92a-2-5p is hsa-miR-92a-2-5p, miR-3940-5p is hsa-miR-3940-5p, miR-4281 is hsa-miR-4281, miR-1260b is hsa-miR-1260b, miR-4758-5p is hsa-miR-4758-5p, miR-1915-5p is hsa-miR-1915-5p, miR-5001-5p is hsa-miR-5001-5p, miR-4286 is hsa-miR-4286, miR-6126 is hsa-miR-6126, miR-6789-5p is hsa-miR-6789-5p, miR-4459 is hsa-miR-4459, miR-1268a is hsa-miR-1268a, miR-6752-5p is hsa-miR-6752-5p, miR-6131 is hsa-miR-6131, miR-6800-5p is hsa-miR-6800-5p, miR-4532 is hsa-miR-4532, miR-6872-3p is hsa-miR-6872-3p, miR-718 is hsa-miR-718, miR-6769a-5p is hsa-miR-6769a-5p, miR-4707-3p is hsa-miR-4707-3p, miR-6765-5p is hsa-miR-6765-5p, miR-4739 is hsa-miR-4739, miR-4525 is hsa-miR-4525, miR-4270 is hsa-miR-4270, miR-4534 is hsa-miR-4534, miR-6785-5p is hsa-miR-6785-5p, miR-6850-5p is hsa-miR-6850-5p, miR-4697-5p is hsa-miR-4697-5p, miR-1260a is hsa-miR-1260a, miR-4486 is hsa-miR-4486, miR-6880-5p is hsa-

miR-6880-5p, miR-6802-5p is hsa-miR-6802-5p, miR-6861-5p is hsa-miR-6861-5p, miR-92b-5p is hsa-miR-92b-5p, miR-1238-5p is hsa-miR-1238-5p, miR-6851-5p is hsa-miR-6851-5p, miR-7704 is hsa-miR-7704, miR-149-3p is hsa-miR-149-3p, miR-4689 is hsa-miR-4689, miR-4688 is hsa-miR-4688, miR-125a-3p is hsa-miR-125a-3p, miR-23b-3p is hsa-miR-23b-3p, miR-614 is hsa-miR-614, miR-1913 is hsa-miR-1913, miR-16-5p is hsa-miR-16-5p, miR-6717-5p is hsa-miR-6717-5p, miR-3648 is hsa-miR-3648, miR-3162-5p is hsa-miR-3162-5p, miR-1909-3p is hsa-miR-1909-3p, miR-8073 is hsa-miR-8073, miR-6769b-5p is hsa-miR-6769b-5p, miR-6836-3p is hsa-miR-6836-3p, miR-4484 is hsa-miR-4484, miR-6819-5p is hsa-miR-6819-5p, and miR-6794-5p is hsa-miR-6794-5p.

(13) The device according to (11) or (12), wherein the nucleic acid(s) is/are 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 115, 117 to 189, and 666 to 675 or a nucleotide sequence 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 115, 117 to 189, and 666 to 675,
(c) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 1 to 115, 117 to 189, and 666 to 675 or a nucleotide sequence 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 115, 117 to 189, and 666 to 675 or a nucleotide sequence 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 nucleic acid(s) capable of specifically binding to polynucleotide(s) selected from other esophageal cancer markers miR-575 and miR-24-3p.

(15) The device according to (14), wherein miR-575 is hsa-miR-575, and miR-24-3p is hsa-miR-24-3p.

(16) The device according to (14) or (15), wherein the nucleic acid(s) is/are polynucleotide(s) 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: 116 and 676 or a nucleotide sequence 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: 116 and 676,
(h) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 116 and 676 or a nucleotide sequence 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: 116 and 676 or a nucleotide sequence 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 polynucleotide selected from the group consisting of the following other esophageal cancer markers: miR-675-5p, miR-486-3p, miR-6777-5p, miR-4497, miR-296-3p, miR-6738-5p, miR-4731-5p, miR-6889-5p, miR-6786-5p, miR-92a-3p, miR-4294, miR-4763-3p, miR-6076, miR-663a, miR-760, miR-4667-5p, miR-6090, miR-4730, miR-7106-5p, miR-3196, miR-5698, miR-6087, miR-4665-5p, miR-8059, and miR-6879-5p.

(18) The device according to (17), wherein miR-675-5p is hsa-miR-675-5p, miR-486-3p is hsa-miR-486-3p, miR-6777-5p is hsa-miR-6777-5p, miR-4497 is hsa-miR-4497, miR-296-3p is hsa-miR-296-3p, miR-6738-5p is hsa-miR-6738-5p, miR-4731-5p is hsa-miR-4731-5p, miR-6889-5p is hsa-miR-6889-5p, miR-6786-5p is hsa-miR-6786-5p, miR-92a-3p is hsa-miR-92a-3p, miR-4294 is hsa-miR-4294, miR-4763-3p is hsa-miR-4763-3p, miR-6076 is hsa-miR-6076, miR-663a is hsa-miR-663a, miR-760 is hsa-miR-760, miR-4667-5p is hsa-miR-4667-5p, miR-6090 is hsa-miR-6090, miR-4730 is hsa-miR-4730, miR-7106-5p is hsa-miR-7106-5p, miR-3196 is hsa-miR-3196, miR-5698 is hsa-miR-5698, miR-6087 is hsa-miR-6087, miR-4665-5p is hsa-miR-4665-5p, miR-8059 is hsa-miR-8059, and miR-6879-5p is hsa-miR-6879-5p.

(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: 190 to 214 or a nucleotide sequence 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: 190 to 214,
(m) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 190 to 214 or a nucleotide sequence 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: 190 to 214 or a nucleotide sequence 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 for measurement based on 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 of (11) to (21), wherein the device comprises at least two nucleic acids capable of specifically binding to at least two polynucleotides, respectively, selected from all of the esophageal cancer markers according to (11) or (12).
(23) A method for detecting esophageal cancer, comprising measuring an expression level of a target nucleic acid in a sample of a subject using a kit according to any of (1) to (10) or a device according to any of (11) to (22), and evaluating the subject *in vitro* as having esophageal cancer or having no esophageal cancer using the measured expression level and a control expression level of a healthy subject measured in the same way as above.
(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>

[0019] The terms used herein are defined as follows.
[0020] 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.
[0021] The term "polynucleotide" used herein refers to a nucleic acid including any of RNA, DNA, and RNA/DNA (chimera). The DNA includes any of cDNA, genomic DNA, and synthetic DNA. The aforementioned 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" used herein 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. The term "polynucleotide" used herein is used interchangeably with the term "nucleic acid".
[0022] 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.
[0023] The term "gene" used herein is intended to include not only RNA and double-stranded DNA but also 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. 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 their transcripts, unless otherwise specified. The "gene" includes not only a "gene" represented by a particular nucleotide sequence (or SEQ ID NO) but also "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 700 or a nucleotide sequence from the nucleotide sequence by the replacement of u with t. Regardless whether or not there is a difference in functional region, the "gene" can comprise, for example, expression regulatory regions, coding regions, exons, or introns. The "gene" may be contained in a cell or may exist alone after being released from a cell. Alternatively, the

"gene" may be in a state enclosed in a vesicle called exosome.

[0024] The term "exosome" used herein is a vesicle that is encapsulated by lipid bilayer and secreted from a cell. The exosome is derived from a multivesicular endosome and may incorporate biomaterials such as "genes" (e.g., RNA or DNA) or proteins when released into an extracellular environment. The exosome is known to be contained in a body fluid such as blood, serum, plasma, serum, or lymph.

[0025] The term "transcript" used herein refers to an RNA synthesized from the DNA sequence of a gene as a template. RNA polymerase binds to a site called a promoter 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 also the whole sequence from a transcription initiation site to the end of a polyA sequence, including expression regulatory regions, coding regions, exons, or introns.

[0026] Unless otherwise specified, the term "microRNA (miRNA)" used herein is intended to mean a 15- to 25-nucleotide non-coding RNA that is involved in the suppression of translation of mRNA, and that transcribed as an RNA precursor having a hairpin-like structure, cleaved by a dsRNA-cleaving enzyme which has RNase III cleavage activity, and integrated into a protein complex called RISC,.

[0027] The term "miRNA" used herein includes not only a "miRNA" represented by a particular nucleotide sequence (or SEQ ID NO) but also a precursor of the "miRNA" (pre-miRNA or pri-miRNA), and miRNAs that have 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 700. 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).

[0028] 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 from the RNA, and/or a polynucleotide complementary thereto.

[0029] The term "primer" used herein includes a polynucleotide that specifically recognizes and amplifies an RNA resulting from the expression of a gene or a polynucleotide from the RNA, and/or a polynucleotide complementary thereto. In this context, the complementary polynucleotide (complementary strand or reverse strand) means a polynucleotide in a complementary 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 700 or a nucleotide sequence 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.

[0030] 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 that is 100% complementary 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.

[0031] 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.

[0032] 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 containing 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 700 or a nucleotide sequence 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.

[0033] The term "several" or "plurality" used herein means an integer of approximately 10, 9, 8, 7, 6, 5, 4, 3, or 2.

[0034] The variant used herein can be prepared by use of a well-known technique such as site-directed mutagenesis or PCR-based mutagenesis.

[0035] The term "identity" used herein can be determined with or without an introduced gap, using a protein or gene search system based on BLAST or FASTA (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).

[0036] The term "derivative" used herein is meant to include a unlimitedly modified nucleic acid, for example, a derivative 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) n.

[0037] The "nucleic acid" used herein capable of specifically binding to a polynucleotide selected from the esophageal 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 esophageal cancer in a subject, for diagnosing the presence or absence of esophageal cancer the severity of esophageal cancer, the presence or absence of amelioration or the degree of amelioration of esophageal cancer, or the therapeutic sensitivity of esophageal cancer, or for screening for a candidate substance useful in the prevention, amelioration, or treatment of esophageal 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 700 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 esophageal 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.*

[0038] The term "detection" used herein is interchangeable with the term "examination", "measurement", "detection", or "decision support". The term "evaluation" used herein is meant to include diagnosing or evaluation-supporting on the basis of examination results or measurement results.

[0039] 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, i.e., esophageal cancer.

[0040] The term "P" or "P value" used herein refers to a probability at which a more extreme statistic than that actually calculated from data under null hypothesis is observed in a statistical test. Thus, smaller "P" or "P value" s regarded as being a more significant difference between subjects to be compared.

[0041] 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 esophageal cancer to be detected early, leading to the complete resection of cancer sites and reduction in the rate of recurrence.

[0042] 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 esophageal cancer patients, leading to reduction in burden on patients and reduction in medical expense.

[0043] 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 identified correctly in the discriminant results to all samples and serves as a primary index for evaluating detection performance.

[0044] The "sample" used herein that is subjected 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 esophageal cancer develops, as esophageal cancer progresses, or as therapeutic effects on esophageal cancer are exerted. Specifically, the "sample" refers to an esophageal tissue, a periesophageal vascular channel, 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.

[0045] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 1, 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: 215) having a hairpin-like structure is known as a precursor of "hsa-miR-204-3p".

[0046] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 2, 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: 216) having a hairpin-like structure is known as a precursor of "hsa-miR-1247-3p".

[0047] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 3, 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: 217) having a hairpin-like structure is known as a precursor of "hsa-miR-6875-5p".

[0048] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 4, 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: 218) having a hairpin-like structure is known as a precursor of "hsa-miR-6857-5p".

[0049] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 5, 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: 219) having a hairpin-like structure is known as a precursor of "hsa-miR-6726-5p".

[0050] The term "hsa-miR-3188 gene" or "hsa-miR-3188" used herein includes the hsa-miR-3188 gene (miRBase Accession No. MIMAT0015070) consisting of the nucleotide sequence represented by SEQ ID NO: 6, 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: 220) having a hairpin-like structure is known as a precursor of "hsa-miR-3188".

[0051] The term "hsa-miR-8069 gene" or "hsa-miR-8069" used herein includes the hsa-miR-8069 gene (miRBase Accession No. MIMAT0030996) consisting of the nucleotide sequence represented by SEQ ID NO: 7, 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: 221) having a hairpin-like structure is known as a precursor of "hsa-miR-8069".

[0052] The term "hsa-miR-4257 gene" or "hsa-miR-4257" used herein includes the hsa-miR-4257 gene (miRBase Accession No. MIMAT0016878) consisting of the nucleotide sequence represented by SEQ ID NO: 8, 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: 222) having a hairpin-like structure is known as a precursor of "hsa-miR-4257".

[0053] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 9, 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: 223) having a hairpin-like structure is known as a precursor of "hsa-miR-1343-3p".

[0054] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 10, 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: 224) having a hairpin-like structure is known as a precursor of "hsa-miR-7108-5p".

[0055] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 11, 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: 225) having a hairpin-like structure is known as a precursor of "hsa-miR-6825-5p".

[0056] The term "hsa-miR-7641 gene" or "hsa-miR-7641" used herein includes the hsa-miR-7641 gene (miRBase Accession No. MIMAT0029782) consisting of the nucleotide sequence represented by 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: 226 and 227) having a hairpin-like structure are known as precursors of "hsa-miR-7641".

[0057] The term "hsa-miR-3185 gene" or "hsa-miR-3185" used herein includes the hsa-miR-3185 gene (miRBase Accession No. MIMAT0015065) consisting of the nucleotide sequence represented by SEQ ID NO: 13, 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: 228) having a hairpin-like structure is known as a precursor of "hsa-miR-3185".

[0058] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 14, 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: 229) having a hairpin-like structure is known as a precursor of "hsa-miR-4746-3p".

[0059] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 15, 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: 230) having a hairpin-like structure is known as a precursor of "hsa-miR-6791-5p".

[0060] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 16, 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: 231) having a hairpin-like structure is known as a precursor of "hsa-miR-6893-5p".

[0061] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 17, 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: 232) having a hairpin-like structure is known as a precursor of "hsa-miR-4433b-3p".

[0062] The term "hsa-miR-3135b gene" or "hsa-miR-3135b" used herein includes the hsa-miR-3135b gene (miRBase Accession No. MIMAT0018985) consisting of the nucleotide sequence represented by SEQ ID NO: 18, 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: 233) having a hairpin-like structure is known as a precursor of "hsa-miR-3135b".

[0063] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 19, 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: 234) having a hairpin-like structure is known as a precursor of "hsa-miR-6781-5p".

[0064] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 20, 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: 235) having a hairpin-like structure is known as a precursor of "hsa-miR-1908-5p".

[0065] The term "hsa-miR-4792 gene" or "hsa-miR-4792" used herein includes the hsa-miR-4792 gene (miRBase Accession No. MIMAT0019964) consisting of the nucleotide sequence represented by SEQ ID NO: 21, 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: 236) having a hairpin-like structure is known as a precursor of "hsa-miR-4792".

[0066] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 22, 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: 237) having a hairpin-like structure is known as a precursor of "hsa-miR-7845-5p".

[0067] The term "hsa-miR-4417 gene" or "hsa-miR-4417" used herein includes the hsa-miR-4417 gene (miRBase Accession No. MIMAT0018929) consisting of the nucleotide sequence represented by SEQ ID NO: 23, 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: 238) having a hairpin-like structure is known as a precursor of "hsa-miR-4417".

[0068] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 24, 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".

[0069] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 25, 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. M0006311, SEQ ID NO: 240) having a hairpin-like structure is known as a precursor of "hsa-miR-1225-5p".

[0070] The term "hsa-miR-1231 gene" or "hsa-miR-1231" used herein includes the hsa-miR-1231 gene (miRBase Accession No. MIMAT0005586) consisting of the nucleotide sequence represented by SEQ ID NO: 26, 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: 241) having a hairpin-like structure is known as a precursor of "hsa-miR-1231".

[0071] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 27, 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. M0006311, SEQ ID NO: 240) having a hairpin-like structure is known as a precursor of "hsa-miR-1225-3p".

[0072] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 28, 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: 242) having a hairpin-like structure is known as a precursor of "hsa-miR-150-3p".

[0073] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 29, 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: 243) having a hairpin-like structure is known as a precursor of "hsa-miR-4433-3p".

[0074] The term "hsa-miR-6125 gene" or "hsa-miR-6125" used herein includes the hsa-miR-6125 gene (miRBase Accession No. MIMAT0024598) consisting of the nucleotide sequence represented by SEQ ID NO: 30, 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: 244) having a hairpin-like structure is known as a precursor of "hsa-miR-6125".

[0075] The term "hsa-miR-4513 gene" or "hsa-miR-4513" used herein includes the hsa-miR-4513 gene (miRBase Accession No. MIMAT0019050) consisting of the nucleotide sequence represented by SEQ ID NO: 31, 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: 245) having a hairpin-like structure is known as a precursor of "hsa-miR-4513".

[0076] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 32, 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: 246) having a hairpin-like structure is known as a precursor of "hsa-miR-6787-5p".

[0077] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 33, 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: 247) having a hairpin-like structure is known as a precursor of "hsa-miR-6784-5p".

[0078] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 34, 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: 248) having a hairpin-like structure is known as a precursor of "hsa-miR-615-5p".

[0079] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 35, 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: 249) having a hairpin-like structure is known as a precursor of "hsa-miR-6765-3p".

[0080] The term "hsa-miR-5572 gene" or "hsa-miR-5572" used herein includes the hsa-miR-5572 gene (miRBase Accession No. MIMAT0022260) consisting of the nucleotide sequence represented by SEQ ID NO: 36, 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: 250) having a hairpin-like structure is known as a precursor of "hsa-miR-5572".

[0081] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 37, 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: 251) having a hairpin-like structure is known as a precursor of "hsa-miR-6842-5p".

[0082] The term "hsa-miR-8063 gene" or "hsa-miR-8063" used herein includes the hsa-miR-8063 gene (miRBase

Accession No. MIMAT0030990) consisting of the nucleotide sequence represented by SEQ ID NO: 38, 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: 252) having a hairpin-like structure is known as a precursor of "hsa-miR-8063".

[0083] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 39, 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: 253) having a hairpin-like structure is known as a precursor of "hsa-miR-6780b-5p".

[0084] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 40, 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: 254) having a hairpin-like structure is known as a precursor of "hsa-miR-187-5p".

[0085] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 41, 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: 255) having a hairpin-like structure is known as a precursor of "hsa-miR-128-1-5p".

[0086] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 42, 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: 256) having a hairpin-like structure is known as a precursor of "hsa-miR-6729-5p".

[0087] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 43, 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: 257) having a hairpin-like structure is known as a precursor of "hsa-miR-6741-5p".

[0088] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 44, 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: 258) having a hairpin-like structure is known as a precursor of "hsa-miR-6757-5p".

[0089] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 45, 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: 259) having a hairpin-like structure is known as a precursor of "hsa-miR-7110-5p".

[0090] The term "hsa-miR-7975 gene" or "hsa-miR-7975" used herein includes the hsa-miR-7975 gene (miRBase Accession No. MIMAT0031178) consisting of the nucleotide sequence represented by SEQ ID NO: 46, 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: 260) having a hairpin-like structure is known as a precursor of "hsa-miR-7975".

[0091] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 47, 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: 261 and 262) having a hairpin-like structure are known as precursors of "hsa-miR-1233-5p".

[0092] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 48, 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: 263) having a hairpin-like structure is known as a precursor of "hsa-miR-6845-5p".

[0093] The term "hsa-miR-3937 gene" or "hsa-miR-3937" used herein includes the hsa-miR-3937 gene (miRBase

Accession No. MIMAT0018352) consisting of the nucleotide sequence represented by SEQ ID NO: 49, 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: 264) having a hairpin-like structure is known as a precursor of "hsa-miR-3937".

[0094] The term "hsa-miR-4467 gene" or "hsa-miR-4467" used herein includes the hsa-miR-4467 gene (miRBase Accession No. MIMAT0018994) consisting of the nucleotide sequence represented by SEQ ID NO: 50, 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: 265) having a hairpin-like structure is known as a precursor of "hsa-miR-4467".

[0095] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 51, 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: 266) having a hairpin-like structure is known as a precursor of "hsa-miR-7109-5p".

[0096] The term "hsa-miR-6088 gene" or "hsa-miR-6088" used herein includes the hsa-miR-6088 gene (miRBase Accession No. MIMAT0023713) consisting of the nucleotide sequence represented by SEQ ID NO: 52, 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: 267) having a hairpin-like structure is known as a precursor of "hsa-miR-6088".

[0097] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 53, 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: 268) having a hairpin-like structure is known as a precursor of "hsa-miR-6782-5p".

[0098] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 54, 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: 269) having a hairpin-like structure is known as a precursor of "hsa-miR-5195-3p".

[0099] The term "hsa-miR-4454 gene" or "hsa-miR-4454" used herein includes the hsa-miR-4454 gene (miRBase Accession No. MIMAT0018976) consisting of the nucleotide sequence represented by SEQ ID NO: 55, 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: 270) having a hairpin-like structure is known as a precursor of "hsa-miR-4454".

[0100] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 56, 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: 271) having a hairpin-like structure is known as a precursor of "hsa-miR-6724-5p".

[0101] The term "hsa-miR-8072 gene" or "hsa-miR-8072" used herein includes the hsa-miR-8072 gene (miRBase Accession No. MIMAT0030999) consisting of the nucleotide sequence represented by SEQ ID NO: 57, 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: 272) having a hairpin-like structure is known as a precursor of "hsa-miR-8072".

[0102] The term "hsa-miR-4516 gene" or "hsa-miR-4516" used herein includes the hsa-miR-4516 gene (miRBase Accession No. MIMAT0019053) consisting of the nucleotide sequence represented by SEQ ID NO: 58, 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: 273) having a hairpin-like structure is known as a precursor of "hsa-miR-4516".

[0103] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 59, 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: 274) having a hairpin-like structure is known as a precursor of "hsa-miR-6756-5p".

[0104] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 60, 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: 275) having a hairpin-like structure is known as a precursor of "hsa-miR-4665-3p".

[0105] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 61, 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: 276) having a hairpin-like structure is known as a precursor of "hsa-miR-6826-5p".

[0106] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 62, 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: 277) having a hairpin-like structure is known as a precursor of "hsa-miR-6820-5p".

[0107] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 63, 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: 278) having a hairpin-like structure is known as a precursor of "hsa-miR-6887-5p".

[0108] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 64, 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: 279) having a hairpin-like structure is known as a precursor of "hsa-miR-3679-5p".

[0109] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 65, 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: 280) having a hairpin-like structure is known as a precursor of "hsa-miR-7847-3p".

[0110] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 66, 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: 281) having a hairpin-like structure is known as a precursor of "hsa-miR-6721-5p".

[0111] The term "hsa-miR-3622a-5p gene" or "hsa-miR-3622a-5p" used herein includes the hsa-miR-3622a-5p gene (miRBase Accession No. MIMAT0018003) consisting of the nucleotide sequence represented by SEQ ID NO: 67, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3622a-5p gene can be obtained by a method described in Witten D et al., 2010, BMC Biol, Vol. 8, p. 58. Also, "hsa-mir-3622a" (miRBase Accession No. MI0016013, SEQ ID NO: 282) having a hairpin-like structure is known as a precursor of "hsa-miR-3622a-5p".

[0112] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 68, 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: 283) having a hairpin-like structure is known as a precursor of "hsa-miR-939-5p".

[0113] The term "hsa-miR-602 gene" or "hsa-miR-602" used herein includes the hsa-miR-602 gene (miRBase Accession No. MIMAT0003270) consisting of the nucleotide sequence represented by SEQ ID NO: 69, 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: 284) having a hairpin-like structure is known as a precursor of "hsa-miR-602".

[0114] The term "hsa-miR-7977 gene" or "hsa-miR-7977" used herein includes the hsa-miR-7977 gene (miRBase Accession No. MIMAT0031180) consisting of the nucleotide sequence represented by SEQ ID NO: 70, 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: 285) having a hairpin-like structure is known as a precursor of "hsa-miR-7977".

[0115] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 71, 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: 286) having a hairpin-like structure is known as a precursor of "hsa-miR-6749-5p".

[0116] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 72, 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: 287) having a hairpin-like structure is known as a precursor of "hsa-miR-1914-3p".

[0117] The term "hsa-miR-4651 gene" or "hsa-miR-4651" used herein includes the hsa-miR-4651 gene (miRBase Accession No. MIMAT0019715) consisting of the nucleotide sequence represented by SEQ ID NO: 73, 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: 288) having a hairpin-like structure is known as a precursor of "hsa-miR-4651".

[0118] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 74, 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: 289) having a hairpin-like structure is known as a precursor of "hsa-miR-4695-5p".

[0119] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 75, 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: 290) having a hairpin-like structure is known as a precursor of "hsa-miR-6848-5p".

[0120] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 76, 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: 291) having a hairpin-like structure is known as a precursor of "hsa-miR-1228-3p".

[0121] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 77, 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: 292) having a hairpin-like structure is known as a precursor of "hsa-miR-642b-3p".

[0122] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 78, 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: 293) having a hairpin-like structure is known as a precursor of "hsa-miR-6746-5p".

[0123] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 79, 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: 294) having a hairpin-like structure is known as a precursor of "hsa-miR-3620-5p".

[0124] The term "hsa-miR-3131 gene" or "hsa-miR-3131" used herein includes the hsa-miR-3131 gene (miRBase Accession No. MIMAT0014996) consisting of the nucleotide sequence represented by SEQ ID NO: 80, 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: 295) having a hairpin-like structure is known as a precursor of "hsa-miR-3131".

[0125] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 81, 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: 296) having a hairpin-like structure is known as a precursor of "hsa-miR-6732-5p".

[0126] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 82, 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: 297) having a hairpin-like structure is known as a precursor of "hsa-miR-7113-3p".

[0127] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 83, 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: 298) having a hairpin-like structure is known as a precursor of "hsa-miR-23a-3p".

[0128] The term "hsa-miR-3154 gene" or "hsa-miR-3154" used herein includes the hsa-miR-3154 gene (miRBase Accession No. MIMAT0015028) consisting of the nucleotide sequence represented by SEQ ID NO: 84, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3154 gene can be obtained by a method described in Berezikov E et al., 2006, Genome Res, Vol. 16, p. 1289-1298. Also, "hsa-mir-3154" (miRBase Accession No. MI0014182, SEQ ID NO: 299) having a hairpin-like structure is known as a precursor of "hsa-miR-3154".

[0129] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 85, 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: 300) having a hairpin-like structure is known as a precursor of "hsa-miR-4723-5p".

[0130] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 86, 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: 301) having a hairpin-like structure is known as a precursor of "hsa-miR-3663-3p".

[0131] The term "hsa-miR-4734 gene" or "hsa-miR-4734" used herein includes the hsa-miR-4734 gene (miRBase Accession No. MIMAT0019859) consisting of the nucleotide sequence represented by SEQ ID NO: 87, 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: 302) having a hairpin-like structure is known as a precursor of "hsa-miR-4734".

[0132] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 88, 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: 303) having a hairpin-like structure is known as a precursor of "hsa-miR-6816-5p".

[0133] The term "hsa-miR-4442 gene" or "hsa-miR-4442" used herein includes the hsa-miR-4442 gene (miRBase Accession No. MIMAT0018960) consisting of the nucleotide sequence represented by SEQ ID NO: 89, 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: 304) having a hairpin-like structure is known as a precursor of "hsa-miR-4442".

[0134] The term "hsa-miR-4476 gene" or "hsa-miR-4476" used herein includes the hsa-miR-4476 gene (miRBase Accession No. MIMAT0019003) consisting of the nucleotide sequence represented by SEQ ID NO: 90, 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: 305) having a hairpin-like structure is known as a precursor of "hsa-miR-4476".

[0135] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 91, 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: 306) having a hairpin-like structure is known as a precursor of "hsa-miR-423-5p".

[0136] The term "hsa-miR-1249 gene" or "hsa-miR-1249" used herein includes the hsa-miR-1249 gene (miRBase Accession No. MIMAT0005901) consisting of the nucleotide sequence represented by SEQ ID NO: 92, 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: 307) having a hairpin-like structure is known as a precursor of "hsa-miR-1249".

[0137] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 93, 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: 308) having a hairpin-like structure is known as a precursor of "hsa-miR-6515-3p".

[0138] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 94, 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: 309) having a hairpin-like structure is known as a precursor of "hsa-miR-887-3p".

[0139] The term "hsa-miR-4741 gene" or "hsa-miR-4741" used herein includes the hsa-miR-4741 gene (miRBase Accession No. MIMAT0019871) consisting of the nucleotide sequence represented by SEQ ID NO: 95, 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: 310) having a hairpin-like structure is known as a precursor of "hsa-miR-4741".

[0140] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 96, 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. M0022611, SEQ ID NO: 311) having a hairpin-like structure is known as a precursor of "hsa-miR-6766-3p".

[0141] The term "hsa-miR-4673 gene" or "hsa-miR-4673" used herein includes the hsa-miR-4673 gene (miRBase Accession No. MIMAT0019755) consisting of the nucleotide sequence represented by SEQ ID NO: 97, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4673 gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4673" (miRBase Accession No. MI0017304, SEQ ID NO: 312) having a hairpin-like structure is known as a precursor of "hsa-miR-4673".

[0142] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 98, 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: 313) having a hairpin-like structure is known as a precursor of "hsa-miR-6779-5p".

[0143] The term "hsa-miR-4706 gene" or "hsa-miR-4706" used herein includes the hsa-miR-4706 gene (miRBase Accession No. MIMAT0019806) consisting of the nucleotide sequence represented by SEQ ID NO: 99, 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: 314) having a hairpin-like structure is known as a precursor of "hsa-miR-4706".

[0144] The term "hsa-miR-1268b gene" or "hsa-miR-1268b" used herein includes the hsa-miR-1268b gene (miRBase Accession No. MIMAT0018925) consisting of the nucleotide sequence represented by SEQ ID NO: 100, 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: 315) having a hairpin-like structure is known as a precursor of "hsa-miR-1268b".

[0145] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 101, 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: 316) having a hairpin-like structure is known as a precursor of "hsa-miR-4632-5p".

[0146] The term "hsa-miR-3197 gene" or "hsa-miR-3197" used herein includes the hsa-miR-3197 gene (miRBase Accession No. MIMAT0015082) consisting of the nucleotide sequence represented by SEQ ID NO: 102, 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: 317) having a hairpin-like structure is known as a precursor of "hsa-miR-3197".

[0147] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 103, 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: 318) having a hairpin-like structure is known as a precursor of "hsa-miR-6798-5p".

[0148] The term "hsa-miR-711 gene" or "hsa-miR-711" used herein includes the hsa-miR-711 gene (miRBase Accession No. MIMAT0012734) consisting of the nucleotide sequence represented by SEQ ID NO: 104, 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: 319) having a hairpin-like structure is known as a precursor of "hsa-miR-711".

[0149] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 105, 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: 320) having a hairpin-like structure is known as a precursor of "hsa-miR-6840-3p".

[0150] The term "hsa-miR-6763-5p gene" or "hsa-miR-6763-5p" used herein includes the hsa-miR-6763-5p gene (miRBase Accession No. MIMAT0027426) consisting of the nucleotide sequence represented by SEQ ID NO: 106, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6763-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6763" (miRBase Accession No. MI0022608, SEQ ID NO: 321) having a hairpin-like structure is known as a precursor of "hsa-miR-6763-5p".

[0151] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 107, 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: 322) having a hairpin-like structure is known as a precursor of "hsa-miR-6727-5p".

[0152] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 108, 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: 323) having a hairpin-like structure is known as a precursor of "hsa-miR-371a-5p".

[0153] The term "hsa-miR-6824-5p gene" or "hsa-miR-6824-5p" used herein includes the hsa-miR-6824-5p gene (miRBase Accession No. MIMAT0027548) consisting of the nucleotide sequence represented by SEQ ID NO: 109, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6824-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6824" (miRBase Accession No. MI0022669, SEQ ID NO: 324) having a hairpin-like structure is known as a precursor of "hsa-miR-6824-5p".

[0154] The term "hsa-miR-4648 gene" or "hsa-miR-4648" used herein includes the hsa-miR-4648 gene (miRBase Accession No. MIMAT0019710) consisting of the nucleotide sequence represented by SEQ ID NO: 110, 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: 325) having a hairpin-like structure is known as a precursor of "hsa-miR-4648".

[0155] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 111, 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: 326) having a hairpin-like structure is known as a precursor of "hsa-miR-1227-5p".

[0156] The term "hsa-miR-564 gene" or "hsa-miR-564" used herein includes the hsa-miR-564 gene (miRBase Accession No. MIMAT0003228) consisting of the nucleotide sequence represented by SEQ ID NO: 112, 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: 327) having a hairpin-like structure is known as a precursor of "hsa-miR-564".

[0157] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 113, 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: 279) having a hairpin-like structure is known as a precursor of "hsa-miR-3679-3p".

[0158] The term "hsa-miR-2861 gene" or "hsa-miR-2861" used herein includes the hsa-miR-2861 gene (miRBase Accession No. MIMAT0013802) consisting of the nucleotide sequence represented by SEQ ID NO: 114, 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: 328) having a hairpin-like structure is known as a precursor of "hsa-miR-2861".

[0159] The term "hsa-miR-6737-5p gene" or "hsa-miR-6737-5p" used herein includes the hsa-miR-6737-5p gene (miRBase Accession No. MIMAT0027375) consisting of the nucleotide sequence represented by SEQ ID NO: 115, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6737-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6737" (miRBase Accession No. MI0022582, SEQ ID NO: 329) having a hairpin-like structure is known as a precursor of "hsa-miR-6737-5p".

[0160] The term "hsa-miR-575 gene" or "hsa-miR-575" used herein includes the hsa-miR-575 gene (miRBase Accession No. MIMAT0003240) consisting of the nucleotide sequence represented by SEQ ID NO: 116, 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: 330) having a hairpin-like structure is known as a precursor of "hsa-miR-575".

[0161] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 117, 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: 331) having a hairpin-like structure is known as a precursor of "hsa-miR-4725-3p".

[0162] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 118, 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: 332) having a hairpin-like structure is known as a precursor of "hsa-miR-6716-5p".

[0163] The term "hsa-miR-4675 gene" or "hsa-miR-4675" used herein includes the hsa-miR-4675 gene (miRBase Accession No. MIMAT0019757) consisting of the nucleotide sequence represented by SEQ ID NO: 119, 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: 333) having a hairpin-like structure is known as a precursor of "hsa-miR-4675".

[0164] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 120, 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: 334) having a hairpin-like structure is known as a precursor of "hsa-miR-1915-3p".

[0165] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 121, 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: 335) having a hairpin-like structure is known as a precursor of "hsa-miR-671-5p".

[0166] The term "hsa-miR-3656 gene" or "hsa-miR-3656" used herein includes the hsa-miR-3656 gene (miRBase Accession No. MIMAT0018076) consisting of the nucleotide sequence represented by SEQ ID NO: 122, 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: 336) having a hairpin-like structure is known as a precursor of "hsa-miR-3656".

[0167] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 123, 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: 337) having a hairpin-like structure is known as a precursor of "hsa-miR-6722-3p".

[0168] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 124, 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: 338) having a hairpin-like structure is known as a precursor of "hsa-miR-4707-5p".

[0169] The term "hsa-miR-4449 gene" or "hsa-miR-4449" used herein includes the hsa-miR-4449 gene (miRBase Accession No. MIMAT0018968) consisting of the nucleotide sequence represented by SEQ ID NO: 125, 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: 339) having a hairpin-like structure is known as a precursor of "hsa-miR-4449".

[0170] The term "hsa-miR-1202 gene" or "hsa-miR-1202" used herein includes the hsa-miR-1202 gene (miRBase Accession No. MIMAT0005865) consisting of the nucleotide sequence represented by SEQ ID NO: 126, 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: 340) having a hairpin-like structure is known as a precursor of "hsa-miR-1202".

[0171] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 127, 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: 341) having a hairpin-like structure is known as a precursor of "hsa-miR-4649-5p".

[0172] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 128, 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: 342) having a hairpin-like structure is known as a precursor of "hsa-miR-744-5p".

[0173] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 129, 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: 343) having a hairpin-like structure is known as a precursor of "hsa-miR-642a-3p".

[0174] The term "hsa-miR-451a gene" or "hsa-miR-451a" used herein includes the hsa-miR-451a gene (miRBase Accession No. MIMAT0001631) consisting of the nucleotide sequence represented by SEQ ID NO: 130, 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: 344) having a hairpin-like structure is known as a precursor of "hsa-miR-451a".

[0175] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 131, 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: 345) having a hairpin-like structure is known as a precursor of "hsa-miR-6870-5p".

[0176] The term "hsa-miR-4443 gene" or "hsa-miR-4443" used herein includes the hsa-miR-4443 gene (miRBase Accession No. MIMAT0018961) consisting of the nucleotide sequence represented by SEQ ID NO: 132, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4443 gene can be obtained by a method described in Jima DD et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4443" (miRBase Accession No. MI0016786, SEQ ID NO: 346) having a hairpin-like structure is known as a precursor of "hsa-miR-4443".

[0177] The term "hsa-miR-6808-5p gene" or "hsa-miR-6808-5p" used herein includes the hsa-miR-6808-5p gene (miRBase Accession No. MIMAT0027516) consisting of the nucleotide sequence represented by SEQ ID NO: 133, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6808-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6808" (miRBase Accession No. MI0022653, SEQ ID NO: 347) having a hairpin-like structure is known as a precursor of "hsa-miR-6808-5p".

[0178] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 134, 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: 348) having a hairpin-like structure is known as a precursor of "hsa-miR-4728-5p".

[0179] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 135, 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: 349) having a hairpin-like structure is known as a precursor of "hsa-miR-937-5p".

[0180] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 136, 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-1" (miRBase Accession No. MI0000452, SEQ ID NO: 350) having a hairpin-like structure is known as a precursor of "hsa-miR-135a-3p".

[0181] The term "hsa-miR-663b gene" or "hsa-miR-663b" used herein includes the hsa-miR-663b gene (miRBase Accession No. MIMAT0005867) consisting of the nucleotide sequence represented by SEQ ID NO: 137, 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: 351) having a hairpin-like structure is known as a precursor of "hsa-miR-663b".

[0182] The term "hsa-miR-1343-5p gene" or "hsa-miR-1343-5p" used herein includes the hsa-miR-1343-5p gene (miRBase Accession No. MIMAT0027038) consisting of the nucleotide sequence represented by SEQ ID NO: 138, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1343-5p gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-1343" (miRBase Accession No. MI0017320, SEQ ID NO: 223) having a hairpin-like structure is known as a precursor of "hsa-miR-1343-5p".

[0183] The term "hsa-miR-6822-5p gene" or "hsa-miR-6822-5p" used herein includes the hsa-miR-6822-5p gene (miRBase Accession No. MIMAT0027544) consisting of the nucleotide sequence represented by SEQ ID NO: 139, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6822-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6822" (miRBase Accession No. MI0022667, SEQ ID NO: 352) having a hairpin-like structure is known as a precursor of "hsa-miR-6822-5p".

[0184] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 140, 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: 353) having a hairpin-like structure is known as a precursor of "hsa-miR-6803-5p".

[0185] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 141, 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: 354) having a hairpin-like structure is known as a precursor of "hsa-miR-6805-3p".

[0186] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 142, 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: 355) having a hairpin-like structure is known as a precursor of "hsa-miR-128-2-5p".

[0187] The term "hsa-miR-4640-5p gene" or "hsa-miR-4640-5p" used herein includes the hsa-miR-4640-5p gene (miRBase Accession No. MIMAT0019699) consisting of the nucleotide sequence represented by SEQ ID NO: 143, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4640-5p gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4640" (miRBase Accession No. MI0017267, SEQ ID NO: 356) having a hairpin-like structure is known as a precursor of "hsa-miR-4640-5p".

[0188] The term "hsa-miR-1469 gene" or "hsa-miR-1469" used herein includes the hsa-miR-1469 gene (miRBase Accession No. MIMAT0007347) consisting of the nucleotide sequence represented by SEQ ID NO: 144, 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: 357) having a hairpin-like structure is known as a precursor of "hsa-miR-1469".

[0189] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 145, 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: 358) having a hairpin-like structure is known as a precursor of "hsa-miR-92a-2-5p".

[0190] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 146, 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: 359) having a hairpin-like structure is known as a precursor of "hsa-miR-3940-5p".

[0191] The term "hsa-miR-4281 gene" or "hsa-miR-4281" used herein includes the hsa-miR-4281 gene (miRBase Accession No. MIMAT0016907) consisting of the nucleotide sequence represented by SEQ ID NO: 147, 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: 360) having a hairpin-like structure is known as a precursor of "hsa-miR-4281".

[0192] The term "hsa-miR-1260b gene" or "hsa-miR-1260b" used herein includes the hsa-miR-1260b gene (miRBase Accession No. MIMAT0015041) consisting of the nucleotide sequence represented by SEQ ID NO: 148, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1260b gene can be obtained by a method described in Stark MS et al., 2010, PLoS One, Vol. 5, e9685. Also, "hsa-mir-1260b" (miRBase Accession No. MI0014197, SEQ ID NO: 361) having a hairpin-like structure is known as a precursor of "hsa-miR-1260b".

[0193] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 149, 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: 362) having a hairpin-like structure is known as a precursor of "hsa-miR-4758-5p".

[0194] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 150, 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: 334) having a hairpin-like structure is known as a precursor of "hsa-miR-1915-5p".

[0195] The term "hsa-miR-5001-5p gene" or "hsa-miR-5001-5p" used herein includes the hsa-miR-5001-5p gene (miRBase Accession No. MIMAT0021021) consisting of the nucleotide sequence represented by SEQ ID NO: 151, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-5001-5p gene can be obtained by a method described in Hansen TB et al., 2011, RNA Biol, Vol. 8, p. 378-383. Also, "hsa-mir-5001" (miRBase Accession No. MI0017867, SEQ ID NO: 363) having a hairpin-like structure is known as a precursor of "hsa-miR-5001-5p".

[0196] The term "hsa-miR-4286 gene" or "hsa-miR-4286" used herein includes the hsa-miR-4286 gene (miRBase Accession No. MIMAT0016916) consisting of the nucleotide sequence represented by SEQ ID NO: 152, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4286 gene can be obtained by a method described in Goff LA et al., 2009, PLoS One, Vol. 4, e7192. Also, "hsa-mir-4286" (miRBase Accession No. MI0015894, SEQ ID

NO: 364) having a hairpin-like structure is known as a precursor of "hsa-miR-4286".

[0197] The term "hsa-miR-6126 gene" or "hsa-miR-6126" used herein includes the hsa-miR-6126 gene (miRBase Accession No. MIMAT0024599) consisting of the nucleotide sequence represented by SEQ ID NO: 153, 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: 365) having a hairpin-like structure is known as a precursor of "hsa-miR-6126".

[0198] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 154, 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: 366) having a hairpin-like structure is known as a precursor of "hsa-miR-6789-5p".

[0199] The term "hsa-miR-4459 gene" or "hsa-miR-4459" used herein includes the hsa-miR-4459 gene (miRBase Accession No. MIMAT0018981) consisting of the nucleotide sequence represented by SEQ ID NO: 155, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4459 gene can be obtained by a method described in Jima DD et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4459" (miRBase Accession No. MI0016805, SEQ ID NO: 367) having a hairpin-like structure is known as a precursor of "hsa-miR-4459".

[0200] The term "hsa-miR-1268a gene" or "hsa-miR-1268a" used herein includes the hsa-miR-1268a gene (miRBase Accession No. MIMAT0005922) consisting of the nucleotide sequence represented by SEQ ID NO: 156, 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: 368) having a hairpin-like structure is known as a precursor of "hsa-miR-1268a".

[0201] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 157, 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: 369) having a hairpin-like structure is known as a precursor of "hsa-miR-6752-5p".

[0202] The term "hsa-miR-6131 gene" or "hsa-miR-6131" used herein includes the hsa-miR-6131 gene (miRBase Accession No. MIMAT0024615) consisting of the nucleotide sequence represented by SEQ ID NO: 158, 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: 370) having a hairpin-like structure is known as a precursor of "hsa-miR-6131".

[0203] The term "hsa-miR-6800-5p gene" or "hsa-miR-6800-5p" used herein includes the hsa-miR-6800-5p gene (miRBase Accession No. MIMAT0027500) consisting of the nucleotide sequence represented by SEQ ID NO: 159, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6800-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6800" (miRBase Accession No. MI0022645, SEQ ID NO: 371) having a hairpin-like structure is known as a precursor of "hsa-miR-6800-5p".

[0204] The term "hsa-miR-4532 gene" or "hsa-miR-4532" used herein includes the hsa-miR-4532 gene (miRBase Accession No. MIMAT0019071) consisting of the nucleotide sequence represented by SEQ ID NO: 160, 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: 372) having a hairpin-like structure is known as a precursor of "hsa-miR-4532".

[0205] The term "hsa-miR-6872-3p gene" or "hsa-miR-6872-3p" used herein includes the hsa-miR-6872-3p gene (miRBase Accession No. MIMAT0027645) consisting of the nucleotide sequence represented by SEQ ID NO: 161, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6872-3p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6872" (miRBase Accession No. MI0022719, SEQ ID NO: 373) having a hairpin-like structure is known as a precursor of "hsa-miR-6872-3p".

[0206] The term "hsa-miR-718 gene" or "hsa-miR-718" used herein includes the hsa-miR-718 gene (miRBase Accession No. MIMAT0012735) consisting of the nucleotide sequence represented by SEQ ID NO: 162, 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: 374) having a hairpin-like structure is known as a precursor of "hsa-miR-718".

[0207] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 163, 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: 375) having a hairpin-like structure is known as a precursor of "hsa-miR-6769a-5p".

[0208] The term "hsa-miR-4707-3p gene" or "hsa-miR-4707-3p" used herein includes the hsa-miR-4707-3p gene

(miRBase Accession No. MIMAT0019808) consisting of the nucleotide sequence represented by SEQ ID NO: 164, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4707-3p gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4707" (miRBase Accession No. MI0017340, SEQ ID NO: 338) having a hairpin-like structure is known as a precursor of "hsa-miR-4707-3p".

[0209] The term "hsa-miR-6765-5p gene" or "hsa-miR-6765-5p" used herein includes the hsa-miR-6765-5p gene (miRBase Accession No. MIMAT0027430) consisting of the nucleotide sequence represented by SEQ ID NO: 165, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6765-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6765" (miRBase Accession No. MI0022610, SEQ ID NO: 249) having a hairpin-like structure is known as a precursor of "hsa-miR-6765-5p".

[0210] The term "hsa-miR-4739 gene" or "hsa-miR-4739" used herein includes the hsa-miR-4739 gene (miRBase Accession No. MIMAT0019868) consisting of the nucleotide sequence represented by SEQ ID NO: 166, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4739 gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4739" (miRBase Accession No. MI0017377, SEQ ID NO: 376) having a hairpin-like structure is known as a precursor of "hsa-miR-4739".

[0211] The term "hsa-miR-4525 gene" or "hsa-miR-4525" used herein includes the hsa-miR-4525 gene (miRBase Accession No. MIMAT0019064) consisting of the nucleotide sequence represented by SEQ ID NO: 167, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4525 gene can be obtained by a method described in Jima DD et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4525" (miRBase Accession No. MI0016892, SEQ ID NO: 377) having a hairpin-like structure is known as a precursor of "hsa-miR-4525".

[0212] The term "hsa-miR-4270 gene" or "hsa-miR-4270" used herein includes the hsa-miR-4270 gene (miRBase Accession No. MIMAT0016900) consisting of the nucleotide sequence represented by SEQ ID NO: 168, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4270 gene can be obtained by a method described in Goff LA et al., 2009, PLoS One, Vol. 4, e7192. Also, "hsa-mir-4270" (miRBase Accession No. MI0015878, SEQ ID NO: 378) having a hairpin-like structure is known as a precursor of "hsa-miR-4270".

[0213] The term "hsa-miR-4534 gene" or "hsa-miR-4534" used herein includes the hsa-miR-4534 gene (miRBase Accession No. MIMAT0019073) consisting of the nucleotide sequence represented by SEQ ID NO: 169, 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: 379) having a hairpin-like structure is known as a precursor of "hsa-miR-4534".

[0214] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 170, 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: 380) having a hairpin-like structure is known as a precursor of "hsa-miR-6785-5p".

[0215] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 171, 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: 381) having a hairpin-like structure is known as a precursor of "hsa-miR-6850-5p".

[0216] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 172, 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: 382) having a hairpin-like structure is known as a precursor of "hsa-miR-4697-5p".

[0217] The term "hsa-miR-1260a gene" or "hsa-miR-1260a" used herein includes the hsa-miR-1260a gene (miRBase Accession No. MIMAT0005911) consisting of the nucleotide sequence represented by SEQ ID NO: 173, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1260a gene can be obtained by a method described in Morin RD et al., 2008, Genome Res, Vol. 18, p. 610-621. Also, "hsa-mir-1260a" (miRBase Accession No. MI0006394, SEQ ID NO: 383) having a hairpin-like structure is known as a precursor of "hsa-miR-1260a".

[0218] The term "hsa-miR-4486 gene" or "hsa-miR-4486" used herein includes the hsa-miR-4486 gene (miRBase Accession No. MIMAT0019020) consisting of the nucleotide sequence represented by SEQ ID NO: 174, 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: 384) having a hairpin-like structure is known as a precursor of "hsa-miR-4486".

[0219] The term "hsa-miR-6880-5p gene" or "hsa-miR-6880-5p" used herein includes the hsa-miR-6880-5p gene (miRBase Accession No. MIMAT0027660) consisting of the nucleotide sequence represented by SEQ ID NO: 175, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6880-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6880" (miRBase

Accession No. MI0022727, SEQ ID NO: 385) having a hairpin-like structure is known as a precursor of "hsa-miR-6880-5p".

[0220] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 176, 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: 386) having a hairpin-like structure is known as a precursor of "hsa-miR-6802-5p".

[0221] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 177, 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: 387) having a hairpin-like structure is known as a precursor of "hsa-miR-6861-5p".

[0222] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 178, 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: 388) having a hairpin-like structure is known as a precursor of "hsa-miR-92b-5p".

[0223] The term "hsa-miR-1238-5p gene" or "hsa-miR-1238-5p" used herein includes the hsa-miR-1238-5p gene (miRBase Accession No. MIMAT0022947) consisting of the nucleotide sequence represented by SEQ ID NO: 179, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1238-5p gene can be obtained by a method described in Berezikov E et al., 2007, Mol Cell, Vol. 28, p. 328-336. Also, "hsa-mir-1238" (miRBase Accession No. MI0006328, SEQ ID NO: 389) having a hairpin-like structure is known as a precursor of "hsa-miR-1238-5p".

[0224] The term "hsa-miR-6851-5p gene" or "hsa-miR-6851-5p" used herein includes the hsa-miR-6851-5p gene (miRBase Accession No. MIMAT0027602) consisting of the nucleotide sequence represented by SEQ ID NO: 180, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6851-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6851" (miRBase Accession No. MI0022697, SEQ ID NO: 390) having a hairpin-like structure is known as a precursor of "hsa-miR-6851-5p".

[0225] The term "hsa-miR-7704 gene" or "hsa-miR-7704" used herein includes the hsa-miR-7704 gene (miRBase Accession No. MIMAT0030019) consisting of the nucleotide sequence represented by SEQ ID NO: 181, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-7704 gene can be obtained by a method described in Swaminathan S et al., 2013, Biochem Biophys Res Commun, Vol. 434, p. 228-234. Also, "hsa-mir-7704" (miRBase Accession No. MI0025240, SEQ ID NO: 391) having a hairpin-like structure is known as a precursor of "hsa-miR-7704".

[0226] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 182, 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: 392) having a hairpin-like structure is known as a precursor of "hsa-miR-149-3p".

[0227] The term "hsa-miR-4689 gene" or "hsa-miR-4689" used herein includes the hsa-miR-4689 gene (miRBase Accession No. MIMAT0019778) consisting of the nucleotide sequence represented by SEQ ID NO: 183, 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: 393) having a hairpin-like structure is known as a precursor of "hsa-miR-4689".

[0228] The term "hsa-miR-4688 gene" or "hsa-miR-4688" used herein includes the hsa-miR-4688 gene (miRBase Accession No. MIMAT0019777) consisting of the nucleotide sequence represented by SEQ ID NO: 184, 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: 394) having a hairpin-like structure is known as a precursor of "hsa-miR-4688".

[0229] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 185, 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: 395) having a hairpin-like structure is known as a precursor of "hsa-miR-125a-3p".

[0230] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 186, 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: 396) having a hairpin-like structure is known as a precursor of "hsa-miR-23b-3p".

[0231] The term "hsa-miR-614 gene" or "hsa-miR-614" used herein includes the hsa-miR-614 gene (miRBase Accession No. MIMAT0003282) consisting of the nucleotide sequence represented by SEQ ID NO: 187, 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: 397) having a hairpin-like structure is known as a precursor of "hsa-miR-614".

[0232] The term "hsa-miR-1913 gene" or "hsa-miR-1913" used herein includes the hsa-miR-1913 gene (miRBase Accession No. MIMAT0007888) consisting of the nucleotide sequence represented by SEQ ID NO: 188, 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: 398) having a hairpin-like structure is known as a precursor of "hsa-miR-1913".

[0233] The term "hsa-miR-16-5p gene" or "hsa-miR-16-5p" used herein includes the hsa-miR-16-5p gene (miRBase Accession No. MIMAT0000069) consisting of the nucleotide sequence represented by SEQ ID NO: 189, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-16-5p gene can be obtained by a method described in Lagos-Quintana M et al., 2001, Science, Vol. 294, p. 853-858. Also, "hsa-mir-16-1 and hsa-mir-16-2" (miRBase Accession Nos. MI0000070 and MI0000115, SEQ ID NOs: 399 and 400) having a hairpin-like structure are known as precursors of "hsa-miR-16-5p".

[0234] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 190, 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: 401) having a hairpin-like structure is known as a precursor of "hsa-miR-675-5p".

[0235] The term "hsa-miR-486-3p gene" or "hsa-miR-486-3p" used herein includes the hsa-miR-486-3p gene (miRBase Accession No. MIMAT0004762) consisting of the nucleotide sequence represented by SEQ ID NO: 191, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-486-3p gene can be obtained by a method described in Fu H et al., 2005, FEBS Lett, Vol. 579, p. 3849-3854. Also, "hsa-mir-486 and hsa-mir-486-2" (miRBase Accession Nos. MI0002470 and MI0023622, SEQ ID NOs: 402 and 403) having a hairpin-like structure are known as precursors of "hsa-miR-486-3p".

[0236] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 192, 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: 404) having a hairpin-like structure is known as a precursor of "hsa-miR-6777-5p".

[0237] The term "hsa-miR-4497 gene" or "hsa-miR-4497" used herein includes the hsa-miR-4497 gene (miRBase Accession No. MIMAT0019032) consisting of the nucleotide sequence represented by SEQ ID NO: 193, 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: 405) having a hairpin-like structure is known as a precursor of "hsa-miR-4497".

[0238] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 194, 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: 406) having a hairpin-like structure is known as a precursor of "hsa-miR-296-3p".

[0239] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 195, 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: 407) having a hairpin-like structure is known as a precursor of "hsa-miR-6738-5p".

[0240] The term "hsa-miR-4731-5p gene" or "hsa-miR-4731-5p" used herein includes the hsa-miR-4731-5p gene (miRBase Accession No. MIMAT0019853) consisting of the nucleotide sequence represented by SEQ ID NO: 196, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4731-5p gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4731" (miRBase Accession No. MI0017368, SEQ ID NO: 408) having a hairpin-like structure is known as a precursor of "hsa-miR-4731-5p".

[0241] The term "hsa-miR-6889-5p gene" or "hsa-miR-6889-5p" used herein includes the hsa-miR-6889-5p gene (miRBase Accession No. MIMAT0027678) consisting of the nucleotide sequence represented by SEQ ID NO: 197, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6889-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6889" (miRBase Accession No. MI0022736, SEQ ID NO: 409) having a hairpin-like structure is known as a precursor of "hsa-miR-6889-5p".

[0242] The term "hsa-miR-6786-5p gene" or "hsa-miR-6786-5p" used herein includes the hsa-miR-6786-5p gene (miRBase Accession No. MIMAT0027472) consisting of the nucleotide sequence represented by SEQ ID NO: 198, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6786-5p gene can be obtained by a

method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6786" (miRBase Accession No. MI0022631, SEQ ID NO: 410) having a hairpin-like structure is known as a precursor of "hsa-miR-6786-5p".

[0243] The term "hsa-miR-92a-3p gene" or "hsa-miR-92a-3p" used herein includes the hsa-miR-92a-3p gene (miRBase Accession No. MIMAT0000092) consisting of the nucleotide sequence represented by SEQ ID NO: 199, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-92a-3p 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-1 and hsa-mir-92a-2" (miRBase Accession Nos. MI0000093 and MI0000094, SEQ ID NOs: 411 and 358) having a hairpin-like structure are known as precursors of "hsa-miR-92a-3p".

[0244] The term "hsa-miR-4294 gene" or "hsa-miR-4294" used herein includes the hsa-miR-4294 gene (miRBase Accession No. MIMAT0016849) consisting of the nucleotide sequence represented by SEQ ID NO: 200, 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: 412) having a hairpin-like structure is known as a precursor of "hsa-miR-4294".

[0245] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 201, 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: 413) having a hairpin-like structure is known as a precursor of "hsa-miR-4763-3p".

[0246] The term "hsa-miR-6076 gene" or "hsa-miR-6076" used herein includes the hsa-miR-6076 gene (miRBase Accession No. MIMAT0023701) consisting of the nucleotide sequence represented by SEQ ID NO: 202, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6076 gene can be obtained by a method described in Voellenkle C et al., 2012, RNA, Vol. 18, p. 472-484. Also, "hsa-mir-6076" (miRBase Accession No. MI0020353, SEQ ID NO: 414) having a hairpin-like structure is known as a precursor of "hsa-miR-6076".

[0247] The term "hsa-miR-663a gene" or "hsa-miR-663a" used herein includes the hsa-miR-663a gene (miRBase Accession No. MIMAT0003326) consisting of the nucleotide sequence represented by SEQ ID NO: 203, 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: 415) having a hairpin-like structure is known as a precursor of "hsa-miR-663a".

[0248] The term "hsa-miR-760 gene" or "hsa-miR-760" used herein includes the hsa-miR-760 gene (miRBase Accession No. MIMAT0004957) consisting of the nucleotide sequence represented by SEQ ID NO: 204, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-760 gene can be obtained by a method described in Berezikov E et al., 2006, Genome Res, Vol. 16, p. 1289-1298. Also, "hsa-mir-760" (miRBase Accession No. MI0005567, SEQ ID NO: 416) having a hairpin-like structure is known as a precursor of "hsa-miR-760".

[0249] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 205, 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: 417) having a hairpin-like structure is known as a precursor of "hsa-miR-4667-5p".

[0250] The term "hsa-miR-6090 gene" or "hsa-miR-6090" used herein includes the hsa-miR-6090 gene (miRBase Accession No. MIMAT0023715) consisting of the nucleotide sequence represented by SEQ ID NO: 206, 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: 418) having a hairpin-like structure is known as a precursor of "hsa-miR-6090".

[0251] The term "hsa-miR-4730 gene" or "hsa-miR-4730" used herein includes the hsa-miR-4730 gene (miRBase Accession No. MIMAT0019852) consisting of the nucleotide sequence represented by SEQ ID NO: 207, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4730 gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4730" (miRBase Accession No. MI0017367, SEQ ID NO: 419) having a hairpin-like structure is known as a precursor of "hsa-miR-4730".

[0252] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 208, 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: 420) having a hairpin-like structure is known as a precursor of "hsa-miR-7106-5p".

[0253] The term "hsa-miR-3196 gene" or "hsa-miR-3196" used herein includes the hsa-miR-3196 gene (miRBase Accession No. MIMAT0015080) consisting of the nucleotide sequence represented by SEQ ID NO: 209, 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: 421) having a hairpin-like structure is known as a precursor of "hsa-miR-3196".

[0254] The term "hsa-miR-5698 gene" or "hsa-miR-5698" used herein includes the hsa-miR-5698 gene (miRBase Accession No. MIMAT0022491) consisting of the nucleotide sequence represented by SEQ ID NO: 210, 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: 422) having a hairpin-like structure is known as a precursor of "hsa-miR-5698".

[0255] The term "hsa-miR-6087 gene" or "hsa-miR-6087" used herein includes the hsa-miR-6087 gene (miRBase Accession No. MIMAT0023712) consisting of the nucleotide sequence represented by SEQ ID NO: 211, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6087 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-6087" (miRBase Accession No. MI0020364, SEQ ID NO: 423) having a hairpin-like structure is known as a precursor of "hsa-miR-6087".

[0256] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 212, 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: 275) having a hairpin-like structure is known as a precursor of "hsa-miR-4665-5p".

[0257] The term "hsa-miR-8059 gene" or "hsa-miR-8059" used herein includes the hsa-miR-8059 gene (miRBase Accession No. MIMAT0030986) consisting of the nucleotide sequence represented by SEQ ID NO: 213, 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: 424) having a hairpin-like structure is known as a precursor of "hsa-miR-8059".

[0258] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 214, 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: 425) having a hairpin-like structure is known as a precursor of "hsa-miR-6879-5p".

[0259] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 666, 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: 677) having a hairpin-like structure is known as a precursor of "hsa-miR-6717-5p".

[0260] The term "hsa-miR-3648 gene" or "hsa-miR-3648" used herein includes the hsa-miR-3648 gene (miRBase Accession No. MIMAT0018068) consisting of the nucleotide sequence represented by SEQ ID NO: 667, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3648 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-3648" (miRBase Accession No. MI0016048, SEQ ID NO: 678) having a hairpin-like structure is known as a precursor of "hsa-miR-3648".

[0261] The term "hsa-miR-3162-5p gene" or "hsa-miR-3162-5p" used herein includes the hsa-miR-3162-5p gene (miRBase Accession No. MIMAT0015036) consisting of the nucleotide sequence represented by SEQ ID NO: 668, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3162-5p gene can be obtained by a method described in Stark MS et al., 2010, PLoS One, Vol. 5, e9685. Also, "hsa-mir-3162" (miRBase Accession No. MI0014192, SEQ ID NO: 679) having a hairpin-like structure is known as a precursor of "hsa-miR-3162-5p".

[0262] The term "hsa-miR-1909-3p gene" or "hsa-miR-1909-3p" used herein includes the hsa-miR-1909-3p gene (miRBase Accession No. MIMAT0007883) consisting of the nucleotide sequence represented by SEQ ID NO: 669, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1909-3p gene can be obtained by a method described in Bar M et al., 2008, Stem Cells, Vol. 26, p. 2496-2505. Also, "hsa-mir-1909" (miRBase Accession No. MI0008330, SEQ ID NO: 680) having a hairpin-like structure is known as a precursor of "hsa-miR-1909-3p".

[0263] The term "hsa-miR-8073 gene" or "hsa-miR-8073" used herein includes the hsa-miR-8073 gene (miRBase Accession No. MIMAT0031000) consisting of the nucleotide sequence represented by SEQ ID NO: 670, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-8073 gene can be obtained by a method described in Wang HJ et al., 2013, Shock, Vol. 39, p. 480-487. Also, "hsa-mir-8073" (miRBase Accession No. MI0025909, SEQ ID NO: 681) having a hairpin-like structure is known as a precursor of "hsa-miR-8073".

[0264] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 671, 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: 682) having a hairpin-like structure is known as a precursor of "hsa-miR-6769b-5p".

[0265] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 672, 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: 683) having a hairpin-like structure is known as a precursor of "hsa-miR-6836-3p".

[0266] The term "hsa-miR-4484 gene" or "hsa-miR-4484" used herein includes the hsa-miR-4484 gene (miRBase Accession No. MIMAT0019018) consisting of the nucleotide sequence represented by SEQ ID NO: 673, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4484 gene can be obtained by a method described in Jima DD et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4484" (miRBase Accession No. MI0016845, SEQ ID NO: 684) having a hairpin-like structure is known as a precursor of "hsa-miR-4484".

[0267] The term "hsa-miR-6819-5p gene" or "hsa-miR-6819-5p" used herein includes the hsa-miR-6819-5p gene (miRBase Accession No. MIMAT0027538) consisting of the nucleotide sequence represented by SEQ ID NO: 674, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6819-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6819" (miRBase Accession No. MI0022664, SEQ ID NO: 685) having a hairpin-like structure is known as a precursor of "hsa-miR-6819-5p".

[0268] The term "hsa-miR-6794-5p gene" or "hsa-miR-6794-5p" used herein includes the hsa-miR-6794-5p gene (miRBase Accession No. MIMAT0027488) consisting of the nucleotide sequence represented by SEQ ID NO: 675, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6794-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6794" (miRBase Accession No. MI0022639, SEQ ID NO: 686) having a hairpin-like structure is known as a precursor of "hsa-miR-6794-5p".

[0269] 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) consisting of the nucleotide sequence represented by SEQ ID NO: 676, 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: 687 and 688) having a hairpin-like structure are known as precursors of "hsa-miR-24-3p".

[0270] A mature miRNA may become a variant due to the sequence cleaved shorter or longer by one to several flanking nucleotides or due to substitution of nucleotides 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 214 and 666 to 676 as well as a large number of the nucleotide sequence variants and fragments represented by SEQ ID NOs: 426 to 665 and 689 to 700, called isomiRs. These variants can also be obtained as miRNAs that have a nucleotide sequence represented by any of SEQ ID NOs: 1 to 214 and 666 to 676.

[0271] Specifically, among the variants of polynucleotides consisting of a nucleotide sequence represented by any of SEQ ID NOs: 1, 2, 6, 9, 13, 18, 20, 21, 23, 28, 29, 30, 31, 34, 36, 40, 41, 46, 47, 50, 52, 54, 55, 56, 58, 64, 66, 67, 68, 72, 73, 74, 76, 77, 79, 80, 83, 84, 85, 87, 89, 90, 91, 92, 93, 94, 95, 97, 99, 100, 101, 102, 104, 108, 110, 112, 113, 114, 117, 118, 120, 121, 122, 124, 125, 126, 127, 128, 129, 130, 132, 134, 135, 136, 137, 142, 143, 145, 146, 147, 148, 149, 150, 151, 152, 153, 155, 156, 158, 160, 162, 164, 166, 167, 173, 174, 178, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 193, 194, 196, 199, 201, 203, 204, 205, 207, 209, 210, 211, 212, 666, 667, 668, 669, 673, and 676 or a nucleotide sequence from the nucleotide sequence by the replacement of u with t according to the present invention, examples of the longest variants registered in miRBase Release 20 include polynucleotides represented by SEQ ID NOs: 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, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 689, 691, 693, 695, 697, and 699, respectively. Also, among the variants of polynucleotides consisting of the nucleotide sequence represented by any of SEQ ID NOs: 1, 2, 6, 9, 13, 18, 20, 21, 23, 28, 29, 30, 31, 34, 36, 40, 41, 46, 47, 50, 52, 54, 55, 56, 58, 64, 66, 67, 68, 72, 73, 74, 76, 77, 79, 80, 83, 84, 85, 87, 89, 90, 91, 92, 93, 94, 95, 97, 99, 100, 101, 102, 104, 108, 110, 112, 113, 114, 117, 118, 120, 121, 122, 124, 125, 126, 127, 128, 129, 130, 132, 134, 135, 136, 137, 142, 143, 145, 146, 147, 148, 149, 150, 151, 152, 153, 155, 156, 158, 160, 162, 164, 166, 167, 173, 174, 178, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 193, 194, 196, 199, 201, 203, 204, 205, 207, 209, 210, 211, 212, 666, 667, 668, 669, 673, and 676 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t according to the present invention, examples of shortest variants registered in the miRBase Release 20 include polynucleotides having sequences represented by SEQ ID NOs: 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, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 690, 692, 694, 696, 698, and 700, respectively. In addition to these variants

and fragments, examples thereof include a large number of isomiR polynucleotides consisting of a nucleotide sequence represented by SEQ ID NOs: 1 to 214 and 666 to 676 registered in the miRBase. Examples of the polynucleotide comprising a nucleotide sequence represented by any of SEQ ID NOs: 1 to 214 and 666 to 676 include a polynucleotide represented by any of SEQ ID NOs: 215 to 425 and 677 to 688, which are their respective precursors.

[0272] The names and miRBase Accession Nos. (registration numbers) of the genes consisting of a nucleotide sequence represented by SEQ ID NOs: 1 to 700 are shown in Table 1.

[0273] 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.

[Table 1]

SEQ ID NO:	Gene name	miRBase registration No.
1	hsa-miR-204-3p	MIMAT0022693
2	hsa-miR-1247-3p	MIMAT0022721
3	hsa-miR-6875-5p	MIMAT0027650
4	hsa-miR-6857-5p	MIMAT0027614
5	hsa-miR-6726-5p	MIMAT0027353
6	hsa-miR-3188	MIMAT0015070
7	hsa-miR-8069	MIMAT0030996
8	hsa-miR-4257	MIMAT0016878
9	hsa-miR-1343-3p	MIMAT0019776
10	hsa-miR-7108-5p	MIMAT0028113
11	hsa-miR-6825-5p	MIMAT0027550
12	hsa-miR-7641	MIMAT0029782
13	hsa-miR-3185	MIMAT0015065
14	hsa-miR-4746-3p	MIMAT0019881
15	hsa-miR-6791-5p	MIMAT0027482
16	hsa-miR-6893-5p	MIMAT0027686
17	hsa-miR-4433b-3p	MIMAT0030414
18	hsa-miR-3135b	MIMAT0018985
19	hsa-miR-6781-5p	MIMAT0027462
20	hsa-miR-1908-5p	MIMAT0007881
21	hsa-miR-4792	MIMAT0019964
22	hsa-miR-7845-5p	MIMAT0030420
23	hsa-miR-4417	MIMAT0018929
24	hsa-miR-3184-5p	MIMAT0015064
25	hsa-miR-1225-5p	MIMAT0005572
26	hsa-miR-1231	MIMAT0005586
27	hsa-miR-1225-3p	MIMAT0005573
28	hsa-miR-150-3p	MIMAT0004610
29	hsa-miR-4433-3p	MIMAT0018949
30	hsa-miR-6125	MIMAT0024598
31	hsa-miR-4513	MIMAT0019050
32	hsa-miR-6787-5p	MIMAT0027474

(continued)

SEQ ID NO:	Gene name	miRBase registration No.
33	hsa-miR-6784-5p	MIMAT0027468
34	hsa-miR-615-5p	MIMAT0004804
35	hsa-miR-6765-3p	MIMAT0027431
36	hsa-miR-5572	MIMAT0022260
37	hsa-miR-6842-5p	MIMAT0027586
38	hsa-miR-8063	MIMAT0030990
39	hsa-miR-6780b-5p	MIMAT0027572
40	hsa-miR-187-5p	MIMAT0004561
41	hsa-miR-128-1-5p	MIMAT0026477
42	hsa-miR-6729-5p	MIMAT0027359
43	hsa-miR-6741-5p	MIMAT0027383
44	hsa-miR-6757-5p	MIMAT0027414
45	hsa-miR-7110-5p	MIMAT0028117
46	hsa-miR-7975	MIMAT0031178
47	hsa-miR-1233-5p	MIMAT0022943
48	hsa-miR-6845-5p	MIMAT0027590
49	hsa-miR-3937	MIMAT0018352
50	hsa-miR-4467	MIMAT0018994
51	hsa-miR-7109-5p	MIMAT0028115
52	hsa-miR-6088	MIMAT0023713
53	hsa-miR-6782-5p	MIMAT0027464
54	hsa-miR-5195-3p	MIMAT0021127
55	hsa-miR-4454	MIMAT0018976
56	hsa-miR-6724-5p	MIMAT0025856
57	hsa-miR-8072	MIMAT0030999
58	hsa-miR-4516	MIMAT0019053
59	hsa-miR-6756-5p	MIMAT0027412
60	hsa-miR-4665-3p	MIMAT0019740
61	hsa-miR-6826-5p	MIMAT0027552
62	hsa-miR-6820-5p	MIMAT0027540
63	hsa-miR-6887-5p	MIMAT0027674
64	hsa-miR-3679-5p	MIMAT0018104
65	hsa-miR-7847-3p	MIMAT0030422
66	hsa-miR-6721-5p	MIMAT0025852
67	hsa-miR-3622a-5p	MIMAT0018003
68	hsa-miR-939-5p	MIMAT0004982
69	hsa-miR-602	MIMAT0003270
70	hsa-miR-7977	MIMAT0031180

(continued)

SEQ ID NO:	Gene name	miRBase registration No.
71	hsa-miR-6749-5p	MIMAT0027398
72	hsa-miR-1914-3p	MIMAT0007890
73	hsa-miR-4651	MIMAT0019715
74	hsa-miR-4695-5p	MIMAT0019788
75	hsa-miR-6848-5p	MIMAT0027596
76	hsa-miR-1228-3p	MIMAT0005583
77	hsa-miR-642b-3p	MIMAT0018444
78	hsa-miR-6746-5p	MIMAT0027392
79	hsa-miR-3620-5p	MIMAT0022967
80	hsa-miR-3131	MIMAT0014996
81	hsa-miR-6732-5p	MIMAT0027365
82	hsa-miR-7113-3p	MIMAT0028124
83	hsa-miR-23a-3p	MIMAT0000078
84	hsa-miR-3154	MIMAT0015028
85	hsa-miR-4723-5p	MIMAT0019838
86	hsa-miR-3663-3p	MIMAT0018085
87	hsa-miR-4734	MIMAT0019859
88	hsa-miR-6816-5p	MIMAT0027532
89	hsa-miR-4442	MIMAT0018960
90	hsa-miR-4476	MIMAT0019003
91	hsa-miR-423-5p	MIMAT0004748
92	hsa-miR-1249	MIMAT0005901
93	hsa-miR-6515-3p	MIMAT0025487
94	hsa-miR-887-3p	MIMAT0004951
95	hsa-miR-4741	MIMAT0019871
96	hsa-miR-6766-3p	MIMAT0027433
97	hsa-miR-4673	MIMAT0019755
98	hsa-miR-6779-5p	MIMAT0027458
99	hsa-miR-4706	MIMAT0019806
100	hsa-miR-1268b	MIMAT0018925
101	hsa-miR-4632-5p	MIMAT0022977
102	hsa-miR-3197	MIMAT0015082
103	hsa-miR-6798-5p	MIMAT0027496
104	hsa-miR-711	MIMAT0012734
105	hsa-miR-6840-3p	MIMAT0027583
106	hsa-miR-6763-5p	MIMAT0027426
107	hsa-miR-6727-5p	MIMAT0027355
108	hsa-miR-371a-5p	MIMAT0004687

(continued)

SEQ ID NO:	Gene name	miRBase registration No.
109	hsa-miR-6824-5p	MIMAT0027548
110	hsa-miR-4648	MIMAT0019710
111	hsa-miR-1227-5p	MIMAT0022941
112	hsa-miR-564	MIMAT0003228
113	hsa-miR-3679-3p	MIMAT0018105
114	hsa-miR-2861	MIMAT0013802
115	hsa-miR-6737-5p	MIMAT0027375
116	hsa-miR-575	MIMAT0003240
117	hsa-miR-4725-3p	MIMAT0019844
118	hsa-miR-6716-5p	MIMAT0025844
119	hsa-miR-4675	MIMAT0019757
120	hsa-miR-1915-3p	MIMAT0007892
121	hsa-miR-671-5p	MIMAT0003880
122	hsa-miR-3656	MIMAT0018076
123	hsa-miR-6722-3p	MIMAT0025854
124	hsa-miR-4707-5p	MIMAT0019807
125	hsa-miR-4449	MIMAT0018968
126	hsa-miR-1202	MIMAT0005865
127	hsa-miR-4649-5p	MIMAT0019711
128	hsa-miR-744-5p	MIMAT0004945
129	hsa-miR-642a-3p	MIMAT0020924
130	hsa-miR-451a	MIMAT0001631
131	hsa-miR-6870-5p	MIMAT0027640
132	hsa-miR-4443	MIMAT0018961
133	hsa-miR-6808-5p	MIMAT0027516
134	hsa-miR-4728-5p	MIMAT0019849
135	hsa-miR-937-5p	MIMAT0022938
136	hsa-miR-135a-3p	MIMAT0004595
137	hsa-miR-663b	MIMAT0005867
138	hsa-miR-1343-5p	MIMAT0027038
139	hsa-miR-6822-5p	MIMAT0027544
140	hsa-miR-6803-5p	MIMAT0027506
141	hsa-miR-6805-3p	MIMAT0027511
142	hsa-miR-128-2-5p	MIMAT0031095
143	hsa-miR-4640-5p	MIMAT0019699
144	hsa-miR-1469	MIMAT0007347
145	hsa-miR-92a-2-5p	MIMAT0004508
146	hsa-miR-3940-5p	MIMAT0019229

(continued)

SEQ ID NO:	Gene name	miRBase registration No.
147	hsa-miR-4281	MIMAT0016907
148	hsa-miR-1260b	MIMAT0015041
149	hsa-miR-4758-5p	MIMAT0019903
150	hsa-miR-1915-5p	MIMAT0007891
151	hsa-miR-5001-5p	MIMAT0021021
152	hsa-miR-4286	MIMAT0016916
153	hsa-miR-6126	MIMAT0024599
154	hsa-miR-6789-5p	MIMAT0027478
155	hsa-miR-4459	MIMAT0018981
156	hsa-miR-1268a	MIMAT0005922
157	hsa-miR-6752-5p	MIMAT0027404
158	hsa-miR-6131	MIMAT0024615
159	hsa-miR-6800-5p	MIMAT0027500
160	hsa-miR-4532	MIMAT0019071
161	hsa-miR-6872-3p	MIMAT0027645
162	hsa-miR-718	MIMAT0012735
163	hsa-miR-6769a-5p	MIMAT0027438
164	hsa-miR-4707-3p	MIMAT0019808
165	hsa-miR-6765-5p	MIMAT0027430
166	hsa-miR-4739	MIMAT0019868
167	hsa-miR-4525	MIMAT0019064
168	hsa-miR-4270	MIMAT0016900
169	hsa-miR-4534	MIMAT0019073
170	hsa-miR-6785-5p	MIMAT0027470
171	hsa-miR-6850-5p	MIMAT0027600
172	hsa-miR-4697-5p	MIMAT0019791
173	hsa-miR-1260a	MIMAT0005911
174	hsa-miR-4486	MIMAT0019020
175	hsa-miR-6880-5p	MIMAT0027660
176	hsa-miR-6802-5p	MIMAT0027504
177	hsa-miR-6861-5p	MIMAT0027623
178	hsa-miR-92b-5p	MIMAT0004792
179	hsa-miR-1238-5p	MIMAT0022947
180	hsa-miR-6851-5p	MIMAT0027602
181	hsa-miR-7704	MIMAT0030019
182	hsa-miR-149-3p	MIMAT0004609
183	hsa-miR-4689	MIMAT0019778
184	hsa-miR-4688	MIMAT0019777

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SEQ ID NO:	Gene name	miRBase registration No.
185	hsa-miR-125a-3p	MIMAT0004602
186	hsa-miR-23b-3p	MIMAT0000418
187	hsa-miR-614	MIMAT0003282
188	hsa-miR-1913	MIMAT0007888
189	hsa-miR-16-5p	MIMAT0000069
190	hsa-miR-675-5p	MIMAT0004284
191	hsa-miR-486-3p	MIMAT0004762
192	hsa-miR-6777-5p	MIMAT0027454
193	hsa-miR-4497	MIMAT0019032
194	hsa-miR-296-3p	MIMAT0004679
195	hsa-miR-6738-5p	MIMAT0027377
196	hsa-miR-4731-5p	MIMAT0019853
197	hsa-miR-6889-5p	MIMAT0027678
198	hsa-miR-6786-5p	MIMAT0027472
199	hsa-miR-92a-3p	MIMAT0000092
200	hsa-miR-4294	MIMAT0016849
201	hsa-miR-4763-3p	MIMAT0019913
202	hsa-miR-6076	MIMAT0023701
203	hsa-miR-663a	MIMAT0003326
204	hsa-miR-760	MIMAT0004957
205	hsa-miR-4667-5p	MIMAT0019743
206	hsa-miR-6090	MIMAT0023715
207	hsa-miR-4730	MIMAT0019852
208	hsa-miR-7106-5p	MIMAT0028109
209	hsa-miR-3196	MIMAT0015080
210	hsa-miR-5698	MIMAT0022491
211	hsa-miR-6087	MIMAT0023712
212	hsa-miR-4665-5p	MIMAT0019739
213	hsa-miR-8059	MIMAT0030986
214	hsa-miR-6879-5p	MIMAT0027658
215	hsa-mir-204	MI0000284
216	hsa-mir-1247	MI0006382
217	hsa-mir-6875	MI0022722
218	hsa-mir-6857	MI0022703
219	hsa-mir-6726	MI0022571
220	hsa-mir-3188	M10014232
221	hsa-mir-8069	MI0025905
222	hsa-mir-4257	MI0015856

(continued)

SEQ ID NO:	Gene name	miRBase registration No.
223	hsa-mir-1343	M10017320
224	hsa-mir-7108	MI0022959
225	hsa-mir-6825	MI0022670
226	hsa-mir-7641-1	MI0024975
227	hsa-mir-7641-2	MI0024976
228	hsa-mir-3185	MI0014227
229	hsa-mir-4746	MI0017385
230	hsa-mir-6791	MI0022636
231	hsa-mir-6893	MI0022740
232	hsa-mir-4433b	MI0025511
233	hsa-mir-3135b	MI0016809
234	hsa-mir-6781	MI0022626
235	hsa-mir-1908	MI0008329
236	hsa-mir-4792	MI0017439
237	hsa-mir-7845	MI0025515
238	hsa-mir-4417	M10016753
239	hsa-mir-3184	MI0014226
240	hsa-mir-1225	MI0006311
241	hsa-mir-1231	MI0006321
242	hsa-mir-150	MI0000479
243	hsa-mir-4433	MI0016773
244	hsa-mir-6125	MI0021259
245	hsa-mir-4513	MI0016879
246	hsa-mir-6787	MI0022632
247	hsa-mir-6784	MI0022629
248	hsa-mir-615	MI0003628
249	hsa-mir-6765	MI0022610
250	hsa-mir-5572	MI0019117
251	hsa-mir-6842	MI0022688
252	hsa-mir-8063	MI0025899
253	hsa-mir-6780b	MI0022681
254	hsa-mir-187	MI0000274
255	hsa-mir-128-1	MI0000447
256	hsa-mir-6729	MI0022574
257	hsa-mir-6741	MI0022586
258	hsa-mir-6757	MI0022602
259	hsa-mir-7110	MI0022961
260	hsa-mir-7975	MI0025751

(continued)

SEQ ID NO:	Gene name	miRBase registration No.
261	hsa-mir-1233-1	MI0006323
262	hsa-mir-1233-2	MI0015973
263	hsa-mir-6845	MI0022691
264	hsa-mir-3937	MI0016593
265	hsa-mir-4467	MI0016818
266	hsa-mir-7109	MI0022960
267	hsa-mir-608	MI0020365
268	hsa-mir-6782	MI0022627
269	hsa-mir-5195	MI0018174
270	hsa-mir-4454	MI0016800
271	hsa-mir-6724	MI0022559
272	hsa-mir-8072	MI0025908
273	hsa-mir-4516	MI0016882
274	hsa-mir-6756	MI0022601
275	hsa-mir-4665	MI0017295
276	hsa-mir-6826	MI0022671
277	hsa-mir-6820	MI0022665
278	hsa-mir-6887	MI0022734
279	hsa-mir-3679	MI0016080
280	hsa-mir-7847	MI0025517
281	hsa-mir-6721	MI0022556
282	hsa-mir-3622a	MI0016013
283	hsa-mir-939	MI0005761
284	hsa-mir-602	MI0003615
285	hsa-mir-7977	MI0025753
286	hsa-mir-6749	MI0022594
287	hsa-mir-1914	MI0008335
288	hsa-mir-4651	MI0017279
289	hsa-mir-4695	MI0017328
290	hsa-mir-6848	MI0022694
291	hsa-mir-1228	MI0006318
292	hsa-mir-642b	MI0016685
293	hsa-mir-6746	MI0022591
294	hsa-mir-3620	MI0016011
295	hsa-mir-3131	MI0014151
296	hsa-mir-6732	MI0022577
297	hsa-mir-7113	MI0022964
298	hsa-mir-23a	MI0000079

(continued)

SEQ ID NO:	Gene name	miRBase registration No.
299	hsa-mir-3154	MI0014182
300	hsa-mir-4723	MI0017359
301	hsa-mir-3663	MI0016064
302	hsa-mir-4734	MI0017371
303	hsa-mir-6816	MI0022661
304	hsa-mir-4442	MI0016785
305	hsa-mir-4476	MI0016828
306	hsa-mir-423	MI0001445
307	hsa-mir-1249	MI0006384
308	hsa-mir-6515	MI0022227
309	hsa-mir-887	MI0005562
310	hsa-mir-4741	MI0017379
311	hsa-mir-6766	MI0022611
312	hsa-mir-4673	MI0017304
313	hsa-mir-6779	MI0022624
314	hsa-mir-4706	MI0017339
315	hsa-mir-1268b	MI0016748
316	hsa-mir-4632	MI0017259
317	hsa-mir-3197	MI0014245
318	hsa-mir-6798	MI0022643
319	hsa-mir-711	MI0012488
320	hsa-mir-6840	MI0022686
321	hsa-mir-6763	MI0022608
322	hsa-mir-6727	MI0022572
323	hsa-mir-371a	MI0000779
324	hsa-mir-6824	MI0022669
325	hsa-mir-4648	MI0017275
326	hsa-mir-1227	MI0006316
327	hsa-mir-564	MI0003570
328	hsa-mir-2861	MI0013006
329	hsa-mir-6737	MI0022582
330	hsa-mir-575	MI0003582
331	hsa-mir-4725	MI0017362
332	hsa-mir-6716	MI0022550
333	hsa-mir-4675	MI0017306
334	hsa-mir-1915	MI0008336
335	hsa-mir-671	MI0003760
336	hsa-mir-3656	MI0016056

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SEQ ID NO:	Gene name	miRBase registration No.
337	hsa-mir-6722	MI0022557
338	hsa-mir-4707	MI0017340
339	hsa-mir-4449	MI0016792
340	hsa-mir-1202	MI0006334
341	hsa-mir-4649	MI0017276
342	hsa-mir-744	MI0005559
343	hsa-mir-642a	MI0003657
344	hsa-mir-451a	MI0001729
345	hsa-mir-6870	MI0022717
346	hsa-mir-4443	MI0016786
347	hsa-mir-6808	MI0022653
348	hsa-mir-4728	MI0017365
349	hsa-mir-937	MI0005759
350	hsa-mir-135a-1	MI0000452
351	hsa-mir-663b	MI0006336
352	hsa-mir-6822	MI0022667
353	hsa-mir-6803	MI0022648
354	hsa-mir-6805	MI0022650
355	hsa-mir-128-2	MI0000727
356	hsa-mir-4640	MI0017267
357	hsa-mir-1469	MI0007074
358	hsa-mir-92a-2	MI0000094
359	hsa-mir-3940	MI0016597
360	hsa-mir-4281	MI0015885
361	hsa-mir-1260b	MI0014197
362	hsa-mir-4758	MI0017399
363	hsa-mir-5001	MI0017867
364	hsa-mir-4286	MI0015894
365	hsa-mir-6126	MI0021260
366	hsa-mir-6789	MI0022634
367	hsa-mir-4459	MI0016805
368	hsa-mir-1268a	MI0006405
369	hsa-mir-6752	MI0022597
370	hsa-mir-6131	MI0021276
371	hsa-mir-6800	MI0022645
372	hsa-mir-4532	MI0016899
373	hsa-mir-6872	MI0022719
374	hsa-mir-718	MI0012489

(continued)

SEQ ID NO:	Gene name	miRBase registration No.
375	hsa-mir-6769a	MI0022614
376	hsa-mir-4739	MI0017377
377	hsa-mir-4525	MI0016892
378	hsa-mir-4270	MI0015878
379	hsa-mir-4534	MI0016901
380	hsa-mir-6785	MI0022630
381	hsa-mir-6850	MI0022696
382	hsa-mir-4697	MI0017330
383	hsa-mir-1260a	MI0006394
384	hsa-mir-4486	MI0016847
385	hsa-mir-6880	MI0022727
386	hsa-mir-6802	MI0022647
387	hsa-mir-6861	MI0022708
388	hsa-mir-92b	MI0003560
389	hsa-mir-1238	MI0006328
390	hsa-mir-6851	MI0022697
391	hsa-mir-7704	MI0025240
392	hsa-mir-149	MI0000478
393	hsa-mir-4689	MI0017322
394	hsa-mir-468	MI0017321
395	hsa-mir-125a	MI0000469
396	hsa-mir-23b	MI0000439
397	hsa-mir-614	MI0003627
398	hsa-mir-1913	MI0008334
399	hsa-mir-16-1	MI0000070
400	hsa-mir-16-2	MI0000115
401	hsa-mir-675	MI0005416
402	hsa-mir-486	MI0002470
403	hsa-mir-486-2	MI0023622
404	hsa-mir-6777	MI0022622
405	hsa-mir-4497	MI0016859
406	hsa-mir-296	MI0000747
407	hsa-mir-6738	MI0022583
408	hsa-mir-4731	MI0017368
409	hsa-mir-6889	MI0022736
410	hsa-mir-6786	MI0022631
411	hsa-mir-92a-1	MI0000093
412	hsa-mir-4294	MI0015827

(continued)

SEQ ID NO:	Gene name	miRBase registration No.
413	hsa-mir-4763	MI0017404
414	hsa-mir-6076	MI0020353
415	hsa-mir-663a	MI0003672
416	hsa-mir-760	MI0005567
417	hsa-mir-4667	MI0017297
418	hsa-mir-6090	MI0020367
419	hsa-mir-4730	MI0017367
420	hsa-mir-7106	MI0022957
421	hsa-mir-3196	MI0014241
422	hsa-mir-5698	MI0019305
423	hsa-mir-6087	MI0020364
424	hsa-mir-8059	MI0025895
425	hsa-mir-6879	MI0022726
426	isomiR example 1 of SEQ ID NO: 1	-
427	isomiR example 2 of SEQ ID NO: 1	-
428	isomiR example 1 of SEQ ID NO: 2	-
429	isomiR example 2 of SEQ ID NO: 2	-
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(continued)

SEQ ID NO:	Gene name	miRBase registration No.
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454	isomiR example 1 of SEQ ID NO: 36	-
455	isomiR example 2 of SEQ ID NO: 36	-
456	isomiR example 1 of SEQ ID NO: 40	-
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458	isomiR example 1 of SEQ ID NO: 41	-
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460	isomiR example 1 of SEQ ID NO: 46	-
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SEQ ID NO:	Gene name	miRBase registration No.
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526	isomiR example 1 of SEQ ID NO: 101	-

(continued)

SEQ ID NO:	Gene name	miRBase registration No.
527	isomiR example 2 of SEQ ID NO: 101	-
528	isomiR example 1 of SEQ ID NO: 102	-
529	isomiR example 2 of SEQ ID NO: 102	-
530	isomiR example 1 of SEQ ID NO: 104	-
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532	isomiR example 1 of SEQ ID NO: 108	-
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535	isomiR example 2 of SEQ ID NO: 110	-
536	isomiR example 1 of SEQ ID NO: 112	-
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540	isomiR example 1 of SEQ ID NO: 114	-
541	isomiR example 2 of SEQ ID NO: 114	-
542	isomiR example 1 of SEQ ID NO: 117	-
543	isomiR example 2 of SEQ ID NO: 117	-
544	isomiR example 1 of SEQ ID NO: 118	-
545	isomiR example 2 of SEQ ID NO: 118	-
546	isomiR example 1 of SEQ ID NO: 120	-
547	isomiR example 2 of SEQ ID NO: 120	-
548	isomiR example 1 of SEQ ID NO: 121	-
549	isomiR example 2 of SEQ ID NO: 121	-
550	isomiR example 1 of SEQ ID NO: 122	-
551	isomiR example 2 of SEQ ID NO: 122	-
552	isomiR example 1 of SEQ ID NO: 124	-
553	isomiR example 2 of SEQ ID NO: 124	-
554	isomiR example 1 of SEQ ID NO: 125	-
555	isomiR example 2 of SEQ ID NO: 125	-
556	isomiR example 1 of SEQ ID NO: 126	-
557	isomiR example 2 of SEQ ID NO: 126	-
558	isomiR example 1 of SEQ ID NO: 127	-
559	isomiR example 2 of SEQ ID NO: 127	-
560	isomiR example 1 of SEQ ID NO: 128	-
561	isomiR example 2 of SEQ ID NO: 128	-
562	isomiR example 1 of SEQ ID NO: 129	-
563	isomiR example 2 of SEQ ID NO: 129	-
564	isomiR example 1 of SEQ ID NO: 130	-

(continued)

SEQ ID NO:	Gene name	miRBase registration No.
565	isomiR example 2 of SEQ ID NO: 130	-
566	isomiR example 1 of SEQ ID NO: 132	-
567	isomiR example 2 of SEQ ID NO: 132	-
568	isomiR example 1 of SEQ ID NO: 134	-
569	isomiR example 2 of SEQ ID NO: 134	-
570	isomiR example 1 of SEQ ID NO: 135	-
571	isomiR example 2 of SEQ ID NO: 135	-
572	isomiR example 1 of SEQ ID NO: 136	-
573	isomiR example 2 of SEQ ID NO: 136	-
574	isomiR example 1 of SEQ ID NO: 137	-
575	isomiR example 2 of SEQ ID NO: 137	-
576	isomiR example 1 of SEQ ID NO: 142	-
577	isomiR example 2 of SEQ ID NO: 142	-
578	isomiR example 1 of SEQ ID NO: 143	-
579	isomiR example 2 of SEQ ID NO: 143	-
580	isomiR example 1 of SEQ ID NO: 145	-
581	isomiR example 2 of SEQ ID NO: 145	-
582	isomiR example 1 of SEQ ID NO: 146	-
583	isomiR example 2 of SEQ ID NO: 146	-
584	isomiR example 1 of SEQ ID NO: 147	-
585	isomiR example 2 of SEQ ID NO: 147	-
586	isomiR example 1 of SEQ ID NO: 148	-
587	isomiR example 2 of SEQ ID NO: 148	-
588	isomiR example 1 of SEQ ID NO: 149	-
589	isomiR example 2 of SEQ ID NO: 149	-
590	isomiR example 1 of SEQ ID NO: 150	-
591	isomiR example 2 of SEQ ID NO: 150	-
592	isomiR example 1 of SEQ ID NO: 151	-
593	isomiR example 2 of SEQ ID NO: 151	-
594	isomiR example 1 of SEQ ID NO: 152	-
595	isomiR example 2 of SEQ ID NO: 152	-
596	isomiR example 1 of SEQ ID NO: 153	-
597	isomiR example 2 of SEQ ID NO: 153	-
598	isomiR example 1 of SEQ ID NO: 155	-
599	isomiR example 2 of SEQ ID NO: 155	-
600	isomiR example 1 of SEQ ID NO: 156	-
601	isomiR example 2 of SEQ ID NO: 156	-
602	isomiR example 1 of SEQ ID NO: 158	-

(continued)

SEQ ID NO:	Gene name	miRBase registration No.
603	isomiR example 2 of SEQ ID NO: 158	-
604	isomiR example 1 of SEQ ID NO: 160	-
605	isomiR example 2 of SEQ ID NO: 160	-
606	isomiR example 1 of SEQ ID NO: 162	-
607	isomiR example 2 of SEQ ID NO: 162	-
608	isomiR example 1 of SEQ ID NO: 164	-
609	isomiR example 2 of SEQ ID NO: 164	-
610	isomiR example 1 of SEQ ID NO: 166	-
611	isomiR example 2 of SEQ ID NO: 166	-
612	isomiR example 1 of SEQ ID NO: 167	-
613	isomiR example 2 of SEQ ID NO: 167	-
614	isomiR example 1 of SEQ ID NO: 173	-
615	isomiR example 2 of SEQ ID NO: 173	-
616	isomiR example 1 of SEQ ID NO: 174	-
617	isomiR example 2 of SEQ ID NO: 174	-
618	isomiR example 1 of SEQ ID NO: 178	-
619	isomiR example 2 of SEQ ID NO: 178	-
620	isomiR example 1 of SEQ ID NO: 182	-
621	isomiR example 2 of SEQ ID NO: 182	-
622	isomiR example 1 of SEQ ID NO: 183	-
623	isomiR example 2 of SEQ ID NO: 183	-
624	isomiR example 1 of SEQ ID NO: 184	-
625	isomiR example 2 of SEQ ID NO: 184	-
626	isomiR example 1 of SEQ ID NO: 185	-
627	isomiR example 2 of SEQ ID NO: 185	-
628	isomiR example 1 of SEQ ID NO: 186	-
629	isomiR example 2 of SEQ ID NO: 186	-
630	isomiR example 1 of SEQ ID NO: 187	-
631	isomiR example 2 of SEQ ID NO: 187	-
632	isomiR example 1 of SEQ ID NO: 188	-
633	isomiR example 2 of SEQ ID NO: 188	-
634	isomiR example 1 of SEQ ID NO: 189	-
635	isomiR example 2 of SEQ ID NO: 189	-
636	isomiR example 1 of SEQ ID NO: 190	-
637	isomiR example 2 of SEQ ID NO: 190	-
638	isomiR example 1 of SEQ ID NO: 191	-
639	isomiR example 2 of SEQ ID NO: 191	-
640	isomiR example 1 of SEQ ID NO: 193	-

(continued)

SEQ ID NO:	Gene name	miRBase registration No.
641	isomiR example 2 of SEQ ID NO: 193	-
642	isomiR example 1 of SEQ ID NO: 194	-
643	isomiR example 2 of SEQ ID NO: 194	-
644	isomiR example 1 of SEQ ID NO: 196	-
645	isomiR example 2 of SEQ ID NO: 196	-
646	isomiR example 1 of SEQ ID NO: 199	-
647	isomiR example 2 of SEQ ID NO: 199	-
648	isomiR example 1 of SEQ ID NO: 201	-
649	isomiR example 2 of SEQ ID NO: 201	-
650	isomiR example 1 of SEQ ID NO: 203	-
651	isomiR example 2 of SEQ ID NO: 203	-
652	isomiR example 1 of SEQ ID NO: 204	-
653	isomiR example 2 of SEQ ID NO: 204	-
654	isomiR example 1 of SEQ ID NO: 205	-
655	isomiR example 2 of SEQ ID NO: 205	-
656	isomiR example 1 of SEQ ID NO: 207	-
657	isomiR example 2 of SEQ ID NO: 207	-
658	isomiR example 1 of SEQ ID NO: 209	-
659	isomiR example 2 of SEQ ID NO: 209	-
660	isomiR example 1 of SEQ ID NO: 210	-
661	isomiR example 2 of SEQ ID NO: 210	-
662	isomiR example 1 of SEQ ID NO: 211	-
663	isomiR example 2 of SEQ ID NO: 211	-
664	isomiR example 1 of SEQ ID NO: 212	-
665	isomiR example 2 of SEQ ID NO: 212	-
666	hsa-miR-6717-5p	MIMAT0025846
667	hsa-miR-3648	MIMAT0018068
668	hsa-miR-3162-5p	MIMAT0015036
669	hsa-miR-1909-3p	MIMAT0007883
670	hsa-miR-8073	MIMAT0031000
671	hsa-miR-6769b-5p	MIMAT0027620
672	hsa-miR-6836-3p	MIMAT0027575
673	hsa-miR-4484	MIMAT0019018
674	hsa-miR-6819-5p	MIMAT0027538
675	hsa-miR-6794-5p	MIMAT0027488
676	hsa-miR-24-3p	MIMAT0000080
677	hsa-mir-6717	MI0022551
678	hsa-mir-3648	MI0016048

(continued)

SEQ ID NO:	Gene name	miRBase registration No.
679	hsa-mir-3162	MI0014192
680	hsa-mir-1909	MI0008330
681	hsa-mir-8073	MI0025909
682	hsa-mir-6769b	MI0022706
683	hsa-mir-6836	MI0022682
684	hsa-mir-4484	MI0016845
685	hsa-mir-6819	MI0022664
686	hsa-mir-6794	MI0022639
687	hsa-mir-24-1	MI0000080
688	hsa-mir-24-2	MI0000081
689	isomiR example 1 of SEQ ID NO: 666	-
690	isomiR example 2 of SEQ ID NO: 666	-
691	isomiR example 1 of SEQ ID NO: 667	-
692	isomiR example 2 of SEQ ID NO: 667	-
693	isomiR example 1 of SEQ ID NO: 668	-
694	isomiR example 2 of SEQ ID NO: 668	-
695	isomiR example 1 of SEQ ID NO: 669	-
696	isomiR example 2 of SEQ ID NO: 669	-
697	isomiR example 1 of SEQ ID NO: 673	-
698	isomiR example 2 of SEQ ID NO: 673	-
699	isomiR example 1 of SEQ ID NO: 676	-
700	isomiR example 2 of SEQ ID NO: 676	-

[0274] The present specification encompasses the contents described in the specifications and/or drawings of Japanese Patent Application No. 2014-125036 and No. 2015-070379 from which the present application claims priority.

Advantageous Effect of Invention

[0275] According to the present invention, esophageal cancer can be detected easily and high accuracy. For example, the presence or absence of esophageal cancer in a patient can be easily detected by using, as indicators, the determined expression levels of several miRNAs in blood, serum, and/or plasma of the patients, which can be collected with limited invasiveness.

Brief Description of Drawings

[0276]

[Figure 1] This figure shows the relationship between hsa-miR-1343-3p consisting of a nucleotide sequence represented by SEQ ID NO: 9 and hsa-miR-1343-5p consisting of a nucleotide sequence represented by SEQ ID NO: 138, which are produced from a precursor hsa-mir-1343 consisting of a nucleotide sequence represented by SEQ ID NO: 223.

[Figure 2] Left diagram: the expression level measurement values of hsa-miR-204-3p (SEQ ID NO: 1) in healthy subjects (100 persons) and esophageal cancer patients (34 persons) selected as a training cohort were each plotted on the ordinate. The horizontal line in the diagram depicts a threshold (12.3) that was optimized by Fisher's discriminant analysis and discriminated between the two groups. Right diagram: the expression level measurement values

of hsa-miR-204-3p (SEQ ID NO: 1) in healthy subjects (50 persons) and esophageal cancer patients (16 persons) selected as a validation cohort were each plotted on the ordinate. The horizontal line in the diagram depicts the threshold (12.3) that was set in the training cohort and discriminated between both of the groups.

[Figure 3] Left diagram: the expression level measurement values of hsa-miR-1247-3p (SEQ ID NO: 2) in healthy subjects (100 persons, circles) and esophageal cancer patients (34 persons, triangles) selected as training cohort were each plotted on the abscissa against their expression level measurement values of hsa-miR-6857-5p (SEQ ID NO: 4) on the ordinate. The line in the diagram depicts a discriminant function (0 = 2.42x + y - 21.17) that was optimized by Fisher's discriminant analysis and discriminated between both of the groups. Right diagram: the expression level measurement values of hsa-miR-1247-3p (SEQ ID NO: 2) in healthy subjects (50 persons, circles) and esophageal cancer patients (34 persons, triangles) selected as validation cohort were each plotted on the abscissa against their expression level measurement values of hsa-miR-6857-5p (SEQ ID NO: 4) on the ordinate. The line in the diagram depicts the threshold (0 = 2.42x + y - 21.17) that was set in the training cohort and discriminated between both of the groups.

[Figure 4] Figure 4A: a discriminant (-2.65 x hsa-miR-4739 - 3.01 x has-miR-1343-5p + 0.69 x hsa-miR-204-3p + 0.95 x hsa-miR-4723-5p - 0.56 x hsa-miR-6726-5p - 0.99 x hsa-miR-6717-5p + 57.33) was prepared by use of Fisher's discriminant analysis from the expression level measurement values of hsa-miR-204-3p (SEQ ID NO: 1), hsa-miR-6726-5p (SEQ ID NO: 5), hsa-miR-4723-5p (SEQ ID NO: 85), hsa-miR-1343-5p (SEQ ID NO: 138), hsa-miR-4739 (SEQ ID NO: 166), and hsa-miR-6717-5p (SEQ ID NO: 666) in 34 esophageal cancer patients, 103 healthy subjects, 69 pancreatic cancer patients, 66 bile duct cancer patients, 30 colorectal cancer patients, 33 stomach cancer patients, 32 liver cancer patients, and 15 benign pancreaticobiliary disease patients selected as training cohorts, 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 discrimination boundary that offered a discriminant score of 0 and discriminated between the groups. Figure 4B: discriminant scores obtained from the discriminant prepared for the training cohort as to the expression level measurement values of hsa-miR-204-3p (SEQ ID NO: 1), hsa-miR-6726-5p (SEQ ID NO: 5), hsa-miR-4723-5p (SEQ ID NO: 85), hsa-miR-1343-5p (SEQ ID NO: 138), hsa-miR-4739 (SEQ ID NO: 166), and hsa-miR-6717-5p (SEQ ID NO: 666) in 16 esophageal cancer patients, 47 healthy subjects, 30 pancreatic cancer patients, 33 bile duct cancer patients, 20 colorectal cancer patients, 17 stomach cancer patients, 20 liver cancer patients, and 6 benign pancreaticobiliary disease patients selected as 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 both of the groups.

Description of Embodiments

[0277] Hereinafter, the present invention will be further described in detail specifically.

1. Target nucleic acid for esophageal cancer

[0278] Primary target nucleic acids that can be used as esophageal cancer markers for detecting the presence and/or absence of esophageal cancer or esophageal cancer cells using the nucleic acid probe or the primer for the detection of esophageal cancer defined above according to the present invention is at least one miRNAs selected from the group consisting of the following miRNAs: hsa-miR-204-3p, hsa-miR-1247-3p, hsa-miR-6875-5p, hsa-miR-6857-5p, hsa-miR-6726-5p, hsa-miR-3188, hsa-miR-8069, hsa-miR-4257, hsa-miR-1343-3p, hsa-miR-7108-5p, hsa-miR-6825-5p, hsa-miR-7641, hsa-miR-3185, hsa-miR-4746-3p, hsa-miR-6791-5p, hsa-miR-6893-5p, hsa-miR-4433b-3p, hsa-miR-3135b, hsa-miR-6781-5p, hsa-miR-1908-5p, hsa-miR-4792, hsa-miR-7845-5p, hsa-miR-4417, hsa-miR-3184-5p, hsa-miR-1225-5p, hsa-miR-1231, hsa-miR-1225-3p, hsa-miR-150-3p, hsa-miR-4433-3p, hsa-miR-6125, hsa-miR-4513, hsa-miR-6787-5p, hsa-miR-6784-5p, hsa-miR-615-5p, hsa-miR-6765-3p, hsa-miR-5572, hsa-miR-6842-5p, hsa-miR-8063, hsa-miR-6780b-5p, hsa-miR-187-5p, hsa-miR-128-1-5p, hsa-miR-6729-5p, hsa-miR-6741-5p, hsa-miR-6757-5p, hsa-miR-7110-5p, hsa-miR-7975, hsa-miR-1233-5p, hsa-miR-6845-5p, hsa-miR-3937, hsa-miR-4467, hsa-miR-7109-5p, hsa-miR-6088, hsa-miR-6782-5p, hsa-miR-5195-3p, hsa-miR-4454, hsa-miR-6724-5p, hsa-miR-8072, hsa-miR-4516, hsa-miR-6756-5p, hsa-miR-4665-3p, hsa-miR-6826-5p, hsa-miR-6820-5p, hsa-miR-6887-5p, hsa-miR-3679-5p, hsa-miR-7847-3p, hsa-miR-6721-5p, hsa-miR-3622a-5p, hsa-miR-939-5p, hsa-miR-602, hsa-miR-7977, hsa-miR-6749-5p, hsa-miR-1914-3p, hsa-miR-4651, hsa-miR-4695-5p, hsa-miR-6848-5p, hsa-miR-1228-3p, hsa-miR-642b-3p, hsa-miR-6746-5p, hsa-miR-3620-5p, hsa-miR-3131, hsa-miR-6732-5p, hsa-miR-7113-3p, hsa-miR-23a-3p, hsa-miR-3154, hsa-miR-4723-5p, hsa-miR-3663-3p, hsa-miR-4734, hsa-miR-6816-5p, hsa-miR-4442, hsa-miR-4476, hsa-miR-423-5p, hsa-miR-1249, hsa-miR-6515-3p, hsa-miR-887-3p, hsa-miR-4741, hsa-miR-6766-3p, hsa-miR-4673, hsa-miR-6779-5p, hsa-miR-4706, hsa-miR-1268b, hsa-miR-4632-5p, hsa-miR-3197, hsa-miR-6798-5p, hsa-miR-711, hsa-miR-6840-3p, hsa-miR-6763-5p, hsa-miR-6727-5p, hsa-miR-371a-5p, hsa-miR-6824-5p, hsa-miR-4648, hsa-miR-1227-5p, hsa-miR-

564, hsa-miR-3679-3p, hsa-miR-2861, hsa-miR-6737-5p, hsa-miR-4725-3p, hsa-miR-6716-5p, hsa-miR-4675, hsa-miR-1915-3p, hsa-miR-671-5p, hsa-miR-3656, hsa-miR-6722-3p, hsa-miR-4707-5p, hsa-miR-4449, hsa-miR-1202, hsa-miR-4649-5p, hsa-miR-744-5p, hsa-miR-642a-3p, hsa-miR-451a, hsa-miR-6870-5p, hsa-miR-4443, hsa-miR-6808-5p, hsa-miR-4728-5p, hsa-miR-937-5p, hsa-miR-135a-3p, hsa-miR-663b, hsa-miR-1343-5p, hsa-miR-6822-5p, hsa-miR-6803-5p, hsa-miR-6805-3p, hsa-miR-128-2-5p, hsa-miR-4640-5p, hsa-miR-1469, hsa-miR-92a-2-5p, hsa-miR-3940-5p, hsa-miR-4281, hsa-miR-1260b, hsa-miR-4758-5p, hsa-miR-1915-5p, hsa-miR-5001-5p, hsa-miR-4286, hsa-miR-6126, hsa-miR-6789-5p, hsa-miR-4459, hsa-miR-1268a, hsa-miR-6752-5p, hsa-miR-6131, hsa-miR-6800-5p, hsa-miR-4532, hsa-miR-6872-3p, hsa-miR-718, hsa-miR-6769a-5p, hsa-miR-4707-3p, hsa-miR-6765-5p, hsa-miR-4739, hsa-miR-4525, hsa-miR-4270, hsa-miR-4534, hsa-miR-6785-5p, hsa-miR-6850-5p, hsa-miR-4697-5p, hsa-miR-1260a, hsa-miR-4486, hsa-miR-6880-5p, hsa-miR-6802-5p, hsa-miR-6861-5p, hsa-miR-92b-5p, hsa-miR-1238-5p, hsa-miR-6851-5p, hsa-miR-7704, hsa-miR-149-3p, hsa-miR-4689, hsa-miR-4688, hsa-miR-125a-3p, hsa-miR-23b-3p, hsa-miR-614, hsa-miR-1913, hsa-miR-16-5p, hsa-miR-6717-5p, hsa-miR-3648, hsa-miR-3162-5p, hsa-miR-1909-3p, hsa-miR-8073, hsa-miR-6769b-5p, hsa-miR-6836-3p, hsa-miR-4484, hsa-miR-6819-5p, and hsa-miR-6794-5p. Furthermore, miRNAs selected from other esophageal cancer markers that can be combined with these miRNAs, i.e., hsa-miR-575 and hsa-miR-24-3p, can also be preferably used as a target nucleic acid. Moreover, at least one miRNA selected from the group consisting of the following other esophageal cancer markers that can be combined with these miRNAs, i.e., hsa-miR-675-5p, hsa-miR-486-3p, hsa-miR-6777-5p, hsa-miR-4497, hsa-miR-296-3p, hsa-miR-6738-5p, hsa-miR-4731-5p, hsa-miR-6889-5p, hsa-miR-6786-5p, hsa-miR-92a-3p, hsa-miR-4294, hsa-miR-4763-3p, hsa-miR-6076, hsa-miR-663a, hsa-miR-760, hsa-miR-4667-5p, hsa-miR-6090, hsa-miR-4730, hsa-miR-7106-5p, hsa-miR-3196, hsa-miR-5698, hsa-miR-6087, hsa-miR-4665-5p, hsa-miR-8059 and hsa-miR-6879-5p can also be preferably used as target nucleic acids.

[0279] These miRNAs include, for example, a human gene comprising a nucleotide sequence represented by any of SEQ ID NOs: 1 to 214 and 666 to 676 (i.e., hsa-miR-204-3p, hsa-miR-1247-3p, hsa-miR-6875-5p, hsa-miR-6857-5p, hsa-miR-6726-5p, hsa-miR-3188, hsa-miR-8069, hsa-miR-4257, hsa-miR-1343-3p, hsa-miR-7108-5p, hsa-miR-6825-5p, hsa-miR-7641, hsa-miR-3185, hsa-miR-4746-3p, hsa-miR-6791-5p, hsa-miR-6893-5p, hsa-miR-4433b-3p, hsa-miR-3135b, hsa-miR-6781-5p, hsa-miR-1908-5p, hsa-miR-4792, hsa-miR-7845-5p, hsa-miR-4417, hsa-miR-3184-5p, hsa-miR-1225-5p, hsa-miR-1231, hsa-miR-1225-3p, hsa-miR-150-3p, hsa-miR-4433-3p, hsa-miR-6125, hsa-miR-4513, hsa-miR-6787-5p, hsa-miR-6784-5p, hsa-miR-615-5p, hsa-miR-6765-3p, hsa-miR-5572, hsa-miR-6842-5p, hsa-miR-8063, hsa-miR-6780b-5p, hsa-miR-187-5p, hsa-miR-128-1-5p, hsa-miR-6729-5p, hsa-miR-6741-5p, hsa-miR-6757-5p, hsa-miR-7110-5p, hsa-miR-7975, hsa-miR-1233-5p, hsa-miR-6845-5p, hsa-miR-3937, hsa-miR-4467, hsa-miR-7109-5p, hsa-miR-6088, hsa-miR-6782-5p, hsa-miR-5195-3p, hsa-miR-4454, hsa-miR-6724-5p, hsa-miR-8072, hsa-miR-4516, hsa-miR-6756-5p, hsa-miR-4665-3p, hsa-miR-6826-5p, hsa-miR-6820-5p, hsa-miR-6887-5p, hsa-miR-3679-5p, hsa-miR-7847-3p, hsa-miR-6721-5p, hsa-miR-3622a-5p, hsa-miR-939-5p, hsa-miR-602, hsa-miR-7977, hsa-miR-6749-5p, hsa-miR-1914-3p, hsa-miR-4651, hsa-miR-4695-5p, hsa-miR-6848-5p, hsa-miR-1228-3p, hsa-miR-642b-3p, hsa-miR-6746-5p, hsa-miR-3620-5p, hsa-miR-3131, hsa-miR-6732-5p, hsa-miR-7113-3p, hsa-miR-23a-3p, hsa-miR-3154, hsa-miR-4723-5p, hsa-miR-3663-3p, hsa-miR-4734, hsa-miR-6816-5p, hsa-miR-4442, hsa-miR-4476, hsa-miR-423-5p, hsa-miR-1249, hsa-miR-6515-3p, hsa-miR-887-3p, hsa-miR-4741, hsa-miR-6766-3p, hsa-miR-4673, hsa-miR-6779-5p, hsa-miR-4706, hsa-miR-1268b, hsa-miR-4632-5p, hsa-miR-3197, hsa-miR-6798-5p, hsa-miR-711, hsa-miR-6840-3p, hsa-miR-6763-5p, hsa-miR-6727-5p, hsa-miR-371a-5p, hsa-miR-6824-5p, hsa-miR-4648, hsa-miR-1227-5p, hsa-miR-564, hsa-miR-3679-3p, hsa-miR-2861, hsa-miR-6737-5p, hsa-miR-4725-3p, hsa-miR-6716-5p, hsa-miR-4675, hsa-miR-1915-3p, hsa-miR-671-5p, hsa-miR-3656, hsa-miR-6722-3p, hsa-miR-4707-5p, hsa-miR-4449, hsa-miR-1202, hsa-miR-4649-5p, hsa-miR-744-5p, hsa-miR-642a-3p, hsa-miR-451a, hsa-miR-6870-5p, hsa-miR-4443, hsa-miR-6808-5p, hsa-miR-4728-5p, hsa-miR-937-5p, hsa-miR-135a-3p, hsa-miR-663b, hsa-miR-1343-5p, hsa-miR-6822-5p, hsa-miR-6803-5p, hsa-miR-6805-3p, hsa-miR-128-2-5p, hsa-miR-4640-5p, hsa-miR-1469, hsa-miR-92a-2-5p, hsa-miR-3940-5p, hsa-miR-4281, hsa-miR-1260b, hsa-miR-4758-5p, hsa-miR-1915-5p, hsa-miR-5001-5p, hsa-miR-4286, hsa-miR-6126, hsa-miR-6789-5p, hsa-miR-4459, hsa-miR-1268a, hsa-miR-6752-5p, hsa-miR-6131, hsa-miR-6800-5p, hsa-miR-4532, hsa-miR-6872-3p, hsa-miR-718, hsa-miR-6769a-5p, hsa-miR-4707-3p, hsa-miR-6765-5p, hsa-miR-4739, hsa-miR-4525, hsa-miR-4270, hsa-miR-4534, hsa-miR-6785-5p, hsa-miR-6850-5p, hsa-miR-4697-5p, hsa-miR-1260a, hsa-miR-4486, hsa-miR-6880-5p, hsa-miR-6802-5p, hsa-miR-6861-5p, hsa-miR-92b-5p, hsa-miR-1238-5p, hsa-miR-6851-5p, hsa-miR-7704, hsa-miR-149-3p, hsa-miR-4689, hsa-miR-4688, hsa-miR-125a-3p, hsa-miR-23b-3p, hsa-miR-614, hsa-miR-1913, hsa-miR-16-5p, hsa-miR-6717-5p, hsa-miR-3648, hsa-miR-3162-5p, hsa-miR-1909-3p, hsa-miR-8073, hsa-miR-6769b-5p, hsa-miR-6836-3p, hsa-miR-4484, hsa-miR-6819-5p, hsa-miR-6794-5phsa-miR-575, hsa-miR-24-3p, hsa-miR-675-5p, hsa-miR-486-3p, hsa-miR-6777-5p, hsa-miR-4497, hsa-miR-296-3p, hsa-miR-6738-5p, hsa-miR-4731-5p, hsa-miR-6889-5p, hsa-miR-6786-5p, hsa-miR-92a-3p, hsa-miR-4294, hsa-miR-4763-3p, hsa-miR-6076, hsa-miR-663a, hsa-miR-760, hsa-miR-4667-5p, hsa-miR-6090, hsa-miR-4730, hsa-miR-7106-5p, hsa-miR-3196, hsa-miR-5698, hsa-miR-6087, hsa-miR-4665-5p, hsa-miR-8059 and hsa-miR-6879-5p, 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.

[0280] The target nucleic acid is preferably a human gene comprising a nucleotide sequence represented by any of SEQ ID NOs: 1 to 700 or a transcript thereof, more preferably the transcript, i.e., a miRNA or its precursor RNA (pri-miRNA or pre-miRNA).

[0281] The first 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 esophageal cancer.

[0282] The second 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 esophageal cancer.

[0283] The third 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 esophageal cancer.

[0284] The fourth 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 esophageal cancer.

[0285] The fifth 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 esophageal cancer.

[0286] The sixth 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 esophageal cancer.

[0287] The seventh 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 esophageal cancer.

[0288] The eighth 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 esophageal cancer.

[0289] The ninth 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 esophageal cancer.

[0290] The 10th 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 esophageal cancer.

[0291] The 11th 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 esophageal cancer.

[0292] 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 esophageal cancer.

[0293] The 13th 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 esophageal cancer.

[0294] The 14th 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 esophageal cancer.

[0295] The 15th 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 esophageal cancer.

[0296] The 16th 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 esophageal cancer.

[0297] The 17th 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 esophageal cancer.

[0298] The 18th 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 esophageal cancer.

[0299] The 19th 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 esophageal cancer.

[0300] The 20th 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 esophageal cancer.

[0301] The 21st 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 esophageal cancer.

[0302] The 22nd 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 esophageal cancer.

[0303] The 23rd 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 esophageal cancer.

[0304] The 24th 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 esophageal cancer.

[0305] The 25th 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 esophageal cancer.

[0306] The 26th target gene is the hsa-miR-1231 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 esophageal cancer.

[0307] The 27th target gene is the hsa-miR-1225-3p 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 esophageal cancer.

[0308] The 28th target gene is the hsa-miR-150-3p 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 esophageal cancer.

[0309] The 29th 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 esophageal cancer.

[0310] The 30th 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 esophageal cancer.

[0311] The 31st 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 esophageal cancer.

[0312] The 32nd 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 esophageal cancer.

[0313] The 33rd 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 esophageal cancer.

[0314] The 34th 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 esophageal cancer.

[0315] The 35th 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 esophageal cancer.

[0316] The 36th 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 esophageal cancer.

[0317] The 37th 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 esophageal cancer.

[0318] The 38th 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 esophageal cancer.

[0319] The 39th 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 esophageal cancer.

[0320] The 40th 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 esophageal cancer.

[0321] The 41st 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 esophageal cancer.

[0322] The 42nd 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 esophageal cancer.

[0323] The 43rd 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 esophageal cancer.

[0324] The 44th 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 esophageal cancer.

[0325] The 45th 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 esophageal cancer.

[0326] The 46th 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 esophageal cancer.

[0327] The 47th target gene is the hsa-miR-1233-5p 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 esophageal cancer.

[0328] The 48th 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 esophageal cancer.

[0329] The 49th 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 esophageal cancer.

[0330] The 50th 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 esophageal cancer.

[0331] The 51st 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 esophageal cancer.

[0332] The 52nd 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 esophageal cancer.

[0333] The 53rd 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 esophageal cancer.

[0334] The 54th 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 esophageal cancer.

[0335] The 55th 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 esophageal cancer.

[0336] The 56th 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 esophageal cancer.

[0337] The 57th 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 esophageal cancer.

[0338] The 58th 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 esophageal cancer.

[0339] The 59th 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 esophageal cancer.

[0340] The 60th 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 esophageal cancer.

[0341] The 61st 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 esophageal cancer.

[0342] The 62nd 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 esophageal cancer.

[0343] The 63rd 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 esophageal cancer.

[0344] The 64th 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 esophageal cancer.

[0345] The 65th 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 esophageal cancer.

[0346] The 66th 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 esophageal cancer.

[0347] The 67th target gene is the hsa-miR-3622a-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 esophageal cancer.

[0348] The 68th 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 esophageal cancer.

[0349] The 69th 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 esophageal cancer.

[0350] The 70th 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 esophageal cancer.

[0351] The 71st 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 esophageal cancer.

[0352] The 72nd 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 esophageal cancer.

[0353] The 73rd 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 esophageal cancer.

[0354] The 74th 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 esophageal cancer.

[0355] The 75th 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 esophageal cancer.

[0356] The 76th 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 esophageal cancer.

[0357] The 77th 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 esophageal cancer.

[0358] The 78th 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 esophageal cancer.

[0359] The 79th 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 esophageal cancer.

[0360] The 80th 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 esophageal cancer.

[0361] The 81st 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 esophageal cancer.

[0362] The 82nd 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 esophageal cancer.

[0363] The 83rd target gene is the hsa-miR-23a-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 esophageal cancer.

[0364] The 84th target gene is the hsa-miR-3154 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 esophageal cancer.

[0365] The 85th 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 esophageal cancer.

[0366] The 86th 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 esophageal cancer.

[0367] The 87th 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 esophageal cancer.

[0368] The 88th 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 esophageal cancer.

[0369] The 89th 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 esophageal cancer.

[0370] The 90th 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 esophageal cancer.

[0371] The 91st target gene is the hsa-miR-423-5p 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 esophageal cancer.

[0372] The 92nd 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 esophageal cancer.

[0373] The 93rd 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 esophageal cancer.

[0374] The 94th 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 esophageal cancer.

[0375] The 95th 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 esophageal cancer.

[0376] The 96th 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 esophageal cancer.

[0377] The 97th target gene is the hsa-miR-4673 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 esophageal cancer.

[0378] The 98th 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 esophageal cancer.

[0379] The 99th 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 esophageal cancer.

[0380] The 100th 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 esophageal cancer.

[0381] The 101st 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 esophageal cancer.

[0382] The 102nd 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 esophageal cancer.

[0383] The 103rd 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 esophageal cancer.

[0384] The 104th 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 esophageal cancer.

[0385] The 105th 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 esophageal cancer.

[0386] The 106th target gene is the hsa-miR-6763-5p 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 esophageal cancer.

[0387] The 107th 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 esophageal cancer.

[0388] The 108th 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 esophageal cancer.

[0389] The 109th target gene is the hsa-miR-6824-5p 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 esophageal cancer.

[0390] The 110th 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 esophageal cancer.

[0391] The 111th 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 esophageal cancer.

[0392] The 112th 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 esophageal cancer.

[0393] The 113th 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 esophageal cancer.

[0394] The 114th 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 esophageal cancer.

[0395] The 115th target gene is the hsa-miR-6737-5p 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 esophageal cancer.

[0396] The 116th target gene is the hsa-miR-575 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 esophageal cancer (Patent Literature 1).

[0397] The 117th 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 esophageal cancer.

[0398] The 118th 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 esophageal cancer.

[0399] The 119th 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 esophageal cancer.

[0400] The 120th 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 esophageal cancer.

[0401] The 121st 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 esophageal cancer.

[0402] The 122nd 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 esophageal cancer.

[0403] The 123rd 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 esophageal cancer.

[0404] The 124th 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 esophageal cancer.

[0405] The 125th 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 esophageal cancer.

[0406] The 126th 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 esophageal cancer.

[0407] The 127th 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 esophageal cancer.

[0408] The 128th 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 esophageal cancer.

[0409] The 129th 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 esophageal cancer.

[0410] The 130th 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 esophageal cancer.

[0411] The 131st 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 esophageal cancer.

[0412] The 132nd target gene is the hsa-miR-4443 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 esophageal cancer.

[0413] The 133rd target gene is the hsa-miR-6808-5p 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 esophageal cancer.

[0414] The 134th 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 esophageal cancer.

[0415] The 135th 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 esophageal cancer.

[0416] The 136th 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 esophageal cancer.

[0417] The 137th 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 esophageal cancer.

[0418] The 138th target gene is the hsa-miR-1343-5p 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 esophageal cancer.

[0419] The 139th target gene is the hsa-miR-6822-5p 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 esophageal cancer.

[0420] The 140th 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 esophageal cancer.

[0421] The 141st 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 esophageal cancer.

[0422] The 142nd target gene is the hsa-miR-128-2-5p 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 esophageal cancer.

[0423] The 143rd target gene is the hsa-miR-4640-5p 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 esophageal cancer.

[0424] The 144th 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 esophageal cancer.

[0425] The 145th target gene is the hsa-miR-92a-2-5p 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 esophageal cancer.

[0426] The 146th 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 esophageal cancer.

[0427] The 147th 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 esophageal cancer.

[0428] The 148th target gene is the hsa-miR-1260b 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 esophageal cancer.

[0429] The 149th 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 esophageal cancer.

[0430] The 150th 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 esophageal cancer.

[0431] The 151st target gene is the hsa-miR-5001-5p 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 esophageal cancer.

[0432] The 152nd target gene is the hsa-miR-4286 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 esophageal cancer.

[0433] The 153rd 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 esophageal cancer.

[0434] The 154th 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 esophageal cancer.

[0435] The 155th target gene is the hsa-miR-4459 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 esophageal cancer.

[0436] The 156th target gene is the hsa-miR-1268a 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 esophageal cancer.

[0437] The 157th 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 esophageal cancer.

[0438] The 158th 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 esophageal cancer.

[0439] The 159th target gene is the hsa-miR-6800-5p 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 esophageal cancer.

[0440] The 160th 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 esophageal cancer.

[0441] The 161st target gene is the hsa-miR-6872-3p 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 esophageal cancer.

[0442] The 162nd 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 esophageal cancer.

[0443] The 163rd 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 esophageal cancer.

[0444] The 164th target gene is the hsa-miR-4707-3p 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 esophageal cancer.

[0445] The 165th target gene is the hsa-miR-6765-5p 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 esophageal cancer.

[0446] The 166th target gene is the hsa-miR-4739 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 esophageal cancer.

[0447] The 167th target gene is the hsa-miR-4525 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 esophageal cancer.

[0448] The 168th target gene is the hsa-miR-4270 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 esophageal cancer.

[0449] The 169th 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 esophageal cancer.

[0450] The 170th 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 esophageal cancer.

[0451] The 171st 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 esophageal cancer.

[0452] The 172nd 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 esophageal cancer.

[0453] The 173rd target gene is the hsa-miR-1260a 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 esophageal cancer.

[0454] The 174th 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 esophageal cancer.

[0455] The 175th target gene is the hsa-miR-6880-5p 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 esophageal cancer.

[0456] The 176th 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 esophageal cancer.

[0457] The 177th 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 esophageal cancer.

[0458] The 178th 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 esophageal cancer.

[0459] The 179th target gene is the hsa-miR-1238-5p 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 esophageal cancer.

[0460] The 180th target gene is the hsa-miR-6851-5p 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 esophageal cancer.

[0461] The 181 st target gene is the hsa-miR-7704 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 esophageal cancer.

[0462] The 182nd 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 esophageal cancer.

[0463] The 183rd 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 esophageal cancer.

[0464] The 184th 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 esophageal cancer.

[0465] The 185th 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 esophageal cancer.

[0466] The 186th 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 esophageal cancer.

[0467] The 187th 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 esophageal cancer.

[0468] The 188th 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 esophageal cancer.

[0469] The 189th target gene is the hsa-miR-16-5p 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 esophageal cancer.

[0470] The 190th 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 esophageal cancer.

[0471] The 191st target gene is the hsa-miR-486-3p 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 esophageal cancer.

[0472] The 192nd 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 esophageal cancer.

[0473] The 193rd 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 esophageal cancer.

[0474] The 194th 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 esophageal cancer.

[0475] The 195th 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 esophageal cancer.

[0476] The 196th target gene is the hsa-miR-4731-5p 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 esophageal cancer.

[0477] The 197th target gene is the hsa-miR-6889-5p 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 esophageal cancer.

[0478] The 198th target gene is the hsa-miR-6786-5p 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 esophageal cancer.

[0479] The 199th target gene is the hsa-miR-92a-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 esophageal cancer (Patent Literature 1).

[0480] The 200th 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 esophageal cancer.

[0481] The 201st 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 esophageal cancer.

[0482] The 202nd target gene is the hsa-miR-6076 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 esophageal cancer.

[0483] The 203rd target gene is the hsa-miR-663a 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 esophageal cancer (Patent Literature 1).

[0484] The 204th target gene is the hsa-miR-760 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 esophageal cancer.

[0485] The 205th 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 esophageal cancer.

[0486] The 206th 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 esophageal cancer.

[0487] The 207th target gene is the hsa-miR-4730 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 esophageal cancer.

[0488] The 208th 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 esophageal cancer.

[0489] The 209th 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 esophageal cancer.

[0490] The 210th 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 esophageal cancer.

[0491] The 211th target gene is the hsa-miR-6087 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 esophageal cancer.

[0492] The 212th 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 esophageal cancer.

[0493] The 213th 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 esophageal cancer.

[0494] The 214th 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 esophageal cancer.

[0495] The 215th 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.

[0496] The 216th target gene is the hsa-miR-3648 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

[0497] The 217th target gene is the hsa-miR-3162-5p 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.

[0498] The 218th target gene is the hsa-miR-1909-3p 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.

[0499] The 219th target gene is the hsa-miR-8073 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.

[0500] The 220th 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.

[0501] The 221st 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.

[0502] The 222nd target gene is the hsa-miR-4484 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.

[0503] The 223rd target gene is the hsa-miR-6819-5p 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.

[0504] The 224th target gene is the hsa-miR-6794-5p 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.

[0505] The 225th 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).

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

[0506] In the present invention, a nucleic acid capable of specifically binding to any of the target nucleic acids as the esophageal 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 esophageal cancer.

[0507] In the present invention, the nucleic acid probes or the primers that can be used for detecting esophageal cancer or for diagnosing esophageal cancer enable qualitative and/or quantitative measurement of the presence, expression level, or existing amount (abundance) of any of the target nucleic acids as the esophageal cancer markers described above, for example, human-derived hsa-miR-204-3p, hsa-miR-1247-3p, hsa-miR-6875-5p, hsa-miR-6857-5p, hsa-miR-6726-5p, hsa-miR-3188, hsa-miR-8069, hsa-miR-4257, hsa-miR-1343-3p, hsa-miR-7108-5p, hsa-miR-6825-5p, hsa-miR-7641, hsa-miR-3185, hsa-miR-4746-3p, hsa-miR-6791-5p, hsa-miR-6893-5p, hsa-miR-4433b-3p, hsa-miR-3135b, hsa-miR-6781-5p, hsa-miR-1908-5p, hsa-miR-4792, hsa-miR-7845-5p, hsa-miR-4417, hsa-miR-3184-5p, hsa-miR-1225-5p, hsa-miR-1231, hsa-miR-1225-3p, hsa-miR-150-3p, hsa-miR-4433-3p, hsa-miR-6125, hsa-miR-4513, hsa-miR-6787-5p, hsa-miR-6784-5p, hsa-miR-615-5p, hsa-miR-6765-3p, hsa-miR-5572, hsa-miR-6842-5p, hsa-miR-8063, hsa-miR-6780b-5p, hsa-miR-187-5p, hsa-miR-128-1-5p, hsa-miR-6729-5p, hsa-miR-6741-5p, hsa-miR-6757-5p, hsa-miR-7110-5p, hsa-miR-7975, hsa-miR-1233-5p, hsa-miR-6845-5p, hsa-miR-3937, hsa-miR-4467, hsa-miR-7109-5p, hsa-miR-6088, hsa-miR-6782-5p, hsa-miR-5195-3p, hsa-miR-4454, hsa-miR-6724-5p, hsa-miR-8072,

hsa-miR-4516, hsa-miR-6756-5p, hsa-miR-4665-3p, hsa-miR-6826-5p, hsa-miR-6820-5p, hsa-miR-6887-5p, hsa-miR-3679-5p, hsa-miR-7847-3p, hsa-miR-6721-5p, hsa-miR-3622a-5p, hsa-miR-939-5p, hsa-miR-602, hsa-miR-7977, hsa-miR-6749-5p, hsa-miR-1914-3p, hsa-miR-4651, hsa-miR-4695-5p, hsa-miR-6848-5p, hsa-miR-1228-3p, hsa-miR-642b-3p, hsa-miR-6746-5p, hsa-miR-3620-5p, hsa-miR-3131, hsa-miR-6732-5p, hsa-miR-7113-3p, hsa-miR-23a-3p, hsa-miR-3154, hsa-miR-4723-5p, hsa-miR-3663-3p, hsa-miR-4734, hsa-miR-6816-5p, hsa-miR-4442, hsa-miR-4476, hsa-miR-423-5p, hsa-miR-1249, hsa-miR-6515-3p, hsa-miR-887-3p, hsa-miR-4741, hsa-miR-6766-3p, hsa-miR-4673, hsa-miR-6779-5p, hsa-miR-4706, hsa-miR-1268b, hsa-miR-4632-5p, hsa-miR-3197, hsa-miR-6798-5p, hsa-miR-711, hsa-miR-6840-3p, hsa-miR-6763-5p, hsa-miR-6727-5p, hsa-miR-371a-5p, hsa-miR-6824-5p, hsa-miR-4648, hsa-miR-1227-5p, hsa-miR-564, hsa-miR-3679-3p, hsa-miR-2861, hsa-miR-6737-5p, hsa-miR-4725-3p, hsa-miR-6716-5p, hsa-miR-4675, hsa-miR-1915-3p, hsa-miR-671-5p, hsa-miR-3656, hsa-miR-6722-3p, hsa-miR-4707-5p, hsa-miR-4449, hsa-miR-1202, hsa-miR-4649-5p, hsa-miR-744-5p, hsa-miR-642a-3p, hsa-miR-451a, hsa-miR-6870-5p, hsa-miR-4443, hsa-miR-6808-5p, hsa-miR-4728-5p, hsa-miR-937-5p, hsa-miR-135a-3p, hsa-miR-663b, hsa-miR-1343-5p, hsa-miR-6822-5p, hsa-miR-6803-5p, hsa-miR-6805-3p, hsa-miR-128-2-5p, hsa-miR-4640-5p, hsa-miR-1469, hsa-miR-92a-2-5p, hsa-miR-3940-5p, hsa-miR-4281, hsa-miR-1260b, hsa-miR-4758-5p, hsa-miR-1915-5p, hsa-miR-5001-5p, hsa-miR-4286, hsa-miR-6126, hsa-miR-6789-5p, hsa-miR-4459, hsa-miR-1268a, hsa-miR-6752-5p, hsa-miR-6131, hsa-miR-6800-5p, hsa-miR-4532, hsa-miR-6872-3p, hsa-miR-718, hsa-miR-6769a-5p, hsa-miR-4707-3p, hsa-miR-6765-5p, hsa-miR-4739, hsa-miR-4525, hsa-miR-4270, hsa-miR-4534, hsa-miR-6785-5p, hsa-miR-6850-5p, hsa-miR-4697-5p, hsa-miR-1260a, hsa-miR-4486, hsa-miR-6880-5p, hsa-miR-6802-5p, hsa-miR-6861-5p, hsa-miR-92b-5p, hsa-miR-1238-5p, hsa-miR-6851-5p, hsa-miR-7704, hsa-miR-149-3p, hsa-miR-4689, hsa-miR-4688, hsa-miR-125a-3p, hsa-miR-23b-3p, hsa-miR-614, hsa-miR-1913, hsa-miR-16-5p, hsa-miR-6717-5p, hsa-miR-3648, hsa-miR-3162-5p, hsa-miR-1909-3p, hsa-miR-8073, hsa-miR-6769b-5p, hsa-miR-6836-3p, hsa-miR-4484, hsa-miR-6819-5p, and hsa-miR-6794-5p or a combination thereof: congeners thereof: transcripts thereof: or variants or derivatives thereof; and, optionally in combination therewith, hsa-miR-575, 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-675-5p, hsa-miR-486-3p, hsa-miR-6777-5p, hsa-miR-4497, hsa-miR-296-3p, hsa-miR-6738-5p, hsa-miR-4731-5p, hsa-miR-6889-5p, hsa-miR-6786-5p, hsa-miR-92a-3p, hsa-miR-4294, hsa-miR-4763-3p, hsa-miR-6076, hsa-miR-663a, hsa-miR-760, hsa-miR-4667-5p, hsa-miR-6090, hsa-miR-4730, hsa-miR-7106-5p, hsa-miR-3196, hsa-miR-5698, hsa-miR-6087, hsa-miR-4665-5p, hsa-miR-8059, and hsa-miR-6879-5p or a combination thereof, congeners thereof, transcripts thereof, or variants or derivatives thereof.

[0508] The expression levels of the target nucleic acids described above are increased or decreased (hereinafter, referred to as "increased/decreased") depending on the types of the target nucleic acids in a subject having esophageal cancer as compared with healthy subjects. Hence, the nucleic acid of the present invention can be effectively used for measuring expression levels of the target nucleic acids described above in body fluids from a subject (e.g., humans) suspected of having esophageal cancer and body fluids from healthy subjects and thereby detecting esophageal cancer through the comparison thereof.

[0509] The nucleic acid probes or the primers that can be used in the present invention is 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: 1 to 115, 117 to 189, and 666 to 675, or a primer for amplifying a polynucleotide consisting of a nucleotide sequence represented by at least one of SEQ ID NOs: 1 to 115, 117 to 189, and 666 to 675.

[0510] The nucleic acid probes or the primers 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 any of SEQ ID NOs: 116 and 676, or a primer for amplifying a polynucleotide consisting of a nucleotide sequence represented by SEQ ID NO: 116.

[0511] The nucleic acid probes or the primers that can be used in the present invention may further 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: 190 to 214, or a primer for amplifying a polynucleotide consisting of a nucleotide sequence represented by at least one of SEQ ID NOs: 190 to 214.

[0512] Specifically, these nucleic acid probes or primers comprise a combination of one or more polynucleotides selected from a group of polynucleotides comprising nucleotide sequences represented by any of SEQ ID NOs: 1 to 700 or nucleotide sequences from the nucleotide sequences by the replacement of u with t, and a complementary polynucleotide group thereof, a group of polynucleotides 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 group of polynucleotides comprising 15 or more, preferably 17 or more consecutive nucleotides that are from the nucleotide sequences of these polynucleotide groups. These polynucleotides can be used as nucleic acid probes and primers for detecting the esophageal cancer markers as target nucleic acids.

[0513] More specifically, examples of the nucleic acid probes or the primers 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 115, 117 to 189, and 666 to 675, or a nucleotide sequence 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 115, 117 to 189, and 666 to 675,
(c) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 1 to 115, 117 to 189, and 666 to 675, or a nucleotide sequence 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 115, 117 to 189, and 666 to 675, or a nucleotide sequence 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).

[0514] In addition to at least one polynucleotides selected from any of the group consisting of the polynucleotides (a) to (e), the nucleic acid probe or the primer that can be used in the present invention may further comprise a polynucleotide selected from the group consisting of the following polynucleotides (f) to (j);

(f) a polynucleotide consisting of a nucleotide sequence represented by SEQ ID NOs: 116 to 676 or a nucleotide sequence 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 SEQ ID NOs: 116 to 676,
(h) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by SEQ ID NOs: 116 to 676 or a nucleotide sequence 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 SEQ ID NOs: 116 to 676 or a nucleotide sequence 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).

[0515] In addition to at least one polynucleotides selected from any of the group consisting of the polynucleotides (a) to (j), the nucleic acid probes or the primers that can be used in the present invention may further comprise 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: 190 to 214 or a nucleotide sequence 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: 190 to 214,
(m) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 190 to 214 or a nucleotide sequence 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: 190 to 214 or a nucleotide sequence 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).

[0516] For the above-mentioned polynucleotides, the "fragment thereof comprising 15 or more consecutive nucleotides" can comprise, but is not limited to, the number of nucleotides in the range from, for example, 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, or the like, and is from the nucleotide sequence of each polynucleotide.

[0517] These polynucleotides or fragments thereof used in the present invention may each be DNA or may each be RNA.

[0518] The polynucleotides that can be used in the present invention can be prepared by use of a general technique such as a DNA recombination technique, a PCR method, or a method using an automatic DNA/RNA synthesizer.

[0519] The DNA recombination technique and the PCR method may employ techniques 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).

[0520] The human-derived hsa-miR-204-3p, hsa-miR-1247-3p, hsa-miR-6875-5p, hsa-miR-6857-5p, hsa-miR-6726-5p, hsa-miR-3188, hsa-miR-8069, hsa-miR-4257, hsa-miR-1343-3p, hsa-miR-7108-5p, hsa-miR-6825-5p, hsa-

miR-7641, hsa-miR-3185, hsa-miR-4746-3p, hsa-miR-6791-5p, hsa-miR-6893-5p, hsa-miR-4433b-3p, hsa-miR-3135b, hsa-miR-6781-5p, hsa-miR-1908-5p, hsa-miR-4792, hsa-miR-7845-5p, hsa-miR-4417, hsa-miR-3184-5p, hsa-miR-1225-5p, hsa-miR-1231, hsa-miR-1225-3p, hsa-miR-150-3p, hsa-miR-4433-3p, hsa-miR-6125, hsa-miR-4513, hsa-miR-6787-5p, hsa-miR-6784-5p, hsa-miR-615-5p, hsa-miR-6765-3p, hsa-miR-5572, hsa-miR-6842-5p, hsa-miR-8063, hsa-miR-6780b-5p, hsa-miR-187-5p, hsa-miR-128-1-5p, hsa-miR-6729-5p, hsa-miR-6741-5p, hsa-miR-6757-5p, hsa-miR-7110-5p, hsa-miR-7975, hsa-miR-1233-5p, hsa-miR-6845-5p, hsa-miR-3937, hsa-miR-4467, hsa-miR-7109-5p, hsa-miR-6088, hsa-miR-6782-5p, hsa-miR-5195-3p, hsa-miR-4454, hsa-miR-6724-5p, hsa-miR-8072, hsa-miR-4516, hsa-miR-6756-5p, hsa-miR-4665-3p, hsa-miR-6826-5p, hsa-miR-6820-5p, hsa-miR-6887-5p, hsa-miR-3679-5p, hsa-miR-7847-3p, hsa-miR-6721-5p, hsa-miR-3622a-5p, hsa-miR-939-5p, hsa-miR-602, hsa-miR-7977, hsa-miR-6749-5p, hsa-miR-1914-3p, hsa-miR-4651, hsa-miR-4695-5p, hsa-miR-6848-5p, hsa-miR-1228-3p, hsa-miR-642b-3p, hsa-miR-6746-5p, hsa-miR-3620-5p, hsa-miR-3131, hsa-miR-6732-5p, hsa-miR-7113-3p, hsa-miR-23a-3p, hsa-miR-3154, hsa-miR-4723-5p, hsa-miR-3663-3p, hsa-miR-4734, hsa-miR-6816-5p, hsa-miR-4442, hsa-miR-4476, hsa-miR-423-5p, hsa-miR-1249, hsa-miR-6515-3p, hsa-miR-887-3p, hsa-miR-4741, hsa-miR-6766-3p, hsa-miR-4673, hsa-miR-6779-5p, hsa-miR-4706, hsa-miR-1268b, hsa-miR-4632-5p, hsa-miR-3197, hsa-miR-6798-5p, hsa-miR-711, hsa-miR-6840-3p, hsa-miR-6763-5p, hsa-miR-6727-5p, hsa-miR-371a-5p, hsa-miR-6824-5p, hsa-miR-4648, hsa-miR-1227-5p, hsa-miR-564, hsa-miR-3679-3p, hsa-miR-2861, hsa-miR-6737-5p, hsa-miR-575, hsa-miR-4725-3p, hsa-miR-6716-5p, hsa-miR-4675, hsa-miR-1915-3p, hsa-miR-671-5p, hsa-miR-3656, hsa-miR-6722-3p, hsa-miR-4707-5p, hsa-miR-4449, hsa-miR-1202, hsa-miR-4649-5p, hsa-miR-744-5p, hsa-miR-642a-3p, hsa-miR-451a, hsa-miR-6870-5p, hsa-miR-4443, hsa-miR-6808-5p, hsa-miR-4728-5p, hsa-miR-937-5p, hsa-miR-135a-3p, hsa-miR-663b, hsa-miR-1343-5p, hsa-miR-6822-5p, hsa-miR-6803-5p, hsa-miR-6805-3p, hsa-miR-128-2-5p, hsa-miR-4640-5p, hsa-miR-1469, hsa-miR-92a-2-5p, hsa-miR-3940-5p, hsa-miR-4281, hsa-miR-1260b, hsa-miR-4758-5p, hsa-miR-1915-5p, hsa-miR-5001-5p, hsa-miR-4286, hsa-miR-6126, hsa-miR-6789-5p, hsa-miR-4459, hsa-miR-1268a, hsa-miR-6752-5p, hsa-miR-6131, hsa-miR-6800-5p, hsa-miR-4532, hsa-miR-6872-3p, hsa-miR-718, hsa-miR-6769a-5p, hsa-miR-4707-3p, hsa-miR-6765-5p, hsa-miR-4739, hsa-miR-4525, hsa-miR-4270, hsa-miR-4534, hsa-miR-6785-5p, hsa-miR-6850-5p, hsa-miR-4697-5p, hsa-miR-1260a, hsa-miR-4486, hsa-miR-6880-5p, hsa-miR-6802-5p, hsa-miR-6861-5p, hsa-miR-92b-5p, hsa-miR-1238-5p, hsa-miR-6851-5p, hsa-miR-7704, hsa-miR-149-3p, hsa-miR-4689, hsa-miR-4688, hsa-miR-125a-3p, hsa-miR-23b-3p, hsa-miR-614, hsa-miR-1913, hsa-miR-16-5p, hsa-miR-6717-5p, hsa-miR-3648, hsa-miR-3162-5p, hsa-miR-1909-3p, hsa-miR-8073, hsa-miR-6769b-5p, hsa-miR-6836-3p, hsa-miR-4484, hsa-miR-6819-5p, hsa-miR-6794-5phsa-miR-675-5p, hsa-miR-24-3p, hsa-miR-486-3p, hsa-miR-6777-5p, hsa-miR-4497, hsa-miR-296-3p, hsa-miR-6738-5p, hsa-miR-4731-5p, hsa-miR-6889-5p, hsa-miR-6786-5p, hsa-miR-92a-3p, hsa-miR-4294, hsa-miR-4763-3p, hsa-miR-6076, hsa-miR-663a, hsa-miR-760, hsa-miR-4667-5p, hsa-miR-6090, hsa-miR-4730, hsa-miR-7106-5p, hsa-miR-3196, hsa-miR-5698, hsa-miR-6087, hsa-miR-4665-5p, hsa-miR-8059 and hsa-miR-6879-5p represented by SEQ ID NOs: 1 to 214 and 666 to 676 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.

[0521] Such nucleic acid probes or primers can be chemically synthesized using an automatic DNA synthesizer. In general, the 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 synthesizer is commercially available from, for example, Polygen GmbH, ABI, or Applied Biosystems, Inc.

[0522] Alternatively, the polynucleotides of the present invention can also be prepared by cDNA cloning methods. The cDNA cloning technique may employ, for example, microRNA Cloning Kit Wako.

[0523] In this context, the sequences of the nucleic acid probes and the primers for detecting the polynucleotide consisting of a nucleotide sequence represented by any of SEQ ID NOs: 1 to 214 and 666 to 676 do not exist as miRNAs or precursors thereof in the living body or *in vivo.* For example, the nucleotide sequences represented by SEQ ID NO: 9 and SEQ ID NO: 138 are produced from the precursor represented by SEQ ID NO: 223. This precursor has a hairpin-like structure as shown in Figure 1, and the nucleotide sequences represented by SEQ ID NO: 9 and SEQ ID NO: 138 have mismatch sequences with each other. Likewise, a nucleotide sequence completely complementary to the nucleotide sequence represented by SEQ ID NO: 9 or SEQ ID NO: 138 is not naturally produced *in vivo.* As such, the nucleic acid probe and the primer for detecting the nucleotide sequence represented by any of SEQ ID NOs: 1 to 214 and 666 to 676 have artificial nucleotide sequences that do not exist in the living body or *in vivo.*

3. Kit or device for detection of esophageal cancer

[0524] The present invention also provides a kit or a device for the detection of esophageal cancer, comprising one or more polynucleotides (which may include a variant, a fragment, or a derivative thereof; hereinafter, also referred to as a polynucleotide for detection) that can be used as nucleic acid probes or primers in the present invention for measuring target nucleic acids as esophageal cancer markers.

[0525] The target nucleic acids as esophageal cancer markers according to the present invention are selected from

the following group A:

(Group A) hsa-miR-204-3p, hsa-miR-1247-3p, hsa-miR-6875-5p, hsa-miR-6857-5p, hsa-miR-6726-5p, hsa-miR-3188, hsa-miR-8069, hsa-miR-4257, hsa-miR-1343-3p, hsa-miR-7108-5p, hsa-miR-6825-5p, hsa-miR-7641, hsa-miR-3185, hsa-miR-4746-3p, hsa-miR-6791-5p, hsa-miR-6893-5p, hsa-miR-4433b-3p, hsa-miR-3135b, hsa-miR-6781-5p, hsa-miR-1908-5p, hsa-miR-4792, hsa-miR-7845-5p, hsa-miR-4417, hsa-miR-3184-5p, hsa-miR-1225-5p, hsa-miR-1231, hsa-miR-1225-3p, hsa-miR-150-3p, hsa-miR-4433-3p, hsa-miR-6125, hsa-miR-4513, hsa-miR-6787-5p, hsa-miR-6784-5p, hsa-miR-615-5p, hsa-miR-6765-3p, hsa-miR-5572, hsa-miR-6842-5p, hsa-miR-8063, hsa-miR-6780b-5p, hsa-miR-187-5p, hsa-miR-128-1-5p, hsa-miR-6729-5p, hsa-miR-6741-5p, hsa-miR-6757-5p, hsa-miR-7110-5p, hsa-miR-7975, hsa-miR-1233-5p, hsa-miR-6845-5p, hsa-miR-3937, hsa-miR-4467, hsa-miR-7109-5p, hsa-miR-6088, hsa-miR-6782-5p, hsa-miR-5195-3p, hsa-miR-4454, hsa-miR-6724-5p, hsa-miR-8072, hsa-miR-4516, hsa-miR-6756-5p, hsa-miR-4665-3p, hsa-miR-6826-5p, hsa-miR-6820-5p, hsa-miR-6887-5p, hsa-miR-3679-5p, hsa-miR-7847-3p, hsa-miR-6721-5p, hsa-miR-3622a-5p, hsa-miR-939-5p, hsa-miR-602, hsa-miR-7977, hsa-miR-6749-5p, hsa-miR-1914-3p, hsa-miR-4651, hsa-miR-4695-5p, hsa-miR-6848-5p, hsa-miR-1228-3p, hsa-miR-642b-3p, hsa-miR-6746-5p, hsa-miR-3620-5p, hsa-miR-3131, hsa-miR-6732-5p, hsa-miR-7113-3p, hsa-miR-23a-3p, hsa-miR-3154, hsa-miR-4723-5p, hsa-miR-3663-3p, hsa-miR-4734, hsa-miR-6816-5p, hsa-miR-4442, hsa-miR-4476, hsa-miR-423-5p, hsa-miR-1249, hsa-miR-6515-3p, hsa-miR-887-3p, hsa-miR-4741, hsa-miR-6766-3p, hsa-miR-4673, hsa-miR-6779-5p, hsa-miR-4706, hsa-miR-1268b, hsa-miR-4632-5p, hsa-miR-3197, hsa-miR-6798-5p, hsa-miR-711, hsa-miR-6840-3p, hsa-miR-6763-5p, hsa-miR-6727-5p, hsa-miR-371a-5p, hsa-miR-6824-5p, hsa-miR-4648, hsa-miR-1227-5p, hsa-miR-564, hsa-miR-3679-3p, hsa-miR-2861, hsa-miR-6737-5p, hsa-miR-4725-3p, hsa-miR-6716-5p, hsa-miR-4675, hsa-miR-1915-3p, hsa-miR-671-5p, hsa-miR-3656, hsa-miR-6722-3p, hsa-miR-4707-5p, hsa-miR-4449, hsa-miR-1202, hsa-miR-4649-5p, hsa-miR-744-5p, hsa-miR-642a-3p, hsa-miR-451a, hsa-miR-6870-5p, hsa-miR-4443, hsa-miR-6808-5p, hsa-miR-4728-5p, hsa-miR-937-5p, hsa-miR-135a-3p, hsa-miR-663b, hsa-miR-1343-5p, hsa-miR-6822-5p, hsa-miR-6803-5p, hsa-miR-6805-3p, hsa-miR-128-2-5p, hsa-miR-4640-5p, hsa-miR-1469, hsa-miR-92a-2-5p, hsa-miR-3940-5p, hsa-miR-4281, hsa-miR-1260b, hsa-miR-4758-5p, hsa-miR-1915-5p, hsa-miR-5001-5p, hsa-miR-4286, hsa-miR-6126, hsa-miR-6789-5p, hsa-miR-4459, hsa-miR-1268a, hsa-miR-6752-5p, hsa-miR-6131, hsa-miR-6800-5p, hsa-miR-4532, hsa-miR-6872-3p, hsa-miR-718, hsa-miR-6769a-5p, hsa-miR-4707-3p, hsa-miR-6765-5p, hsa-miR-4739, hsa-miR-4525, hsa-miR-4270, hsa-miR-4534, hsa-miR-6785-5p, hsa-miR-6850-5p, hsa-miR-4697-5p, hsa-miR-1260a, hsa-miR-4486, hsa-miR-6880-5p, hsa-miR-6802-5p, hsa-miR-6861-5p, hsa-miR-92b-5p, hsa-miR-1238-5p, hsa-miR-6851-5p, hsa-miR-7704, hsa-miR-149-3p, hsa-miR-4689, hsa-miR-4688, hsa-miR-125a-3p, hsa-miR-23b-3p, hsa-miR-614, hsa-miR-1913, hsa-miR-16-5p, hsa-miR-6717-5p, hsa-miR-3648, hsa-miR-3162-5p, hsa-miR-1909-3p, hsa-miR-8073, hsa-miR-6769b-5p, hsa-miR-6836-3p, hsa-miR-4484, hsa-miR-6819-5p and hsa-miR-6794-5p.

[0526] Additional target nucleic acids that may be optionally used in the measurement are selected from the following group B:

(Group B) hsa-miR-575 and hsa-miR-24-3p.

[0527] Additional target nucleic acids that may be further optionally used in the measurement are selected from the following group C:

(Group C) hsa-miR-675-5p, hsa-miR-486-3p, hsa-miR-6777-5p, hsa-miR-4497, hsa-miR-296-3p, hsa-miR-6738-5p, hsa-miR-4731-5p, hsa-miR-6889-5p, hsa-miR-6786-5p, hsa-miR-92a-3p, hsa-miR-4294, hsa-miR-4763-3p, hsa-miR-6076, hsa-miR-663a, hsa-miR-760, hsa-miR-4667-5p, hsa-miR-6090, hsa-miR-4730, hsa-miR-7106-5p, hsa-miR-3196, hsa-miR-5698, hsa-miR-6087, hsa-miR-4665-5p, hsa-miR-8059 and hsa-miR-6879-5p.

[0528] 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 esophageal cancer markers described above, preferably one or more polynucleotide(s) selected from the polynucleotides described in the preceding Section 2, or variant(s) thereof, etc.

[0529] Specifically, the kit or the device of the present invention can comprise at least one polynucleotide comprising (or consisting of) a nucleotide sequence represented by any of SEQ ID NOs: 1 to 115, 117 to 189, and 666 to 675 or a nucleotide sequence 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.

[0530] The kit or the device of the present invention can further comprise one or more polynucleotides comprising (or consisting of) a nucleotide sequence represented by SEQ ID NOs: 116 and 676 or a nucleotide sequence 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.

[0531] The kit or the device of the present invention can further comprise one or more polynucleotides comprising (or consisting of) a nucleotide sequence represented by any of SEQ ID NOs: 190 to 214 or a nucleotide sequence 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.

[0532] The fragment(s) that can be comprised in the kit or the device of the present invention is/are, for example, one or more polynucleotides, 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 that are from a nucleotide sequence derived from a nucleotide sequence represented by any of SEQ ID NOs: 1 to 115, 117 to 189, and 666 to 675 by the replacement of u with t, or a complementary sequence thereof;
(2) a polynucleotide comprising 15 or more consecutive nucleotides that are from a nucleotide sequence derived from a nucleotide sequence represented by SEQ ID NOs: 116 and 676 by the replacement of u with t, or a complementary sequence thereof; and
(3) a polynucleotide comprising 15 or more consecutive nucleotides that are from a nucleotide sequence derived from a nucleotide sequence represented by any of SEQ ID NOs: 190 to 214 by the replacement of u with t, or a complementary sequence thereof.

[0533] In a preferred embodiment, the polynucleotide is a polynucleotide consisting of a nucleotide sequence represented by any of SEQ ID NOs: 1 to 115, 117 to 189, and 666 to 675 or a nucleotide sequence 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.

[0534] In a preferred embodiment, the polynucleotide is a polynucleotide consisting of a nucleotide sequence represented by any of SEQ ID NOs: 116 and 676 or a nucleotide sequence 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.

[0535] In a preferred embodiment, the polynucleotide is a polynucleotide consisting of a nucleotide sequence represented by any of SEQ ID NOs: 190 to 214 or a nucleotide sequence 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.

[0536] 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.

[0537] In the present invention, the size of the polynucleotide fragment is the number of nucleotides in the range of from, for example, 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 19 consecutive nucleotides to less than the total number of nucleotides of the sequence, in the nucleotide sequence of each polynucleotide.

[0538] Specific examples of the combination of aforementioned polynucleotides constituting the kit or the device of the present invention can include a combination of 2, 3, 4, 5, 6, 7, 8, 9, 10 or more of the polynucleotides as relevant to the combinations of SEQ ID NOs: 1 to 214 and 666 to 676 shown in Table 1. However, these are given merely for illustrative purposes, and all of various other possible combinations are included in the present invention.

[0539] The aforementioned combination constituting the kit or the device for discriminating an esophageal cancer patient from a healthy subject according to the present invention is desirably, for example, a combination of two or more aforementioned polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 214 and 666 to 676 shown in Table 1. Usually, a combination of two of these polynucleotides can produce adequate performance.

[0540] The combination of two polynucleotides for specifically discriminating an esophageal cancer patient from a healthy subject is preferably a combination comprising at least one of newly found polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 115, 117 to 189 and 666 to 675, among the combinations constituted by two of the polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 214 and 666 to 676.

[0541] The combination of polynucleotides with cancer type specificity capable of discriminating an esophageal cancer patient not only from a healthy subject but also from other cancer patients is preferably, for example, a combination of

a plurality of polynucleotides comprising at least one polynucleotide selected from the group consisting of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1, 2, 5, 8, 22, 32, 33, 35, 43, 44, 56, 85, 98, 106, 109, 115, 121, 126, 133, 138, 155, 157, 166, 177, 179, 185, 202, 212, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675 and 676 (hereinafter, this group is referred to as "cancer type-specific polynucleotide group 1"); and any of the polynucleotides of the other SEQ ID NOs.

[0542] The combination of polynucleotides with cancer type specificity is more preferably a combination of multiple polynucleotides selected from cancer type-specific polynucleotide group 1.

[0543] The combination of polynucleotides with cancer type specificity is further preferably a combination comprising at least one polynucleotide selected from the group consisting of or more for polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1, 22, 85, 109, 121, 126, 133, 138, 166, and 666 (hereinafter, this group is referred to as "cancer type-specific polynucleotide group 2") included in cancer type-specific polynucleotide group 1, among the combinations of multiple polynucleotides selected from the cancer type-specific polynucleotide group 1.

[0544] The number of the polynucleotides with cancer type specificity may be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more in the combination and is more preferably 6 or more in the combination. Usually, the combination of 6 polynucleotides of these polynucleotides can produce adequate performance.

[0545] Non-limiting examples of the combination of the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 1 or a complementary sequence thereof with polynucleotides consisting of nucleotide sequences represented by SEQ ID NOs of five polynucleotides selected from the cancer type-specific polynucleotide group 1 or complementary sequences thereof are listed below.

(1) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1, 85, 138, 166, 666, and 668 (markers: hsa-miR-4739, hsa-miR-1343-5p, hsa-miR-204-3p, hsa-miR-4723-5p, hsa-miR-3162-5p, and hsa-miR-6717-5p);
(2) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1, 85, 98, 138, 166, and 666 (markers: hsa-miR-4739, hsa-miR-1343-5p, hsa-miR-6779-5p, hsa-miR-204-3p, hsa-miR-4723-5p, and hsa-miR-6717-5p);
(3) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1, 85, 138, 155, 166, and 666 (markers: hsa-miR-4739, hsa-miR-1343-5p, hsa-miR-204-3p, hsa-miR-4723-5p, hsa-miR-4459, and hsa-miR-6717-5p);
(4) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1, 5, 85, 138, 166, and 666 (markers: hsa-miR-4739, hsa-miR-1343-5p, hsa-miR-204-3p, hsa-miR-4723-5p, hsa-miR-6726-5p, and hsa-miR-6717-5p); and
(5) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1, 35, 85, 138, 166, and 666 (markers: hsa-miR-4739, hsa-miR-1343-5p, hsa-miR-204-3p, hsa-miR-4723-5p, hsa-miR-6765-3p, and hsa-miR-6717-5p).

[0546] Non-limiting examples of the combination of the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 22 or a complementary sequence thereof with polynucleotides consisting of nucleotide sequences represented by SEQ ID NOs of five polynucleotides selected from the cancer type-specific polynucleotide group 1 or complementary sequences thereof are further listed.

(1) a combination of SEQ ID NOs: 1, 22, 85, 138, 166 and 666 (markers: hsa-miR-4739, hsa-miR-1343-5p, hsa-miR-7845-5p, hsa-miR-204-3p, hsa-miR-4273-5p, and hsa-miR-6717-5p);
(2) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 22, 32, 121, 133, 166, and 666 (markers: hsa-miR-4739, hsa-miR-7845-5p, hsa-miR-671-5p, hsa-miR-6787-5p, hsa-miR-6808-5p, and hsa-miR-6717-5p);
(3) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1, 22, 126, 138, 166, and 666 (markers: hsa-miR-4739, hsa-miR-1202, hsa-miR-1343-5p, hsa-miR-7845-5p, hsa-miR-204-3p, and hsa-miR-6717-5p);
(4) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1, 22, 121, 155, 166, and 666 (markers: hsa-miR-4739, hsa-miR-7845-5p, hsa-miR-671-5p, hsa-miR-204-3p, hsa-miR-4459, and hsa-miR-6717-5p);and
(5) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 22, 32, 109, 121, 666, and 667 (markers: hsa-miR-7845-5p, hsa-miR-671-5p, hsa-miR-3648, hsa-miR-6787-5p, hsa-miR-6824-5p, and hsa-miR-6717-5p).

[0547] Non-limiting examples of the combination of the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 85 or a complementary sequence thereof with polynucleotides consisting of nucleotide sequences

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

(1) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 85, 138, 166, 185, 666, and 669 (markers: miR-4739, miR-1343-5p, miR-125a-3p, miR-4723-5p, miR-1909-3p, and miR-6717-5p);
(2) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 85, 138, 166, 185, 666, and 676 (markers: miR-4739, miR-1343-5p, miR-125a-3p, miR-4723-5p, miR-6717-5p, and miR-24-3p);
(3) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 85, 138, 166, 177, 185, and 666 (markers: miR-4739, miR-1343-5p, miR-125a-3p, miR-4723-5p, miR-6861-5p, and miR-6717-5p);
(4) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 85, 138, 166, 185, 666, and 667 (markers: miR-4739, miR-1343-5p, miR-3648, miR-125a-3p, miR-4723-5p, and miR-6717-5p); and
(5) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 33, 85, 138, 166, 185, and 666 (markers: miR-6784-5p, miR-4739, miR-1343-5p, miR-125a-3p, miR-4723-5p, and miR-6717-5p).

[0548] Non-limiting examples of the combination of the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 109 or a complementary sequence thereof with polynucleotides consisting of nucleotide sequences represented by SEQ ID NOs of five polynucleotides selected from the cancer type-specific polynucleotide group 1 or complementary sequences thereof are further listed below.

(1) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 109, 121, 126, 138, 166, and 666 (markers: miR-4739, miR-1202, miR-1343-5p, miR-671-5p, miR-6824-5p, and miR-6717-5p);
(2) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1, 85, 109, 138, 166, and 666 (markers: miR-4739, miR-1343-5p, miR-204-3p, miR-4723-5p, miR-6824-5p, miR-6717-5p);
(3) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1, 109, 121, 138, 166, and 666 (markers: miR-4739, miR-1343-5p, miR-671-5p, miR-204-3p, miR-6824-5p, and miR-6717-5p);
(4) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 109, 126, 138, 166, 666, and 676 (markers: miR-4739, miR-1202, miR-1343-5p, miR-6824-5p, miR-6717-5p, and miR-24-3p); and
(5) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 109, 126, 138, 166, 202, and 666 (markers: miR-4739, miR-1202, miR-1343-5p, miR-6824-5p, miR-6076, and miR-6717-5p).

[0549] Non-limiting examples of the combination of the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 121 or a complementary sequence thereof with polynucleotides consisting of nucleotide sequences represented by SEQ ID NOs of five polynucleotides selected from the cancer type-specific polynucleotide group 1 or complementary sequences thereof are further listed below.

(1) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1, 121, 138, 166, 666, and 668 (markers: miR-4739, miR-1343-5p, miR-671-5p, miR-204-3p, miR-3162-5p, and miR-6717-5p);
(2) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1, 33, 121, 138, 166, and 666 (markers: miR-6784-5p, miR-4739, miR-1343-5p, miR-671-5p, miR-204-3p, and miR-6717-5p);
(3) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1, 85, 121, 138, 166, and 666 (markers: miR-4739, miR-1343-5p, miR-671-5p, miR-204-3p, miR-4723-5p, and miR-6717-5p);
(4) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1, 121, 138, 166, 179, and 666 (markers: miR-4739, miR-1343-5p, miR-671-5p, miR-204-3p, miR-1238-5p, and miR-6717-5p); and
(5) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1, 121, 138, 166, 177, and 666 (markers: miR-4739, miR-1343-5p, miR-671-5p, miR-204-3p, miR-6861-5p, and miR-6717-5p).

[0550] Non-limiting examples of the combination of the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 126 or a complementary sequence thereof with polynucleotides consisting of nucleotide sequences represented by SEQ ID NOs of five polynucleotides selected from the cancer type-specific polynucleotide group 1 or complementary sequences thereof are further listed below.

(1) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 32, 109, 126, 138, 166, and 666 (markers: miR-4739, miR-1202, miR-1343-5p, miR-6787-5p, miR-6824-5p, and miR-6717-5p);
(2) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1, 85, 126, 138, 166, and 666 (markers: miR-4739, miR-1202, miR-1343-5p, miR-204-3p, miR-4723-5p, and miR-6717-5p);
(3) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1, 109, 126, 138, 166, and 666 (markers: miR-4739, miR-1202, miR-1343-5p, miR-204-3p, miR-6824-5p, and miR-6717-5p);
(4) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 22, 109, 126, 138, 166, and 666 (markers: miR-4739, miR-1202, miR-1343-5p, miR-7845-5p, miR-6824-5p, and miR-6717-5p); and
(5) a combination of SEQ ID NOs: 109, 126, 138, 157, 166, and 666 (markers: miR-4739, miR-1202, miR-6752-5p, miR-1343-5p, miR-6824-5p, and miR-6717-5p).

[0551] Non-limiting examples of the combination of the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 133 or a complementary sequence thereof with polynucleotides consisting of nucleotide sequences represented by SEQ ID NOs of five polynucleotides selected from the cancer type-specific polynucleotide group 1 or complementary sequences thereof are further listed below.

(1) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 126, 133, 138, 166, 666, and 672 (markers: miR-4739, miR-1202, miR-1343-5p, miR-6808-5p, miR-6836-3p, and miR-6717-5p);
(2) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 126, 133, 138, 166, 666 (markers: miR-4739, miR-1202, miR-1343-5p, miR-6808-5p, and miR-6717-5p);
(3) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 109, 126, 133, 138, 166, and 666 (markers: miR-4739, miR-1202, miR-1343-5p, miR-6824-5p, miR-6808-5p, and miR-6717-5p);
(4) a combination of SEQ ID NOs: 126, 133, 138, 166, 666, and 673 (markers: miR-4739, miR-1202, miR-1343-5p, miR-4484, miR-6808-5p, and miR-6717-5p); and
(5) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 126, 133, 138, 166, 666, and 675 (markers: miR-4739, miR-1202, miR-1343-5p, miR-6794-5p, miR-6808-5p, and miR-6717-5p).

[0552] Non-limiting examples of the combination of the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 138 or a complementary sequence thereof with polynucleotides consisting of nucleotide sequences represented by SEQ ID NOs of five polynucleotides selected from the cancer type-specific polynucleotide group 1 or complementary sequences thereof are further listed below.

(1) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1, 85,138, 166, 666, and 669 (markers: miR-4739, miR-1343-5p, miR-204-3p, miR-4723-5p, miR-1909-3p, and miR-6717-5p);
(2) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 8, 85, 138, 166, 185, and 666 (markers: miR-4739, miR-1343-5p, miR-125a-3p, miR-4723-5p, miR-4257, and miR-6717-5p);
(3) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1, 35, 121, 138, 166, and 666 (markers: miR-4739, miR-1343-5p, miR-671-5p, miR-204-3p, miR-6765-3p, and miR-6717-5p);
(4) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1, 121, 126, 138, 166, and 666 (markers: miR-4739, miR-1202, miR-1343-5p, miR-671-5p, miR-204-3p, and miR-6717-5p); and
(5) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1, 121, 138, 166, 666, and 672 (markers: miR-4739, miR-1343-5p, miR-671-5p, miR-204-3p, miR-6836-3p, and miR-6717-5p).

[0553] Non-limiting examples of the combination of the polynucleotide consisting of the nucleotide sequence repre-

sented by SEQ ID NO: 166 or a complementary sequence thereof with polynucleotides consisting of nucleotide sequences represented by SEQ ID NOs of five polynucleotides selected from the cancer type-specific polynucleotide group 1 or complementary sequences thereof are further listed below.

(1) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1, 85, 138, 166, 666, and 672 (markers: miR-4739, miR-1343-5p, miR-204-3p, miR-4723-5p, miR-6836-3p, and miR-6717-5p);
(2) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 56, 85, 138, 166, 185, and 666 (markers: miR-4739, miR-1343-5p, miR-125a-3p, miR-6724-5p, miR-4723-5p, and miR-6717-5p);
(3) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1, 32, 121, 138, 166, and 666 (markers: miR-4739, miR-1343-5p, miR-671-5p, miR-204-3p, miR-6787-5p, and miR-6717-5p);
(4) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1, 22, 121, 138, 166, and 666 (markers: miR-4739, miR-1343-5p, miR-7845-5p, miR-671-5p, miR-204-3p, and miR-6717-5p); and
(5) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 5, 85, 138, 166, 185, and 666 (markers: miR-4739, miR-1343-5p, miR-125a-3p, miR-4723-5p, miR-6726-5p, and miR-6717-5p).

[0554] Non-limiting examples of the combination of the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 666 or a complementary sequence thereof with polynucleotides consisting of nucleotide sequences represented by SEQ ID NOs of five polynucleotides selected from the cancer type-specific polynucleotide group 1 or complementary sequences thereof are further listed below.

(1) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1, 121, 138, 157, 166, and 666 (markers: miR-4739, miR-6752-5p, miR-1343-5p, miR-671-5p, miR-204-3p, and miR-6717-5p);
(2) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1, 85,133, 138, 166, and 666 (markers: miR-4739, miR-1343-5p, miR-204-3p, miR-4723-5p, miR-6808-5p, and miR-6717-5p);
(3) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1, 121, 138, 166, 185, and 666 (markers: miR-4739, miR-1343-5p, miR-671-5p, miR-204-3p, miR-125a-3p, and miR-6717-5p);
(4) a combination of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1, 121, 138, 166, 666, and 667 (markers: miR-4739, miR-1343-5p, miR-671-5p, miR-3648, miR-204-3p, and miR-6717-5p); and
(5) a combination of SEQ ID NOs: 85, 138, 166, 185, and 666 (markers: miR-4739, miR-1343-5p, miR-125a-3p, miR-4723-5p, and miR-6717-5p).

[0555] The kit or the device of the present invention can also comprise a polynucleotide that is already known or that will be found in the future, to enable detection of esophageal cancer in addition to the polynucleotide(s) (which can include a variant, a fragment, and a derivative) according to the present invention.

[0556] The kit of the present invention can also comprise an antibody for measuring marker(s) for esophageal cancer examination known in the art, such as CEA or SCC, in addition to the polynucleotide(s), etc., according to the present invention described above.

[0557] These polynucleotides comprised in the kit of the present invention may be packaged in different containers either individually or in any combination.

[0558] The kit of the present invention may comprise a kit for extracting nucleic acids (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.

[0559] 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).

[0560] The nucleic acid array technique is a technique which involves bonding 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 target nucleic acids through the use of hybridization using this array.

[0561] The kit or the device of the present invention comprises nucleic acids capable of specifically binding to the polynucleotides of at least one, preferably at least two, more preferably at least three, most preferably at least five to any of the esophageal cancer marker miRNAs, respectively, of the 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, preferably at least two, more preferably at least three, most preferably at least five to any of the esophageal cancer marker miRNAs, respectively, of the group 2 described above.

[0562] The kit or the device of the present invention can be used for detecting esophageal cancer as described in the Section 4 below.

4. Method for detecting esophageal cancer

[0563] The present invention further provides a method for detecting esophageal cancer, comprising using the kit or the device of the present invention (comprising the above-mentioned nucleic acid(s) that can be used in the present invention) described in the preceding Section "3. Kit or device for detection of esophageal cancer" to measure expression levels of one or more esophageal cancer-derived genes represented by an expression level(s) of esophageal cancer-derived gene(s) selected from the following group 1 of miRNAs, i.e., hsa-miR-204-3p, hsa-miR-1247-3p, hsa-miR-6875-5p, hsa-miR-6857-5p, hsa-miR-6726-5p, hsa-miR-3188, hsa-miR-8069, hsa-miR-4257, hsa-miR-1343-3p, hsa-miR-7108-5p, hsa-miR-6825-5p, hsa-miR-7641, hsa-miR-3185, hsa-miR-4746-3p, hsa-miR-6791-5p, hsa-miR-6893-5p, hsa-miR-4433b-3p, hsa-miR-3135b, hsa-miR-6781-5p, hsa-miR-1908-5p, hsa-miR-4792, hsa-miR-7845-5p, hsa-miR-4417, hsa-miR-3184-5p, hsa-miR-1225-5p, hsa-miR-1231, hsa-miR-1225-3p, hsa-miR-150-3p, hsa-miR-4433-3p, hsa-miR-6125, hsa-miR-4513, hsa-miR-6787-5p, hsa-miR-6784-5p, hsa-miR-615-5p, hsa-miR-6765-3p, hsa-miR-5572, hsa-miR-6842-5p, hsa-miR-8063, hsa-miR-6780b-5p, hsa-miR-187-5p, hsa-miR-128-1-5p, hsa-miR-6729-5p, hsa-miR-6741-5p, hsa-miR-6757-5p, hsa-miR-7110-5p, hsa-miR-7975, hsa-miR-1233-5p, hsa-miR-6845-5p, hsa-miR-3937, hsa-miR-4467, hsa-miR-7109-5p, hsa-miR-6088, hsa-miR-6782-5p, hsa-miR-5195-3p, hsa-miR-4454, hsa-miR-6724-5p, hsa-miR-8072, hsa-miR-4516, hsa-miR-6756-5p, hsa-miR-4665-3p, hsa-miR-6826-5p, hsa-miR-6820-5p, hsa-miR-6887-5p, hsa-miR-3679-5p, hsa-miR-7847-3p, hsa-miR-6721-5p, hsa-miR-3622a-5p, hsa-miR-939-5p, hsa-miR-602, hsa-miR-7977, hsa-miR-6749-5p, hsa-miR-1914-3p, hsa-miR-4651, hsa-miR-4695-5p, hsa-miR-6848-5p, hsa-miR-1228-3p, hsa-miR-642b-3p, hsa-miR-6746-5p, hsa-miR-3620-5p, hsa-miR-3131, hsa-miR-6732-5p, hsa-miR-7113-3p, hsa-miR-23a-3p, hsa-miR-3154, hsa-miR-4723-5p, hsa-miR-3663-3p, hsa-miR-4734, hsa-miR-6816-5p, hsa-miR-4442, hsa-miR-4476, hsa-miR-423-5p, hsa-miR-1249, hsa-miR-6515-3p, hsa-miR-887-3p, hsa-miR-4741, hsa-miR-6766-3p, hsa-miR-4673, hsa-miR-6779-5p, hsa-miR-4706, hsa-miR-1268b, hsa-miR-4632-5p, hsa-miR-3197, hsa-miR-6798-5p, hsa-miR-711, hsa-miR-6840-3p, hsa-miR-6763-5p, hsa-miR-6727-5p, hsa-miR-371a-5p, hsa-miR-6824-5p, hsa-miR-4648, hsa-miR-1227-5p, hsa-miR-564, hsa-miR-3679-3p, hsa-miR-2861, hsa-miR-6737-5p, hsa-miR-4725-3p, hsa-miR-6716-5p, hsa-miR-4675, hsa-miR-1915-3p, hsa-miR-671-5p, hsa-miR-3656, hsa-miR-6722-3p, hsa-miR-4707-5p, hsa-miR-4449, hsa-miR-1202, hsa-miR-4649-5p, hsa-miR-744-5p, hsa-miR-642a-3p, hsa-miR-451a, hsa-miR-6870-5p, hsa-miR-4443, hsa-miR-6808-5p, hsa-miR-4728-5p, hsa-miR-937-5p, hsa-miR-135a-3p, hsa-miR-663b, hsa-miR-1343-5p, hsa-miR-6822-5p, hsa-miR-6803-5p, hsa-miR-6805-3p, hsa-miR-128-2-5p, hsa-miR-4640-5p, hsa-miR-1469, hsa-miR-92a-2-5p, hsa-miR-3940-5p, hsa-miR-4281, hsa-miR-1260b, hsa-miR-4758-5p, hsa-miR-1915-5p, hsa-miR-5001-5p, hsa-miR-4286, hsa-miR-6126, hsa-miR-6789-5p, hsa-miR-4459, hsa-miR-1268a, hsa-miR-6752-5p, hsa-miR-6131, hsa-miR-6800-5p, hsa-miR-4532, hsa-miR-6872-3p, hsa-miR-718, hsa-miR-6769a-5p, hsa-miR-4707-3p, hsa-miR-6765-5p, hsa-miR-4739, hsa-miR-4525, hsa-miR-4270, hsa-miR-4534, hsa-miR-6785-5p, hsa-miR-6850-5p, hsa-miR-4697-5p, hsa-miR-1260a, hsa-miR-4486, hsa-miR-6880-5p, hsa-miR-6802-5p, hsa-miR-6861-5p, hsa-miR-92b-5p, hsa-miR-1238-5p, hsa-miR-6851-5p, hsa-miR-7704, hsa-miR-149-3p, hsa-miR-4689, hsa-miR-4688, hsa-miR-125a-3p, hsa-miR-23b-3p, hsa-miR-614, hsa-miR-1913, hsa-miR-16-5p, hsa-miR-6717-5p, hsa-miR-3648, hsa-miR-3162-5p, hsa-miR-1909-3p, hsa-miR-8073, hsa-miR-6769b-5p, hsa-miR-6836-3p, hsa-miR-4484, hsa-miR-6819-5p, and hsa-miR-6794-5p; and optionally expression levels of esophageal cancer-derived gene(s) selected from the following group 2: i.e., hsa-miR-575 and hsa-miR-24-3p; and optionally expression levels of esophageal cancer-derived gene(s) selected from the following group 3: i.e., hsa-miR-675-5p, hsa-miR-486-3p, hsa-miR-6777-5p, hsa-miR-4497, hsa-miR-296-3p, hsa-miR-6738-5p, hsa-miR-4731-5p, hsa-miR-6889-5p, hsa-miR-6786-5p, hsa-miR-92a-3p, hsa-miR-4294, hsa-miR-4763-3p, hsa-miR-6076, hsa-miR-663a, hsa-miR-760, hsa-miR-4667-5p, hsa-miR-6090, hsa-miR-4730, hsa-miR-7106-5p, hsa-miR-3196, hsa-miR-5698, hsa-miR-6087, hsa-miR-4665-5p, hsa-miR-8059, and hsa-miR-6879-5p in a sample *in vitro,* further comparing, for example, the expression level of the gene described above in the sample

(e.g., blood, serum, or plasma) collected from a subject suspected of having esophageal cancer with a control expression level in the sample collected from a healthy subject (including a non-esophageal cancer patient), and evaluating the subject as having esophageal cancer when the expression level of the target nucleic acid is different between the samples.

[0564] This method of the present invention enables a limitedly invasive, early diagnosis of the cancer with high sensitivity and high 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.

[0565] The method for extracting the esophageal cancer-derived gene(s) from the sample such as blood, serum, or plasma according to the present invention is/are 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 esophageal cancer-derived gene(s) 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.) may be used, though the method is not limited thereto.

[0566] The present invention also provides use of the kit or the device of the present invention for detecting *in vitro* an expression product(s) of an esophageal cancer-derived miRNA gene(s) in a sample from a subject.

[0567] In the method of the present invention, the kit or the device described above comprising a single polynucleotide or any possible combination of polynucleotides that can be used in the present invention as described above.

[0568] In the detection or (gentice) diagnosis of esophageal 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.

[0569] 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.

[0570] The kit or the device of the present invention is useful for the diagnosis of esophageal cancer or the detection of the presence or absence of esophageal cancer. Specifically, the detection of esophageal cancer using the kit or the device can be performed by detecting *in vitro* expression level(s) of gene(s) using the nucleic acid probe(s) or the primer(s) contained in the kit or the device in a sample such as blood, serum, plasma, or urine from a subject suspected of having esophageal cancer. The subject suspected of having esophageal cancer can be evaluated as having esophageal cancer when the expression level(s) of target miRNA marker(s) measured using polynucleotide(s) (including variant(s), fragment(s), and derivative(s) thereof) consisting of a nucleotide sequence(s) represented by at least one of SEQ ID NOs: 1 to 115, 117 to 189, and 666 to 675 or a complementary sequence(s) thereof, and optionally nucleotide sequence(s) represented by one or more of SEQ ID NOs: 116 and 676 or a complementary sequence thereof, and optionally a nucleotide sequence(s) represented by one or more of SEQ ID NOs: 190 to 214 or a complementary sequence(s) thereof, in the sample such as blood, serum, plasma, or urine of the subject has a statistically significantly higher than the expression level(s) thereof in the sample such as blood, serum, or plasma, or urine of a healthy subject.

[0571] The method of the present invention can be combined with a diagnostic imaging method such as esophagography, endoscopy, CT scan, MRI scan, endosonography, or ultrasonography. The method of the present invention is capable of specifically detecting esophageal cancer and can substantially discriminate esophageal cancer from the other cancers.

[0572] The method for detecting the absence of an expression product of esophageal cancer-derived gene(s) or the presence of the expression product(s) of esophageal cancer-derived gene(s) 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 of a subject, and measuring the expression level(s) of the target gene(s) contained therein using one or more polynucleotides (including variant(s), fragment(s), and derivative(s)) selected from the polynucleotide group of the present invention, to evaluate the presence or absence of esophageal cancer or to detect esophageal cancer. Using the method for detecting esophageal cancer according to the present invention, for example, the presence or absence of amelioration of the disease or the degree of amelioration thereof in an esophageal cancer patient given a therapeutic drug for the amelioration of the disease can be also evaluated or diagnosed.

[0573] The method of the present invention can comprise, for example, the following steps (a), (b), and (c):

(a) a step of contacting *in vitro* a sample from a subject with polynucleotide(s) contained in the kit or the device of the present invention;

(b) a step of measuring expression level(s) of the target nucleic acid in the sample using the polynucleotide(s) as

nucleic acid probe(s) or primer(s); and
(c) a step of evaluating the presence or absence of esophageal cancer (cells) in the subject on the basis of the measurement results in the step (b).

[0574] Specifically, the present invention provides a method for detecting esophageal cancer, comprising measuring expression level(s) of target nucleic acid(s) in a sample of a subject using a nucleic acid(s) capable of specifically binding to at least one (preferably at least two) polynucleotides selected from the group consisting of miR-204-3p, miR-1247-3p, miR-6875-5p, miR-6857-5p, miR-6726-5p, miR-3188, miR-8069, miR-4257, miR-1343-3p, miR-7108-5p, miR-6825-5p, miR-7641, miR-3185, miR-4746-3p, miR-6791-5p, miR-6893-5p, miR-4433b-3p, miR-3135b, miR-6781-5p, miR-1908-5p, miR-4792, miR-7845-5p, miR-4417, miR-3184-5p, miR-1225-5p, miR-1231, miR-1225-3p, miR-150-3p, miR-4433-3p, miR-6125, miR-4513, miR-6787-5p, miR-6784-5p, miR-615-5p, miR-6765-3p, miR-5572, miR-6842-5p, miR-8063, miR-6780b-5p, miR-187-5p, miR-128-1-5p, miR-6729-5p, miR-6741-5p, miR-6757-5p, miR-7110-5p, miR-7975, miR-1233-5p, miR-6845-5p, miR-3937, miR-4467, miR-7109-5p, miR-6088, miR-6782-5p, miR-5195-3p, miR-4454, miR-6724-5p, miR-8072, miR-4516, miR-6756-5p, miR-4665-3p, miR-6826-5p, miR-6820-5p, miR-6887-5p, miR-3679-5p, miR-7847-3p, miR-6721-5p, miR-3622a-5p, miR-939-5p, miR-602, miR-7977, miR-6749-5p, miR-1914-3p, miR-4651, miR-4695-5p, miR-6848-5p, miR-1228-3p, miR-642b-3p, miR-6746-5p, miR-3620-5p, miR-3131, miR-6732-5p, miR-7113-3p, miR-23a-3p, miR-3154, miR-4723-5p, miR-3663-3p, miR-4734, miR-6816-5p, miR-4442, miR-4476, miR-423-5p, miR-1249, miR-6515-3p, miR-887-3p, miR-4741, miR-6766-3p, miR-4673, miR-6779-5p, miR-4706, miR-1268b, miR-4632-5p, miR-3197, miR-6798-5p, miR-711, miR-6840-3p, miR-6763-5p, miR-6727-5p, miR-371a-5p, miR-6824-5p, miR-4648, miR-1227-5p, miR-564, miR-3679-3p, miR-2861, miR-6737-5p, miR-4725-3p, miR-6716-5p, miR-4675, miR-1915-3p, miR-671-5p, miR-3656, miR-6722-3p, miR-4707-5p, miR-4449, miR-1202, miR-4649-5p, miR-744-5p, miR-642a-3p, miR-451 a, miR-6870-5p, miR-4443, miR-6808-5p, miR-4728-5p, miR-937-5p, miR-135a-3p, miR-663b, miR-1343-5p, miR-6822-5p, miR-6803-5p, miR-6805-3p, miR-128-2-5p, miR-4640-5p, miR-1469, miR-92a-2-5p, miR-3940-5p, miR-4281, miR-1260b, miR-4758-5p, miR-1915-5p, miR-5001-5p, miR-4286, miR-6126, miR-6789-5p, miR-4459, miR-1268a, miR-6752-5p, miR-6131, miR-6800-5p, miR-4532, miR-6872-3p, miR-718, miR-6769a-5p, miR-4707-3p, miR-6765-5p, miR-4739, miR-4525, miR-4270, miR-4534, miR-6785-5p, miR-6850-5p, miR-4697-5p, miR-1260a, miR-4486, miR-6880-5p, miR-6802-5p, miR-6861-5p, miR-92b-5p, miR-1238-5p, miR-6851-5p, miR-7704, miR-149-3p, miR-4689, miR-4688, miR-125a-3p, miR-23b-3p, miR-614, miR-1913, miR-16-5p, miR-6717-5p, miR-3648, miR-3162-5p, miR-1909-3p, miR-8073, miR-6769b-5p, miR-6836-3p, miR-4484, miR-6819-5p and miR-6794-5p; and evaluating *in vitro* whether or not the subject has esophageal cancer in the subject using the above-measured expression levels and a control expression level of healthy subject(s)measured in the same way as above.

[0575] The term "evaluation" used herein is evaluation support based on results of *in vitro* examination, not physician's judgment.

[0576] As described above, in a preferred embodiment of the method of the present invention, specifically, miR-204-3p is hsa-miR-204-3p, miR-1247-3p is hsa-miR-1247-3p, miR-6875-5p is hsa-miR-6875-5p, miR-6857-5p is hsa-miR-6857-5p, miR-6726-5p is hsa-miR-6726-5p, miR-3188 is hsa-miR-3188, miR-8069 is hsa-miR-8069, miR-4257 is hsa-miR-4257, miR-1343-3p is hsa-miR-1343-3p, miR-7108-5p is hsa-miR-7108-5p, miR-6825-5p is hsa-miR-6825-5p, miR-7641 is hsa-miR-7641, miR-3185 is hsa-miR-3185, miR-4746-3p is hsa-miR-4746-3p, miR-6791-5p is hsa-miR-6791-5p, miR-6893-5p is hsa-miR-6893-5p, miR-4433b-3p is hsa-miR-4433b-3p, miR-3135b is hsa-miR-3135b, miR-6781-5p is hsa-miR-6781-5p, miR-1908-5p is hsa-miR-1908-5p, miR-4792 is hsa-miR-4792, miR-7845-5p is hsa-miR-7845-5p, miR-4417 is hsa-miR-4417, miR-3184-5p is hsa-miR-3184-5p, miR-1225-5p is hsa-miR-1225-5p, miR-1231 is hsa-miR-1231, miR-1225-3p is hsa-miR-1225-3p, miR-150-3p is hsa-miR-150-3p, miR-4433-3p is hsa-miR-4433-3p, miR-6125 is hsa-miR-6125, miR-4513 is hsa-miR-4513, miR-6787-5p is hsa-miR-6787-5p, miR-6784-5p is hsa-miR-6784-5p, miR-615-5p is hsa-miR-615-5p, miR-6765-3p is hsa-miR-6765-3p, miR-5572 is hsa-miR-5572, miR-6842-5p is hsa-miR-6842-5p, miR-8063 is hsa-miR-8063, miR-6780b-5p is hsa-miR-6780b-5p, miR-187-5p is hsa-miR-187-5p, miR-128-1-5p is hsa-miR-128-1-5p, miR-6729-5p is hsa-miR-6729-5p, miR-6741-5p is hsa-miR-6741-5p, miR-6757-5p is hsa-miR-6757-5p, miR-7110-5p is hsa-miR-7110-5p, miR-7975 is hsa-miR-7975, miR-1233-5p is hsa-miR-1233-5p, miR-6845-5p is hsa-miR-6845-5p, miR-3937 is hsa-miR-3937, miR-4467 is hsa-miR-4467, miR-7109-5p is hsa-miR-7109-5p, miR-6088 is hsa-miR-6088, miR-6782-5p is hsa-miR-6782-5p, miR-5195-3p is hsa-miR-5195-3p, miR-4454 is hsa-miR-4454, miR-6724-5p is hsa-miR-6724-5p, miR-8072 is hsa-miR-8072, miR-4516 is hsa-miR-4516, miR-6756-5p is hsa-miR-6756-5p, miR-4665-3p is hsa-miR-4665-3p, miR-6826-5p is hsa-miR-6826-5p, miR-6820-5p is hsa-miR-6820-5p, miR-6887-5p is hsa-miR-6887-5p, miR-3679-5p is hsa-miR-3679-5p, miR-7847-3p is hsa-miR-7847-3p, miR-6721-5p is hsa-miR-6721-5p, miR-3622a-5p is hsa-miR-3622a-5p, miR-939-5p is hsa-miR-939-5p, miR-602 is hsa-miR-602, miR-7977 is hsa-miR-7977, miR-6749-5p is hsa-miR-6749-5p, miR-1914-3p is hsa-miR-1914-3p, miR-4651 is hsa-miR-4651, miR-4695-5p is hsa-miR-4695-5p, miR-6848-5p is hsa-miR-6848-5p, miR-1228-3p is hsa-miR-1228-3p, miR-642b-3p is hsa-miR-642b-3p, miR-6746-5p is hsa-miR-6746-5p, miR-3620-5p is hsa-miR-3620-5p, miR-3131 is hsa-miR-3131, miR-6732-5p is hsa-miR-6732-5p, miR-7113-3p is hsa-miR-7113-3p, miR-23a-3p is hsa-miR-23a-3p, miR-3154 is hsa-miR-3154, miR-4723-5p is hsa-miR-4723-5p, miR-3663-3p is hsa-miR-3663-3p, miR-4734 is

hsa-miR-4734, miR-6816-5p is hsa-miR-6816-5p, miR-4442 is hsa-miR-4442, miR-4476 is hsa-miR-4476, miR-423-5p is hsa-miR-423-5p, miR-1249 is hsa-miR-1249, miR-6515-3p is hsa-miR-6515-3p, miR-887-3p is hsa-miR-887-3p, miR-4741 is hsa-miR-4741, miR-6766-3p is hsa-miR-6766-3p, miR-4673 is hsa-miR-4673, miR-6779-5p is hsa-miR-6779-5p, miR-4706 is hsa-miR-4706, miR-1268b is hsa-miR-1268b, miR-4632-5p is hsa-miR-4632-5p, miR-3197 is hsa-miR-3197, miR-6798-5p is hsa-miR-6798-5p, miR-711 is hsa-miR-711, miR-6840-3p is hsa-miR-6840-3p, miR-6763-5p is hsa-miR-6763-5p, miR-6727-5p is hsa-miR-6727-5p, miR-371a-5p is hsa-miR-371a-5p, miR-6824-5p is hsa-miR-6824-5p, miR-4648 is hsa-miR-4648, miR-1227-5p is hsa-miR-1227-5p, miR-564 is hsa-miR-564, miR-3679-3p is hsa-miR-3679-3p, miR-2861 is hsa-miR-2861, miR-6737-5p is hsa-miR-6737-5p, miR-4725-3p is hsa-miR-4725-3p, miR-6716-5p is hsa-miR-6716-5p, miR-4675 is hsa-miR-4675, miR-1915-3p is hsa-miR-1915-3p, miR-671-5p is hsa-miR-671-5p, miR-3656 is hsa-miR-3656, miR-6722-3p is hsa-miR-6722-3p, miR-4707-5p is hsa-miR-4707-5p, miR-4449 is hsa-miR-4449, miR-1202 is hsa-miR-1202, miR-4649-5p is hsa-miR-4649-5p, miR-744-5p is hsa-miR-744-5p, miR-642a-3p is hsa-miR-642a-3p, miR-451a is hsa-miR-451a, miR-6870-5p is hsa-miR-6870-5p, miR-4443 is hsa-miR-4443, miR-6808-5p is hsa-miR-6808-5p, miR-4728-5p is hsa-miR-4728-5p, miR-937-5p is hsa-miR-937-5p, miR-135a-3p is hsa-miR-135a-3p, miR-663b is hsa-miR-663b, miR-1343-5p is hsa-miR-1343-5p, miR-6822-5p is hsa-miR-6822-5p, miR-6803-5p is hsa-miR-6803-5p, miR-6805-3p is hsa-miR-6805-3p, miR-128-2-5p is hsa-miR-128-2-5p, miR-4640-5p is hsa-miR-4640-5p, miR-1469 is hsa-miR-1469, miR-92a-2-5p is hsa-miR-92a-2-5p, miR-3940-5p is hsa-miR-3940-5p, miR-4281 is hsa-miR-4281, miR-1260b is hsa-miR-1260b, miR-4758-5p is hsa-miR-4758-5p, miR-1915-5p is hsa-miR-1915-5p, miR-5001-5p is hsa-miR-5001-5p, miR-4286 is hsa-miR-4286, miR-6126 is hsa-miR-6126, miR-6789-5p is hsa-miR-6789-5p, miR-4459 is hsa-miR-4459, miR-1268a is hsa-miR-1268a, miR-6752-5p is hsa-miR-6752-5p, miR-6131 is hsa-miR-6131, miR-6800-5p is hsa-miR-6800-5p, miR-4532 is hsa-miR-4532, miR-6872-3p is hsa-miR-6872-3p, miR-718 is hsa-miR-718, miR-6769a-5p is hsa-miR-6769a-5p, miR-4707-3p is hsa-miR-4707-3p, miR-6765-5p is hsa-miR-6765-5p, miR-4739 is hsa-miR-4739, miR-4525 is hsa-miR-4525, miR-4270 is hsa-miR-4270, miR-4534 is hsa-miR-4534, miR-6785-5p is hsa-miR-6785-5p, miR-6850-5p is hsa-miR-6850-5p, miR-4697-5p is hsa-miR-4697-5p, miR-1260a is hsa-miR-1260a, miR-4486 is hsa-miR-4486, miR-6880-5p is hsa-miR-6880-5p, miR-6802-5p is hsa-miR-6802-5p, miR-6861-5p is hsa-miR-6861-5p, miR-92b-5p is hsa-miR-92b-5p, miR-1238-5p is hsa-miR-1238-5p, miR-6851-5p is hsa-miR-6851-5p, miR-7704 is hsa-miR-7704, miR-149-3p is hsa-miR-149-3p, miR-4689 is hsa-miR-4689, miR-4688 is hsa-miR-4688, miR-125a-3p is hsa-miR-125a-3p, miR-23b-3p is hsa-miR-23b-3p, miR-614 is hsa-miR-614, miR-1913 is hsa-miR-1913, miR-16-5p is hsa-miR-16-5p, miR-6717-5p is hsa-miR-6717-5p, miR-3648 is hsa-miR-3648, miR-3162-5p is hsa-miR-3162-5p, miR-1909-3p is hsa-miR-1909-3p, miR-8073 is hsa-miR-8073, miR-6769b-5p is hsa-miR-6769b-5p, miR-6836-3p is hsa-miR-6836-3p, miR-4484 is hsa-miR-4484, miR-6819-5p is hsa-miR-6819-5p, and miR-6794-5p is hsa-miR-6794-5p.

[0577] In a preferred embodiment of the method of the present invention, specifically, the nucleic acid(s) (specifically, probe(s) or primer(s)) 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 115, 117 to 189, and 666 to 675 or a nucleotide sequence 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 115, 117 to 189, and 666 to 675,

(c) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 1 to 115, 117 to 189, and 666 to 675 or a nucleotide sequence 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 115, 117 to 189, and 666 to 675 or a nucleotide sequence 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).

[0578] In the method of the present invention, a nucleic acid capable of specifically binding to a polynucleotide selected from miR-575 and miR-24-3p can be further used.

[0579] Specifically, miR-575 is hsa-miR-575, and miR-24-3p is hsa-miR-24-3p.

[0580] Specifically, the nucleic acid(s) is/are further 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: 116 and 676 or a nucleotide sequence 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: 116 and 676,

(h) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 116 and 676 or a nucleotide sequence 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: 116 and 676 or a nucleotide sequence 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).

[0581] The nucleic acid(s) in the method of the present invention can further comprise a nucleic acid capable of specifically binding to at least one polynucleotides selected from the following miRNAs: miR-675-5p, miR-486-3p, miR-6777-5p, miR-4497, miR-296-3p, miR-6738-5p, miR-4731-5p, miR-6889-5p, miR-6786-5p, miR-92a-3p, miR-4294, miR-4763-3p, miR-6076, miR-663a, miR-760, miR-4667-5p, miR-6090, miR-4730, miR-7106-5p, miR-3196, miR-5698, miR-6087, miR-4665-5p, miR-8059 and miR-6879-5p.

[0582] In a preferred embodiment, as for such nucleic acids, specifically, miR-675-5p is hsa-miR-675-5p, miR-486-3p is hsa-miR-486-3p, miR-6777-5p is hsa-miR-6777-5p, miR-4497 is hsa-miR-4497, miR-296-3p is hsa-miR-296-3p, miR-6738-5p is hsa-miR-6738-5p, miR-4731-5p is hsa-miR-4731-5p, miR-6889-5p is hsa-miR-6889-5p, miR-6786-5p is hsa-miR-6786-5p, miR-92a-3p is hsa-miR-92a-3p, miR-4294 is hsa-miR-4294, miR-4763-3p is hsa-miR-4763-3p, miR-6076 is hsa-miR-6076, miR-663a is hsa-miR-663a, miR-760 is hsa-miR-760, miR-4667-5p is hsa-miR-4667-5p, miR-6090 is hsa-miR-6090, miR-4730 is hsa-miR-4730, miR-7106-5p is hsa-miR-7106-5p, miR-3196 is hsa-miR-3196, miR-5698 is hsa-miR-5698, miR-6087 is hsa-miR-6087, miR-4665-5p is hsa-miR-4665-5p, miR-8059 is hsa-miR-8059, and miR-6879-5p is hsa-miR-6879-5p.

[0583] In a preferred embodiment, such nucleic acid(s) is specifically polynucleotide(s) 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: 190 to 214 or a nucleotide sequence 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,
(1) a polynucleotide comprising a nucleotide sequence represented by any of SEQ ID NOs: 190 to 214,
(m) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 190 to 214 or a nucleotide sequence 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: 190 to 214 or a nucleotide sequence 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).

[0584] Examples of the sample used in the method of the present invention can include samples prepared from living tissues (preferably esophageal tissues) or body fluids such as blood, serum, plasma, and urine from 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.

[0585] The subject used herein refers to a mammal, for example, a human, a monkey, a mouse or a rat without any limitation, and is preferably a human.

[0586] The steps of the method of the present invention can be changed according to the type of the sample to be assayed.

[0587] In the case of using RNA as an analyte, the detection of esophageal cancer (cells) can comprise, for example, the following steps (a), (b), and (c):

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

[0588] For example, various hybridization methods can be used for detecting, examining, evaluating, or diagnosing

esophageal cancer (or esophageal 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.

[0589] 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(s) that can be used in the present invention. Specific examples thereof can include a method which comprises labeling the nucleic acid probe (or a complementary strand) with a radioisotope (^{32}P, ^{33}P, ^{35}S, etc.), a fluorescent material, or the like, hybridizing the labeled product with the tissue-derived RNA from a subject, which is transferred to a nylon membrane or the like according to a routine method, and then detecting and measuring a signal 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.)).

[0590] 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 comprises preparing cDNA from the 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.

[0591] 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 having the attached nucleic acid probes are referred to as probe spots, and regions having no attached nucleic acid probe are referred to as blank spots. A group of genes 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 any 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.

[0592] Examples of the measurement using the DNA chip can include, but are not limited to, a method of detecting and measuring a signal from the label on the nucleic acid probes using an image detector (examples thereof can include Typhoon 9410 (GE Healthcare) and 3D-Gene(™) scanner (Toray Industries, Inc.)).

[0593] 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.

[0594] The stringent conditions are defined by hybridization and subsequent washing conditions. Examples of the hybridization conditions include, but not limited to, 30°C to 60°C for 1 to 24 hours in a solution containing SSC, a surfactant, formamide, dextran sulfate, blocking agent(s), 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 comprise 3-10 x SSC and 0.1-1% SDS. Examples of the conditions for the washing, following the hybridization, which is another condition to define the stringent conditions, can include conditions comprising 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 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.

[0595] 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.

[0596] Examples of the conditions for carrying out PCR using polynucleotide fragments in the kit of the present invention as primers include treatment for approximately 15 seconds to 1 minute at 5 to 10°C plus a Tm value calculated from the sequences of the primers, using a PCR buffer having composition such as 10 mM Tris-HCL (pH 8.3), 50 mM KCL, and 1 to 2 mM MgCl2. Examples of the method for calculating such a Tm value include Tm value = 2 x (the number of adenine residues + the number of thymine residues) + 4 x (the number of guanine residues + the number of cytosine residues).

[0597] 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.

[0598] For the calculation of gene expression levels, statistical treatment 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).

[0599] The present invention also provides a method comprising measuring target genes or gene expression levels in a sample 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 from an esophageal cancer patient and a sample from a healthy subject as supervising samples, and determining or evaluating the presence and/or absence of the esophageal cancer-derived genes in the sample.

[0600] Specifically, the present invention further provides the method comprising: a first step of measuring *in vitro* expression levels of target genes (target nucleic acid) in multiple samples that were known to be able to determine or evaluate the presence and/or absence of the esophageal cancer-derived gene in the samples, using the polynucleotides, the kit, or the device (e.g., chip) for detection of the present invention, or a combination thereof; a second step of constructing a discriminant with the measurement values of the expression levels of the target genes that was obtained in the first step as supervising samples; a third step of measuring *in vitro* expression levels of the target gene in a sample from a subject in the same way as in the first step; and a fourth step of assigning the measurement values of the expression levels 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 esophageal 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 the detection, that was contained in the polynucleotide, 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.

[0601] 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 this formula, x represents an explanatory variable, w represents a coefficient of the explanatory variable, and w0 represents a constant term.

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

[0602] Values obtained from the discriminant are referred to as discriminant scores. The measurement values of a newly offered data set can be assined as explanatory variables to the discriminant to determine clusters by the signs of the discriminant scores.

[0603] 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 a highly discriminating synthetic variable by focusing on the variance of the 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 associate with class g, and μg represents an average input of the data associate with class g. The numerator and the denominator are the interclass variance and the intraclass 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).

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

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

[0604] 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 in which a data point belongs to, based on a short Mahalanobis' distance from the data point to that cluster. In this formula, 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.

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

[0605] 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 data to be 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)).

[0606] C-support vector classification (C-SVC), one type of SVM, comprises preparing a hyperplane by supervising a data set 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).

[0607] 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., an esophageal cancer patient group and a healthy subject group. For example, esophageal tissue examination can be used for each subject to be confirmed either as an esophageal cancer patient or as a healthy subject.

[0608] 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 genes that were found to differ clearly in their gene expression levels between the two groups as explanatory variables and using this grouping as objective variables (e.g., -1 and +1). 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.

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

[0609] Formula 5 is a finally obtained discriminant, and a group in which the data point belongs to 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.

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

[0610] For example, a RBF kernel defined by Formula 6 can be used as the kernel function. In this context, x represents a support vector, and y represents a kernel parameter for adjusting the complexity of the hyperplane.

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

[0611] 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 an esophageal cancer-derived target gene in a sample from a subject, or for evaluating the expression level thereof by comparison with a control from a healthy subject.

[0612] The method of the present invention can comprise, for example, the following steps (a), (b), and (c):

(a) a step of measuring expression level(s) of target gene(s) in tissues containing esophageal cancer-derived genes from esophageal cancer patients and/or samples already known to be tissues containing no esophageal cancer-derived gene(s) 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) a step of measuring an expression level of the target gene in a sample from a subject using the polynucleotide, the kit, or the device (e.g., DNA chip) for diagnosis (detection) according to the present invention, assigning the obtained measurement value(s) into the discriminants prepared in the step (b), and determining or evaluating the presence and/or absence of expression of the esophageal 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 above in the Section 2 above, or a fragment thereof. Specifically, the explanatory variable for discriminating an esophageal cancer patient from a healthy subject according to the present invention is gene expression level(s) selected from, for example, the following expression levels (1) to (3):

(1) gene expression level(s) in the serum of an esophageal 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 115, 117 to 189, and 666 to 675 or a complementary sequence thereof,

(2) gene expression level(s) in the serum of an esophageal cancer patient or a healthy subject measured by any DNA comprising 15 or more consecutive nucleotides in a nucleotide sequence represented by SEQ ID NOs: 116 and 676 or a complementary sequence thereof, and

(3) gene expression level(s) in the serum of an esophageal 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: 190 to 214 or a complementary sequence thereof.

[0613] As described above, for the method for determining or evaluating the presence and/or absence of esophageal cancer-derived gene(s) in a sample from a subject, the preparation of a discriminant requires a discriminant prepared in a training cohort. For enhancing the discrimination accuracy of the discriminant, it is necessary for the discriminant to use genes that show clear difference between two groups in the training cohort.

[0614] Each gene that is used for an explanatory variable in a discriminant is preferably determined as follows. First, comprehensive gene expression levels of an esophageal cancer patient group and comprehensive gene expression levels of a healthy subject group, both of which are 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.

[0615] The gene can be regarded as being statistically significant when the critical rate (significance level) as the P value obtained by the test is smaller than, for example, 5%, 1%, or 0.01 %.

[0616] 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.

[0617] 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 an esophageal 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 an esophageal 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.

[0618] Next, a discriminant that can be calculated by various methods described above is prepared using any number of genes having 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 being P value, and a method of repetitively evaluating a discriminant while increasing the number of genes for use one by one in a descending order of difference in gene expression level (Furey TS. et al., 2000, Bioinformatics., Vol. 16, p. 906-14). A gene expression level of another independent esophageal cancer patient or healthy subject is assigned as an explanatory variable to this discriminant to calculate discriminant Specifically, the found gene set for diagnosis and the discriminant constructed using the gene set for diagnosis can be evaluated in an independent sample cohort to find a more universal gene set for diagnosis capable of detecting esophageal cancer and a more universal method for discriminating esophageal cancer.

[0619] Split-sample method is preferably used for evaluating the discriminant performance (generality). Specifically, a data set is divided into a training cohort andgenes in serum from a patient confirmed to be negative using CEA but finally found to have esophageal cancer by detailed examination such as computed tomography using a contrast medium, with genes expressed in serum from a patient having no esophageal cancer.

[0620] 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 115, 177 to 189, and 666 to 675 or a complementary sequence thereof as described above; and optionally one or two or more of the polynucleotides based on a nucleotide sequence represented by SEQ ID NOs: 116 and 676 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: 190 to 214 or a complementary sequence thereof. Further, a discriminant is constructed using expression levels of the gene set for diagnosis in samples from class I esophageal cancer patients as a result of tissue diagnosis and samples from class II healthy subjects as a result of tissue diagnosis. As a result, the presence or absence of esophageal 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 an unknown sample.

Examples

[0621] 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 esophageal cancer patient and healthy subject>

[0622] Sera were collected using VENOJECT II vacuum blood collecting tube VP-AS109K60 (Terumo Corp.) from 100 healthy subjects and 34 esophageal cancer patients (3 cases with stage IB, 1 case with stage IIA, 5 cases with stage IIB, 4 cases with stage IIIA, 7 cases with stage IIIB, 2 cases with stage IIIC, and 1 case with yp stage IA, 3 cases with yp stage IIA, 2 cases with yp stage IIB, 5 cases with yp stage IIIA, and 1 case with yp stage IIIC as samples (yp) stage-classified by pathological examination after treatment) with no primary cancer found other than esophageal cancer after acquisition of informed consent, and used as a training cohort. Likewise, sera were collected using VENOJECT II vacuum blood collecting tube VP-AS109K60 (Terumo Corp.) from 50 healthy subjects and 16 esophageal cancer patients (3 cases with stage IIA, 2 cases with stage IIIA, 2 cases with stage IIIC, and 1 case with yp stage 0, 1 case with yp stage

IA, 2 cases with yp stage IIA, 2 cases with yp stage IIIA, 1 case with yp stage IIIB, 1 case with yp stage IIIC, and 1 case with yp stage IV as samples (yp) stage-classified by pathological examination after treatment) with no primary cancer found other than esophageal cancer after acquision of informed consent, and used as a validation cohort.

<Extraction of total RNA>

[0623] 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 esophageal cancer patients included in the training cohort and the validation cohort, using areagent for RNA extraction in 3D-Gene(TM) RNA extraction reagent from liquid sample kit (Toray Industries, Inc.) according to the protocol provided by the manufacturer.

<Measurement of gene expression level>

[0624] miRNAs in the total RNA obtained from the serum samples of each of 200 persons in total of 150 healthy subjects and 50 esophageal 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 having a nucleotide 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 sera were obtained for the 50 esophageal 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 Development 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 of cancers other than esophageal cancer>

[0625] Serum was collected using VENOJECT II vacuum blood collecting tube VP-AS109K60 (Terumo Corp.) from each of 69 pancreatic cancer patients, 66 bile duct cancer patients, 30 colorectal cancer patients, 33 stomach cancer patients, 32 liver cancer patients, and 15 benign pancreaticobiliary disease patients 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 esophageal cancer patients and 103 healthy subjects of Reference Example 1.

[0626] Likewise, Sera were 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 colorectal cancer patients, 17 stomach cancer patients, 20 liver cancer patients, and 6 benign pancreaticobiliary disease patients 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 esophageal cancer patients confirmed to have no cancer in organs other than the esophagus 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 markers using samples of training cohort, and method for evaluating esophageal cancer discriminant performance of the single gene marker using the validation cohort>

[0627] In this Example, a gene marker for discriminating an esophageal cancer patient from a healthy subject was selected from the training cohort and studied in samples of the validation cohort independent of the training cohort, for a method for evaluating the esophageal cancer discriminant performance of each selected gene marker alone.

[0628] 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.

[0629] Next, genes for diagnosis were selected using the training cohort. Here, in order to acquire diagnostic markers

with higher reliability, only genes having the expression level of 2^6 or higher in 50% or more of the samples in either of the esophageal cancer patient group of the training cohort or the healthy subject group of the training cohort were selected. In order to further acquire statistically significant genes for discriminating an esophageal 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 result is described in Table 2 mentioned later.

[0630] In this way, hsa-miR-204-3p, hsa-miR-1247-3p, hsa-miR-6875-5p, hsa-miR-6857-5p, hsa-miR-6726-5p, hsa-miR-3188, hsa-miR-8069, hsa-miR-4257, hsa-miR-1343-3p, hsa-miR-7108-5p, hsa-miR-6825-5p, hsa-miR-7641, hsa-miR-3185, hsa-miR-4746-3p, hsa-miR-6791-5p, hsa-miR-6893-5p, hsa-miR-4433b-3p, hsa-miR-3135b, hsa-miR-6781-5p, hsa-miR-1908-5p, hsa-miR-4792, hsa-miR-7845-5p, hsa-miR-4417, hsa-miR-3184-5p, hsa-miR-1225-5p, hsa-miR-1231, hsa-miR-1225-3p, hsa-miR-150-3p, hsa-miR-4433-3p, hsa-miR-6125, hsa-miR-4513, hsa-miR-6787-5p, hsa-miR-6784-5p, hsa-miR-615-5p, hsa-miR-6765-3p, hsa-miR-5572, hsa-miR-6842-5p, hsa-miR-8063, hsa-miR-6780b-5p, hsa-miR-187-5p, hsa-miR-128-1-5p, hsa-miR-6729-5p, hsa-miR-6741-5p, hsa-miR-6757-5p, hsa-miR-7110-5p, hsa-miR-7975, hsa-miR-1233-5p, hsa-miR-6845-5p, hsa-miR-3937, hsa-miR-4467, hsa-miR-7109-5p, hsa-miR-6088, hsa-miR-6782-5p, hsa-miR-5195-3p, hsa-miR-4454, hsa-miR-6724-5p, hsa-miR-8072, hsa-miR-4516, hsa-miR-6756-5p, hsa-miR-4665-3p, hsa-miR-6826-5p, hsa-miR-6820-5p, hsa-miR-6887-5p, hsa-miR-3679-5p, hsa-miR-7847-3p, hsa-miR-6721-5p, hsa-miR-3622a-5p, hsa-miR-939-5p, hsa-miR-602, hsa-miR-7977, hsa-miR-6749-5p, hsa-miR-1914-3p, hsa-miR-4651, hsa-miR-4695-5p, hsa-miR-6848-5p, hsa-miR-1228-3p, hsa-miR-642b-3p, hsa-miR-6746-5p, hsa-miR-3620-5p, hsa-miR-3131, hsa-miR-6732-5p, hsa-miR-7113-3p, hsa-miR-23a-3p, hsa-miR-3154, hsa-miR-4723-5p, hsa-miR-3663-3p, hsa-miR-4734, hsa-miR-6816-5p, hsa-miR-4442, hsa-miR-4476, hsa-miR-423-5p, hsa-miR-1249, hsa-miR-6515-3p, hsa-miR-887-3p, hsa-miR-4741, hsa-miR-6766-3p, hsa-miR-4673, hsa-miR-6779-5p, hsa-miR-4706, hsa-miR-1268b, hsa-miR-4632-5p, hsa-miR-3197, hsa-miR-6798-5p, hsa-miR-711, hsa-miR-6840-3p, hsa-miR-6763-5p, hsa-miR-6727-5p, hsa-miR-371a-5p, hsa-miR-6824-5p, hsa-miR-4648, hsa-miR-1227-5p, hsa-miR-564, hsa-miR-3679-3p, hsa-miR-2861, hsa-miR-6737-5p, hsa-miR-575, hsa-miR-4725-3p, hsa-miR-6716-5p, hsa-miR-4675, hsa-miR-1915-3p, hsa-miR-671-5p, hsa-miR-3656, hsa-miR-6722-3p, hsa-miR-4707-5p, hsa-miR-4449, hsa-miR-1202, hsa-miR-4649-5p, hsa-miR-744-5p, hsa-miR-642a-3p, hsa-miR-451a, hsa-miR-6870-5p, hsa-miR-4443, hsa-miR-6808-5p, hsa-miR-4728-5p, hsa-miR-937-5p, hsa-miR-135a-3p, hsa-miR-663b, hsa-miR-1343-5p, hsa-miR-6822-5p, hsa-miR-6803-5p, hsa-miR-6805-3p, hsa-miR-128-2-5p, hsa-miR-4640-5p, hsa-miR-1469, hsa-miR-92a-2-5p, hsa-miR-3940-5p, hsa-miR-4281, hsa-miR-1260b, hsa-miR-4758-5p, hsa-miR-1915-5p, hsa-miR-5001-5p, hsa-miR-4286, hsa-miR-6126, hsa-miR-6789-5p, hsa-miR-4459, hsa-miR-1268a, hsa-miR-6752-5p, hsa-miR-6131, hsa-miR-6800-5p, hsa-miR-4532, hsa-miR-6872-3p, hsa-miR-718, hsa-miR-6769a-5p, hsa-miR-4707-3p, hsa-miR-6765-5p, hsa-miR-4739, hsa-miR-4525, hsa-miR-4270, hsa-miR-4534, hsa-miR-6785-5p, hsa-miR-6850-5p, hsa-miR-4697-5p, hsa-miR-1260a, hsa-miR-4486, hsa-miR-6880-5p, hsa-miR-6802-5p, hsa-miR-6861-5p, hsa-miR-92b-5p, hsa-miR-1238-5p, hsa-miR-6851-5p, hsa-miR-7704, hsa-miR-149-3p, hsa-miR-4689, hsa-miR-4688, hsa-miR-125a-3p, hsa-miR-23b-3p, hsa-miR-614, hsa-miR-1913 and hsa-miR-16-5p genes, and polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 189 related thereto were found.

[0631] Among them, genes newly found as markers for examining the presence or absence of esophageal cancer are polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 115 and 117 to 189.

[0632] A discriminant for determining the presence or absence of esophageal cancer was further prepared by Fisher's discriminant analysis with the expression levels of these genes as indicators. Specifically, any polynucleotide consisting of a nucleotide sequence represented by any of SEQ ID NOs: 1 to 189 found in the training cohort was apply for Formula 2 above to construct a discriminant. Calculated accuracy, sensitivity, and specificity are shown in Table 3 mentioned later. In this respect, a discriminant coefficient and a constant term are shown in Table 4.

[0633] In this context, for example, 42 polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1, 3, 4, 5, 6, 9, 10, 13, 15, 17, 18, 19, 26, 28, 29, 30, 32, 33, 35, 40, 41, 43, 55, 58, 61, 63, 67, 68, 70, 76, 77, 80, 90, 92, 93, 95, 109, 116, 119, 122, 127 and 150 were selected as markers capable of determining esophageal cancer even in any of 3 stage I samples included in the training cohort.

[0634] Accuracy, sensitivity, and specificity for 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 gene expression level measurement value of the nucleotide sequence represented by SEQ ID NO: 1 was compared between the healthy subjects (100 persons) and the esophageal cancer patients (34 persons) in the training cohort. As a result, the expression level measurement values were found to be significantly lower in the esophageal 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 esophageal 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 189 showed that the expression level measurement values were significantly lower (-) or higher (+) in the esophageal 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

correctly or incorrectly identified samples in the detection of esophageal cancer in the validation cohort was calculated using the threshold (12.3) that was set in the training cohort and discriminated between the two groups. As a result, 13 true positives, 48 true negatives, 2 false positives, and 3 false negatives were obtained. From these values, 92.4% accuracy, 81.2% sensitivity, and 96% specificity were obtained as detection performance. In this way, the detection performance was calculated as to any of the polynucleotides shown in SEQ ID NOs: 1 to 189, and described in Table 3. Likewise, 129 polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 1l, 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, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 106, 107, 109, 110, 112, 113, 114, 115, 116, 117, 119, 120, 130, 131, 134, 139, 143, 151, 159, 173, 182, 185, 186, 187, 188 and 189 shown in Table 2 exhibited sensitivity of 81.2%, 87.5%, 93.8%, 100%, 87.5%, 87.5%, 81.2%, 75%, 87.5%, 100%, 100%, 87.5%, 81.2%, 75%, 87.5%, 87.5%, 81.2%, 93.8%, 93.8%, 81.2%, 100%, 87.5%, 68.8%, 87.5%, 81.2%, 75%, 87.5%, 81.2%, 81.2%, 87.5%, 75%, 68.8%, 81.2%, 75%, 68.8%, 100%, 68.8%, 87.5%, 87.5%, 81.2%, 68.8%, 75%, 75%, 87.5%, 68.8%, 62.5%, 93.8%, 75%, 81.2%, 62.5%, 56.2%, 56.2%, 56.2%, 75%, 68.8%, 62.5%, 62.5%, 62.5%, 68.8%, 68.8%, 68.8%, 56.2%, 56.2%, 56.2%, 81.2%, 56.2%, 50%, 68.8%, 75%, 56.2%, 56.2%, 56.2%, 62.5%, 43.8%, 50%, 56.2%, 56.2%, 68.8%, 62.5%, 62.5%, 68.8%, 56.2%, 43.8%, 62.5%, 56.2%, 43.8%, 43.8%, 75%, 56.2%, 56.2%, 62.5%, 56.2%, 87.5%, 43.8%, 50%, 43.8%, 50%, 56.2%, 43.8%, 50%, 43.8%, 68.8%, 62.5%, 56.2%, 43.8%, 43.8%, 56.2%, 56.2%, 62.5%, 56.2%, 62.5%, 50%, 68.8%, 56.2%, 43.8%, 62.5%, 43.8%, 43.8%, 43.8%, 43.8%, 50%, 56.2%, 43.8%, 43.8%, 75%, 62.5%, 43.8%, 50% and 62.5%, respectively, in the validation cohort (Table 3). As seen from Comparative Example mentioned later, the existing marker SCC for esophageal cancer had sensitivity of 37.5% in the validation cohort (Table 5-2), demonstrating that the 129 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, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 106, 107, 109, 110, 112, 113, 114, 115, 116, 117, 119, 120, 130, 131, 134, 139, 143, 151, 159, 173, 182, 185, 186, 187, 188 and 189 can discriminate, each alone, esophageal cancer in the validation cohort with sensitivity beyond CEA.

[0635] Thus, these polynucleotides can detect even early esophageal cancer and contribute to the early diagnosis of esophageal cancer.

[Example 2]

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

[0636] In this Example, a method for evaluating esophageal 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 17,766 combinations of any two of the expression level measurement values of the newly found polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 115 and 117 to 189 among the polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 189 selected in Example 1, to construct a discriminant for determining the presence or absence of esophageal 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 the independent samples.

[0637] For example, the gene expression level measurement values of the nucleotide sequences represented by SEQ ID NO: 2 and SEQ ID NO: 4 were compared between the healthy subjects (100 persons) and the esophageal cancer patients (34 persons) in the training cohort. As a result, a variance diagram that significantly separated the measurement values of the esophageal 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 esophageal cancer patients (16 persons) in the validation cohort (see the right diagram of Figure 3). Likewise, a variance diagram that significantly separated the measurement values of the esophageal cancer patient group from those of the healthy subject group was also obtained as to the other combinations of any two of the gene expression level measurement values of the newly found polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 115 and 117 to 189. These results were able to be validated in the validation cohort. As shown in Figure 3, for example, as for these nucleotide sequences represented by SEQ ID NO: 2 and SEQ ID NO: 4, the number of samples that were correctly or incorrectly identified esophageal cancer was calculated using the function (0 = 2.42x + y - 21.17) that was set in the training cohort and discriminated between the two groups. As a result, 15 true positives, 49 true negatives, 1 false positive, and 1 false negative were obtained. From these values, 97% accuracy, 93.8% sensitivity, and 98% specificity were obtained as the detection performance. In this way, the detection performance was calculated for the combinations

of two of the polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 189. Among them, 188 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, any of combinations of the expression level measurement values of the polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 and 6, SEQ ID NOs: 1 and 9, SEQ ID NOs: 1 and 13, and SEQ ID NOs: 1 and 14 exhibited sensitivity of 100% in the validation cohort. Likewise, any of the remaining combinations of two polynucleotides consisting of the nucleotide sequences represented by SEQ ID NO: 1 and any of SEQ ID NOs: 2 to 189 also exhibited sensitivity of 81% or higher, which was beyond the sensitivity (37.5%) of the existing marker SCC for esophageal cancer (Table 5-2). The 17,096 combinations that showed sensitivity beyond SCC were obtained for the validation cohort. All of the nucleotide sequences 1 to 189 described in Table 2 obtained in Example 1 were employed at least once in these combinations. Thus, a combination of the expression level measurement values of two of the polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 189 also produced excellent esophageal cancer detection sensitivity.

[0638] Markers for the detection of esophageal cancer with better sensitivity are obtained by further 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 189. For example, the newly found polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 115 and 117 to 189 among the polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 189 selected in Example 1 were measured to obtain their expression levels between the healthy subject group and the esophageal cancer group in the validation cohort. All of the polynucleotides were ranked in the descending order of their P values based on 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 esophageal cancer detection sensitivity was evaluated using combinations of one or more polynucleotides to which the polynucleotides were added 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: 189 to SEQ ID NOs: 188, 187, ... shown in Table 2. As a result, the sensitivity in the validation cohort was 31.2% for 1 polynucleotide (SEQ ID NO: 189), 56.2% for 2 polynucleotides (SEQ ID NOs: 188 and 189), 75.0% for 3 polynucleotides (SEQ ID NOs: 187 to 189), 93.8% for 5 polynucleotides (SEQ ID NOs: 185 to 189), 100% for 11 polynucleotides (SEQ ID NOs: 179 to 189), 100% for 30 polynucleotides (SEQ ID NOs: 160 to 189), 100% for 50 polynucleotides (SEQ ID NOs: 140 to 189), 100% for 100 polynucleotides (SEQ ID NOs: 89 to 115 and 117 to 189), 100% for 150 polynucleotides (SEQ ID NOs: 39 to 115 and 117 to 189), and 100% for 189 polynucleotides (SEQ ID NOs: 1 to 115 and 117 to 189).

[0639] These results demonstrated that a combination of multiple polynucleotides can produce higher esophageal 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 esophageal cancer.

[0640] From these results, it can be concluded that all of the polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 189 serve as excellent markers for the detection of esophageal cancer.

[Table 2]

SEQ ID NO:	Gene name	P value after Bonferroni correction	Expression level in esophageal cancer patient relative to healthy subject
1	hsa-miR-204-3p	3.17E-32	-
2	hsa-miR-1247-3p	5.11E-32	+
3	hsa-miR-6875-5p	5.55E-29	+
4	hsa-miR-6857-5p	3.05E-27	+
5	hsa-miR-6726-5p	2.44E-26	-
6	hsa-miR-3188	1.00E-24	+
7	hsa-miR-8069	1.45E-24	+
8	hsa-miR-4257	2.73E-23	-
9	hsa-miR-1343-3p	4.31E-23	-
10	hsa-miR-7108-5p	4.94E-23	+
11	hsa-miR-6825-5p	5.79E-23	+

(continued)

SEQ ID NO:	Gene name	P value after Bonferroni correction	Expression level in esophageal cancer patient relative to healthy subject
12	hsa-miR-7641	7.55E-23	-
13	hsa-miR-3185	7.72E-22	+
14	hsa-miR-4746-3p	1.19E-21	+
15	hsa-miR-6791-5p	7.82E-21	+
16	hsa-miR-6893-5p	7.89E-21	-
17	hsa-miR-4433b-3p	8.03E-21	+
18	hsa-miR-3135b	1.34E-20	-
19	hsa-miR-6781-5p	2.01E-20	+
20	hsa-miR-1908-5p	2.19E-20	+
21	hsa-miR-4792	2.39E-20	+
22	hsa-miR-7845-5p	3.30E-20	+
23	hsa-miR-4417	7.21E-20	+
24	hsa-miR-3184-5p	1.29E-19	+
25	hsa-miR-1225-5p	1.55E-19	+
26	hsa-miR-1231	3.51E-19	+
27	hsa-miR-1225-3p	3.85E-19	+
28	hsa-miR-150-3p	6.30E-19	-
29	hsa-miR-4433-3p	7.27E-19	+
30	hsa-miR-6125	2.07E-18	+
31	hsa-miR-4513	2.51E-18	-
32	hsa-miR-6787-5p	2.87E-18	-
33	hsa-miR-6784-5p	3.57E-18	+
34	hsa-miR-615-5p	8.70E-18	-
35	hsa-miR-6765-3p	1.34E-17	-
36	hsa-miR-5572	1.62E-17	+
37	hsa-miR-6842-5p	2.45E-17	+
38	hsa-miR-8063	2.69E-17	-
39	hsa-miR-6780b-5p	3.33E-17	+
40	hsa-miR-187-5p	9.41E-17	-
41	hsa-miR-128-1-5p	9.79E-17	+
42	hsa-miR-6729-5p	1.08E-16	+
43	hsa-miR-6741-5p	9.63E-16	-
44	hsa-miR-6757-5p	1.95E-15	-
45	hsa-miR-7110-5p	2.20E-15	+
46	hsa-miR-7975	2.43E-15	-
47	hsa-miR-1233-5p	2.66E-15	-
48	hsa-miR-6845-5p	3.62E-15	+

(continued)

SEQ ID NO:	Gene name	P value after Bonferroni correction	Expression level in esophageal cancer patient relative to healthy subject
49	hsa-miR-3937	1.05E-14	+
50	hsa-miR-4467	1.31E-14	+
51	hsa-miR-7109-5p	1.80E-14	-
52	hsa-miR-6088	1.95E-14	-
53	hsa-miR-6782-5p	2.52E-14	+
54	hsa-miR-5195-3p	2.64E-14	-
55	hsa-miR-4454	3.79E-14	-
56	hsa-miR-6724-5p	5.19E-14	+
57	hsa-miR-8072	6.32E-14	+
58	hsa-miR-4516	1.64E-13	-
59	hsa-miR-6756-5p	2.32E-13	-
60	hsa-miR-4665-3p	2.91E-13	+
61	hsa-miR-6826-5p	4.31E-13	-
62	hsa-miR-6820-5p	6.77E-13	-
63	hsa-miR-6887-5p	9.53E-13	-
64	hsa-miR-3679-5p	1.05E-12	+
65	hsa-miR-7847-3p	1.11E-12	-
66	hsa-miR-6721-5p	1.24E-12	+
67	hsa-miR-3622a-5p	2.38E-12	-
68	hsa-miR-939-5p	2.39E-12	+
69	hsa-miR-602	3.03E-12	+
70	hsa-miR-7977	5.99E-12	-
71	hsa-miR-6749-5p	8.45E-12	-
72	hsa-miR-1914-3p	8.68E-12	-
73	hsa-miR-4651	9.05E-12	-
74	hsa-miR-4695-5p	9.79E-12	+
75	hsa-miR-6848-5p	1.17E-11	+
76	hsa-miR-1228-3p	1.56E-11	+
77	hsa-miR-642b-3p	1.71E-11	-
78	hsa-miR-6746-5p	2.34E-11	-
79	hsa-miR-3620-5p	2.79E-11	+
80	hsa-miR-3131	2.99E-11	-
81	hsa-miR-6732-5p	3.68E-11	+
82	hsa-miR-7113-3p	5.38E-11	+
83	hsa-miR-23a-3p	5.53E-11	-
84	hsa-miR-3154	6.89E-11	+
85	hsa-miR-4723-5p	9.65E-11	-

(continued)

SEQ ID NO:	Gene name	P value after Bonferroni correction	Expression level in esophageal cancer patient relative to healthy subject
86	hsa-miR-3663-3p	3.45E-10	-
87	hsa-miR-4734	3.66E-10	+
88	hsa-miR-6816-5p	4.49E-10	+
89	hsa-miR-4442	5.02E-10	-
90	hsa-miR-4476	5.16E-10	-
91	hsa-miR-423-5p	6.10E-10	-
92	hsa-miR-1249	6.19E-10	+
93	hsa-miR-6515-3p	6.91E-10	+
94	hsa-miR-887-3p	7.28E-10	+
95	hsa-miR-4741	9.08E-10	+
96	hsa-miR-6766-3p	1.13E-09	+
97	hsa-miR-4673	2.76E-09	+
98	hsa-miR-6779-5p	2.82E-09	-
99	hsa-miR-4706	3.75E-09	-
100	hsa-miR-1268b	5.40E-09	+
101	hsa-miR-4632-5p	5.60E-09	+
102	hsa-miR-3197	6.35E-09	+
103	hsa-miR-6798-5p	9.47E-09	+
104	hsa-miR-711	9.91E-09	+
105	hsa-miR-6840-3p	1.16E-08	-
106	hsa-miR-6763-5p	1.21E-08	+
107	hsa-miR-6727-5p	1.25E-08	-
108	hsa-miR-371a-5p	1.88E-08	-
109	hsa-miR-6824-5p	2.00E-08	+
110	hsa-miR-4648	2.81E-08	+
111	hsa-miR-1227-5p	2.85E-08	+
112	hsa-miR-564	5.06E-08	-
113	hsa-miR-3679-3p	5.14E-08	+
114	hsa-miR-2861	6.22E-08	-
115	hsa-miR-6737-5p	6.48E-08	+
116	hsa-miR-575	1.06E-07	-
117	hsa-miR-4725-3p	1.31E-07	+
118	hsa-miR-6716-5p	1.39E-07	+
119	hsa-miR-4675	1.85E-07	-
120	hsa-miR-1915-3p	1.89E-07	+
121	hsa-miR-671-5p	1.89E-07	-
122	hsa-miR-3656	2.14E-07	+

(continued)

SEQ ID NO:	Gene name	P value after Bonferroni correction	Expression level in esophageal cancer patient relative to healthy subject
123	hsa-miR-6722-3p	2.15E-07	+
124	hsa-miR-4707-5p	2.32E-07	+
125	hsa-miR-4449	2.73E-07	+
126	hsa-miR-1202	4.73E-07	-
127	hsa-miR-4649-5p	1.23E-06	-
128	hsa-miR-744-5p	1.53E-06	+
129	hsa-miR-642a-3p	1.70E-06	-
130	hsa-miR-451a	2.39E-06	-
131	hsa-miR-6870-5p	2.74E-06	+
132	hsa-miR-4443	3.08E-06	+
133	hsa-miR-6808-5p	3.57E-06	+
134	hsa-miR-4728-5p	4.15E-06	-
135	hsa-miR-937-5p	4.83E-06	-
136	hsa-miR-135a-3p	7.39E-06	+
137	hsa-miR-663b	8.35E-06	-
138	hsa-miR-1343-5p	9.72E-06	+
139	hsa-miR-6822-5p	1.03E-05	+
140	hsa-miR-6803-5p	1.05E-05	+
141	hsa-miR-6805-3p	1.86E-05	+
142	hsa-miR-128-2-5p	2.08E-05	-
143	hsa-miR-4640-5p	2.71E-05	+
144	hsa-miR-1469	2.75E-05	+
145	hsa-miR-92a-2-5p	3.53E-05	+
146	hsa-miR-3940-5p	4.11E-05	+
147	hsa-miR-4281	4.74E-05	-
148	hsa-miR-1260b	7.11E-05	-
149	hsa-miR-4758-5p	7.66E-05	-
150	hsa-miR-1915-5p	7.76E-05	-
151	hsa-miR-5001-5p	9.17E-05	-
152	hsa-miR-4286	1.58E-04	-
153	hsa-miR-6126	1.61E-04	+
154	hsa-miR-6789-5p	1.64E-04	+
155	hsa-miR-4459	2.00E-04	+
156	hsa-miR-1268a	2.18E-04	+
157	hsa-miR-6752-5p	2.64E-04	+
158	hsa-miR-6131	2.95E-04	-
159	hsa-miR-6800-5p	3.49E-04	+

(continued)

SEQ ID NO:	Gene name	P value after Bonferroni correction	Expression level in esophageal cancer patient relative to healthy subject
160	hsa-miR-4532	4.53E-04	-
161	hsa-miR-6872-3p	5.66E-04	-
162	hsa-miR-718	6.77E-04	+
163	hsa-miR-6769a-5p	7.66E-04	-
164	hsa-miR-4707-3p	7.90E-04	+
165	hsa-miR-6765-5p	8.10E-04	+
166	hsa-miR-4739	1.05E-03	+
167	hsa-miR-4525	1.09E-03	-
168	hsa-miR-4270	1.26E-03	-
169	hsa-miR-4534	1.51E-03	-
170	hsa-miR-6785-5p	1.53E-03	-
171	hsa-miR-6850-5p	1.54E-03	+
172	hsa-miR-4697-5p	1.57E-03	-
173	hsa-miR-1260a	1.69E-03	-
174	hsa-miR-4486	1.83E-03	+
175	hsa-miR-6880-5p	2.43E-03	+
176	hsa-miR-6802-5p	2.70E-03	-
177	hsa-miR-6861-5p	3.25E-03	-
178	hsa-miR-92b-5p	4.09E-03	+
179	hsa-miR-1238-5p	4.13E-03	+
180	hsa-miR-6851-5p	4.42E-03	+
181	hsa-miR-7704	5.64E-03	-
182	hsa-miR-149-3p	5.75E-03	-
183	hsa-miR-4689	6.06E-03	-
184	hsa-miR-4688	9.69E-03	-
185	hsa-miR-125a-3p	2.00E-28	-
186	hsa-miR-23b-3p	7.47E-11	-
187	hsa-miR-614	1.25E-08	-
188	hsa-miR-1913	4.37E-08	+
189	hsa-miR-16-5p	3.26E-04	-

[Table 3]

	Training cohort			Validation cohort		
SEQ ID NO:	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
1	94	79.4	99	92.4	81.2	96
2	96.3	91.2	98	93.9	87.5	96
3	95.5	91.2	97	90.9	93.8	90

(continued)

	Training cohort			Validation cohort		
SEQ ID NO:	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
4	94	94.1	94	97	100	96
5	91	73.5	97	92.4	87.5	94
6	94	88.2	96	95.5	87.5	98
7	91.8	82.4	95	92.4	81.2	96
8	91.8	76.5	97	89.4	75	94
9	93.3	88.2	95	93.9	87.5	96
10	91	79.4	95	92.4	100	90
11	88.8	82.4	91	93.9	100	92
12	89.6	79.4	93	93.9	87.5	96
13	92.5	88.2	94	92.4	81.2	96
14	92.5	88.2	94	90.9	75	96
15	90.3	88.2	91	95.5	87.5	98
16	91.8	73.5	98	93.9	87.5	96
17	90.3	79.4	94	83.3	81.2	84
18	97	97.1	97	97	93.8	98
19	91.8	73.5	98	92.4	93.8	92
20	91	85.3	93	90.9	81.2	94
21	91.8	85.3	94	98.5	100	98
22	94	85.3	97	90.9	87.5	92
23	92.5	79.4	97	87.9	68.8	94
24	91.8	88.2	93	92.4	87.5	94
25	93.3	85.3	96	90.9	81.2	94
26	89.6	76.5	94	87.9	75	92
27	93.3	85.3	96	97	87.5	100
28	88.8	76.5	93	86.4	81.2	88
29	88.1	82.4	90	89.4	81.2	92
30	93.3	91.2	94	93.9	87.5	96
31	88.8	67.6	96	90.9	75	96
32	91	76.5	96	87.9	68.8	94
33	86.6	79.4	89	86.4	81.2	88
34	90.3	76.5	95	92.4	75	98
35	89.6	70.6	96	89.4	68.8	96
36	87.3	82.4	89	92.4	100	90
37	89.6	73.5	95	89.4	68.8	96
38	86.6	76.5	90	92.4	87.5	94
39	88.1	67.6	95	97	87.5	100
40	89.6	82.4	92	92.4	81.2	96

(continued)

	Training cohort			Validation cohort		
SEQ ID NO:	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
41	88.1	76.5	92	81.8	68.8	86
42	89.6	64.7	98	92.4	75	98
43	91	73.5	97	87.9	75	92
44	85.8	70.6	91	97	87.5	100
45	84.3	64.7	91	84.8	68.8	90
46	88.1	64.7	96	84.8	62.5	92
47	88.1	67.6	95	93.9	93.8	94
48	88.1	64.7	96	86.4	75	90
49	87.3	67.6	94	92.4	81.2	96
50	83.6	73.5	87	87.9	62.5	96
51	83.6	64.7	90	81.8	56.2	90
52	83.6	61.8	91	83.3	56.2	92
53	88.8	73.5	94	84.8	56.2	94
54	89.6	76.5	94	90.9	75	96
55	86.6	67.6	93	87.9	68.8	94
56	87.3	73.5	92	81.8	62.5	88
57	88.1	64.7	96	80.3	62.5	86
58	88.1	64.7	96	87.9	62.5	96
59	89.6	70.6	96	81.8	68.8	86
60	87.3	70.6	93	83.3	68.8	88
61	85.1	58.8	94	92.4	68.8	100
62	91	69.7	98	81.8	56.2	90
63	85.1	58.8	94	84.8	56.2	94
64	84.3	58.8	93	86.4	56.2	96
65	81.3	55.9	90	87.9	81.2	90
66	84.3	67.6	90	77.3	56.2	84
67	86.6	55.9	97	84.8	50	96
68	79.1	61.8	85	83.3	68.8	88
69	84.3	58.8	93	89.4	75	94
70	85.8	52.9	97	84.8	56.2	94
71	83.6	61.8	91	86.4	56.2	96
72	85.1	61.8	93	80.3	56.2	88
73	84.3	50	96	89.4	62.5	98
74	79.9	52.9	89	81.8	43.8	94
75	84.3	58.8	93	78.8	50	88
76	86.6	64.7	94	81.8	56.2	90
77	85.1	58.8	94	87.9	56.2	98

(continued)

	Training cohort			Validation cohort		
SEQ ID NO:	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
78	81.3	55.9	90	86.4	68.8	92
79	84.3	58.8	93	84.8	62.5	92
80	82.8	55.9	92	89.4	62.5	98
81	82.8	64.7	89	80.3	68.8	84
82	81.3	58.8	89	83.3	56.2	92
83	85.8	55.9	96	78.8	43.8	90
84	85.8	58.8	95	83.3	62.5	90
85	83.6	50	95	81.8	56.2	90
86	79.1	32.4	95	83.3	43.8	96
87	76.9	26.5	94	81.8	43.8	94
88	85.1	70.6	90	87.9	75	92
89	81.3	52.9	91	83.3	56.2	92
90	85.8	52.9	97	84.8	56.2	94
91	83.6	58.8	92	71.2	31.2	84
92	80.5	41.2	93.9	83.3	62.5	90
93	79.1	38.2	93	75.8	56.2	82
94	79.1	50	89	87.9	87.5	88
95	85.1	55.9	95	81.8	43.8	94
96	85.8	58.8	95	80.3	50	90
97	85.8	55.9	96	83.3	43.8	96
98	76.9	38.2	90	86.4	50	98
99	82.8	50	94	84.8	56.2	94
100	77.6	44.1	89	74.2	43.8	84
101	85.8	52.9	97	86.4	50	98
102	85.8	64.7	93	81.8	43.8	94
103	80.6	52.9	90	80.3	68.8	84
104	85.8	61.8	94	89.4	62.5	98
105	79.1	38.2	93	78.8	31.2	94
106	79.9	50	90	83.3	56.2	92
107	83.6	55.9	93	84.8	43.8	98
108	79.9	44.1	92	72.7	31.2	86
109	84.3	47.1	97	83.3	43.8	96
110	79.1	41.2	92	89.4	56.2	100
111	79.9	38.2	94	75.8	31.2	90
112	85.1	50	97	87.9	56.2	98
113	82.1	47.1	94	83.3	62.5	90
114	80.6	44.1	93	86.4	56.2	96

(continued)

	Training cohort			Validation cohort		
SEQ ID NO:	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
115	79.9	50	90	83.3	62.5	90
116	88.1	55.9	99	84.8	50	96
117	82.8	61.8	90	86.4	68.8	92
118	82.1	47.1	94	77.3	31.2	92
119	79.1	38.2	93	89.4	56.2	100
120	78.4	29.4	95	81.8	43.8	94
121	80.6	41.2	94	77.3	31.2	92
122	79.9	38.2	94	78.8	18.8	98
123	80.6	44.1	93	78.8	37.5	92
124	79.9	50	90	77.3	37.5	90
125	79.1	32.4	95	81.8	37.5	96
126	81.3	35.3	97	80.3	37.5	94
127	78.4	44.1	90	81.8	37.5	96
128	80.6	38.2	95	83.3	37.5	98
129	74.6	26.5	91	72.7	18.8	90
130	84.3	47.1	97	86.4	62.5	94
131	79.9	32.4	96	86.4	43.8	100
132	82.8	47.1	95	80.3	31.2	96
133	80.6	35.3	96	72.7	12.5	92
134	76.9	32.4	92	80.3	43.8	92
135	79.9	35.3	95	80.3	31.2	96
136	79.9	44.1	92	71.2	31.2	84
137	74.6	23.5	92	80.3	18.8	100
138	81.3	44.1	94	81.8	37.5	96
139	76.9	26.5	94	84.8	43.8	98
140	76.9	35.3	91	69.7	25	84
141	76.9	35.3	91	80.3	31.2	96
142	79.1	29.4	96	83.3	31.2	100
143	79.1	29.4	96	86.4	43.8	100
144	77.6	26.5	95	74.2	25	90
145	78.4	32.4	94	78.8	37.5	92
146	76.9	29.4	93	77.3	31.2	92
147	75.4	23.5	93	78.8	25	96
148	81.3	38.2	96	80.3	37.5	94
149	82.8	38.2	98	78.8	18.8	98
150	79.1	29.4	96	78.8	31.2	94
151	80.6	38.2	95	81.8	50	92

(continued)

	Training cohort			Validation cohort		
SEQ ID NO:	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
152	76.1	23.5	94	77.3	31.2	92
153	73.9	23.5	91	75.8	12.5	96
154	73.1	11.8	94	75.8	31.2	90
155	81.3	38.2	96	80.3	25	98
156	73.1	26.5	89	71.2	31.2	84
157	73.9	17.6	93	66.7	6.2	86
158	79.9	35.3	95	80.3	31.2	96
159	76.9	23.5	95	83.3	56.2	92
160	77.6	23.5	96	80.3	25	98
161	79.1	29.4	96	81.8	37.5	96
162	73.1	14.7	93	69.7	0	92
163	76.1	23.5	94	75.8	12.5	96
164	76.1	17.6	96	77.3	31.2	92
165	78.4	23.5	97	78.8	25	96
166	79.9	29.4	97	80.3	31.2	96
167	76.9	26.5	94	77.3	6.2	100
168	80.6	35.3	96	77.3	25	94
169	77.6	23.5	96	69.7	6.2	90
170	79.1	29.4	96	83.1	26.7	100
171	81.3	38.2	96	75.8	31.2	90
172	76.1	23.5	94	78.8	31.2	94
173	77.6	26.5	95	81.8	43.8	94
174	76.1	20.6	95	81.8	31.2	98
175	80.6	29.4	98	78.8	18.8	98
176	79.9	26.5	98	80.3	25	98
177	79.9	29.4	97	81.8	31.2	98
178	73.1	11.8	94	78.8	18.8	98
179	76.1	17.6	96	77.3	12.5	98
180	73.1	8.8	95	78.8	12.5	100
181	76.1	29.4	92	69.7	25	84
182	76.1	20.6	95	77.3	43.8	88
183	76.9	17.6	97	78.8	12.5	100
184	77.6	20.6	97	81.8	31.2	98
185	95.5	85.3	99	93.9	75	100
186	83.6	50	95	86.4	62.5	94
187	79.1	47.1	90	80.3	43.8	92
188	79.1	41.2	92	83.1	50	93.9

(continued)

	Training cohort			Validation cohort		
SEQ ID NO:	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
189	82.1	41.2	96	87.9	62.5	96

[Table 4]

SEQ ID NO:	Discriminant coefficient	Constant term
1	1.728	21.253
2	4.247	27.391
3	4.025	37.004
4	1.997	11.064
5	3.142	30.220
6	3.455	21.479
7	7.377	95.667
8	2.889	18.733
9	2.480	18.013
10	4.837	44.847
11	2.182	14.705
12	1.260	8.443
13	2.577	18.611
14	2.990	19.980
15	5.216	48.423
16	2.157	17.534
17	3.898	31.927
18	2.959	22.467
19	5.747	60.613
20	4.475	52.095
21	2.037	14.005
22	3.204	21.819
23	5.663	46.868
24	2.397	19.749
25	3.533	26.374
26	3.637	24.242
27	3.134	17.788
28	2.259	14.444
29	3.890	28.987
30	5.510	66.435
31	3.218	18.273
32	4.013	33.740

(continued)

SEQ ID NO:	Discriminant coefficient	Constant term
33	3.829	48.615
34	2.368	14.866
35	1.648	13.802
36	2.478	16.783
37	3.608	21.816
38	2.700	21.869
39	3.045	27.546
40	2.276	22.213
41	2.830	21.434
42	8.628	108.988
43	4.284	28.951
44	2.953	20.892
45	1.831	14.542
46	2.058	19.942
47	2.788	30.680
48	3.787	36.710
49	4.284	37.394
50	2.351	23.417
51	5.582	40.862
52	3.374	33.771
53	3.304	20.643
54	3.097	20.730
55	2.087	23.779
56	4.807	48.256
57	5.366	66.548
58	4.590	60.012
59	5.385	44.281
60	4.425	25.890
61	2.238	13.151
62	3.068	21.797
63	3.019	18.844
64	2.848	19.631
65	3.913	24.472
66	4.110	31.289
67	2.450	13.850
68	2.535	19.310
69	3.143	20.245
70	2.050	19.680

(continued)

SEQ ID NO:	Discriminant coefficient	Constant term
71	5.003	49.921
72	4.868	36.163
73	5.151	55.976
74	4.628	34.855
75	4.911	36.605
76	4.102	25.952
77	2.468	22.972
78	3.620	23.145
79	4.177	33.363
80	2.569	17.652
81	3.560	30.479
82	3.219	18.791
83	1.409	7.771
84	4.626	27.715
85	2.981	26.017
86	4.075	49.126
87	5.860	70.045
88	4.518	45.735
89	3.376	31.771
90	1.504	10.293
91	2.408	17.120
92	3.741	22.446
93	4.216	28.494
94	2.433	17.718
95	3.691	36.766
96	4.011	23.884
97	2.738	15.840
98	6.279	44.218
99	3.821	29.214
100	3.138	31.313
101	4.137	33.060
102	3.184	30.108
103	3.013	31.561
104	3.467	28.752
105	3.228	28.241
106	3.979	27.890
107	6.059	77.100
108	3.680	26.849

(continued)

SEQ ID NO:	Discriminant coefficient	Constant term
109	4.631	30.402
110	1.394	8.449
111	6.759	64.607
112	1.409	7.968
113	3.162	19.071
114	5.990	73.977
115	5.334	38.106
116	1.456	8.354
117	4.005	39.314
118	3.960	26.029
119	2.965	22.212
120	4.191	46.456
121	3.073	19.231
122	4.802	55.520
123	6.630	56.690
124	4.376	32.100
125	3.860	25.003
126	2.820	18.115
127	2.803	28.773
128	2.467	17.131
129	2.799	21.018
130	1.014	8.569
131	3.279	24.306
132	2.463	15.756
133	5.281	36.256
134	4.856	33.829
135	4.127	34.385
136	2.446	18.351
137	3.464	30.213
138	3.758	39.142
139	3.002	17.723
140	6.638	74.011
141	2.417	18.061
142	2.771	29.864
143	4.044	31.341
144	5.475	55.815
145	1.996	18.798
146	4.966	60.960

(continued)

SEQ ID NO:	Discriminant coefficient	Constant term
147	3.897	45.041
148	2.189	18.504
149	5.725	48.947
150	1.479	9.192
151	4.007	30.769
152	2.375	17.501
153	3.148	34.147
154	4.614	45.732
155	3.496	28.749
156	3.223	36.168
157	3.880	43.759
158	2.161	22.836
159	4.249	36.373
160	3.372	40.014
161	2.156	12.836
162	3.830	25.976
163	4.148	26.395
164	3.013	19.353
165	4.848	51.132
166	3.658	41.969
167	2.809	19.310
168	5.360	42.861
169	3.044	20.270
170	2.349	21.153
171	5.182	58.972
172	4.905	38.453
173	2.327	16.003
174	2.883	20.522
175	2.041	15.621
176	4.697	39.475
177	3.841	27.790
178	3.535	28.077
179	3.283	21.183
180	4.096	26.607
181	7.491	103.673
182	5.921	55.473
183	3.240	30.496
184	3.873	27.506

(continued)

SEQ ID NO:	Discriminant coefficient	Constant term
185	1.385	7.776
186	1.393	7.911
187	1.816	11.959
188	3.362	20.857
189	1.031	6.129

[Table 5-1]

Training cohort			
Sample name	Cancer stage	CEA(ng/mL)	SCC(ng/mL)
EC03	IIIB	4	42.2
EC04	IIIB	3.1	1
EC05	IB	6.2	1.9
EC06	(yp) IIA	3.3	1
EC07	IIB	0.7	1
EC09	IIB	2	14.7
EC10	(yp) IIB	1.6	0.9
EC12	IIB	3.3	1.2
EC13	IIIB	1	6
EC15	IIIA	2.7	2.4
EC17	IIIC	4	2.1
EC18	IIIA	4.6	3.2
EC19	IIIC	1.3	3.8
EC20	IIIB	2.5	1.5
EC23	(yp) IIIC	4	0.7
EC24	IIIB	5	1
EC25	IIA	なし	なし
EC26	(yp) IIB	1.4	0.9
EC27	(yp) IIIA	4.8	2.1
EC29	(yp) IIIA	3.1	0.8
EC30	IIIB	3.6	0.6
EC31	IB	4.7	0.9
EC32	(yp) IIIA	0.5	1.3
EC34	IIIA	3.6	0.7
EC36	IIIA	4.1	1.2
EC38	(yp) IIA	2.3	3.4
EC40	IIB	6.6	1.6
EC41	(yp) IIIA	14.2	1.3

(continued)

Training cohort			
Sample name	Cancer stage	CEA(ng/mL)	SCC(ng/mL)
EC42	IIB	5.2	1.2
EC45	(yp) IA	3.1	0.6
EC47	IIIB	2.9	1
EC48	IB	4	1.5
EC49	(yp) IIA	1.8	8
EC50	(yp) IIIA	1.7	1.2
	Sensitivity	12.1%	36.4%

[Table 5-2]

Validation cohort			
Sample name	Cancer stage	CEA(ng/mL)	SCC(ng/mL)
EC01	(yp) IIA	1.6	1.3
EC02	IIA	1.3	2.4
EC08	IIIA	2.1	1.1
EC11	(yp) IV	1.8	1
EC14	IIA	7.2	1.2
EC16	(yp) IIIA	6.3	0.9
EC21	IIA	3.2	2.4
EC22	(yp) IIA	4.3	2.9
EC28	IIIA	1.6	0.1
EC33	(yp) IIIC	2.1	1.9
EC35	IIIC	1.6	0.6
EC37	(yp) IIIA	2.1	1
EC39	(yp) IA	1.8	9.1
EC43	IIIC	6.6	1.3
EC44	(yp) IIIB	2.2	11.2
EC46	(yp) 0	0.7	0.6
	Sensitivity	18.8%	37.5%

Each sample that exhibited a value equal to or higher than the reference value of each tumor marker (for CEA: 5 ng/mL, SCC: 1.5 ng/mL) was confirmed to be positive (+), and each sample that exhibited a value equal to or lower than the reference value was confirmed to be negative (-). The cancer stages were classified using samples collected before treatment, as a rule, except that samples stage-classified by pathological examination after treatment were represented by "yp".

[Table 6]

	Training cohort			Validation cohort		
SEQ ID NO:	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
1_2	98.5	94.1	100	98.5	93.8	100

(continued)

	Training cohort			Validation cohort		
SEQ ID NO:	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
1_3	96.3	88.2	99	92.4	87.5	94
1_4	95.5	85.3	99	93.9	93.8	94
1_5	95.5	88.2	98	93.9	87.5	96
1_6	95.5	82.4	100	98.5	100	98
1_7	96.3	85.3	100	93.9	93.8	94
1_8	99.3	97.1	100	93.9	93.8	94
1_9	98.5	100	98	95.5	100	94
1_10	96.3	88.2	99	97	93.8	98
1_11	97	88.2	100	97	93.8	98
1_12	94.8	82.4	99	93.9	87.5	96
1_13	94	82.4	98	95.5	100	94
1_14	96.3	88.2	99	97	100	96
1_15	94	82.4	98	95.5	93.8	96
1_16	94	79.4	99	93.9	87.5	96
1_17	96.3	85.3	100	92.4	87.5	94
1_18	97	88.2	100	95.5	87.5	98
1_19	96.3	85.3	100	95.5	93.8	96
1_20	96.3	88.2	99	97	93.8	98
1_21	97	88.2	100	98.5	93.8	100
1_22	98.5	94.1	100	92.4	93.8	92
1_23	96.3	85.3	100	92.4	87.5	94
1_24	96.3	85.3	100	93.9	87.5	96
1_25	95.5	82.4	100	92.4	87.5	94
1_26	94.8	82.4	99	92.4	87.5	94
1_27	95.5	85.3	99	95.5	93.8	96
1_28	93.3	76.5	99	93.9	87.5	96
1_29	94.8	79.4	100	92.4	87.5	94
1_30	97.8	91.2	100	95.5	93.8	96
1_31	95.5	85.3	99	92.4	87.5	94
1_32	95.5	85.3	99	93.9	87.5	96
1_33	95.5	82.4	100	89.4	87.5	90
1_34	97.8	91.2	100	97	87.5	100
1_35	96.3	85.3	100	93.9	87.5	96
1_36	94.8	82.4	99	93.9	87.5	96
1_37	95.5	85.3	99	93.9	87.5	96
1_38	95.5	85.3	99	93.9	93.8	94
1_39	97.8	94.1	99	95.5	87.5	98

(continued)

	Training cohort			Validation cohort		
SEQ ID NO:	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
1_40	99.3	97.1	100	98.5	93.8	100
1_41	94.8	82.4	99	93.9	87.5	96
1_42	94.8	85.3	98	95.5	87.5	98
1_43	94.8	85.3	98	93.9	93.8	94
1_44	97.8	91.2	100	97	93.8	98
1_45	95.5	85.3	99	92.4	87.5	94
1_46	95.5	82.4	100	95.5	87.5	98
1_47	97	88.2	100	93.9	87.5	96
1_48	95.5	82.4	100	93.9	87.5	96
1_49	94	79.4	99	95.5	87.5	98
1_50	95.5	85.3	99	92.4	93.8	92
1_51	95.5	82.4	100	92.4	87.5	94
1_52	95.5	82.4	100	95.5	93.8	96
1_53	97	88.2	100	90.9	87.5	92
1_54	96.3	88.2	99	95.5	87.5	98
1_55	95.5	82.4	100	95.5	87.5	98
1_56	96.3	88.2	99	93.9	93.8	94
1_57	95.5	85.3	99	89.4	93.8	88
1_58	97.8	94.1	99	97	100	96
1_59	96.3	85.3	100	95.5	100	94
1_60	94.8	82.4	99	87.9	81.2	90
1_61	97.8	91.2	100	98.5	93.8	100
1_62	95.5	84.8	99	93.9	87.5	96
1_63	96.3	88.2	99	93.9	87.5	96
1_64	97	88.2	100	93.9	87.5	96
1_65	97	91.2	99	92.4	93.8	92
1_66	94	79.4	99	90.9	87.5	92
1_67	94	79.4	99	92.4	81.2	96
1_68	94.8	82.4	99	92.4	87.5	94
1_69	96.3	85.3	100	92.4	87.5	94
1_70	94.8	79.4	100	95.5	87.5	98
1_71	96.3	88.2	99	95.5	93.8	96
1_72	94.8	85.3	98	90.9	93.8	90
1_73	94.8	85.3	98	92.4	87.5	94
1_74	94.8	82.4	99	93.9	93.8	94
1_75	94	82.4	98	92.4	87.5	94
1_76	94	79.4	99	95.5	93.8	96

(continued)

	Training cohort			Validation cohort		
SEQ ID NO:	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
1_77	96.3	85.3	100	90.9	87.5	92
1_78	95.5	85.3	99	93.9	93.8	94
1_79	94.8	79.4	100	89.4	87.5	90
1_80	96.3	85.3	100	93.9	87.5	96
1_81	94	79.4	99	89.4	87.5	90
1_82	94.8	85.3	98	92.4	93.8	92
1_83	94	79.4	99	95.5	87.5	98
1_84	94.8	82.4	99	93.9	87.5	96
1_85	96.3	85.3	100	92.4	87.5	94
1_86	96.3	88.2	99	95.5	93.8	96
1_87	95.5	82.4	100	90.9	81.2	94
1_88	95.5	82.4	100	93.9	87.5	96
1_89	95.5	85.3	99	90.9	87.5	92
1_90	94	79.4	99	93.9	87.5	96
1_91	94.8	79.4	100	93.9	87.5	96
1_92	93.2	76.5	99	92.4	87.5	94
1_93	94.8	82.4	99	92.4	87.5	94
1_94	94.8	79.4	100	89.4	87.5	90
1_95	96.3	85.3	100	90.9	87.5	92
1_96	94	79.4	99	92.4	81.2	96
1_97	96.3	85.3	100	93.9	87.5	96
1_98	95.5	82.4	100	95.5	93.8	96
1_99	95.5	85.3	99	93.9	93.8	94
1_100	94.8	79.4	100	92.4	87.5	94
1_101	95.5	85.3	99	95.5	93.8	96
1_102	95.5	82.4	100	92.4	93.8	92
1_103	96.3	85.3	100	89.4	93.8	88
1_104	96.3	85.3	100	97	93.8	98
1_105	95.5	88.2	98	92.4	87.5	94
1_106	94.8	82.4	99	92.4	87.5	94
1_107	95.5	85.3	99	90.9	81.2	94
1_108	95.5	85.3	99	89.4	93.8	88
1_109	96.3	85.3	100	93.9	87.5	96
1_110	94	79.4	99	95.5	93.8	96
1_111	94	79.4	99	90.9	81.2	94
1_112	94	79.4	99	93.9	87.5	96
1_113	93.3	79.4	98	93.9	87.5	96

(continued)

	Training cohort			Validation cohort		
SEQ ID NO:	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
1_114	97	88.2	100	93.9	87.5	96
1_115	95.5	82.4	100	90.9	87.5	92
1_116	94	79.4	99	92.4	81.2	96
1_117	94.8	82.4	99	93.9	87.5	96
1_118	94.8	82.4	99	93.9	87.5	96
1_119	95.5	85.3	99	95.5	93.8	96
1_120	94.8	82.4	99	95.5	93.8	96
1_121	94	79.4	99	90.9	87.5	92
1_122	94	79.4	99	92.4	87.5	94
1_123	94.8	79.4	100	93.9	87.5	96
1_124	94	79.4	99	93.9	87.5	96
1_125	94.8	82.4	99	92.4	87.5	94
1_126	96.3	85.3	100	93.9	87.5	96
1_127	96.3	85.3	100	92.4	93.8	92
1_128	96.3	88.2	99	92.4	87.5	94
1_129	95.5	82.4	100	89.4	81.2	92
1_130	94	79.4	99	92.4	87.5	94
1_131	94	79.4	99	95.5	87.5	98
1_132	95.5	82.4	100	93.9	93.8	94
1_133	94	79.4	99	95.5	87.5	98
1_134	97	91.2	99	93.9	87.5	96
1_135	94.8	82.4	99	93.9	87.5	96
1_136	95.5	82.4	100	95.5	87.5	98
1_137	97.8	91.2	100	92.4	87.5	94
1_138	96.3	85.3	100	97	93.8	98
1_139	95.5	82.4	100	90.9	81.2	94
1_140	94	79.4	99	92.4	81.2	96
1_141	94.8	82.4	99	92.4	87.5	94
1_142	95.5	85.3	99	90.9	87.5	92
1_143	95.5	82.4	100	92.4	87.5	94
1_144	94	79.4	99	92.4	81.2	96
1_145	94.8	82.4	99	95.5	87.5	98
1_146	94	79.4	99	92.4	87.5	94
1_147	95.5	85.3	99	93.9	93.8	94
1_148	94.8	79.4	100	93.9	87.5	96
1_149	94	79.4	99	95.5	87.5	98
1_150	96.3	85.3	100	90.9	81.2	94

(continued)

	Training cohort			Validation cohort		
SEQ ID NO:	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
1_151	95.5	82.4	100	93.9	87.5	96
1_152	93.3	79.4	98	93.9	87.5	96
1_153	96.3	88.2	99	95.5	87.5	98
1_154	94.8	82.4	99	89.4	81.2	92
1_155	97	88.2	100	98.5	93.8	100
1_156	94	79.4	99	90.9	81.2	94
1_157	93.3	79.4	98	90.9	87.5	92
1_158	94	82.4	98	95.5	87.5	98
1_159	94.8	79.4	100	92.4	87.5	94
1_160	95.5	82.4	100	92.4	93.8	92
1_161	94	79.4	99	93.9	87.5	96
1_162	94	79.4	99	93.9	87.5	96
1_163	94.8	82.4	99	93.9	87.5	96
1_164	94.8	82.4	99	92.4	87.5	94
1_165	95.5	82.4	100	93.9	87.5	96
1_166	94.8	79.4	100	95.5	87.5	98
1_167	96.3	85.3	100	93.9	81.2	98
1_168	94.8	79.4	100	92.4	87.5	94
1_169	96.3	85.3	100	92.4	81.2	96
1_170	96.3	88.2	99	92.3	86.7	94
1_171	94.8	82.4	99	92.4	81.2	96
1_172	95.5	85.3	99	95.5	87.5	98
1_173	94.8	79.4	100	92.4	81.2	96
1_174	95.5	85.3	99	95.5	93.8	96
1_175	95.5	82.4	100	90.9	81.2	94
1_176	94.8	82.4	99	93.9	93.8	94
1_177	95.5	82.4	100	93.9	93.8	94
1_178	94	79.4	99	92.4	81.2	96
1_179	94	79.4	99	92.4	87.5	94
1_180	94.8	82.4	99	92.4	81.2	96
1_181	94	79.4	99	93.9	87.5	96
1_182	94.8	85.3	98	92.4	87.5	94
1_183	94	79.4	99	95.5	93.8	96
1_184	94.8	79.4	100	93.9	87.5	96
1_185	95.5	85.3	99	97	87.5	100
1_186	94.8	79.4	100	95.5	87.5	98
1_187	94	79.4	99	93.9	87.5	96

(continued)

	Training cohort			Validation cohort		
SEQ ID NO:	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
1_188	94	79.4	99	93.8	93.8	93.9
1_189	94.8	79.4	100	93.9	87.5	96

[Example 3]

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

[0641] In this Example, the samples of 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 esophageal cancer discriminant performance were conducted using any of the samples.

[0642] Specifically, the miRNA expression levels in the sera of the 50 esophageal cancer patients and the 150 healthy subjects obtained in the preceding Reference Examples were normalized by quantile normalization. In order to acquire diagnosis 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 esophageal cancer patient group or the healthy subject group were selected in the gene marker selection. In order to further acquire statistical significance for discriminating an esophageal 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 described in Table 7. In this way, hsa-miR-675-5p, hsa-miR-486-3p, hsa-miR-6777-5p, hsa-miR-4497, hsa-miR-296-3p, hsa-miR-6738-5p, hsa-miR-4731-5p, hsa-miR-6889-5p, hsa-miR-6786-5p, hsa-miR-92a-3p, hsa-miR-4294, hsa-miR-4763-3p, hsa-miR-6076, hsa-miR-663a, hsa-miR-760, hsa-miR-4667-5p, hsa-miR-6090, hsa-miR-4730, hsa-miR-7106-5p, hsa-miR-3196, hsa-miR-5698, hsa-miR-6087, hsa-miR-4665-5p, hsa-miR-8059 and hsa-miR-6879-5p genes, and the nucleotide sequences represented by SEQ ID NOs: 190 to 214 related thereto were found in addition to the genes described in Table 2. As with the nucleotide sequences of SEQ ID NOs: 1 to 189, the results obtained about the polynucleotides shown in the nucleotide sequences of SEQ ID NOs: 190 to 214 also showed that the gene measurement values were significantly lower (-) or higher (+) in the esophageal cancer patient group than in the healthy subject group (Table 7). These results were able to be validated in the validation cohort. Thus, the presence or absence of esophageal 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 7 either alone or in combination with the gene expression level measurement values described in Table 2.

[Table 7]

SEQ ID NO:	Gene name	P value after Bonferroni correction	Expression level in esophageal cancer patient relative to healthy subject
1	hsa-miR-204-3p	8.14E-45	+
2	hsa-miR-1247-3p	1.36E-45	-
3	hsa-miR-6875-5p	6.12E-37	-
4	hsa-miR-6857-5p	1.04E-39	+
5	hsa-miR-6726-5p	7.48E-40	+
6	hsa-miR-3188	6.76E-39	-
7	hsa-miR-8069	1.65E-29	+
8	hsa-miR-4257	1.79E-35	-
9	hsa-miR-1343-3p	1.95E-36	+
10	hsa-miR-7108-5p	1.78E-35	+
11	hsa-miR-6825-5p	4.35E-36	-
12	hsa-miR-7641	1.73E-34	-

(continued)

SEQ ID NO:	Gene name	P value after Bonferroni correction	Expression level in esophageal cancer patient relative to healthy subject
13	hsa-miR-3185	1.35E-33	+
14	hsa-miR-4746-3p	4.69E-34	+
15	hsa-miR-6791-5p	5.41E-32	+
16	hsa-miR-6893-5p	6.65E-32	+
17	hsa-miR-4433b-3p	7.92E-29	+
18	hsa-miR-3135b	9.14E-25	-
19	hsa-miR-6781-5p	1.02E-32	+
20	hsa-miR-1908-5p	1.06E-32	+
21	hsa-miR-4792	7.47E-32	+
22	hsa-miR-7845-5p	6.13E-29	+
23	hsa-miR-4417	1.23E-29	+
24	hsa-miR-3184-5p	1.98E-30	+
25	hsa-miR-1225-5p	1.13E-30	+
26	hsa-miR-1231	1.73E-26	+
27	hsa-miR-1225-3p	4.81E-30	+
28	hsa-miR-150-3p	9.61E-24	+
29	hsa-miR-4433-3p	1.64E-27	+
30	hsa-miR-6125	7.40E-28	+
31	hsa-miR-4513	1.69E-23	+
32	hsa-miR-6787-5p	3.22E-27	-
33	hsa-miR-6784-5p	4.73E-27	+
34	hsa-miR-615-5p	9.34E-26	-
35	hsa-miR-6765-3p	7.95E-27	+
36	hsa-miR-5572	1.59E-27	-
37	hsa-miR-6842-5p	2.94E-27	-
38	hsa-miR-8063	1.48E-26	+
39	hsa-miR-6780b-5p	3.59E-29	-
40	hsa-miR-187-5p	8.52E-25	-
41	hsa-miR-128-1-5p	5.67E-21	-
42	hsa-miR-6729-5p	1.04E-26	-
43	hsa-miR-6741-5p	7.62E-23	+
44	hsa-miR-6757-5p	1.84E-26	+
45	hsa-miR-7110-5p	1.82E-24	+
46	hsa-miR-7975	8.82E-24	-
47	hsa-miR-1233-5p	1.28E-26	-
48	hsa-miR-6845-5p	3.06E-24	-
49	hsa-miR-3937	7.00E-24	-

(continued)

SEQ ID NO:	Gene name	P value after Bonferroni correction	Expression level in esophageal cancer patient relative to healthy subject
50	hsa-miR-4467	5.02E-23	+
51	hsa-miR-7109-5p	2.70E-17	-
52	hsa-miR-6088	3.91E-22	-
53	hsa-miR-6782-5p	1.72E-19	-
54	hsa-miR-5195-3p	8.97E-24	-
55	hsa-miR-4454	9.04E-23	+
56	hsa-miR-6724-5p	5.74E-19	-
57	hsa-miR-8072	6.96E-19	+
58	hsa-miR-4516	6.08E-22	-
59	hsa-miR-6756-5p	5.52E-19	-
60	hsa-miR-4665-3p	3.30E-20	-
61	hsa-miR-6826-5p	2.65E-21	+
62	hsa-miR-6820-5p	1.83E-18	+
63	hsa-miR-6887-5p	7.93E-19	-
64	hsa-miR-3679-5p	1.14E-21	-
65	hsa-miR-7847-3p	2.20E-20	-
66	hsa-miR-6721-5p	3.96E-16	+
67	hsa-miR-3622a-5p	1.78E-18	+
68	hsa-miR-939-5p	1.12E-17	-
69	hsa-miR-602	9.30E-19	+
70	hsa-miR-7977	4.08E-19	-
71	hsa-miR-6749-5p	2.11E-19	-
72	hsa-miR-1914-3p	3.49E-15	-
73	hsa-miR-4651	9.97E-21	-
74	hsa-miR-4695-5p	1.01E-17	+
75	hsa-miR-6848-5p	1.96E-16	+
76	hsa-miR-1228-3p	1.45E-17	+
77	hsa-miR-642b-3p	3.30E-17	+
78	hsa-miR-6746-5p	2.40E-18	-
79	hsa-miR-3620-5p	3.16E-15	+
80	hsa-miR-3131	1.67E-20	-
81	hsa-miR-6732-5p	3.23E-17	+
82	hsa-miR-7113-3p	6.47E-18	+
83	hsa-miR-23a-3p	1.75E-15	+
84	hsa-miR-3154	3.86E-14	+
85	hsa-miR-4723-5p	4.11E-15	-
86	hsa-miR-3663-3p	6.62E-16	-

(continued)

SEQ ID NO:	Gene name	P value after Bonferroni correction	Expression level in esophageal cancer patient relative to healthy subject
87	hsa-miR-4734	9.47E-16	+
88	hsa-miR-6816-5p	1.28E-16	-
89	hsa-miR-4442	9.49E-16	+
90	hsa-miR-4476	9.75E-16	-
91	hsa-miR-423-5p	6.53E-13	+
92	hsa-miR-1249	3.05E-15	-
93	hsa-miR-6515-3p	9.05E-12	-
94	hsa-miR-887-3p	1.74E-15	+
95	hsa-miR-4741	9.67E-16	+
96	hsa-miR-6766-3p	2.28E-14	-
97	hsa-miR-4673	2.15E-14	-
98	hsa-miR-6779-5p	3.15E-13	+
99	hsa-miR-4706	8.59E-16	+
100	hsa-miR-1268b	1.75E-14	+
101	hsa-miR-4632-5p	4.72E-14	-
102	hsa-miR-3197	6.20E-15	+
103	hsa-miR-6798-5p	1.13E-12	+
104	hsa-miR-711	1.63E-16	-
105	hsa-miR-6840-3p	1.79E-12	+
106	hsa-miR-6763-5p	1.13E-12	+
107	hsa-miR-6727-5p	1.88E-15	+
108	hsa-miR-371a-5p	5.18E-12	+
109	hsa-miR-6824-5p	1.52E-13	+
110	hsa-miR-4648	8.82E-15	-
111	hsa-miR-1227-5p	3.56E-11	-
112	hsa-miR-564	4.80E-13	-
113	hsa-miR-3679-3p	1.57E-12	-
114	hsa-miR-2861	7.34E-13	+
115	hsa-miR-6737-5p	5.72E-09	+
116	hsa-miR-575	2.07E-11	-
117	hsa-miR-4725-3p	1.06E-13	+
118	hsa-miR-6716-5p	2.52E-11	+
119	hsa-miR-4675	2.03E-14	-
120	hsa-miR-1915-3p	1.35E-13	+
121	hsa-miR-671-5p	1.87E-11	+
122	hsa-miR-3656	7.58E-11	-
123	hsa-miR-6722-3p	9.17E-11	+

(continued)

SEQ ID NO:	Gene name	P value after Bonferroni correction	Expression level in esophageal cancer patient relative to healthy subject
124	hsa-miR-4707-5p	1.41E-12	-
125	hsa-miR-4449	4.22E-12	+
126	hsa-miR-1202	1.28E-12	-
127	hsa-miR-4649-5p	8.69E-11	-
128	hsa-miR-744-5p	9.90E-11	-
129	hsa-miR-642a-3p	1.42E-09	+
130	hsa-miR-451a	3.46E-12	+
131	hsa-miR-6870-5p	2.08E-12	+
132	hsa-miR-4443	5.77E-08	-
133	hsa-miR-6808-5p	9.18E-07	+
134	hsa-miR-4728-5p	2.27E-11	+
135	hsa-miR-937-5p	1.97E-08	+
136	hsa-miR-135a-3p	1.01E-07	+
137	hsa-miR-663b	1.89E-09	+
138	hsa-miR-1343-5p	1.68E-10	+
139	hsa-miR-6822-5p	2.82E-09	-
140	hsa-miR-6803-5p	8.05E-07	-
141	hsa-miR-6805-3p	6.65E-10	-
142	hsa-miR-128-2-5p	8.46E-10	+
143	hsa-miR-4640-5p	1.16E-10	+
144	hsa-miR-1469	2.15E-07	+
145	hsa-miR-92a-2-5p	4.30E-10	-
146	hsa-miR-3940-5p	2.18E-07	-
147	hsa-miR-4281	2.04E-08	-
148	hsa-miR-1260b	1.61E-08	-
149	hsa-miR-4758-5p	3.25E-08	-
150	hsa-miR-1915-5p	1.01E-07	+
151	hsa-miR-5001-5p	1.96E-08	-
152	hsa-miR-4286	4.72E-07	+
153	hsa-miR-6126	3.16E-09	+
154	hsa-miR-6789-5p	8.38E-08	-
155	hsa-miR-4459	3.24E-08	-
156	hsa-miR-1268a	5.97E-07	+
157	hsa-miR-6752-5p	5.95E-06	-
158	hsa-miR-6131	1.52E-07	+
159	hsa-miR-6800-5p	1.75E-07	+
160	hsa-miR-4532	2.82E-05	+

(continued)

SEQ ID NO:	Gene name	P value after Bonferroni correction	Expression level in esophageal cancer patient relative to healthy subject
161	hsa-miR-6872-3p	5.54E-07	-
162	hsa-miR-718	3.56E-05	-
163	hsa-miR-6769a-5p	2.25E-06	-
164	hsa-miR-4707-3p	5.95E-07	-
165	hsa-miR-6765-5p	6.88E-07	-
166	hsa-miR-4739	5.13E-06	+
167	hsa-miR-4525	1.01E-06	+
168	hsa-miR-4270	2.71E-05	+
169	hsa-miR-4534	0.000121	-
170	hsa-miR-6785-5p	1.06E-06	+
171	hsa-miR-6850-5p	6.01E-05	+
172	hsa-miR-4697-5p	9.68E-08	+
173	hsa-miR-1260a	7.59E-07	-
174	hsa-miR-4486	6.56E-06	-
175	hsa-miR-6880-5p	8.38E-07	-
176	hsa-miR-6802-5p	4.43E-06	-
177	hsa-miR-6861-5p	4.72E-06	-
178	hsa-miR-92b-5p	5.54E-05	+
179	hsa-miR-1238-5p	1.21E-05	+
180	hsa-miR-6851-Sp	6.80E-06	+
182	hsa-miR-149-3p	4.63E-07	-
183	hsa-miR-4689	6.67E-06	+
184	hsa-miR-4688	4.38E-07	+
185	hsa-miR-125a-3p	7.44E-39	-
186	hsa-miR-23b-3p	4.37E-18	-
187	hsa-miR-614	3.43E-14	+
188	hsa-miR-1913	2.99E-12	+
189	hsa-miR-16-5p	1.45E-08	+
190	hsa-miR-675-5p	5.72E-07	-
191	hsa-miR-486-3p	2.23E-04	-
192	hsa-miR-6777-5p	3.28E-04	-
193	hsa-miR-4497	3.90E-04	-
194	hsa-miR-296-3p	4.06E-04	-
195	hsa-miR-6738-5p	4.53E-04	-
196	hsa-miR-4731-5p	5.31E-04	-
197	hsa-miR-6889-5p	6.59E-04	+
198	hsa-miR-6786-5p	6.60E-04	+

(continued)

SEQ ID NO:	Gene name	P value after Bonferroni correction	Expression level in esophageal cancer patient relative to healthy subject
199	hsa-miR-92a-3p	1.13E-03	-
200	hsa-miR-4294	1.17E-03	-
201	hsa-miR-4763-3p	1.35E-03	+
202	hsa-miR-6076	1.38E-03	+
203	hsa-miR-663a	1.52E-03	+
204	hsa-miR-760	2.13E-03	+
205	hsa-miR-4667-5p	2.18E-03	+
206	hsa-miR-6090	2.38E-03	+
207	hsa-miR-4730	2.79E-03	+
208	hsa-miR-7106-5p	2.80E-03	-
209	hsa-miR-3196	3.86E-03	+
210	hsa-miR-5698	4.60E-03	-
211	hsa-miR-6087	5.73E-03	-
212	hsa-miR-4665-5p	5.91E-03	-
213	hsa-miR-8059	8.38E-03	-
214	hsa-miR-6879-5p	8.44E-03	+

[Example 4]

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

[0643] In this Example, gene markers for diagnosis were selected by comparing gene expression levels of miRNAs in serum of esophageal cancer patients with that of a control group consisting of healthy subjects, pancreatic cancer patients, bile duct cancer patients, colorectal cancer patients, stomach 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 described in Reference Example 2. The polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 666 to 676 thus newly selected were further combined with the polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 214 to study a method for evaluating pancreatic cancer-specific discriminant performance.

[0644] Specifically, first, the miRNA expression levels in the training cohort and the validation cohort obtained in Reference Example 2 mentioned above 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 of the expression level measurement values of the polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 214 and 666 to 676, to construct a discriminant for determining the presence or absence of esophageal cancer. Next, accuracy, sensitivity, and specificity in the validation cohort were calculated using the discriminant thus prepared, with the esophageal 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 colorectal cancer patient group, the stomach cancer patient group, the liver cancer patient group, and the benign pancreaticobiliary disease patient group as a negative sample groups. The discriminant performance of the selected polynucleotides was validated using the independent samples.

[0645] Most of polynucleotides consisting of the nucleotide sequences represented by these SEQ ID NOs: 1 to 214 and 666 to 676 or complementary sequences thereof were able to provide relatively high accuracy, sensitivity, and specificity in the determination of the presence or absence of esophageal cancer, and furthermore, were able to specifically discriminate esophageal cancer from the other cancers. For example, at least one polynucleotide selected from the group consisting of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1, 2, 5, 8,

22, 32, 33, 35, 43, 44, 56, 85, 98, 106, 109, 115, 121, 126, 133, 138, 155, 157, 166, 177, 179, 185, 202, 212, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675 and 676 or complementary sequences thereof (the cancer type-specific polynucleotide group 1) was able to specifically bind to the target marker.

[0646] Among the combinations of multiple polynucleotides selected from cancer type-specific polynucleotide group 1, particularly, combinations comprising at least one polynucleotide selected from the group consisting of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1, 22, 85, 109, 121, 126, 133, 138, 166, and 666 or complementary sequences thereof (the cancer type-specific polynucleotide group 2) were able to specifically discriminate esophageal cancer from the other cancers with high accuracy.

[0647] The number of the polynucleotides with cancer type specificity in the combination described above 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 85% or higher. Specific results about the discrimination accuracy of the measurement using each polynucleotide in the cancer type-specific polynucleotide group 2 will be described below.

[0648] The discriminant accuracy of the measurement using the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 1 or a complementary sequence thereof is shown in Table 8-1. The measurement using the combination of one polynucleotide comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 1 or a complementary sequence thereof exhibited accuracy of 65.4% in the training cohort and accuracy of 65.4% 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: 1 or a complementary sequence thereof exhibited the highest accuracy of 78.3% in the training cohort and accuracy of 77.7% 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: 1 or a complementary sequence thereof exhibited the highest accuracy of 85.9% in the training cohort and accuracy of 79.8% 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: 1 or a complementary sequence thereof exhibited the highest accuracy of 89.2% in the training cohort and accuracy of 88.8% 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: 1 or a complementary sequence thereof exhibited the highest accuracy of 91.1% in the training cohort and accuracy of 90.4% 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: 1 or a complementary sequence thereof exhibited the highest accuracy of 92.7% in the training cohort and accuracy of 93.1 % in the validation cohort.

[0649] The discriminant accuracy of the measurement using the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 22 or a complementary sequence thereof is shown in Table 8-2. The measurement using the combination of one polynucleotide comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 22 or a complementary sequence thereof exhibited accuracy of 70.9% in the training cohort and accuracy of 69.1% 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: 22 or a complementary sequence thereof exhibited the highest accuracy of 83.0% in the training cohort and accuracy of 77.7% 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: 22 or a complementary sequence thereof exhibited the highest accuracy of 86.9% in the training cohort and accuracy of 81.9% 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: 22 or a complementary sequence thereof exhibited the highest accuracy of 89.3% in the training cohort and accuracy of 87.2% 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: 22 or a complementary sequence thereof exhibited the highest accuracy of 91.4% in the training cohort and accuracy of 86.7% 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: 22 or a complementary sequence thereof exhibited the highest accuracy of 91.9% in the training cohort and accuracy of 90.4% in the validation cohort.

[0650] The discriminant accuracy of the measurement using the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 85 or a complementary sequence thereof is shown in Table 8-3. The measurement using the combination of one polynucleotide comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 85 or a complementary sequence thereof exhibited accuracy of 65.2% in the training cohort and accuracy of 61.2% 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: 85 or a complementary sequence thereof exhibited the highest accuracy of 79.1% in the training cohort and accuracy of 77.1% 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: 85 or a complementary sequence thereof exhibited the highest accuracy of 84.3% in the training cohort and accuracy of 78.1% 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: 85 or a complementary sequence thereof exhibited the highest accuracy of 88.5% in the training cohort and accuracy of 88.8% 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: 85 or a complementary sequence thereof exhibited the highest accuracy of 90.8% in the training cohort and accuracy of 91.0% 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: 85 or a complementary sequence thereof exhibited the highest accuracy of 91.6% in the training cohort and accuracy of 91.0% in the validation cohort.

[0651] The discriminant accuracy of the measurement using the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 109 or a complementary sequence thereof is shown in Table 8-4. The measurement using the combination of one polynucleotide comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 109 or a complementary sequence thereof exhibited accuracy of 57.6% in the training cohort and accuracy of 54.8% 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: 109 or a complementary sequence thereof exhibited the highest accuracy of 83.0% in the training cohort and accuracy of 76.1% 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: 109 or a complementary sequence thereof exhibited the highest accuracy of 85.9% in the training cohort and accuracy of 81.9% 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: 109 or a complementary sequence thereof exhibited the highest accuracy of 88.7% in the training cohort and accuracy of 84.5% 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: 109 or a complementary sequence thereof exhibited the highest accuracy of 91.1% in the training cohort and accuracy of 90.4% 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: 109 or a complementary sequence thereof exhibited the highest accuracy of 91.9% in the training cohort and accuracy of 90.4% in the validation cohort.

[0652] The discriminant accuracy of the measurement using the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 121 or a complementary sequence thereof is shown in Table 8-5. The measurement using the combination of one polynucleotide comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 121 or a complementary sequence thereof exhibited accuracy of 72.3% in the training cohort and accuracy of 67.6% 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: 121 or a complementary sequence thereof exhibited the highest accuracy of 81.9% in the training cohort and accuracy of 73.9% 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: 121 or a complementary sequence thereof exhibited the highest accuracy of 86.1% in the training cohort and accuracy of 79.7% 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: 121 or a complementary sequence thereof exhibited the highest accuracy of 89.0% in the training cohort and accuracy of 83.0% 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: 121 or a complementary sequence thereof exhibited the highest accuracy of 91.4% in the training cohort and accuracy of 86.2% 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: 121 or a complementary sequence thereof exhibited the highest accuracy of 91.6% in the training cohort and accuracy of 89.9% in the validation cohort.

[0653] The discriminant accuracy of the measurement using the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 126 or a complementary sequence thereof is shown in Table 8-6. The measurement using the combination of one polynucleotide comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 126 or a complementary sequence thereof exhibited accuracy of 73.6% in the training

cohort and accuracy of 66.0% 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: 126 or a complementary sequence thereof exhibited the highest accuracy of 83.5% in the training cohort and accuracy of 76.1% 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: 126 or a complementary sequence thereof exhibited the highest accuracy of 88.5% in the training cohort and accuracy of 79.8% 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: 126 or a complementary sequence thereof exhibited the highest accuracy of 89.8% in the training cohort and accuracy of 84.0% 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: 126 or a complementary sequence thereof exhibited the highest accuracy of 91.1% in the training cohort and accuracy of 91.5% 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: 126 or a complementary sequence thereof exhibited the highest accuracy of 92.7% in the training cohort and accuracy of 90.4% in the validation cohort.

[0654] The discriminant accuracy of the measurement using the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 133 or a complementary sequence thereof is shown in Table 8-7. The measurement using the combination of one polynucleotide comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 133 or a complementary sequence thereof exhibited accuracy of 52.9% in the training cohort and accuracy of 54.8% 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: 133 or a complementary sequence thereof exhibited the highest accuracy of 81.7% in the training cohort and accuracy of 79.3% 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: 133 or a complementary sequence thereof exhibited the highest accuracy of 86.1% in the training cohort and accuracy of 83.5% 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: 133 or a complementary sequence thereof exhibited the highest accuracy of 89.0% in the training cohort and accuracy of 86.1% 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: 133 or a complementary sequence thereof exhibited the highest accuracy of 90.8% in the training cohort and accuracy of 89.4% 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: 133 or a complementary sequence thereof exhibited the highest accuracy of 91.3% in the training cohort and accuracy of 89.4% in the validation cohort.

[0655] The discriminant accuracy of the measurement using the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 138 or a complementary sequence thereof is shown in Table 8-8. The measurement using the combination of one polynucleotide comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 138 or a complementary sequence thereof exhibited accuracy of 70.1% in the training cohort and accuracy of 68.1% 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: 138 or a complementary sequence thereof exhibited the highest accuracy of 80.1% in the training cohort and accuracy of 77.7% 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: 138 or a complementary sequence thereof exhibited the highest accuracy of 85.8% in the training cohort and accuracy of 92.0% 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: 138 or a complementary sequence thereof exhibited the highest accuracy of 89.5% in the training cohort and accuracy of 88.8% 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: 138 or a complementary sequence thereof exhibited the highest accuracy of 91.6% in the training cohort and accuracy of 90.4% 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: 138 or a complementary sequence thereof exhibited the highest accuracy of 91.9% in the training cohort and accuracy of 90.4% in the validation cohort.

[0656] The discriminant accuracy of the measurement using the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 166 or a complementary sequence thereof is shown in Table 8-9. The measurement using

the combination of one polynucleotide comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 166 or a complementary sequence thereof exhibited accuracy of 71.7% in the training cohort and accuracy of 72.3% 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: 166 or a complementary sequence thereof exhibited the highest accuracy of 80.9% in the training cohort and accuracy of 77.7% 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: 166 or a complementary sequence thereof exhibited the highest accuracy of 86.9% in the training cohort and accuracy of 81.9% 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: 166 or a complementary sequence thereof exhibited the highest accuracy of 90.1 % in the training cohort and accuracy of 87.2% 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: 166 or a complementary sequence thereof exhibited the highest accuracy of 92.1% in the training cohort and accuracy of 90.4% 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: 166 or a complementary sequence thereof exhibited the highest accuracy of 91.6% in the training cohort and accuracy of 91.5% in the validation cohort.

[0657] The discriminant accuracy of the measurement using the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 666 or a complementary sequence thereof is shown in Table 8-10. The measurement using the combination of one polynucleotide comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 666 or a complementary sequence thereof exhibited accuracy of 56.0% in the training cohort and accuracy of 53.2% 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: 666 or a complementary sequence thereof exhibited the highest accuracy of 81.2% in the training cohort and accuracy of 78.2% 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: 666 or a complementary sequence thereof exhibited the highest accuracy of 85.9% in the training cohort and accuracy of 81.4% 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: 666 or a complementary sequence thereof exhibited the highest accuracy of 89.2% in the training cohort and accuracy of 89.9% 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: 666 or a complementary sequence thereof exhibited the highest accuracy of 91.3% in the training cohort and accuracy of 91.0% 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: 666 or a complementary sequence thereof exhibited the highest accuracy of 92.1% in the training cohort and accuracy of 91.5% in the validation cohort.

[0658] The expression level measurement values of the polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1, 5, 85, 138, 166, and 666 were compared among 34 esophageal cancer patients, 103 healthy subjects, 69 pancreatic cancer patients, 66 bile duct cancer patients, 30 colorectal cancer patients, 33 stomach cancer patients, 32 liver cancer patients, and 15 benign pancreaticobiliary disease patients in the training cohort. As a result, a variance 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 Figure 4A). These results were also reproducible for the validation cohort (see Figure 4B).

[Table 8-1]

	Training cohort			Validation cohort		
SEQ ID NO:	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
1	65.4	76.5	64.4	65.4	62.5	65.7
1_22	78.3	85.3	77.6	77.7	87.5	76.7
1_22_126	85.9	100	84.5	79.8	87.5	79.1
1_138_166_666	89.2	94.1	88.8	88.8	81.2	89.5

(continued)

SEQ ID NO:	Training cohort			Validation cohort		
	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
1_121_138_166_666	91.1	94.1	90.8	90.4	87.5	90.7
1_85_138_166_666_668	90.6	94.1	90.2	91.5	81.2	92.4
1_85_98_138_166_666	90.8	97.1	90.2	92	87.5	92.4
1_85_138_155_166_666	91.9	97.1	91.4	91.5	81.2	92.4
1_5_85_138_166_666	92.7	91.2	92.8	93.1	81.2	94.2
1_35_85_138_166_666	90.8	97.1	90.2	91	81.2	91.9

[Table 8-2]

SEQ ID NO:	Training cohort			Validation cohort		
	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
22	70.9	76.5	70.4	69.1	75	68.6
22_126	83	88.2	82.5	77.7	75	77.9
22_126_166	86.9	100	85.6	81.9	81.2	82
22_98_166_666	89.3	94.1	88.8	87.2	100	86
22_98_166_666_668	91.4	94.1	91.1	86.7	81.2	87.2
1_22_85_138_166_666	91.3	94.1	91.1	91.5	81.2	92.4
22_32_121_133_166_666	91.6	100	90.8	88.3	81.2	89
1_22_126_138_166_666	91.3	100	90.5	92	87.5	92.4
1_22_121_155_166_666	90.1	91.2	89.9	89.9	93.8	89.5
22_32_109_121_666_667	91.9	97.1	91.4	90.4	81.2	91.2

[Table 8-3]

SEQ ID NO:	Training cohort			Validation cohort		
	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
85	65.2	73.5	64.4	61.2	12.5	65.7
2_85	79.1	91.2	77.9	77.1	68.8	77.9
85_138_667	84.3	94.1	83.3	78.1	56.2	80.1
22_85_166_666	88.5	94.1	87.9	88.8	81.2	89.5
1_85_138_166_666	90.8	97.1	90.2	91	81.2	91.9
85_138_166_185_666_669	91.1	97.1	90.5	90.4	75	91.9
85_138_166_185_666_676	91.3	97.1	90.8	91	87.5	91.3
85_138_166_177_185_666	91.3	97.1	90.8	89.9	75	91.3
85_138_166_185_666_667	91.6	97.1	91.1	89.8	75	91.2
33_85_138_166_185_666	91.6	97.1	91.1	91	81.2	91.9

[Table 8-4]

SEQ ID NO:	Training cohort			Validation cohort		
	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
109	57.6	64.7	56.9	54.8	56.2	54.7
33_109	83	100	81.3	76.1	81.2	75.6
22_109_126	85.9	94.1	85.1	81.9	75	82.6
33_109_121_667	88.7	94.1	88.2	84.5	81.2	84.8
109_126_138_166_666	91.1	97.1	90.5	90.4	81.2	91.3
109_121_126_138_166_666	91.6	97.1	91.1	90.4	87.5	90.7
1_85_109_138_166_666	91.1	97.1	90.5	91	81.2	91.9
1_109_121_138_166_666	90.8	91.2	90.8	89.9	87.5	90.1
109_126_138_166_666_676	91.9	100	91.1	90.4	81.2	91.3
109_126_138_166_202_666	91.1	97.1	90.5	90.4	81.2	91.3

[Table 8-5]

SEQ ID NO:	Training cohort			Validation cohort		
	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
121	72.3	73.5	72.1	67.6	43.8	69.8
2_121	81.9	91.2	81	73.9	75	73.8
22_121_667	86.1	94.1	85.3	79.7	87.5	78.9
22_109_121_126	89	91.2	88.8	83	81.2	83.1
22_32_109_121_666	91.4	100	90.5	86.2	68.8	87.8
1_121_138_166_666_668	90.3	91.2	90.2	89.9	75	91.3
1_33_121_138_166_666	91.6	100	90.8	89.9	87.5	90.1
1_85_121_138_166_666	90.6	94.1	90.2	92	87.5	92.4
1_121_138_166_179_666	90.6	94.1	90.2	91	87.5	91.3
1_121_138_166_177_666	91.1	94.1	90.8	91	87.5	91.3

[Table 8-6]

SEQ ID NO:	Training cohort			Validation cohort		
	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
126	73.6	76.5	73.3	66	25	69.8
126_138	83.5	88.2	83	76.1	43.8	79.1
109_126_138	88.5	94.1	87.9	79.8	68.8	80.8
22_126_166_202	89.8	100	88.8	84	81.2	84.3
1_126_138_166_666	91.1	97.1	90.5	91.5	87.5	91.9

(continued)

SEQ ID NO:	Training cohort			Validation cohort		
	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
32_109_126_138_166_666	91.9	100	91.1	92	87.5	92.4
1_85_126_138_166_666	90.8	97.1	90.2	91	81.2	91.9
1_109_126_138_166_666	92.7	100	91.9	90.4	81.2	91.3
22_109_126_138_166_666	91.3	100	90.5	89.9	81.2	90.7
109_126_138_157_166_666	91.1	97.1	90.5	90.4	81.2	91.3

[Table 8-7]

SEQ ID NO:	Training cohort			Validation cohort		
	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
133	52.9	50	53.2	54.8	56.2	54.7
33_133	81.7	94.1	80.5	79.3	81.2	79.1
22_126_133	86.1	94.1	85.3	83.5	93.8	82.6
22_126_133_667	89	100	87.9	86.1	93.8	85.4
126_133_138_166_666	90.8	97.1	90.2	89.4	87.5	89.5
126_133_138_166_666_672	90.8	97.1	90.2	89.4	87.5	89.5
126_133_138_166_666_	90.8	97.1	90.2	89.4	87.5	89.5
109_126_133_138_166_666	91.3	97.1	90.8	89.4	81.2	90.1
126_133_138_166_666_673	91.1	97.1	90.5	89.4	87.5	89.5
126_133_138_166_666_675	91.1	97.1	90.5	89.4	87.5	89.5

[Table 8-8]

SEQ ID NO:	Training cohort			Validation cohort		
	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
138	70.1	70.6	70	68.1	68.8	68
33_138	80.1	94.1	78.7	77.7	75	77.9
138_166_666	85.8	94.1	85	92	93.8	91.9
138_166_185_666	89.5	97.1	88.8	88.8	93.8	88.4
85_138_166_185_666	91.6	97.1	91.1	90.4	75	91.9
1_85_138_166_666_669	90.8	97.1	90.2	91	81.2	91.9
8_85_138_166_185_666	91.6	97.1	91.1	91	81.2	91.9
1_35_121_138_166_666	91.9	97.1	91.4	90.4	87.5	90.7
1_121_126_138_166_666	90.8	97.1	90.2	90.4	87.5	90.7
1_121_138_166_666_672	91.3	94.1	91.1	89.9	87.5	90.1

[Table 8-9]

	Training cohort			Validation cohort		
SEQ ID NO:	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
166	71.7	91.2	69.8	72.3	75	72.1
33_166	80.9	94.1	79.6	77.7	68.8	78.5
22_126_166	86.9	100	85.6	81.9	81.2	82
22_121_166_666	90.1	97.1	89.4	87.2	93.8	86.6
121_138_166_185_666	92.1	97.1	91.6	90.4	93.8	90.1
1_85_138_166_666_672	91.6	97.1	91.1	91.5	81.2	92.4
56_85_138_166_185_666	91.6	97.1	91.1	89.4	75	90.7
1_32_121_138_166_666	91.3	100	90.5	91	81.2	91.9
1_22_121_138_166_666	91.3	100	90.5	89.9	87.5	90.1
5_85_138_166_185_666	90.8	97.1	90.2	89.4	87.5	89.5

[Table 8-10]

	Training cohort			Validation cohort		
SEQ ID NO:	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
666	56	41.2	57.5	53.2	75	51.2
33_666	81.2	85.3	80.7	78.2	62.5	79.7
2_32_666	85.9	97.1	84.8	81.4	68.8	82.6
98_138_166_666	89.2	91.2	89	89.9	87.5	90.1
98_138_166_666_668	91.3	91.2	91.4	91	87.5	91.3
1_121_138_157_166_666	90.8	94.1	90.5	90.4	87.5	90.7
1_85_133_138_166_666	92.1	97.1	91.6	91.5	81.2	92.4
1_121_138_166_185_666	91.3	100	90.5	91	87.5	91.3
1_121_138_166_666_667	91.1	97.1	90.5	90.4	87.5	90.6
85_138_166_185_666	91.6	97.1	91.1	90.4	75	91.9

[Comparative Example 1]

<Esophageal cancer discriminant performance of existing tumor marker in blood>

[0659] The concentrations of the existing esophageal cancer tumor markers CEA and SCC in blood were measured in the training cohort and the validation cohort obtained in the preceding Reference Examples. When the concentrations of these tumor markers in blood are higher than the reference values described in Non-Patent Literature 3 above (CEA: 5 ng/mL, SCC: 1.5 ng/mL), subjects are suspected of having cancer, as a rule. Thus, whether or not the concentrations of CEA in blood exceeded their reference values was confirmed for each sample, and the results were assessed for the ability of these tumor markers to detect cancer in esophageal cancer patients. The sensitivity of each existing marker in the training cohort and the validation cohort was calculated. The results are shown in Table 5. The sensitivity of CEA was as low as 12.1% in the training cohort, and was as low as 18.8% in the validation cohort, whereas the sensitivity of SCC remained at 36.4% in the training cohort and 37.5% in the validation cohort, demonstrating that neither of the markers are useful in the detection of esophageal cancer (Tables 5-1 and 5-2).

[0660] 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 189, combinations of 1 or 2 polynucleotides exhibiting sensitivity beyond the existing esophageal cancer markers are presented and thus such polynucleotides serve as excellent diagnosis markers.

[0661] As shown in these Examples and Comparative Example, the kit, etc., and the method of the present invention can detect esophageal cancer with higher sensitivity than the existing tumor markers and therefore permit early detection and treatment of esophageal cancer. As a result, survival rates can be improved, and a therapeutic option of endoscopic therapy or photo dynamic therapy, which places less burden on patients, can also be applied.

Industrial Applicability

[0662] According to the present invention, esophageal cancer can be effectively detected by a simple and inexpensive method. This enables early detection, diagnosis and treatment of esophageal cancer. The method of the present invention can detect esophageal cancer with limited invasiveness using the blood of a patient and therefore allows esophageal cancer to be detected conveniently and rapidly.

[0663] All publications, patents, and patent applications cited herein are incorporated herein by reference in their entirety.

SEQUENCE LISTING

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National Cancer Center

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cgcag 65

<210> 252
<211> 81
<212> RNA
<213> Homo sapiens

<400> 252
uagaggcagu uucaacagau guguagacuu uugauaugag aaauugguuu caaaaucagg 60

agucggggcu uuacugcuuu u 81

<210> 253
<211> 79
<212> RNA
<213> Homo sapiens

<400> 253
cagccugggg aaggcuuggc agggaagaca caugagcagu gccuccacuu cacgccucuc 60

ccuugucucc uuucccuag 79

<210> 254
<211> 109
<212> RNA
<213> Homo sapiens

<400> 254
ggucgggcuc accaugacac agugugagac cucgggcuac aacacaggac ccgggcgcug 60

cucugacccc ucgugucuug uguugcagcc ggagggacgc agguccgca 109

<210> 255
<211> 82
<212> RNA
<213> Homo sapiens

<400> 255
ugagcuguug gauucggggc cguagcacug ucugagaggu uuacauuucu cacagugaac 60

cggucucuuu uucagcugcu uc 82

<210> 256
<211> 65
<212> RNA
<213> Homo sapiens

<400> 256
gagggugggc gagggcggcu gagcggcucc auccccggc cugcucaucc cccucgcccu 60
cucag 65

<210> 257
<211> 63
<212> RNA
<213> Homo sapiens

<400> 257
aaugggguggg ugcuggguggg agccgugccc uggccacuca uucggcucuc ucccucaccc 60
uag 63

<210> 258
<211> 69
<212> RNA
<213> Homo sapiens

<400> 258
gggcuuaggg augggaggcc aggaugaaga uuaaucccua auccccaaca cuggccuugc 60
uaucccccag 69

<210> 259
<211> 86
<212> RNA
<213> Homo sapiens

<400> 259
ggggcugggg gugugggggag agagagugca cagccagcuc agggauuaaa gcucuuucuc 60
ucucucucuc ucccacuucc cugcag 86

<210> 260
<211> 68
<212> RNA
<213> Homo sapiens

<400> 260
gugcaaagag caggaggaca ggggauuuau cucccaaggg aggucccccug auccuaguca 60
cggcacca 68

<210> 261
<211> 82
<212> RNA
<213> Homo sapiens

<400> 261
gugaguggga ggccagggca cggcaggggg agcugcaggg cuaugggagg ggccccagcg 60

ucugagcccu guccuccccgc ag 82

<210> 262
<211> 82
<212> RNA
<213> Homo sapiens

<400> 262
gugaguggga ggccagggca cggcaggggg agcugcaggg cuaugggagg ggccccagcg 60

ucugagcccu guccuccccgc ag 82

<210> 263
<211> 61
<212> RNA
<213> Homo sapiens

<400> 263
aacugcgggg ccagagcaga gagcccuugc acaccaccag ccucuccucc cugugcccca 60

g 61

<210> 264
<211> 106
<212> RNA
<213> Homo sapiens

<400> 264
agaagaaugc ccaaccagcc cucaguugcu acaguucccu guuguuucag cucgacaaca 60

acaggcggcu guagcaaugg ggggcuggau gggcaucuca augugc 106

<210> 265
<211> 63
<212> RNA
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<400> 265
ugguggcggc gguaguuaug ggcuucucuu ucucaccagc agccccuggg ccgccgccuc 60

ccu 63

<210> 266
<211> 65
<212> RNA
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<400> 266
gucuccuggg gggaggagac ccugcucucc cuggcagcaa gccucuccug cccuuccaga 60

uuagc 65

<210> 267

<211> 51
<212> RNA
<213> Homo sapiens

<400> 267
agagaugaag cgggggggcg gggucuugcu cuauugccua cgcugaucuc a 51

<210> 268
<211> 69
<212> RNA
<213> Homo sapiens

<400> 268
uggggguaggg gugggggaau ucaggggugu cgaacucaug gcugccaccu uugugucccc 60

auccugcag 69

<210> 269
<211> 115
<212> RNA
<213> Homo sapiens

<400> 269
gagcaaaaac cagagaacaa caugggagcg uuccuaaccc cuaaggcaac uggaugggag 60

accugaccca uccaguucuc ugagggggcu cuuguguguu cuacaagguu guuca 115

<210> 270
<211> 55
<212> RNA
<213> Homo sapiens

<400> 270
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<210> 271
<211> 92
<212> RNA
<213> Homo sapiens

<400> 271
cgcugcgcuu cugggcccgc ggcgggcgug gggcugcccg ggccggucga ccagcgcgcc 60

guagcucccg aggcccgagc cgcgacccgc gg 92

<210> 272
<211> 80
<212> RNA
<213> Homo sapiens

<400> 272
gcgucaagau ggcggcgggg agguaggcag agcaggacgc cgcugcugcc gccgccaccg 60

ccgccuccgc uccagucgcc 80

<210> 273
<211> 86

<212> RNA
<213> Homo sapiens

<400> 273
agggagaagg gucggggcag ggagggcagg gcaggcucug ggguggggggg ucugugaguc 60

agccacggcu cugcccacgu cucccc 86

<210> 274
<211> 63
<212> RNA
<213> Homo sapiens

<400> 274
acccuagggu ggggcuggag gugggggcuga ggcugagucu uccucccccuu ccucccugcc 60

cag 63

<210> 275
<211> 79
<212> RNA
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<400> 275
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uagcccccgc cacaucggg 79

<210> 276
<211> 98
<212> RNA
<213> Homo sapiens

<400> 276
cuuggucaau aggaaagagg ugggaccucc uggcuuuucc ucugcagcau ggcucggacc 60

uagugcaaug uuuaagcucc ccucucuuuc cuguucag 98

<210> 277
<211> 62
<212> RNA
<213> Homo sapiens

<400> 277
ccuucugcgg cagagcuggg gucaccagcc cucauguacu ugugacuucu ccccugccac 60

ag 62

<210> 278
<211> 65
<212> RNA
<213> Homo sapiens

<400> 278
gagaaugggg ggacagaugg agaggacaca ggcuggcacu gaggucccccu ccacuuuccu 60

ccuag 65

<210> 279
<211> 68
<212> RNA
<213> Homo sapiens

<400> 279
cguggugagg auauggcagg gaaggggagu uucccucuau ucccuucccc ccaguaaucu 60

ucaucaug 68

<210> 280
<211> 103
<212> RNA
<213> Homo sapiens

<400> 280
gugucggcug uggcgugacu gucccucugu gucccccacu aggcccacug cucaguggag 60

cguggaggac gaggaggagg ccguccacga gcaaugccag cau 103

<210> 281
<211> 87
<212> RNA
<213> Homo sapiens

<400> 281
cccucaucuc ugggcagggg cuuauuguag gagucucuga agagagcugu ggacugaccu 60

gcuuuaaccc uucccccaggu ucccauu 87

<210> 282
<211> 83
<212> RNA
<213> Homo sapiens

<400> 282
aauagagggu gcacaggcac gggagcucag gugaggcagg gagcugagcu caccugaccu 60

cccaugccug ugcacccucu auu 83

<210> 283
<211> 82
<212> RNA
<213> Homo sapiens

<400> 283
uguggggcagg gcccuggggga gcugaggcuc ugggggguggc cggggcugac ccugggccuc 60

ugcucccccag ugucugaccg cg 82

<210> 284
<211> 98
<212> RNA
<213> Homo sapiens

<400> 284
uucucacccc cgccugacac gggcgacagc ugcggcccgc uguguucacu cgggccgagu 60

gcgucuccug ucaggcaagg gagagcagag ccccccug 98

<210> 285
<211> 49
<212> RNA
<213> Homo sapiens

<400> 285
uucccagcca acgcaccaaa aaugauaugg gucuguuguc uggagaaac 49

<210> 286
<211> 69
<212> RNA
<213> Homo sapiens

<400> 286
ggcccucggg ccuggggguug ggggagcucu guccugucuc acucauugcu ccucccccugc 60

cuggcccag 69

<210> 287
<211> 80
<212> RNA
<213> Homo sapiens

<400> 287
cgugugagcc cgcccugugc ccggcccacu ucugcuuccu cuuagcgcag gaggggcccc 60

gcacugggag gggcccucac 80

<210> 288
<211> 73
<212> RNA
<213> Homo sapiens

<400> 288
cggcgacggc ggggugggug aggucgggcc ccaagacucg ggguuugccg ggcgccucag 60

uucaccgcgg ccg 73

<210> 289
<211> 74
<212> RNA
<213> Homo sapiens

<400> 289
ccugcaggag gcagugggcg agcaggcggg gcagcccaau gccaugggcc ugaucucacc 60

gcugccuccu uccc 74

<210> 290
<211> 70
<212> RNA
<213> Homo sapiens

<400> 290

gucccugggg gcugggaugg gccauggugu gcucugaucc cccugugguc ucuuggcccc 60

caggaacucc 70

<210> 291
<211> 73
<212> RNA
<213> Homo sapiens

<400> 291
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ccucgccccc cag 73

<210> 292
<211> 77
<212> RNA
<213> Homo sapiens

<400> 292
gaguugggag guucccucuc caaaauguguc uugaucccccc accccaagac acauuuggag 60

agggacccuc ccaacuc 77

<210> 293
<211> 63
<212> RNA
<213> Homo sapiens

<400> 293
cuugcccggg agaaggaggu ggccuggaga gcugcugucu ccagccgccg ccugucucca 60

cag 63

<210> 294
<211> 79
<212> RNA
<213> Homo sapiens

<400> 294
gugagguggg ggccagcagg gaguggggcug ggcugggcug ggccaaggua caaggccuca 60

cccugcaucc cgcacccag 79

<210> 295
<211> 63
<212> RNA
<213> Homo sapiens

<400> 295
gagucgagga cugguggaag ggccuuuccc cucagaccaa ggcccuggcc ccagcuucuu 60

cuc 63

<210> 296
<211> 60
<212> RNA

<213> Homo sapiens

<400> 296
aggccuaggg gguggcaggc uggccaucag uguggggcuaa cccuguccuc ucccucccag 60

<210> 297
<211> 59
<212> RNA
<213> Homo sapiens

<400> 297
cuccagggag acagugugug aggccucuug ccauggccuc ccugcccgcc ucucugcag 59

<210> 298
<211> 73
<212> RNA
<213> Homo sapiens

<400> 298
ggccggcugg gguuccuggg gaugggauuu gcuuccuguc acaaaucaca uugccaggga 60

uuuccaaccg acc 73

<210> 299
<211> 84
<212> RNA
<213> Homo sapiens

<400> 299
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ggaguuggga gcagagaggg gacc 84

<210> 300
<211> 81
<212> RNA
<213> Homo sapiens

<400> 300
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cucucuggcu ccucccccaaa g 81

<210> 301
<211> 97
<212> RNA
<213> Homo sapiens

<400> 301
cccgggaccu ugguccaggc gcuggucugc guggugcucg gguggauaag ucugaucuga 60

gcaccacaca ggccgggcgc cgggaccaag ggggcuc 97

<210> 302
<211> 70
<212> RNA
<213> Homo sapiens

<400> 302
cucgggcccg accgcgccgg cccgcaccuc ccggcccgga gcugcgggcu gcggucaggg 60

cgaucccggg 70

<210> 303
<211> 66
<212> RNA
<213> Homo sapiens

<400> 303
ccgagugggg cggggcaggu cccugcaggg acugugacac ugaaggaccu gcaccuucgc 60

ccacag 66

<210> 304
<211> 67
<212> RNA
<213> Homo sapiens

<400> 304
gcgcccuccc ucucucccgg gugugcaaau gugugugugc gguguuaugc cggacaagag 60

ggaggug 67

<210> 305
<211> 70
<212> RNA
<213> Homo sapiens

<400> 305
aaaagccugu cccuaagucc cucccagccu uccagaguug gugccaggaa ggauuuaggg 60

acaggcuuug 70

<210> 306
<211> 94
<212> RNA
<213> Homo sapiens

<400> 306
auaaaggaag uuaggcugag gggcagagag cgagacuuuu cuauuuucca aaagcucggu 60

cugaggcccc ucagucuugc uuccuaaccc gcgc 94

<210> 307
<211> 66
<212> RNA
<213> Homo sapiens

<400> 307
gggaggaggg aggagauggg ccaaguuccc ucuggcugga acgcccuucc cccccuucuu 60

caccug 66

<210> 308

<211> 57
<212> RNA
<213> Homo sapiens

<400> 308
cauuggaggg uguggaagac aucugggcca acucugaucu cuucaucuac cccccag 57

<210> 309
<211> 79
<212> RNA
<213> Homo sapiens

<400> 309
gugcagaucc uugggagccc uguuagacuc uggauuuuac acuuggagug aacgggcgcc 60

aucccgaggc uuugcacag 79

<210> 310
<211> 90
<212> RNA
<213> Homo sapiens

<400> 310
cgggcggggc ggguccggcc gccuccgagc ccggccggca gcccccggcc uuaaagcgcg 60

ggcuguccgg aggggucggc uuucccaccg 90

<210> 311
<211> 72
<212> RNA
<213> Homo sapiens

<400> 311
augagcgggu gggagcagau cuuauugaga guuccuucuc cugcuccuga uugucuuccc 60

ccacccucac ag 72

<210> 312
<211> 59
<212> RNA
<213> Homo sapiens

<400> 312
guccaggcag gagccggacu ggaccucagg gaagaggcug acccggcccc ucuugcggc 59

<210> 313
<211> 64
<212> RNA
<213> Homo sapiens

<400> 313
gagcucuggg aggggcuggg uuuggcagga caguuuccaa gcccugucuc cucccaucuu 60

ccag 64

<210> 314
<211> 82

<212> RNA
<213> Homo sapiens

<400> 314
gcuacgggga gcggggagga agugggcgcu gcuucugcgu uaucuggaag gagcagccca 60

cuccuguccu gggcucugug gu 82

<210> 315
<211> 50
<212> RNA
<213> Homo sapiens

<400> 315
acccgggcgu gguggugggg gugggugccu guaauuccag cuaguuggga 50

<210> 316
<211> 61
<212> RNA
<213> Homo sapiens

<400> 316
gagggcagcg uggguguggc ggaggcaggc gugaccguuu gccgcccucu cgcugcucua 60

g 61

<210> 317
<211> 73
<212> RNA
<213> Homo sapiens

<400> 317
ggcgagggga ggcgcaggcu cggaaaggcg cgcgaggcuc caggcuccuu cccgauccac 60

cgcucuccuc gcu 73

<210> 318
<211> 67
<212> RNA
<213> Homo sapiens

<400> 318
ggcagccagg gggaugggcg agcuugggcc cauuccuuuc cuuacccuac cccccauccc 60

ccuguag 67

<210> 319
<211> 76
<212> RNA
<213> Homo sapiens

<400> 319
acugacuuug agucucuccu cagggugcug caggcaaagc uggggaccca gggagagacg 60

uaagugaggg gagaug 76

<210> 320

<211> 71
<212> RNA
<213> Homo sapiens

<400> 320
ugaccacccc cgggcaaaga ccugcagauc cccuguuaga gacgggccca ggacuuugug 60

cggggugccc a 71

<210> 321
<211> 65
<212> RNA
<213> Homo sapiens

<400> 321
uucuccuggg gaguggcugg ggagcagaca gacccaaccu caugcucccc ggccucugcc 60

cccag 65

<210> 322
<211> 65
<212> RNA
<213> Homo sapiens

<400> 322
gggugcucgg ggcaggcggc ugggagcggc ccucacauug auggcuccug ccaccuccuc 60

cgcag 65

<210> 323
<211> 67
<212> RNA
<213> Homo sapiens

<400> 323
guggcacuca aacugugggg gcacuuucug cucucuggug aaagugccgc caucuuuuga 60

guguuac 67

<210> 324
<211> 63
<212> RNA
<213> Homo sapiens

<400> 324
gagguguagg ggagguuggg ccagggaugc cuucacugug ucucucuggu cuugccaccc 60

cag 63

<210> 325
<211> 72
<212> RNA
<213> Homo sapiens

<400> 325
ugugggacug caaaugggag cucagcaccu gccugccacc cacgcagacc agccccugcu 60

cuguucccac ag 72

<210> 326
<211> 88
<212> RNA
<213> Homo sapiens

<400> 326
gugggggccag gcgguggugg gcacugcugg ggugggcaca gcagccaugc agagcgggca 60

uuugaccccg ugccacccuu uuccccag 88

<210> 327
<211> 94
<212> RNA
<213> Homo sapiens

<400> 327
cgggcagcgg gugccaggca cggugucagc aggcaacaug gccgagaggc cggggccucc 60

gggcggcgcc guguccgcga ccgcguaccc ugac 94

<210> 328
<211> 90
<212> RNA
<213> Homo sapiens

<400> 328
ggcgccucug cagcuccggc ucccccuggc cucucgggaa cuacaagucc cagggggccu 60

ggcgguggggc ggcgggcgga agaggcgggg 90

<210> 329
<211> 70
<212> RNA
<213> Homo sapiens

<400> 329
uuggguuggg guggucggcc cuggaggggg uuuguuugcu uauuccccuc ugugcuucac 60

cccuacccag 70

<210> 330
<211> 94
<212> RNA
<213> Homo sapiens

<400> 330
aauucagccc ugccacuggc uuaugucaug accuugggcu acucaggcug ucugcacaau 60

gagccaguug gacaggagca gugccacuca acuc 94

<210> 331
<211> 90
<212> RNA
<213> Homo sapiens

<400> 331

gugucucucu ggagacccug cagccuuccc acccaccagg gagcuuucca ugggcugugg 60

ggaaggcguc agugucgggu gagggaacac 90

<210> 332
<211> 80
<212> RNA
<213> Homo sapiens

<400> 332
gagaggccaa gaccuuggga auggggguaa gggccuucug agcccagguc cgaacucucc 60

auuccucugc agagcgcucu 80

<210> 333
<211> 77
<212> RNA
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<400> 333
caugagaaau ccugcugguc aaccauagcc cuggucagac ucuccggggc ugugauugac 60

cagcaggacu ucucaug 77

<210> 334
<211> 80
<212> RNA
<213> Homo sapiens

<400> 334
ugagaggccg caccuugccu ugcugcccgg gccgugcacc cgugggcccc agggcgacgc 60

ggcgggggcg gcccuagcga 80

<210> 335
<211> 118
<212> RNA
<213> Homo sapiens

<400> 335
gcaggugaac uggcaggcca ggaagaggag gaagcccugg aggggcugga ggugauggau 60

guuuuccucc gguucucagg gcuccaccuc uuucgggccg uagagccagg gcuggugc 118

<210> 336
<211> 69
<212> RNA
<213> Homo sapiens

<400> 336
cuuucggcca gcgggacggc auccgaggug ggcuaggcuc gggcccgugg cgggugcggg 60

ggugggagg 69

<210> 337
<211> 78
<212> RNA

<213> Homo sapiens

<400> 337
ggccucaggc aggcgcaccc gaccacaugc auggcuggug gcggcgugca ggggucgggu 60

gggccaggcu gugggggcg 78

<210> 338
<211> 80
<212> RNA
<213> Homo sapiens

<400> 338
gguuccggag ccccggcgcg ggcggguucu ggggguguaga cgcugcuggc cagcccgccc 60

cagccgaggu ucucggcacc 80

<210> 339
<211> 66
<212> RNA
<213> Homo sapiens

<400> 339
agcagcccuc ggcggcccgg ggggcgggcg gcggugcccg ucccggggcu gcgcgaggca 60

caggcg 66

<210> 340
<211> 83
<212> RNA
<213> Homo sapiens

<400> 340
ccugcugcag aggugccagc ugcaguggggg gaggcacugc cagggcugcc cacucugcuu 60

agccagcagg ugccaagaac agg 83

<210> 341
<211> 64
<212> RNA
<213> Homo sapiens

<400> 341
ucugggcgag ggguggggcuc ucagaggggc uggcaguacu gcucugaggc cugccucucc 60

ccag 64

<210> 342
<211> 98
<212> RNA
<213> Homo sapiens

<400> 342
uuggggcaagg ugcggggcua gggcuaacag cagucuuacu gaagguuucc uggaaaccac 60

gcacaugcug uugccacuaa ccucaaccuu acucgguc 98

<210> 343
<211> 97
<212> RNA
<213> Homo sapiens

<400> 343
aucugaguug ggaggguccc ucuccaaaug ugucuugggg ugggggauca agacacauuu 60

ggagagggaa ccucccaacu cggccucugc caucauu 97

<210> 344
<211> 72
<212> RNA
<213> Homo sapiens

<400> 344
cuugggaaug gcaaggaaac cguuaccauu acugaguuua guaaugguaa ugguucucuu 60

gcuauaccca ga 72

<210> 345
<211> 60
<212> RNA
<213> Homo sapiens

<400> 345
caaggugggg gagaugggggg uugaacuuca uuucucaugc ucaucccccau cuccuuucag 60

<210> 346
<211> 53
<212> RNA
<213> Homo sapiens

<400> 346
gguggggguu ggaggcgugg guuuuagaac cuaucccuuu cuagcccuga gca 53

<210> 347
<211> 59
<212> RNA
<213> Homo sapiens

<400> 347
ggggccaggc agggaggugg gaccaugggg gccuugcugu gugaccaccg uuccugcag 59

<210> 348
<211> 67
<212> RNA
<213> Homo sapiens

<400> 348
gugggagggg agaggcagca agcacacagg gccugggacu agcaugcuga ccucccuccu 60

gccccag 67

<210> 349
<211> 86
<212> RNA

<213> Homo sapiens

<400> 349
agcacugccc ccggugaguc agggugggggc uggcccccug cuucgugccc auccgcgcuc 60

ugacucucug cccaccugca ggagcu 86

<210> 350
<211> 90
<212> RNA
<213> Homo sapiens

<400> 350
aggccucgcu guucucuaug gcuuuuuauu ccuaugugau ucuacugcuc acucauauag 60

ggauuggagc cguggcgcac ggcggggaca 90

<210> 351
<211> 115
<212> RNA
<213> Homo sapiens

<400> 351
ggugccgagg gccguccggc auccuaggcg ggucgcugcg guaccucccu ccugucugug 60

gcgggugggau cccguggccg uguuuuccug guggcccggc cgugccugag guuuc 115

<210> 352
<211> 61
<212> RNA
<213> Homo sapiens

<400> 352
uggcccaggg aaccaguugg ggcuuccgcu cugcagaggc ucuaacuggc uuucccugca 60

g 61

<210> 353
<211> 65
<212> RNA
<213> Homo sapiens

<400> 353
cuccucuggg gguggggggc ugggcguggu ggacagcgau gcaucccucg ccuucucacc 60

cucag 65

<210> 354
<211> 62
<212> RNA
<213> Homo sapiens

<400> 354
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accggucucu uucccuacug uguc 84

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cccacccacc cccuguuucc uggcccacag 90

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ccggccugug gaaga 75

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<212> RNA
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ccggauccca gcccacuuac cuugguuacu cuccuuccuu cu 102

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ag 62

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ugauggugau agucuggugg gggcggugg 89

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ccacccuccc c 71

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ucugccucug uccagguccu ugugacccgc ccgcucuccu 100

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guaccaugac uuaagugugg uggcuuaaac aug 93

<210> 365
<211> 89
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cccacacccu gccuaugggc cacacagcu 89

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<211> 98
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ugcucacugc cccgucccgg cgcccguguc uccuccag 98

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cugggg 66

<210> 368
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<210> 369
<211> 71
<212> RNA
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cauacuccca g 71

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gguggguucu ggcuggucag augggagugg acagagaccc gggguccuc 109

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<212> RNA
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ccucuccugg caucgccccc ag 82

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<210> 373
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ag 62

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<212> RNA
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cgcacgaggc 70

<210> 375
<211> 73
<212> RNA
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cucugcucuc cag 73

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<211> 74
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ccccucccc uccc 74

<210> 377
<211> 75
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cuucccacc cugaa 75

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<211> 70
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aaaaguggguc 70

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<211> 60
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acaucgcccc accuucccca g 81

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<211> 61
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acuccugccc cuuggucu 78

<210> 383
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ccaaaaaagg uaa 73

<210> 384
<211> 63
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<210> 385
<211> 62
<212> RNA
<213> Homo sapiens

<400> 385
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<210> 386
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<211> 64
<212> RNA
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caca 64

<210> 388
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<212> RNA
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uauugcacuc gucccggccu ccggcccccc cggccc 96

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<211> 83
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ccuuccucgu cugucugccc cag 83

<210> 390

<211> 67
<212> RNA
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ccuccag 67

<210> 391
<211> 59
<212> RNA
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<400> 391
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<210> 392
<211> 89
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gggacggggg cugugcuggg gcagcugga 89

<210> 393
<211> 70
<212> RNA
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uggagaggcc 70

<210> 394
<211> 83
<212> RNA
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cagcagagga ccugggccug gac 83

<210> 395
<211> 86
<212> RNA
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<400> 395
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gguucuuggg agccuggcgu cuggcc 86

<210> 396
<211> 97
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<400> 396
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acauugccag ggauuaccac gcaaccacga ccuuggc 97

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<400> 397
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uguucuugcc agguggcaga agguugcugc 90

<210> 398
<211> 80
<212> RNA
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gcugcugcca aguggcuggu 80

<210> 399
<211> 89
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auuaacugug cugcugaagu aagguugac 89

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acugugcugc uuuaguguga c 81

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cucagccccu ggg 73

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caggauac 68

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gaug 64

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<211> 66
<212> RNA
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ccccag 66

<210> 405
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<212> RNA
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cccgcccggc gcccguccgc ccgcgggguc 89

<210> 406
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aggcucuccu gaagggcucu 80

<210> 407
<211> 64
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ccag 64

<210> 408
<211> 70
<212> RNA
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acuggcaggg 70

<210> 409
<211> 59
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<210> 410
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<212> RNA
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<400> 410
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gccggagggg cgucacgugc acccaaguga cgccccuucu gauucugccu cag 113

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<212> RNA
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<400> 411
cuuucuacac agguugggau cgguugcaau gcuguguuuc uguaugguau ugcacuuguc 60

ccggccuguu gaguuugg 78

<210> 412
<211> 76
<212> RNA
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ucccagguuu cggugc 76

<210> 413
<211> 92
<212> RNA
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<400> 413
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gcaggggcug gugcugggcg gggggcggcg gg 92

<210> 414
<211> 113
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ccgcggccgu guuuuccugg uggcccggcc aug 93

<210> 416
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uguggggagc gaaaugcaac 80

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cuccacaggc cuggug 76

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ccaggugcac ag 72

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uucucauuuu gcucaccugu u 81

<210> 425
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<212> RNA
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<210> 429
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ggaaaaaggc gggagaagcc cca 83

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Claims

1. A kit for the detection of esophageal cancer, comprising nucleic acid(s) capable of specifically binding to at least one polynucleotide selected from the group consisting of the following esophageal cancer markers: miR-204-3p, miR-1247-3p, miR-6875-5p, miR-6857-5p, miR-6726-5p, miR-3188, miR-8069, miR-4257, miR-1343-3p, miR-7108-5p, miR-6825-5p, miR-7641, miR-3185, miR-4746-3p, miR-6791-5p, miR-6893-5p, miR-4433b-3p, miR-3135b, miR-6781-5p, miR-1908-5p, miR-4792, miR-7845-5p, miR-4417, miR-3184-5p, miR-1225-5p, miR-1231, miR-1225-3p, miR-150-3p, miR-4433-3p, miR-6125, miR-4513, miR-6787-5p, miR-6784-5p, miR-615-5p, miR-

6765-3p, miR-5572, miR-6842-5p, miR-8063, miR-6780b-5p, miR-187-5p, miR-128-1-5p, miR-6729-5p, miR-6741-5p, miR-6757-5p, miR-7110-5p, miR-7975, miR-1233-5p, miR-6845-5p, miR-3937, miR-4467, miR-7109-5p, miR-6088, miR-6782-5p, miR-5195-3p, miR-4454, miR-6724-5p, miR-8072, miR-4516, miR-6756-5p, miR-4665-3p, miR-6826-5p, miR-6820-5p, miR-6887-5p, miR-3679-5p, miR-7847-3p, miR-6721-5p, miR-3622a-5p, miR-939-5p, miR-602, miR-7977, miR-6749-5p, miR-1914-3p, miR-4651, miR-4695-5p, miR-6848-5p, miR-1228-3p, miR-642b-3p, miR-6746-5p, miR-3620-5p, miR-3131, miR-6732-5p, miR-7113-3p, miR-23a-3p, miR-3154, miR-4723-5p, miR-3663-3p, miR-4734, miR-6816-5p, miR-4442, miR-4476, miR-423-5p, miR-1249, miR-6515-3p, miR-887-3p, miR-4741, miR-6766-3p, miR-4673, miR-6779-5p, miR-4706, miR-1268b, miR-4632-5p, miR-3197, miR-6798-5p, miR-711, miR-6840-3p, miR-6763-5p, miR-6727-5p, miR-371a-5p, miR-6824-5p, miR-4648, miR-1227-5p, miR-564, miR-3679-3p, miR-2861, miR-6737-5p, miR-4725-3p, miR-6716-5p, miR-4675, miR-1915-3p, miR-671-5p, miR-3656, miR-6722-3p, miR-4707-5p, miR-4449, miR-1202, miR-4649-5p, miR-744-5p, miR-642a-3p, miR-451a, miR-6870-5p, miR-4443, miR-6808-5p, miR-4728-5p, miR-937-5p, miR-135a-3p, miR-663b, miR-1343-5p, miR-6822-5p, miR-6803-5p, miR-6805-3p, miR-128-2-5p, miR-4640-5p, miR-1469, miR-92a-2-5p, miR-3940-5p, miR-4281, miR-1260b, miR-4758-5p, miR-1915-5p, miR-5001-5p, miR-4286, miR-6126, miR-6789-5p, miR-4459, miR-1268a, miR-6752-5p, miR-6131, miR-6800-5p, miR-4532, miR-6872-3p, miR-718, miR-6769a-5p, miR-4707-3p, miR-6765-5p, miR-4739, miR-4525, miR-4270, miR-4534, miR-6785-5p, miR-6850-5p, miR-4697-5p, miR-1260a, miR-4486, miR-6880-5p, miR-6802-5p, miR-6861-5p, miR-92b-5p, miR-1238-5p, miR-6851-5p, miR-7704, miR-149-3p, miR-4689, miR-4688, miR-125a-3p, miR-23b-3p, miR-614, miR-1913, miR-16-5p, miR-6717-5p, miR-3648, miR-3162-5p, miR-1909-3p, miR-8073, miR-6769b-5p, miR-6836-3p, miR-4484, miR-6819-5p, and miR-6794-5p.

2. The kit according to claim 1, wherein miR-204-3p is hsa-miR-204-3p, miR-1247-3p is hsa-miR-1247-3p, miR-6875-5p is hsa-miR-6875-5p, miR-6857-5p is hsa-miR-6857-5p, miR-6726-5p is hsa-miR-6726-5p, miR-3188 is hsa-miR-3188, miR-8069 is hsa-miR-8069, miR-4257 is hsa-miR-4257, miR-1343-3p is hsa-miR-1343-3p, miR-7108-5p is hsa-miR-7108-5p, miR-6825-5p is hsa-miR-6825-5p, miR-7641 is hsa-miR-7641, miR-3185 is hsa-miR-3185, miR-4746-3p is hsa-miR-4746-3p, miR-6791-5p is hsa-miR-6791-5p, miR-6893-5p is hsa-miR-6893-5p, miR-4433b-3p is hsa-miR-4433b-3p, miR-3135b is hsa-miR-3135b, miR-6781-5p is hsa-miR-6781-5p, miR-1908-5p is hsa-miR-1908-5p, miR-4792 is hsa-miR-4792, miR-7845-5p is hsa-miR-7845-5p, miR-4417 is hsa-miR-4417, miR-3184-5p is hsa-miR-3184-5p, miR-1225-5p is hsa-miR-1225-5p, miR-1231 is hsa-miR-1231, miR-1225-3p is hsa-miR-1225-3p, miR-150-3p is hsa-miR-150-3p, miR-4433-3p is hsa-miR-4433-3p, miR-6125 is hsa-miR-6125, miR-4513 is hsa-miR-4513, miR-6787-5p is hsa-miR-6787-5p, miR-6784-5p is hsa-miR-6784-5p, miR-615-5p is hsa-miR-615-5p, miR-6765-3p is hsa-miR-6765-3p, miR-5572 is hsa-miR-5572, miR-6842-5p is hsa-miR-6842-5p, miR-8063 is hsa-miR-8063, miR-6780b-5p is hsa-miR-6780b-5p, miR-187-5p is hsa-miR-187-5p, miR-128-1-5p is hsa-miR-128-1-5p, miR-6729-5p is hsa-miR-6729-5p, miR-6741-5p is hsa-miR-6741-5p, miR-6757-5p is hsa-miR-6757-5p, miR-7110-5p is hsa-miR-7110-5p, miR-7975 is hsa-miR-7975, miR-1233-5p is hsa-miR-1233-5p, miR-6845-5p is hsa-miR-6845-5p, miR-3937 is hsa-miR-3937, miR-4467 is hsa-miR-4467, miR-7109-5p is hsa-miR-7109-5p, miR-6088 is hsa-miR-6088, miR-6782-5p is hsa-miR-6782-5p, miR-5195-3p is hsa-miR-5195-3p, miR-4454 is hsa-miR-4454, miR-6724-5p is hsa-miR-6724-5p, miR-8072 is hsa-miR-8072, miR-4516 is hsa-miR-4516, miR-6756-5p is hsa-miR-6756-5p, miR-4665-3p is hsa-miR-4665-3p, miR-6826-5p is hsa-miR-6826-5p, miR-6820-5p is hsa-miR-6820-5p, miR-6887-5p is hsa-miR-6887-5p, miR-3679-5p is hsa-miR-3679-5p, miR-7847-3p is hsa-miR-7847-3p, miR-6721-5p is hsa-miR-6721-5p, miR-3622a-5p is hsa-miR-3622a-5p, miR-939-5p is hsa-miR-939-5p, miR-602 is hsa-miR-602, miR-7977 is hsa-miR-7977, miR-6749-5p is hsa-miR-6749-5p, miR-1914-3p is hsa-miR-1914-3p, miR-4651 is hsa-miR-4651, miR-4695-5p is hsa-miR-4695-5p, miR-6848-5p is hsa-miR-6848-5p, miR-1228-3p is hsa-miR-1228-3p, miR-642b-3p is hsa-miR-642b-3p, miR-6746-5p is hsa-miR-6746-5p, miR-3620-5p is hsa-miR-3620-5p, miR-3131 is hsa-miR-3131, miR-6732-5p is hsa-miR-6732-5p, miR-7113-3p is hsa-miR-7113-3p, miR-23a-3p is hsa-miR-23a-3p, miR-3154 is hsa-miR-3154, miR-4723-5p is hsa-miR-4723-5p, miR-3663-3p is hsa-miR-3663-3p, miR-4734 is hsa-miR-4734, miR-6816-5p is hsa-miR-6816-5p, miR-4442 is hsa-miR-4442, miR-4476 is hsa-miR-4476, miR-423-5p is hsa-miR-423-5p, miR-1249 is hsa-miR-1249, miR-6515-3p is hsa-miR-6515-3p, miR-887-3p is hsa-miR-887-3p, miR-4741 is hsa-miR-4741, miR-6766-3p is hsa-miR-6766-3p, miR-4673 is hsa-miR-4673, miR-6779-5p is hsa-miR-6779-5p, miR-4706 is hsa-miR-4706, miR-1268b is hsa-miR-1268b, miR-4632-5p is hsa-miR-4632-5p, miR-3197 is hsa-miR-3197, miR-6798-5p is hsa-miR-6798-5p, miR-711 is hsa-miR-711, miR-6840-3p is hsa-miR-6840-3p, miR-6763-5p is hsa-miR-6763-5p, miR-6727-5p is hsa-miR-6727-5p, miR-371a-5p is hsa-miR-371a-5p, miR-6824-5p is hsa-miR-6824-5p, miR-4648 is hsa-miR-4648, miR-1227-5p is hsa-miR-1227-5p, miR-564 is hsa-miR-564, miR-3679-3p is hsa-miR-3679-3p, miR-2861 is hsa-miR-2861, miR-6737-5p is hsa-miR-6737-5p, miR-4725-3p is hsa-miR-4725-3p, miR-6716-5p is hsa-miR-6716-5p, miR-4675 is hsa-miR-4675, miR-1915-3p is hsa-miR-1915-3p, miR-671-5p is hsa-miR-671-5p, miR-3656 is hsa-miR-3656, miR-6722-3p is hsa-miR-6722-3p, miR-4707-5p is hsa-miR-4707-5p, miR-4449 is hsa-miR-4449, miR-1202 is hsa-miR-1202, miR-4649-5p is hsa-miR-4649-5p, miR-744-5p is hsa-miR-744-5p, miR-642a-3p is hsa-miR-642a-3p, miR-451a is hsa-miR-451a, miR-6870-5p is hsa-miR-6870-5p, miR-4443 is hsa-miR-4443, miR-6808-5p is hsa-miR-6808-5p, miR-

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3. The kit according to claim 1 or 2, wherein the nucleic acid(s) is/are 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 115, 117 to 189, and 666 to 675 or a nucleotide sequence 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 115, 117 to 189, and 666 to 675,
(c) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 1 to 115, 117 to 189, and 666 to 675 or a nucleotide sequence 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 115, 117 to 189, and 666 to 675 or a nucleotide sequence 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 polynucleotide(s) selected from other esophageal cancer markers miR-575 and miR-24-3p.

5. The kit according to claim 4, wherein miR-575 is hsa-miR-575, and miR-24-3p is hsa-miR-24-3p.

6. The kit according to claim 4 or 5, wherein the nucleic acid(s) is/are polynucleotide(s) 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: 116 and 676 or a nucleotide sequence 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: 116 and 676,
(h) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 116 and 676 or a nucleotide sequence 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: 116 and 676 or a nucleotide sequence 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(s) capable of specifically binding to at least one polynucleotide selected from the group consisting of the following other esophageal cancer markers miR-675-5p, miR-486-3p, miR-6777-5p, miR-4497, miR-296-3p, miR-6738-5p, miR-4731-5p, miR-6889-5p, miR-6786-5p, miR-92a-3p, miR-4294, miR-4763-3p, miR-6076, miR-663a, miR-760, miR-4667-5p, miR-6090, miR-4730, miR-7106-5p, miR-3196, miR-5698, miR-6087, miR-4665-5p, miR-8059 and miR-6879-5p.

8. The kit according to claim 7, wherein miR-675-5p is hsa-miR-675-5p, miR-486-3p is hsa-miR-486-3p, miR-6777-5p is hsa-miR-6777-5p, miR-4497 is hsa-miR-4497, miR-296-3p is hsa-miR-296-3p, miR-6738-5p is hsa-miR-6738-5p, miR-4731-5p is hsa-miR-4731-5p, miR-6889-5p is hsa-miR-6889-5p, miR-6786-5p is hsa-miR-6786-5p, miR-92a-3p is hsa-miR-92a-3p, miR-4294 is hsa-miR-4294, miR-4763-3p is hsa-miR-4763-3p, miR-6076 is hsa-miR-6076, miR-663a is hsa-miR-663a, miR-760 is hsa-miR-760, miR-4667-5p is hsa-miR-4667-5p, miR-6090 is hsa-miR-6090, miR-4730 is hsa-miR-4730, miR-7106-5p is hsa-miR-7106-5p, miR-3196 is hsa-miR-3196, miR-5698 is hsa-miR-5698, miR-6087 is hsa-miR-6087, miR-4665-5p is hsa-miR-4665-5p, miR-8059 is hsa-miR-8059, and miR-6879-5p is hsa-miR-6879-5p.

9. The kit according to claim 7 or 8, wherein the nucleic acid(s) is/are polynucleotide(s) 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: 190 to 214 or a nucleotide sequence 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: 190 to 214,
(m) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 190 to 214 or a nucleotide sequence 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: 190 to 214 or a nucleotide sequence 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 nucleic acids capable of specifically binding to at least two polynucleotides, respectively, selected from all of the esophageal cancer markers according to claim 1 or 2.

11. A device for the detection of esophageal cancer, comprising a nucleic acid capable of specifically binding to at least one polynucleotide selected from the group consisting of the following esophageal cancer markers: miR-204-3p, miR-1247-3p, miR-6875-5p, miR-6857-5p, miR-6726-5p, miR-3188, miR-8069, miR-4257, miR-1343-3p, miR-7108-5p, miR-6825-5p, miR-7641, miR-3185, miR-4746-3p, miR-6791-5p, miR-6893-5p, miR-4433b-3p, miR-3135b, miR-6781-5p, miR-1908-5p, miR-4792, miR-7845-5p, miR-4417, miR-3184-5p, miR-1225-5p, miR-1231, miR-1225-3p, miR-150-3p, miR-4433-3p, miR-6125, miR-4513, miR-6787-5p, miR-6784-5p, miR-615-5p, miR-6765-3p, miR-5572, miR-6842-5p, miR-8063, miR-6780b-5p, miR-187-5p, miR-128-1-5p, miR-6729-5p, miR-6741-5p, miR-6757-5p, miR-7110-5p, miR-7975, miR-1233-5p, miR-6845-5p, miR-3937, miR-4467, miR-7109-5p, miR-6088, miR-6782-5p, miR-5195-3p, miR-4454, miR-6724-5p, miR-8072, miR-4516, miR-6756-5p, miR-4665-3p, miR-6826-5p, miR-6820-5p, miR-6887-5p, miR-3679-5p, miR-7847-3p, miR-6721-5p, miR-3622a-5p, miR-939-5p, miR-602, miR-7977, miR-6749-5p, miR-1914-3p, miR-4651, miR-4695-5p, miR-6848-5p, miR-1228-3p, miR-642b-3p, miR-6746-5p, miR-3620-5p, miR-3131, miR-6732-5p, miR-7113-3p, miR-23a-3p, miR-3154, miR-4723-5p, miR-3663-3p, miR-4734, miR-6816-5p, miR-4442, miR-4476, miR-423-5p, miR-1249, miR-6515-3p, miR-887-3p, miR-4741, miR-6766-3p, miR-4673, miR-6779-5p, miR-4706, miR-1268b, miR-4632-5p, miR-3197, miR-6798-5p, miR-711, miR-6840-3p, miR-6763-5p, miR-6727-5p, miR-371a-5p, miR-6824-5p, miR-4648, miR-1227-5p, miR-564, miR-3679-3p, miR-2861, miR-6737-5p, miR-4725-3p, miR-6716-5p, miR-4675, miR-1915-3p, miR-671-5p, miR-3656, miR-6722-3p, miR-4707-5p, miR-4449, miR-1202, miR-4649-5p, miR-744-5p, miR-642a-3p, miR-451a, miR-6870-5p, miR-4443, miR-6808-5p, miR-4728-5p, miR-937-5p, miR-135a-3p, miR-663b, miR-1343-5p, miR-6822-5p, miR-6803-5p, miR-6805-3p, miR-128-2-5p, miR-4640-5p, miR-1469, miR-92a-2-5p, miR-3940-5p, miR-4281, miR-1260b, miR-4758-5p, miR-1915-5p, miR-5001-5p, miR-4286, miR-6126, miR-6789-5p, miR-4459, miR-1268a, miR-6752-5p, miR-6131, miR-6800-5p, miR-4532, miR-6872-3p, miR-718, miR-6769a-5p, miR-4707-3p, miR-6765-5p, miR-4739, miR-4525, miR-4270, miR-4534, miR-6785-5p, miR-6850-5p, miR-4697-5p, miR-1260a, miR-4486, miR-6880-5p, miR-6802-5p, miR-6861-5p, miR-92b-5p, miR-1238-5p, miR-6851-5p, miR-7704, miR-149-3p, miR-4689,

miR-4688, miR-125a-3p, miR-23b-3p, miR-614, miR-1913, miR-16-5p, miR-6717-5p, miR-3648, miR-3162-5p, miR-1909-3p, miR-8073, miR-6769b-5p, miR-6836-3p, miR-4484, miR-6819-5p, and miR-6794-5p.

12. The device according to claim 11, wherein miR-204-3p is hsa-miR-204-3p, miR-1247-3p is hsa-miR-1247-3p, miR-6875-5p is hsa-miR-6875-5p, miR-6857-5p is hsa-miR-6857-5p, miR-6726-5p is hsa-miR-6726-5p, miR-3188 is hsa-miR-3188, miR-8069 is hsa-miR-8069, miR-4257 is hsa-miR-4257, miR-1343-3p is hsa-miR-1343-3p, miR-7108-5p is hsa-miR-7108-5p, miR-6825-5p is hsa-miR-6825-5p, miR-7641 is hsa-miR-7641, miR-3185 is hsa-miR-3185, miR-4746-3p is hsa-miR-4746-3p, miR-6791-5p is hsa-miR-6791-5p, miR-6893-5p is hsa-miR-6893-5p, miR-4433b-3p is hsa-miR-4433b-3p, miR-3135b is hsa-miR-3135b, miR-6781-5p is hsa-miR-6781-5p, miR-1908-5p is hsa-miR-1908-5p, miR-4792 is hsa-miR-4792, miR-7845-5p is hsa-miR-7845-5p, miR-4417 is hsa-miR-4417, miR-3184-5p is hsa-miR-3184-5p, miR-1225-5p is hsa-miR-1225-5p, miR-1231 is hsa-miR-1231, miR-1225-3p is hsa-miR-1225-3p, miR-150-3p is hsa-miR-150-3p, miR-4433-3p is hsa-miR-4433-3p, miR-6125 is hsa-miR-6125, miR-4513 is hsa-miR-4513, miR-6787-5p is hsa-miR-6787-5p, miR-6784-5p is hsa-miR-6784-5p, miR-615-5p is hsa-miR-615-5p, miR-6765-3p is hsa-miR-6765-3p, miR-5572 is hsa-miR-5572, miR-6842-5p is hsa-miR-6842-5p, miR-8063 is hsa-miR-8063, miR-6780b-5p is hsa-miR-6780b-5p, miR-187-5p is hsa-miR-187-5p, miR-128-1-5p is hsa-miR-128-1-5p, miR-6729-5p is hsa-miR-6729-5p, miR-6741-5p is hsa-miR-6741-5p, miR-6757-5p is hsa-miR-6757-5p, miR-7110-5p is hsa-miR-7110-5p, miR-7975 is hsa-miR-7975, miR-1233-5p is hsa-miR-1233-5p, miR-6845-5p is hsa-miR-6845-5p, miR-3937 is hsa-miR-3937, miR-4467 is hsa-miR-4467, miR-7109-5p is hsa-miR-7109-5p, miR-6088 is hsa-miR-6088, miR-6782-5p is hsa-miR-6782-5p, miR-5195-3p is hsa-miR-5195-3p, miR-4454 is hsa-miR-4454, miR-6724-5p is hsa-miR-6724-5p, miR-8072 is hsa-miR-8072, miR-4516 is hsa-miR-4516, miR-6756-5p is hsa-miR-6756-5p, miR-4665-3p is hsa-miR-4665-3p, miR-6826-5p is hsa-miR-6826-5p, miR-6820-5p is hsa-miR-6820-5p, miR-6887-5p is hsa-miR-6887-5p, miR-3679-5p is hsa-miR-3679-5p, miR-7847-3p is hsa-miR-7847-3p, miR-6721-5p is hsa-miR-6721-5p, miR-3622a-5p is hsa-miR-3622a-5p, miR-939-5p is hsa-miR-939-5p, miR-602 is hsa-miR-602, miR-7977 is hsa-miR-7977, miR-6749-5p is hsa-miR-6749-5p, miR-1914-3p is hsa-miR-1914-3p, miR-4651 is hsa-miR-4651, miR-4695-5p is hsa-miR-4695-5p, miR-6848-5p is hsa-miR-6848-5p, miR-1228-3p is hsa-miR-1228-3p, miR-642b-3p is hsa-miR-642b-3p, miR-6746-5p is hsa-miR-6746-5p, miR-3620-5p is hsa-miR-3620-5p, miR-3131 is hsa-miR-3131, miR-6732-5p is hsa-miR-6732-5p, miR-7113-3p is hsa-miR-7113-3p, miR-23a-3p is hsa-miR-23a-3p, miR-3154 is hsa-miR-3154, miR-4723-5p is hsa-miR-4723-5p, miR-3663-3p is hsa-miR-3663-3p, miR-4734 is hsa-miR-4734, miR-6816-5p is hsa-miR-6816-5p, miR-4442 is hsa-miR-4442, miR-4476 is hsa-miR-4476, miR-423-5p is hsa-miR-423-5p, miR-1249 is hsa-miR-1249, miR-6515-3p is hsa-miR-6515-3p, miR-887-3p is hsa-miR-887-3p, miR-4741 is hsa-miR-4741, miR-6766-3p is hsa-miR-6766-3p, miR-4673 is hsa-miR-4673, miR-6779-5p is hsa-miR-6779-5p, miR-4706 is hsa-miR-4706, miR-1268b is hsa-miR-1268b, miR-4632-5p is hsa-miR-4632-5p, miR-3197 is hsa-miR-3197, miR-6798-5p is hsa-miR-6798-5p, miR-711 is hsa-miR-711, miR-6840-3p is hsa-miR-6840-3p, miR-6763-5p is hsa-miR-6763-5p, miR-6727-5p is hsa-miR-6727-5p, miR-371a-5p is hsa-miR-371a-5p, miR-6824-5p is hsa-miR-6824-5p, miR-4648 is hsa-miR-4648, miR-1227-5p is hsa-miR-1227-5p, miR-564 is hsa-miR-564, miR-3679-3p is hsa-miR-3679-3p, miR-2861 is hsa-miR-2861, miR-6737-5p is hsa-miR-6737-5p, miR-4725-3p is hsa-miR-4725-3p, miR-6716-5p is hsa-miR-6716-5p, miR-4675 is hsa-miR-4675, miR-1915-3p is hsa-miR-1915-3p, miR-671-5p is hsa-miR-671-5p, miR-3656 is hsa-miR-3656, miR-6722-3p is hsa-miR-6722-3p, miR-4707-5p is hsa-miR-4707-5p, miR-4449 is hsa-miR-4449, miR-1202 is hsa-miR-1202, miR-4649-5p is hsa-miR-4649-5p, miR-744-5p is hsa-miR-744-5p, miR-642a-3p is hsa-miR-642a-3p, miR-451a is hsa-miR-451a, miR-6870-5p is hsa-miR-6870-5p, miR-4443 is hsa-miR-4443, miR-6808-5p is hsa-miR-6808-5p, miR-4728-5p is hsa-miR-4728-5p, miR-937-5p is hsa-miR-937-5p, miR-135a-3p is hsa-miR-135a-3p, miR-663b is hsa-miR-663b, miR-1343-5p is hsa-miR-1343-5p, miR-6822-5p is hsa-miR-6822-5p, miR-6803-5p is hsa-miR-6803-5p, miR-6805-3p is hsa-miR-6805-3p, miR-128-2-5p is hsa-miR-128-2-5p, miR-4640-5p is hsa-miR-4640-5p, miR-1469 is hsa-miR-1469, miR-92a-2-5p is hsa-miR-92a-2-5p, miR-3940-5p is hsa-miR-3940-5p, miR-4281 is hsa-miR-4281, miR-1260b is hsa-miR-1260b, miR-4758-5p is hsa-miR-4758-5p, miR-1915-5p is hsa-miR-1915-5p, miR-5001-5p is hsa-miR-5001-5p, miR-4286 is hsa-miR-4286, miR-6126 is hsa-miR-6126, miR-6789-5p is hsa-miR-6789-5p, miR-4459 is hsa-miR-4459, miR-1268a is hsa-miR-1268a, miR-6752-5p is hsa-miR-6752-5p, miR-6131 is hsa-miR-6131, miR-6800-5p is hsa-miR-6800-5p, miR-4532 is hsa-miR-4532, miR-6872-3p is hsa-miR-6872-3p, miR-718 is hsa-miR-718, miR-6769a-5p is hsa-miR-6769a-5p, miR-4707-3p is hsa-miR-4707-3p, miR-6765-5p is hsa-miR-6765-5p, miR-4739 is hsa-miR-4739, miR-4525 is hsa-miR-4525, miR-4270 is hsa-miR-4270, miR-4534 is hsa-miR-4534, miR-6785-5p is hsa-miR-6785-5p, miR-6850-5p is hsa-miR-6850-5p, miR-4697-5p is hsa-miR-4697-5p, miR-1260a is hsa-miR-1260a, miR-4486 is hsa-miR-4486, miR-6880-5p is hsa-miR-6880-5p, miR-6802-5p is hsa-miR-6802-5p, miR-6861-5p is hsa-miR-6861-5p, miR-92b-5p is hsa-miR-92b-5p, miR-1238-5p is hsa-miR-1238-5p, miR-6851-5p is hsa-miR-6851-5p, miR-7704 is hsa-miR-7704, miR-149-3p is hsa-miR-149-3p, miR-4689 is hsa-miR-4689, miR-4688 is hsa-miR-4688, miR-125a-3p is hsa-miR-125a-3p, miR-23b-3p is hsa-miR-23b-3p, miR-614 is hsa-miR-614, miR-1913 is hsa-miR-1913, miR-16-5p is hsa-miR-16-5p, miR-6717-5p is hsa-miR-6717-5p, miR-3648 is hsa-miR-3648, miR-3162-5p is hsa-miR-3162-5p, miR-1909-3p is hsa-

miR-1909-3p, miR-8073 is hsa-miR-8073, miR-6769b-5p is hsa-miR-6769b-5p, miR-6836-3p is hsa-miR-6836-3p, miR-4484 is hsa-miR-4484, miR-6819-5p is hsa-miR-6819-5p, and miR-6794-5p is hsa-miR-6794-5p.

13. The device according to claim 11 or 12, wherein the nucleic acid(s) is/are 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 115, 117 to 189, and 666 to 675 or a nucleotide sequence 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 115, 117 to 189, and 666 to 675,
(c) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 1 to 115, 117 to 189, and 666 to 675 or a nucleotide sequence 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 115, 117 to 189, and 666 to 675 or a nucleotide sequence 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 nucleic acid(s) capable of specifically binding to polynucleotide(s) selected from other esophageal cancer markers miR-575 and miR-24-3p.

15. The device according to claim 14, wherein miR-575 is hsa-miR-575, and miR-24-3p is hsa-miR-24-3p.

16. The device according to claim 14 or 15, wherein the nucleic acid(s) is/are polynucleotide(s) 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: 116 and 676 or a nucleotide sequence 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: 116 and 676,
(h) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 116 and 676 or a nucleotide sequence 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: 116 and 676 or a nucleotide sequence 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 nucleic acid(s) capable of specifically binding to at least one polynucleotide selected from the group consisting of the following other esophageal cancer markers: miR-675-5p, miR-486-3p, miR-6777-5p, miR-4497, miR-296-3p, miR-6738-5p, miR-4731-5p, miR-6889-5p, miR-6786-5p, miR-92a-3p, miR-4294, miR-4763-3p, miR-6076, miR-663a, miR-760, miR-4667-5p, miR-6090, miR-4730, miR-7106-5p, miR-3196, miR-5698, miR-6087, miR-4665-5p, miR-8059, and miR-6879-5p.

18. The device according to claim 17, wherein miR-675-5p is hsa-miR-675-5p, miR-486-3p is hsa-miR-486-3p, miR-6777-5p is hsa-miR-6777-5p, miR-4497 is hsa-miR-4497, miR-296-3p is hsa-miR-296-3p, miR-6738-5p is hsa-miR-6738-5p, miR-4731-5p is hsa-miR-4731-5p, miR-6889-5p is hsa-miR-6889-5p, miR-6786-5p is hsa-miR-6786-5p, miR-92a-3p is hsa-miR-92a-3p, miR-4294 is hsa-miR-4294, miR-4763-3p is hsa-miR-4763-3p, miR-6076 is hsa-miR-6076, miR-663a is hsa-miR-663a, miR-760 is hsa-miR-760, miR-4667-5p is hsa-miR-4667-5p, miR-6090 is hsa-miR-6090, miR-4730 is hsa-miR-4730, miR-7106-5p is hsa-miR-7106-5p, miR-3196 is hsa-miR-3196, miR-5698 is hsa-miR-5698, miR-6087 is hsa-miR-6087, miR-4665-5p is hsa-miR-4665-5p, miR-8059 is hsa-miR-8059, and miR-6879-5p is hsa-miR-6879-5p.

19. The device according to claim 17 or 18, wherein the nucleic acid(s) is/are polynucleotide(s) 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: 190 to 214 or a nucleotide sequence 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: 190 to 214,
(m) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 190 to 214 or a nucleotide sequence 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: 190 to 214 or a nucleotide sequence 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 nucleic acids capable of specifically binding to at least two polynucleotides, respectively, selected from all of the esophageal cancer markers according to claim 11 or 12.

23. A method for detecting esophageal cancer, comprising measuring expression level(s) of target nucleic acid(s) in a sample of 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 the *in vitro* whether or not the subject has esophageal cancer using both of the measured expression level(s) and control expression level(s) 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

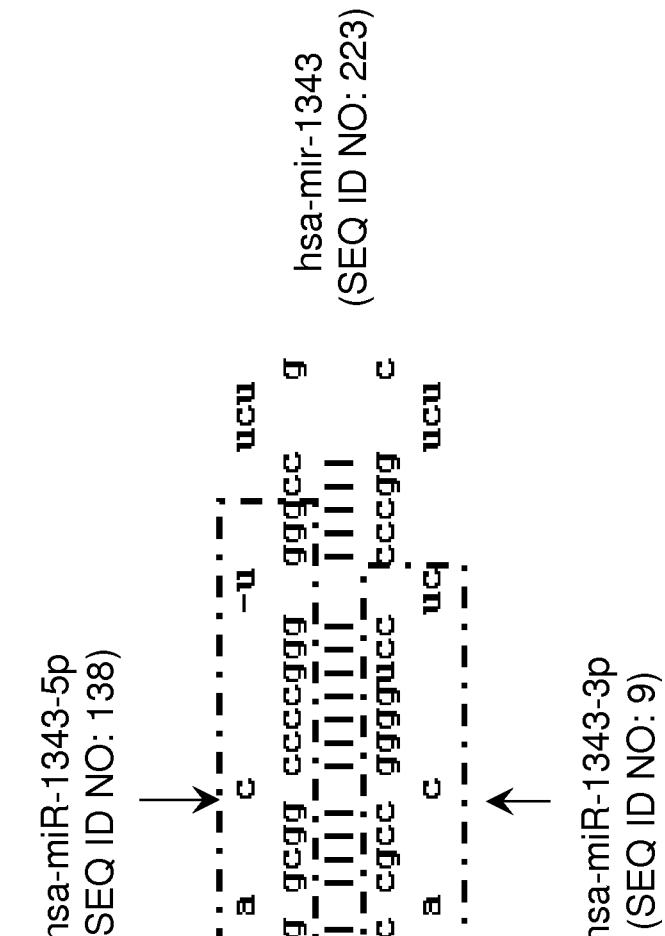

hsa-miR-1343-5p
(SEQ ID NO: 138)
hsa-miR-1343-3p
(SEQ ID NO: 9)
hsa-mir-1343
(SEQ ID NO: 223)

Fig. 2

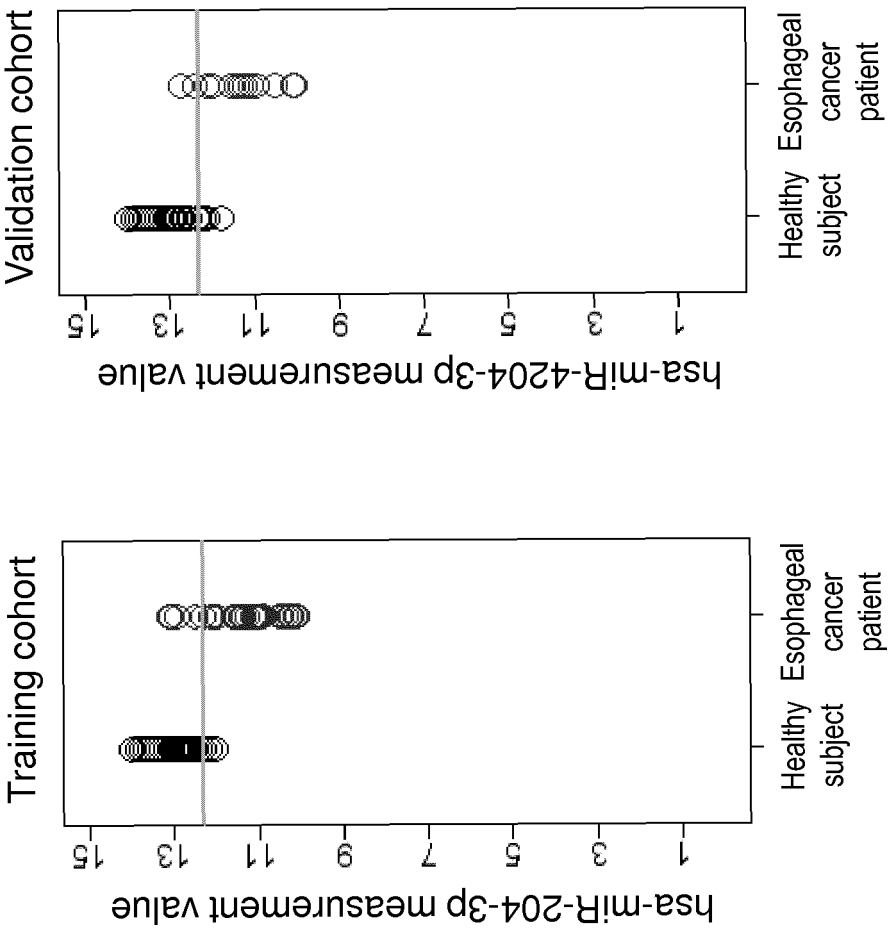

Validation cohort
hsa-miR-4204-3p measurement value
1
3
5
7
9
11
13
15
Healthy subject
Esophageal cancer patient
Training cohort
hsa-miR-204-3p measurement value
1
3
5
7
9
11
13
15
Healthy subject
Esophageal cancer patient

Fig. 3

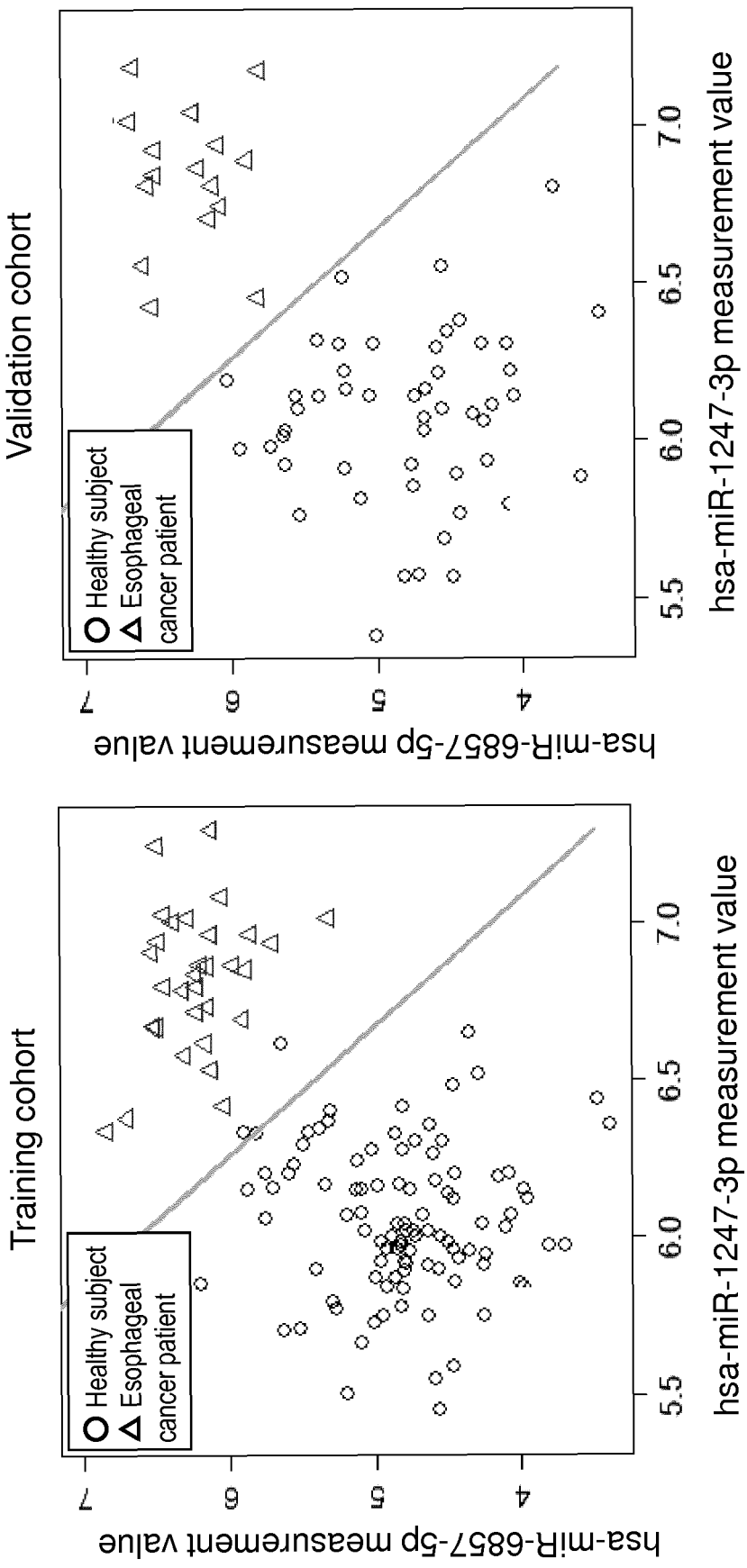
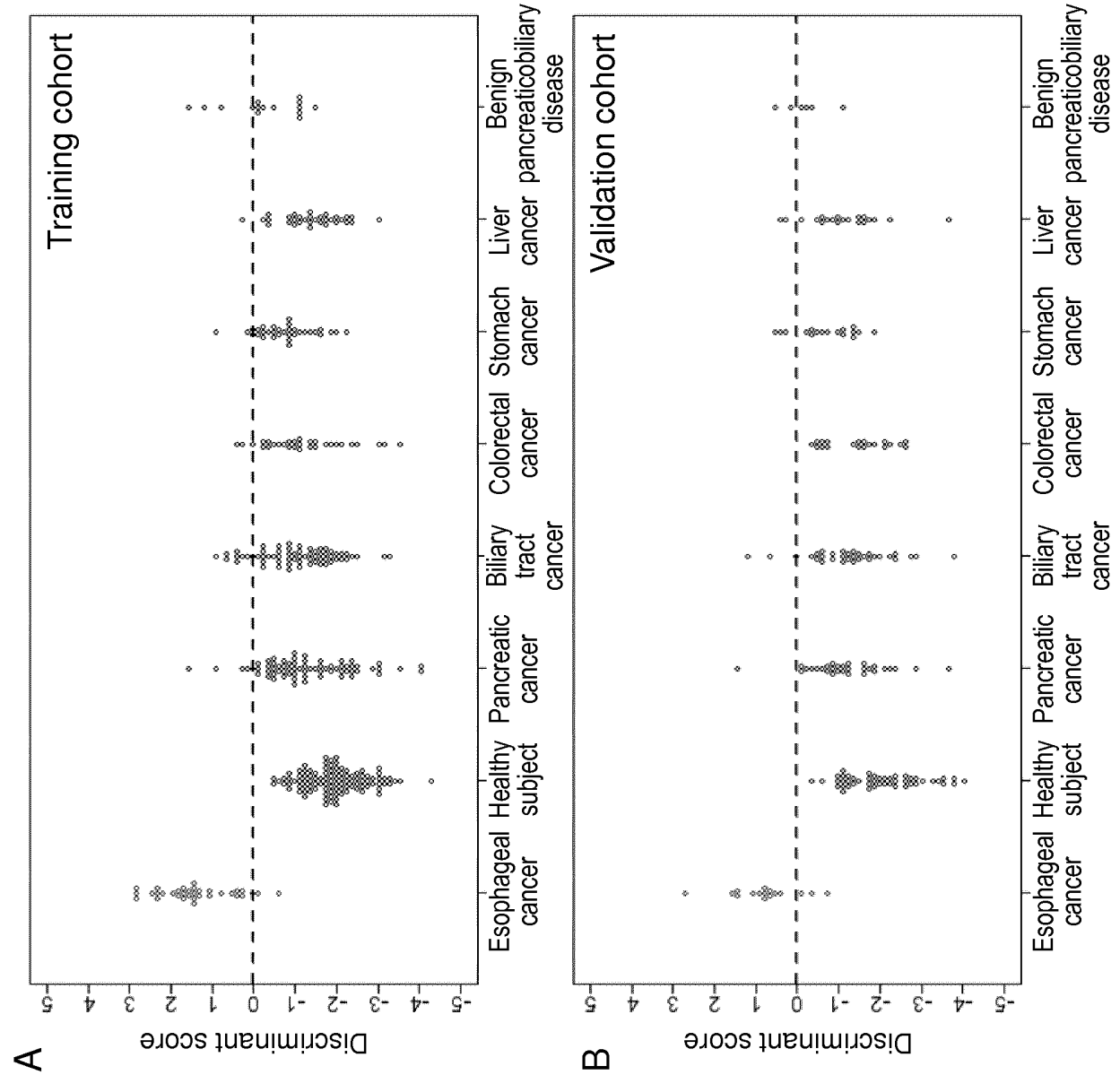

Training cohort
Validation cohort
Healthy subject
Esophageal cancer patient
hsa-miR-6857-5p measurement value
hsa-miR-1247-3p measurement value
4
5
6
7
5.5
6.0
6.5
7.0

Fig. 4


A
Training cohort
Discriminant score
5
4
3
2
1
0
-1
-2
-3
-4
-5
Esophageal cancer
Healthy subject
Pancreatic cancer
Biliary tract cancer
Colorectal cancer
Stomach cancer
Liver cancer
Benign pancreaticobiliary disease
B
Validation cohort
Discriminant score
5
4
3
2
1
0
-1
-2
-3
-4
-5
Esophageal cancer
Healthy subject
Pancreatic cancer
Biliary tract cancer
Colorectal cancer
Stomach cancer
Liver cancer
Benign pancreaticobiliary disease

INTERNATIONAL SEARCH REPORT

International application No.
PCT/JP2015/067580

A. CLASSIFICATION OF SUBJECT MATTER
C12N15/09(2006.01)i, *C12Q1/68*(2006.01)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)
C12N15/09, C12Q1/68, 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/REGISTRY/MEDLINE/BIOSIS(STN), DWPI(Thomson Innovation), GenBank/EMBL/DDBJ/GeneSeq

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X Y	Noami S. SAKAI, "A review of the current understanding and clinical utility of miRNAs in esophageal cancer", Seminars in Cancer Biology, 2013, Vol.23P, p.512-521	1-3,7-13, 17-25 4-6,14-16
X Y	JP 2011-501943 A (The Ohio State University Research Foundation), 20 January 2011 (20.01.2011), claims & US 2010/0285471 A1 & WO 2009/029129 A1 & EP 2212440 A1 & CA 2702241 A & CN 101861401 A & CN 103937876 A	1-3,7-13, 17-25 4-6,14-16
X Y	JP 2010-510769 A (Capitalbio Corp.), 08 April 2010 (08.04.2010), claims; examples & WO 2008/064519 A1 & CN 101316935 A	1-3,7-13, 17-25 4-6,14-16

☒ 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
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"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
03 September 2015 (03.09.15)	15 September 2015 (15.09.15)
Name and mailing address of the ISA/ Japan Patent Office 3-4-3,Kasumigaseki,Chiyoda-ku, Tokyo 100-8915,Japan	Authorized officer Telephone No.

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INTERNATIONAL SEARCH REPORT

International application No.
PCT/JP2015/067580

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X Y	Hiroshi ITO, "Cancer and MicroRNA as a Diagnostic and Therapeutic Marker", Yamaguchi Medical Journal, 2013, vol.62, no.4, pages 191 to 197	1-3,7-13, 17-25 4-6,14-16
Y	US 2014/0031246 A1 (THE JOHNS HOPKINS UNIVERSITY), 30 June 2014 (30.06.2014), claims & WO 2012/012689 A2	4-6,14-16

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REFERENCES CITED IN THE DESCRIPTION

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Patent documents cited in the description

- US 2014031246 A **[0009]**
- JP 2014125036 A **[0274]**
- JP 2015070379 A **[0274]**

Non-patent literature cited in the description

- Esophagus Cancer. American Cancer Society, 2014, 2-8, 19-20, 29-41 **[0010]**
- **SOBIN, L. et al.** *TNM Classification of Malignant Tumours, the 7th edition, Japanese version,* 2009, 63-68 **[0010]**
- **TERADA, T. et al.** *International Journal of Clinical and Experimental Medicine,* 2013, vol. 6 (3), 219-26 **[0010]**
- **ZHENG ZHANG et al.** *J. Comput. Biol.,* 2000, vol. 7, 203-214 **[0035]**
- **ALTSCHUL, S.F. et al.** *Journal of Molecular Biology,* 1990, vol. 215, 403-410 **[0035]**
- **PEARSON, W.R. et al.** *Proc. Natl. Acad. Sci. U. S. A.,* 1988, vol. 85, 2444-2448 **[0035]**
- **NIELSEN, P.E. et al.** *Science,* 1991, vol. 254, 1497-500 **[0036]**
- **OBIKA, S. et al.** *Tetrahedron Lett.,* 1998, vol. 39, 5401-5404 **[0036]**
- **LIM LP et al.** *Science,* 2003, vol. 299, 1540 **[0045] [0084]**
- **MORIN RD et al.** *Genome Res,* 2008, vol. 18, 610-621 **[0046] [0136] [0200] [0217]**
- **LADEWIG E et al.** *Genome Res,* 2012, vol. 22, 1634-1645 **[0047] [0048] [0049] [0054] [0055] [0059] [0060] [0063] [0076] [0077] [0079] [0081] [0083] [0086] [0087] [0088] [0089] [0092] [0095] [0097] [0103] [0105] [0106] [0107] [0115] [0119] [0122] [0125] [0126] [0132] [0140] [0142] [0147] [0149] [0150] [0151] [0153] [0159] [0175] [0177] [0183] [0184] [0185] [0198] [0201] [0203] [0205] [0207] [0209] [0214] [0215] [0219] [0220] [0221] [0224] [0236] [0239] [0241] [0242] [0252] [0258] [0264] [0265] [0267] [0268]**
- **STARK MS et al.** *PLoS One,* 2010, vol. 5, e9685 **[0050] [0057] [0068] [0124] [0146] [0192] [0253] [0261]**
- **WANG HJ et al.** *Shock,* 2013, vol. 39, 480-487 **[0051] [0082] [0101] [0257] [0263]**
- **GOFF LA et al.** *PLoS One,* 2009, vol. 4, e7192 **[0052] [0191] [0196] [0212] [0244]**
- **PERSSON H et al.** *Cancer Res,* 2011, vol. 71, 78-86 **[0053] [0058] [0065] [0104] [0117] [0118] [0129] [0131] [0139] [0141] [0143] [0145] [0154] [0161] [0163] [0168] [0171] [0178] [0182] [0187] [0193] [0208] [0210] [0216] [0227] [0228] [0240] [0245] [0249] [0251] [0256]**
- **YOO JK et al.** *Arch Pharm Res,* 2013, vol. 36, 353-358 **[0056]**
- **PLE H et al.** *PLoS One,* 2012, vol. 7, e50746 **[0061] [0066] [0109]**
- **JIMA DD et al.** *Blood,* 2010, vol. 116, e118-e127 **[0062] [0067] [0073] [0075] [0094] [0099] [0102] [0133] [0134] [0144] [0169] [0176] [0199] [0204] [0211] [0213] [0218] [0237] [0266]**
- **BAR M et al.** *Stem Cells,* 2008, vol. 26, 2496-2505 **[0064] [0116] [0164] [0194] [0232] [0262]**
- **BEREZIKOV E et al.** *Mol Cell,* 2007, vol. 28, 328-336 **[0069] [0070] [0071] [0091] [0120] [0155] [0223]**
- **LAGOS-QUINTANA M et al.** *Curr Biol,* 2002, vol. 12, 735-739 **[0072] [0180] [0186] [0226] [0229] [0230]**
- **SMITH JL et al.** *J Virol,* 2012, vol. 86, 5278-5287 **[0074] [0197]**
- **CUMMINS JM et al.** *Proc Natl Acad Sci USA,* 2006, vol. 103, 3687-3692 **[0078] [0113] [0156] [0160] [0173] [0222] [0231] [0247]**
- **TANDON M et al.** *Oral Dis,* 2012, vol. 18, 127-131 **[0080]**
- **QUINTANA M et al.** *Curr Biol,* 2002, vol. 12, 735-739 **[0085]**
- **VELTHUT-MEIKAS A et al.** *Mol Endocrinol,* 2013 **[0090] [0114]**
- **LIAO JY et al.** *PLoS One,* 2010, vol. 5, e10563 **[0093] [0130] [0190]**
- **YOO JK et al.** *Stem Cells Dev,* 2012, vol. 21, 2049-2057 **[0096] [0250] [0255]**
- **SCHOTTE D et al.** *Leukemia,* 2011, vol. 25, 1389-1399 **[0098]**
- **LI Y et al.** *Gene,* 2012, vol. 497, 330-335 **[0100] [0110] [0162] [0167] [0259]**
- **CREIGHTON CJ et al.** *PLoS One,* 2010, vol. 5, e9637 **[0108] [0157]**
- **WITTEN D et al.** *BMC Biol,* 2010, vol. 8, 58 **[0111] [0121] [0123]**

- **LUI WO et al.** *Cancer Res,* 2007, vol. 67, 6031-6043 **[0112] [0179]**
- **LAGOS-QUINTANA M et al.** *Science,* 2001, vol. 294, 853-858 **[0127] [0233] [0269]**
- **BEREZIKOV E et al.** *Genome Res,* 2006, vol. 16, 1289-1298 **[0128] [0138] [0165] [0172] [0248]**
- **KASASHIMA K et al.** *Biochem Biophys Res Commun,* 2004, vol. 322, 403-410 **[0135]**
- **JOYCE CE et al.** *Hum Mol Genet,* 2011, vol. 20, 4025-4040 **[0137]**
- **ARTZI S et al.** *BMC Bioinformatics,* 2008, vol. 9, 39 **[0148] [0206]**
- **SUH MR et al.** *Dev Biol,* 2004, vol. 270, 488-498 **[0152]**
- **LI H ; 2009 et al.** *J Clin Invest,* vol. 119, 3666-3677 **[0158]**
- **MEIRI E et al.** *Nucleic Acids Res,* 2010, vol. 38, 6234-6246 **[0166] [0260]**
- **MARTON S et al.** *Leukemia,* 2008, vol. 22, 330-338 **[0170]**
- **ALTUVIA Y et al.** *Nucleic Acids Res,* 2005, vol. 33, 2697-2706 **[0174]**
- **TAKADA S et al.** *Leukemia,* 2008, vol. 22, 1274-1278 **[0181]**
- **KAWAJI H et al.** *BMC Genomics,* 2008, vol. 9, 157 **[0188]**
- **MOURELATOS Z et al.** *Genes Dev,* 2002, vol. 16, 720-728 **[0189] [0243]**
- **HANSEN TB et al.** *RNA Biol,* 2011, vol. 8, 378-383 **[0195]**
- **DANNEMANN M et al.** *Genome Biol Evol,* 2012, vol. 4, 552-564 **[0202]**
- **SWAMINATHAN S et al.** *Biochem Biophys Res Commun,* 2013, vol. 434, 228-234 **[0225]**
- **CAI X et al.** *RNA,* 2007, vol. 13, 313-316 **[0234]**
- **FU H et al.** *FEBS Lett,* 2005, vol. 579, 3849-3854 **[0235]**
- **HOUBAVIY HB et al.** *Dev Cell,* 2003, vol. 5, 351-358 **[0238]**
- **VOELLENKLE C et al.** *RNA,* 2012, vol. 18, 472-484 **[0246]**
- **WATAHIKI A et al.** *PLoS One,* 2011, vol. 6, e24950 **[0254]**
- **MORIN RD. et al.** *Genome Res.,* 2008, vol. 18, 610-621 **[0270]**
- **AUSUBEL et al.** Current Protocols in Molecular Biology. John Willey & Sons, 1993 **[0519]**
- **SAMBROOK et al.** Molecular Cloning - A Laboratory Manual. Cold Spring Harbor Laboratory Press, 1989 **[0519]**
- Molecular Cloning. **SAMBROOK, J. ; RUSSEL, D.** A LABORATORY MANUAL. Cold Spring Harbor Laboratory Press, 15 January 2001, vol. 1, 7.42-7.45 **[0595]**
- A LABORATORY MANUAL. vol. 2, 8.9-8.17 **[0595]**
- **BOLSTAD, B. M. et al.** *Bioinformatics,* 2003, vol. 19, 185-193 **[0598]**
- **VENABLES, W.N. et al.** Modern Applied Statistics with S. Fourth edition. Springer, 2002 **[0603]**
- **TAKAFUMI KANAMORI et al.** Pattern Recognition. Kyoritsu Shuppan Co., Ltd, 2009 **[0603]**
- **RICHARD O. et al.** Pattern Classification Second Edition. Wiley-Interscience, 2000 **[0603]**
- **V. VAPNIK.** The Nature of Statistical Leaning Theory. Springer, 1995 **[0605]**
- Statistics of pattern recognition and learning - New concepts and approaches. **HIDEKI ASO et al.** Frontier of Statistical Science 6. Iwanami Shoten, Publishers, 2004 **[0605]**
- **NELLO CRISTIANINI et al.** Introduction to SVM. Kyoritsu Shuppan Co., Ltd, 2008 **[0605]**
- **C. CORTES et al.** *Machine Learning,* 1995, vol. 20, 273-297 **[0606]**
- **YASUSHI NAGATA et al.** Basics of statistical multiple comparison methods. Scientist Press Co., Ltd, 2007 **[0616]**
- **FUREY TS. et al.** *Bioinformatics.,* 2000, vol. 16, 906-14 **[0618]**
- **VENABLES, W. N. ; RIPLEY, B. D.** Modern Applied Statistics with S. Springer, 2002 **[0624]**

专利名称(译)	食道癌检测试剂盒或装置，以及检测方法		
公开(公告)号	EP3159406A1	公开(公告)日	2017-04-26
申请号	EP2015809775	申请日	2015-06-18
[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	SUDO HIROKO NOBUMASA HITOSHI KOZONO SATOKO KONDOU SATOSHI KAWAUCHI JUNPEI OCHIAI ATSUSHI KOJIMA MOTOHIRO		
发明人	SUDO, HIROKO NOBUMASA, HITOSHI KOZONO, SATOKO KONDOU, SATOSHI KAWAUCHI, JUNPEI OCHIAI, ATSUSHI KOJIMA, MOTOHIRO		
IPC分类号	C12N15/09 C12Q1/68 G01N33/53 G01N33/574		
CPC分类号	C12N15/09 C12Q1/68 G01N33/53 G01N33/574 C12Q1/6837 C12Q1/6886 C12Q2600/158 C12Q2600/178		
优先权	2014125036 2014-06-18 JP 2015070379 2015-03-30 JP		
其他公开文献	EP3159406A4		
外部链接	Espacenet		

摘要(译)

旨在提供用于检测食道癌的试剂盒或装置以及用于检测食道癌的方法。本发明提供用于检测食道癌的试剂盒或装置，其包含能够特异性结合受试者样品中的miRNA的核酸，以及用于检测食道癌的方法，包括测量miRNA。体外。