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(54) **METHOD AND NUCLEIC ACIDS FOR THE ANALYSIS OF COLON CELL PROLIFERATIVE DISORDERS**

(76) Inventors: **Peter Adorjan**, Berlin (DE); **Matthias Burger**, Berlin (DE); **Sabine Maier**, Berlin (DE); **Ralf Lesche**, Berlin (DE); **Susan Cottrell**, Seattle, WA (US); **Suzanne Mooney**, Seattle, WA (US)

Correspondence Address:
DAVIS WRIGHT TREMAINE, LLP
2600 CENTURY SQUARE
1501 FOURTH AVENUE
SEATTLE, WA 98101-1688 (US)

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C07K 14/47 (2006.01)

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(57) **ABSTRACT**

The invention provides methods and nucleic acids for detecting, differentiating or distinguishing between colon cell proliferative disorders by analysis of one or more of the genes Versican, TPEF, H-Cadherin, Calcitonin, and EYA4. The invention further provides novel nucleic acid sequences useful for the cell proliferative disorder specific analysis of said genes as well as methods, assays and kits thereof.

FIGURE 1

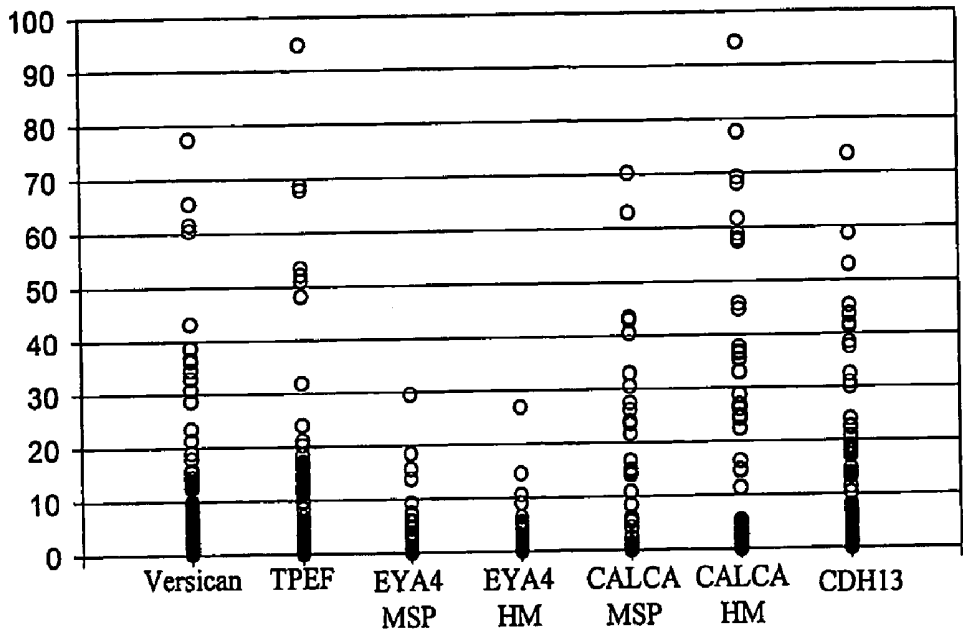

100
90
80
70
60
50
40
30
20
10
0
Versican
TPEF
EYA4 MSP
EYA4 HM
CALCA MSP
CALCA HM
CDH13

FIGURE 2

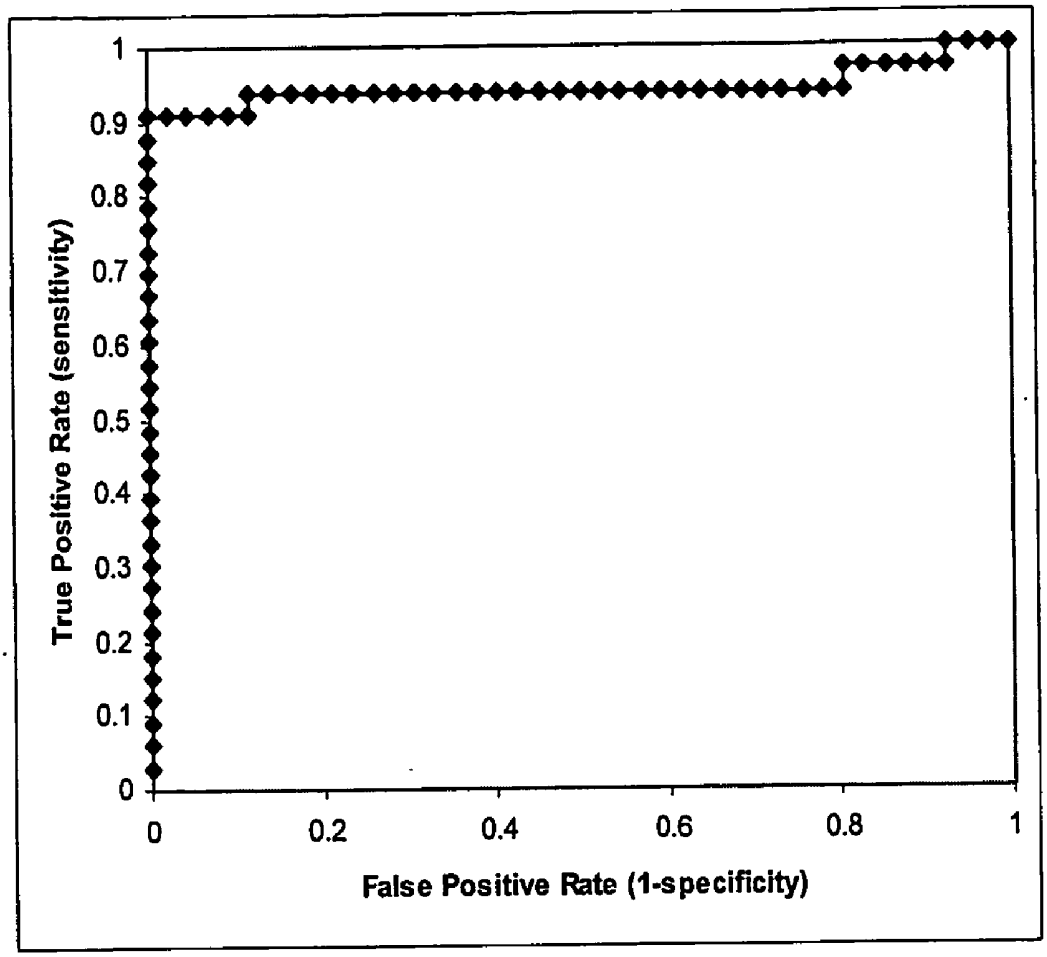

True Positive Rate (sensitivity)
False Positive Rate (1-specificity)
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1
0
0.2
0.4
0.6
0.8
1

FIGURE 3

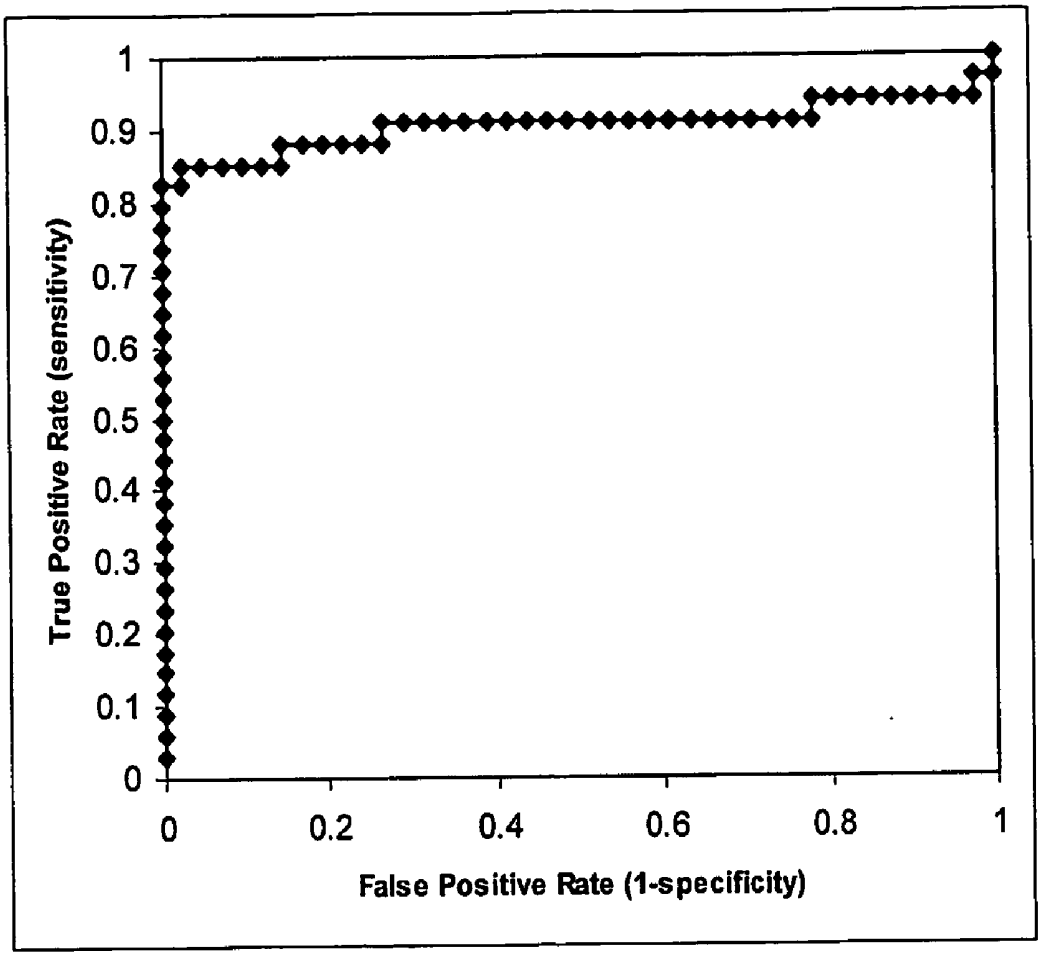

True Positive Rate (sensitivity)
False Positive Rate (1-specificity)
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1
0
0.2
0.4
0.6
0.8
1

FIGURE 4

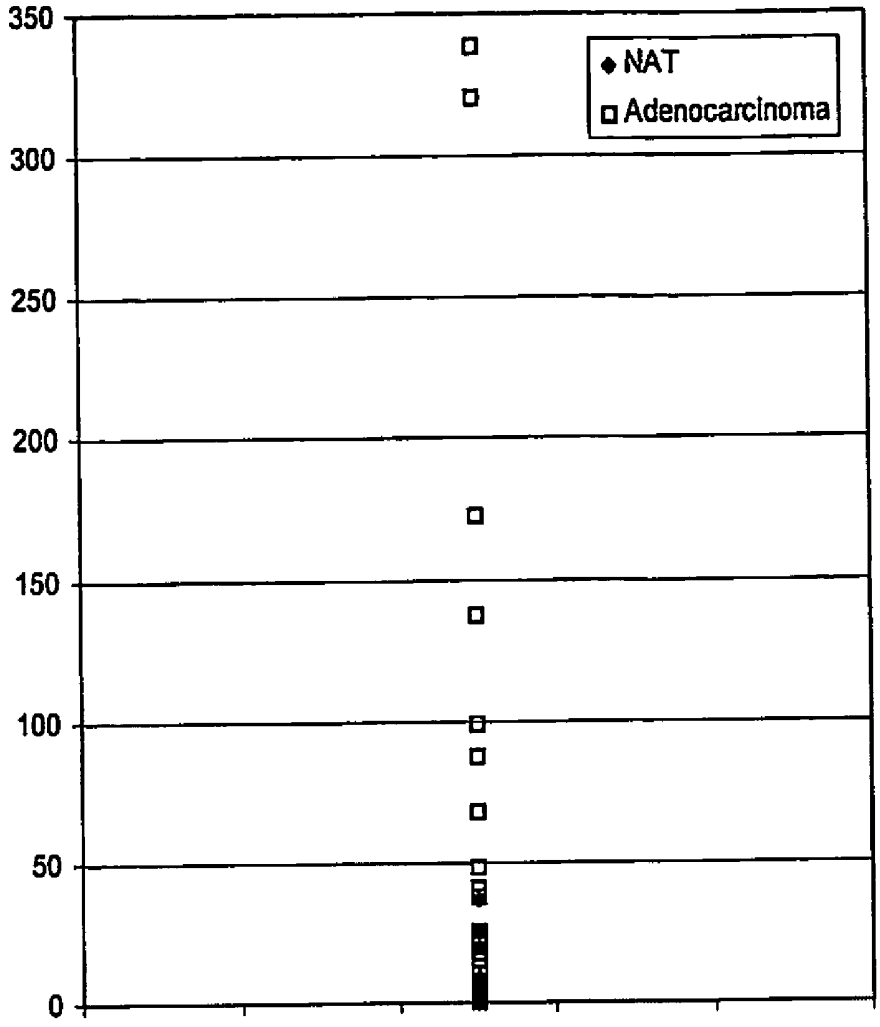


FIGURE 5

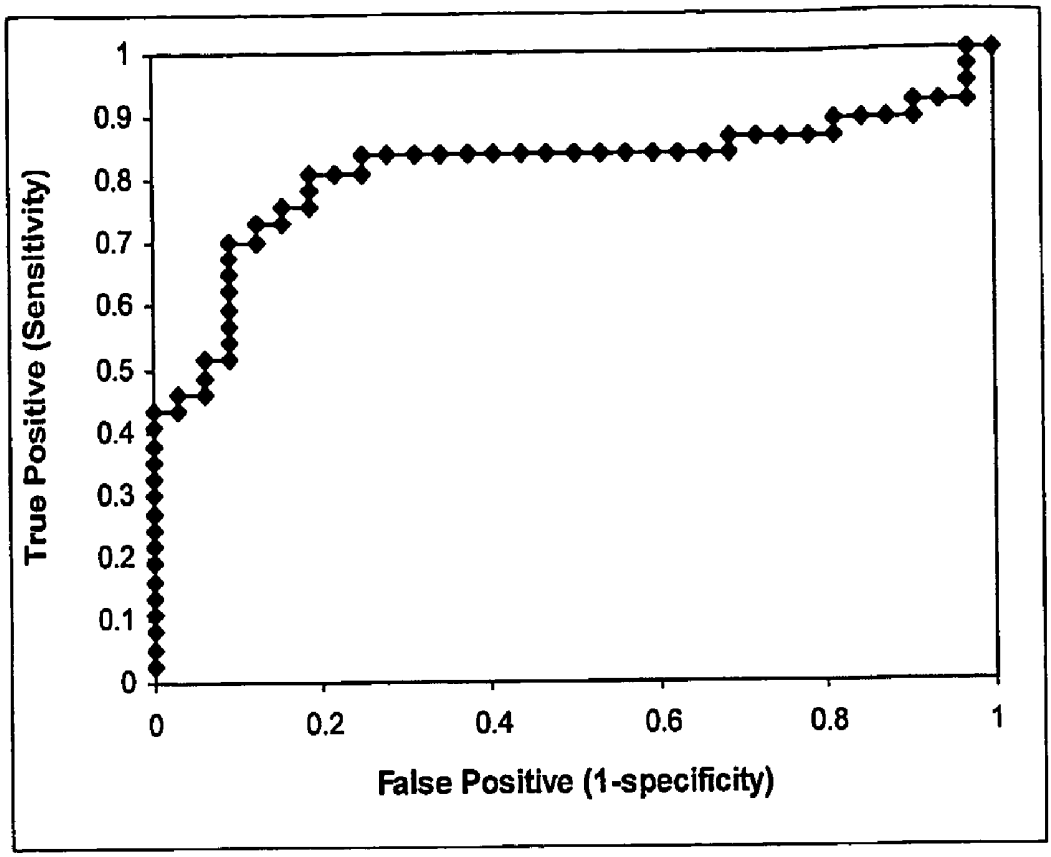

True Positive (Sensitivity)
False Positive (1-specificity)
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1
0
0.2
0.4
0.6
0.8
1

FIGURE 6

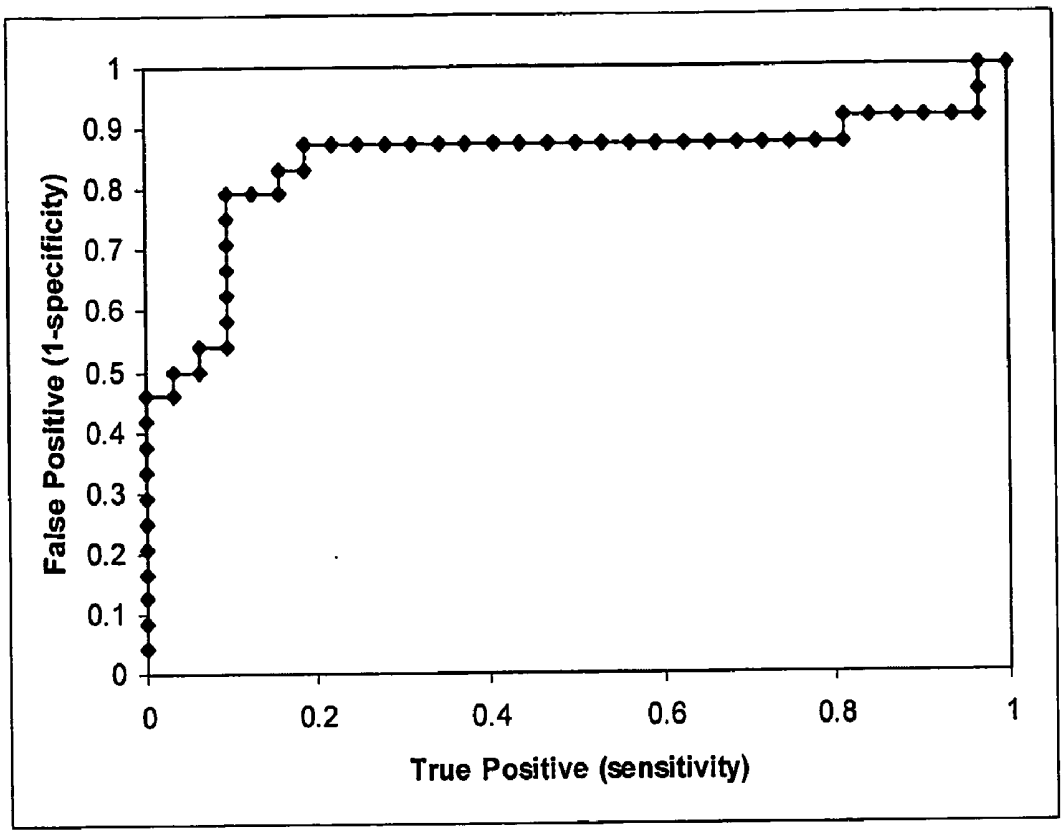

False Positive (1-specificity)
True Positive (sensitivity)
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1
0
0.2
0.4
0.6
0.8
1

FIGURE 7

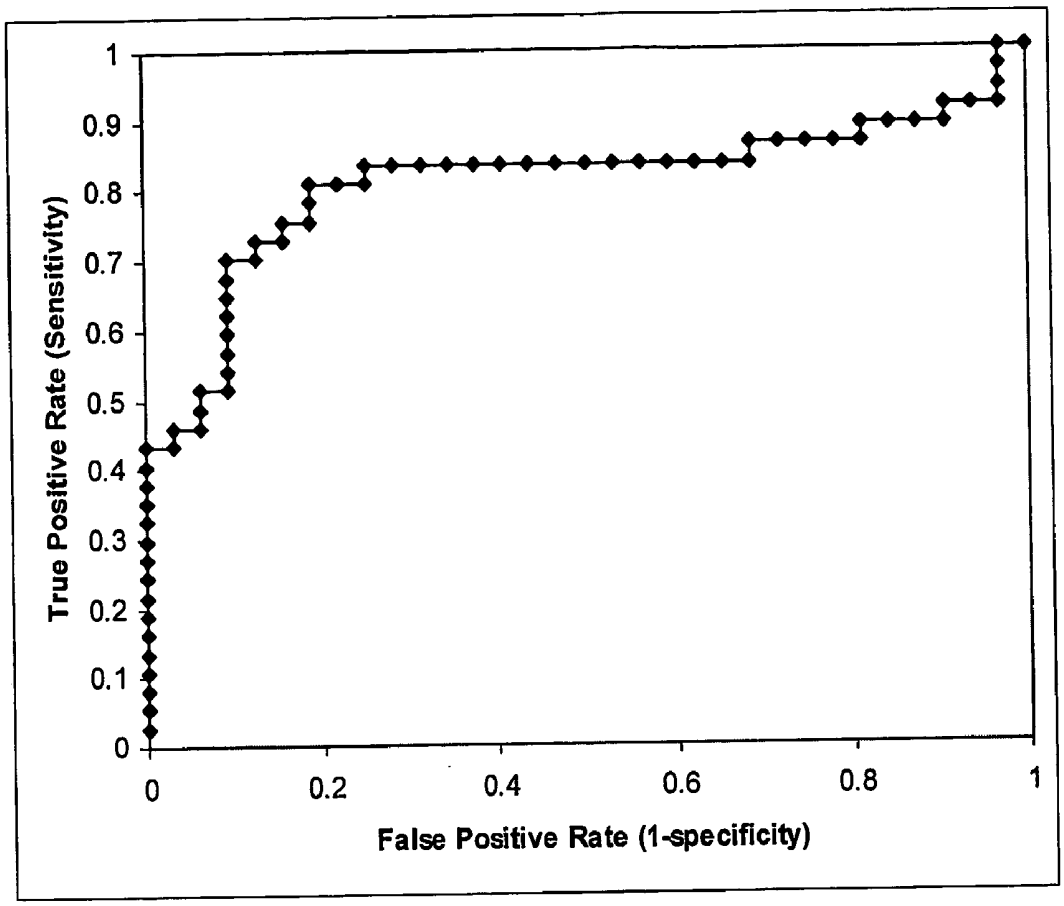

True Positive Rate (Sensitivity)
False Positive Rate (1-specificity)
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1
0
0.2
0.4
0.6
0.8
1

FIGURE 8

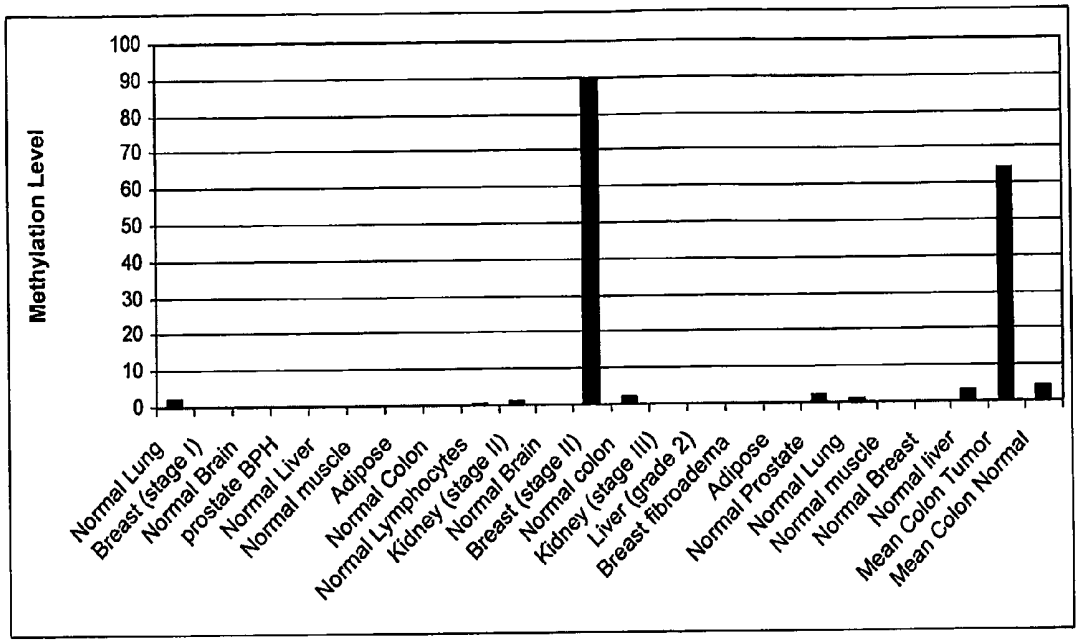

Methylation Level
100
90
80
70
60
50
40
30
20
10
0
Normal Lung
Breast (stage I)
Normal Brain
prostate BPH
Normal Liver
Normal muscle
Adipose
Normal Colon
Normal Lymphocytes
Kidney (stage II)
Normal Brain
Breast (stage II)
Normal colon
Kidney (stage III)
Liver (grade 2)
Breast fibroadema
Adipose
Normal Prostate
Normal Lung
Normal muscle
Normal Breast
Normal liver
Mean Colon Tumor
Mean Colon Normal

FIGURE 9

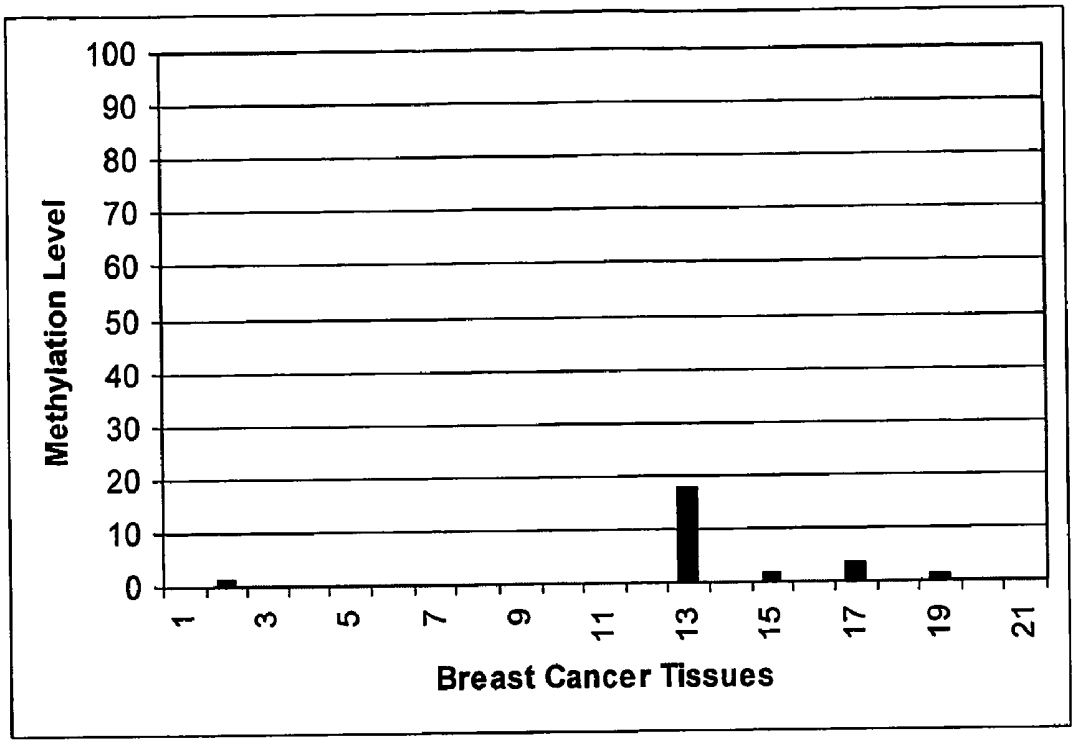

Methylation Level
100
90
80
70
60
50
40
30
20
10
0
1
3
5
7
9
11
13
15
17
19
21
Breast Cancer Tissues

FIGURE 10

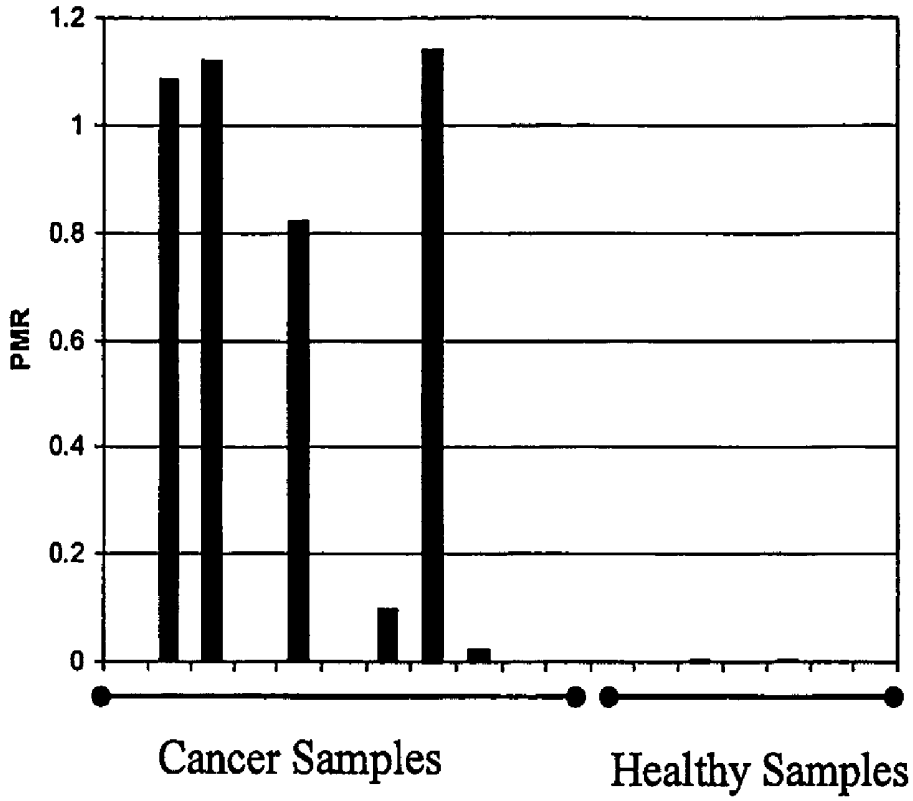


FIGURE 11

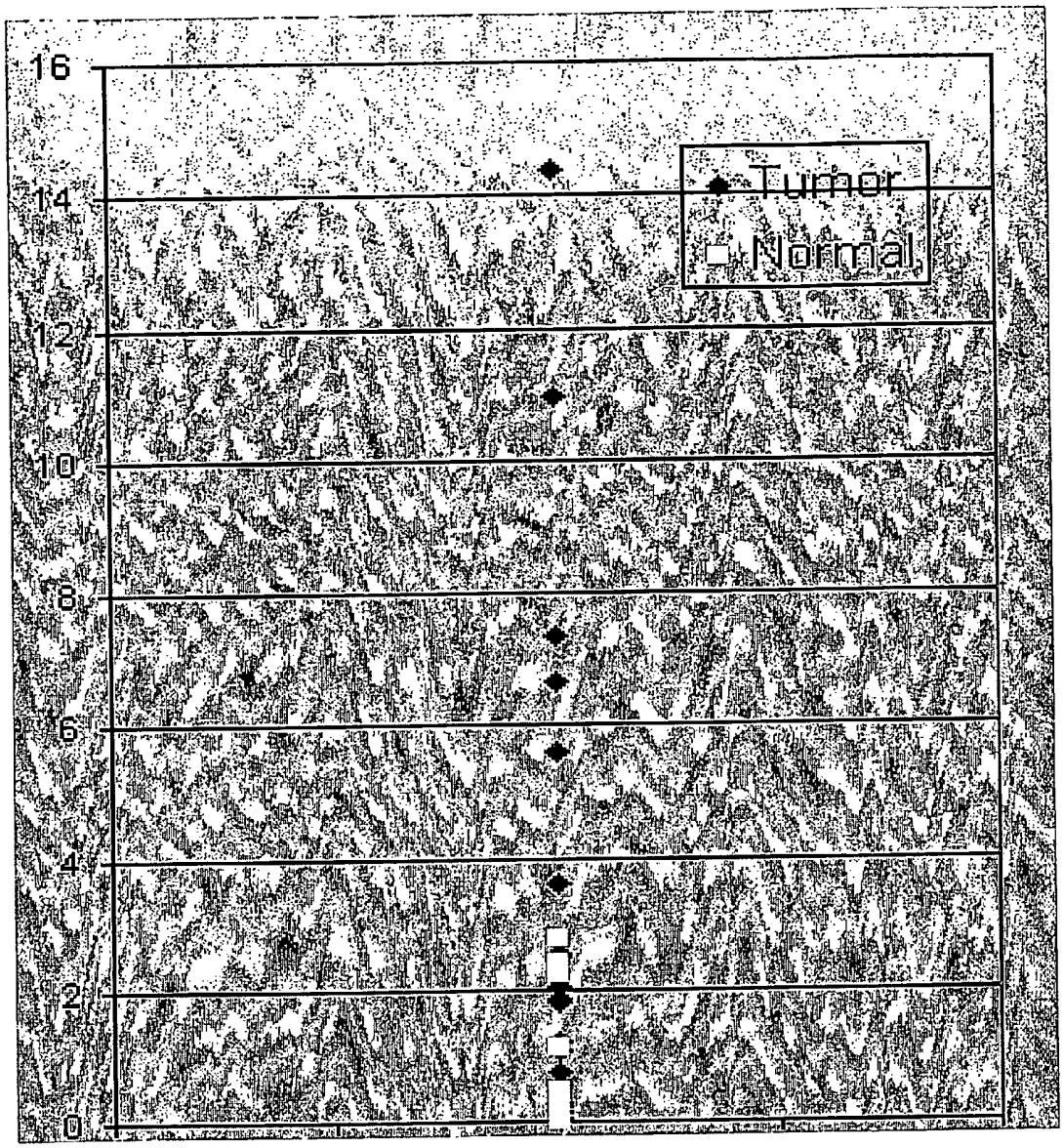


FIGURE 12

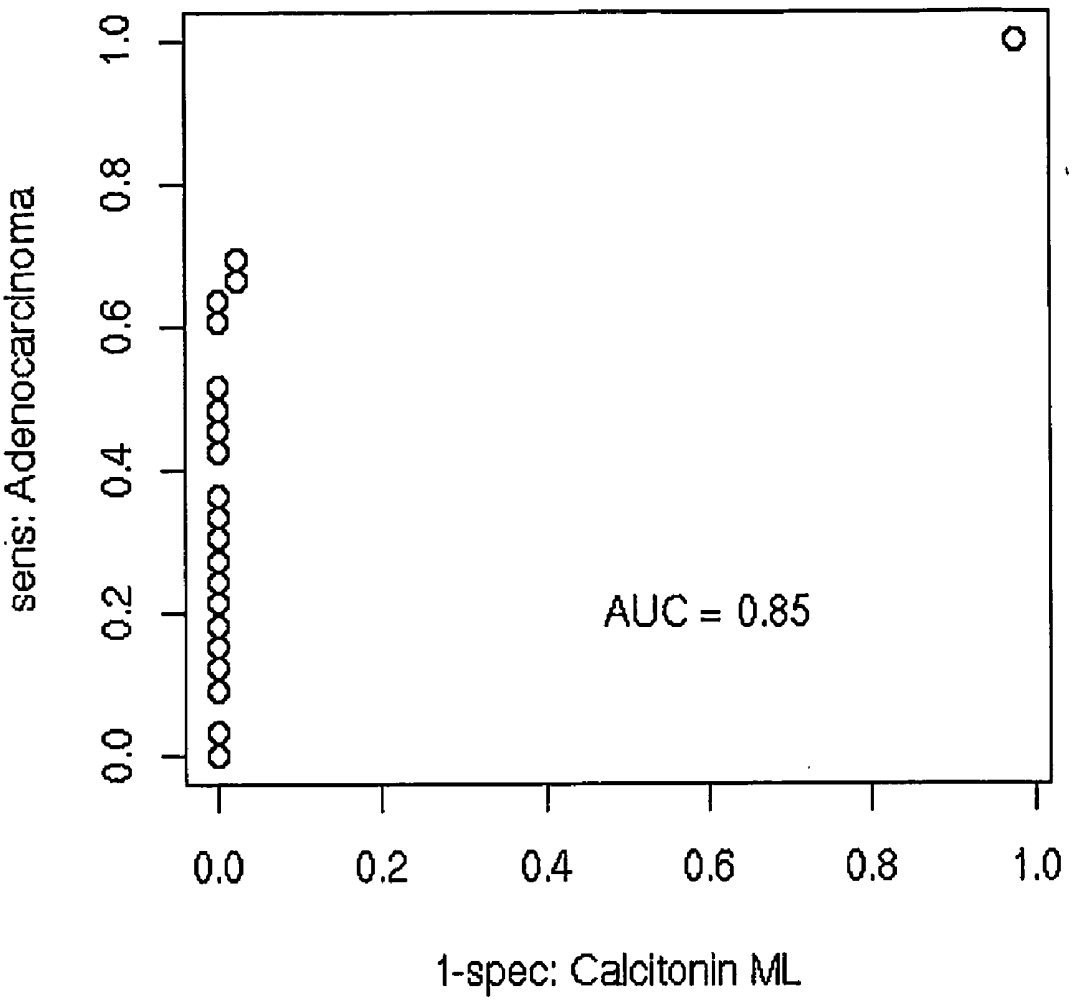

sens: Adenocarcinoma
0.0
0.2
0.4
0.6
0.8
1.0
AUC = 0.85
0.0
0.2
0.4
0.6
0.8
1.0
1-spec: Calcitonin ML

FIGURE 13

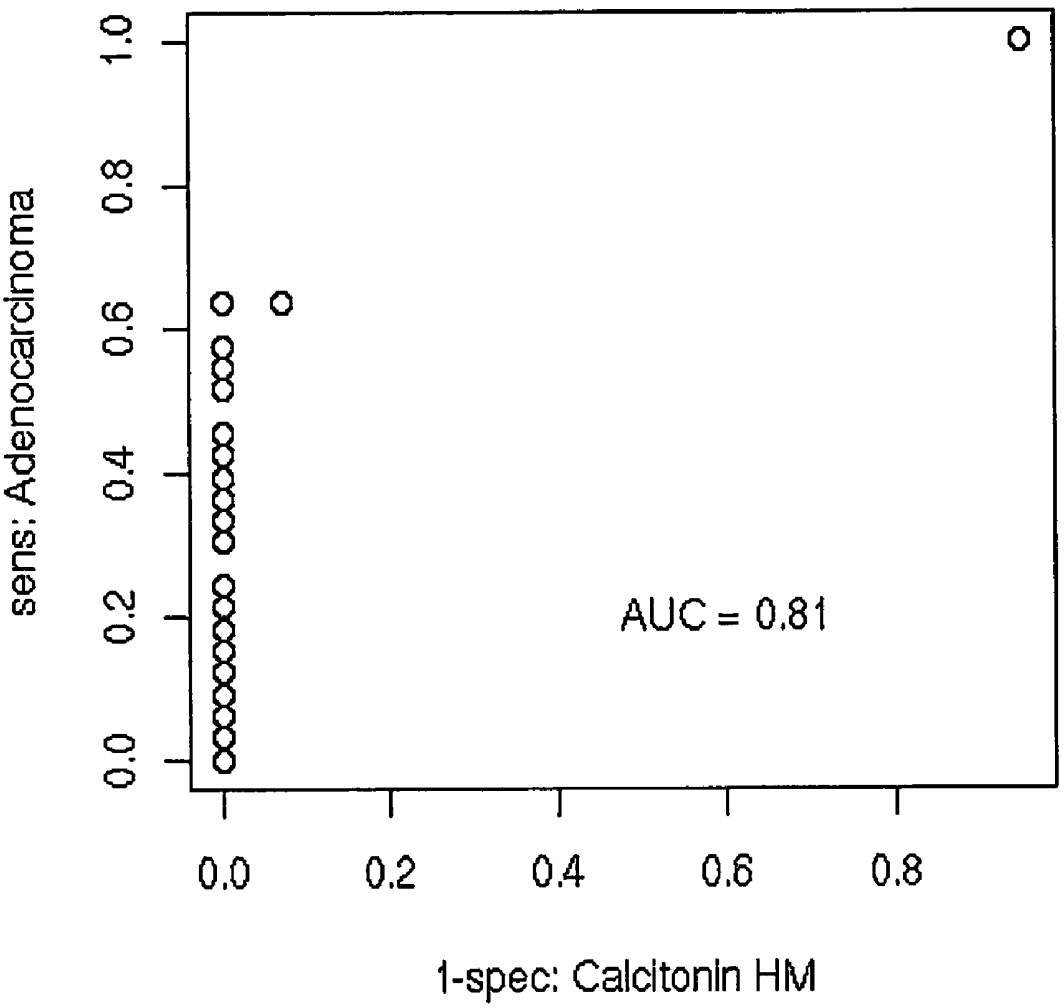

sens: Adenocarcinoma
0.0
0.2
0.4
0.6
0.8
1.0
AUC = 0.81
0.0
0.2
0.4
0.6
0.8
1-spec: Calcitonin HM

Figure 14

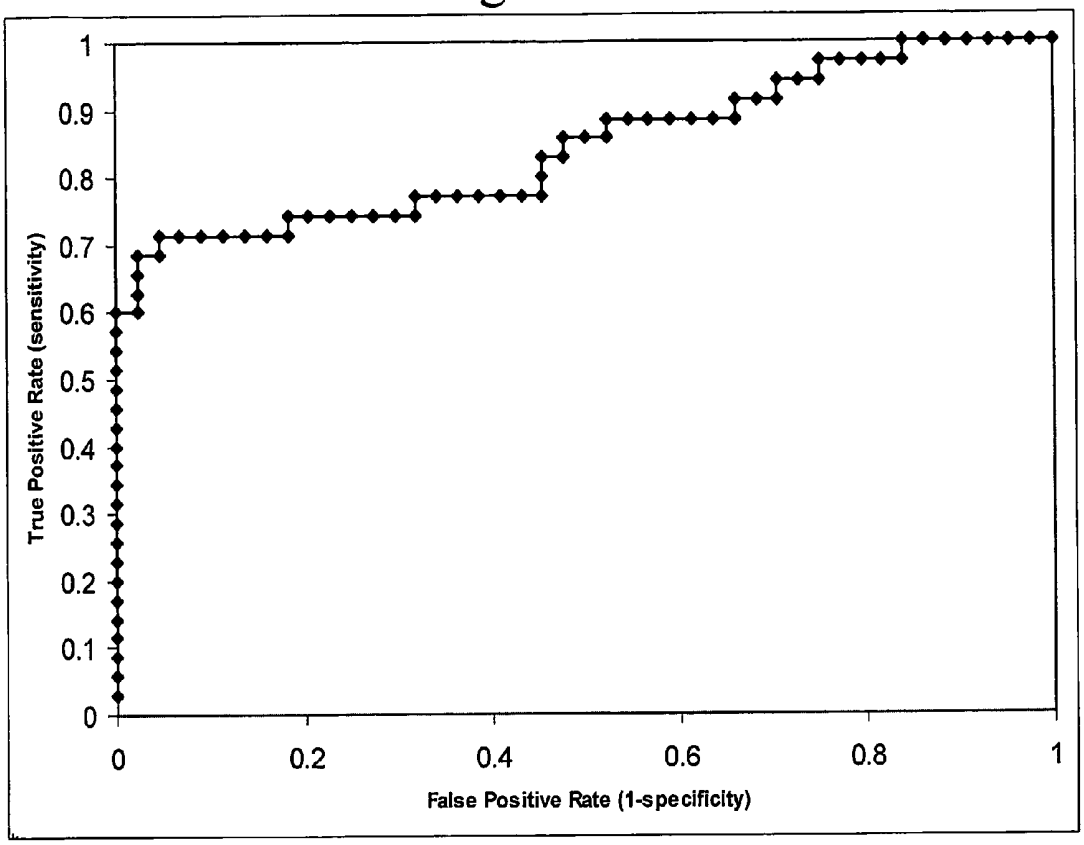

True Positive Rate (sensitivity)
False Positive Rate (1-specificity)
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1
0
0.2
0.4
0.6
0.8
1

Figure 15

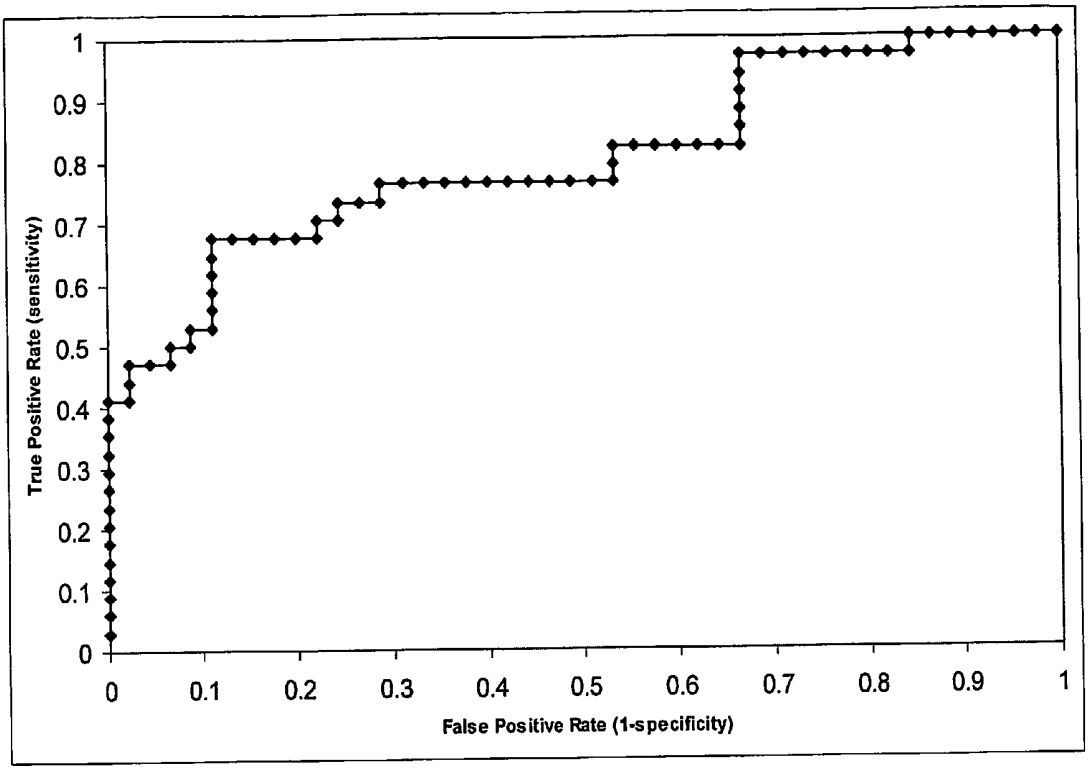

True Positive Rate (sensitivity)
False Positive Rate (1-specificity)
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1

Figure 16

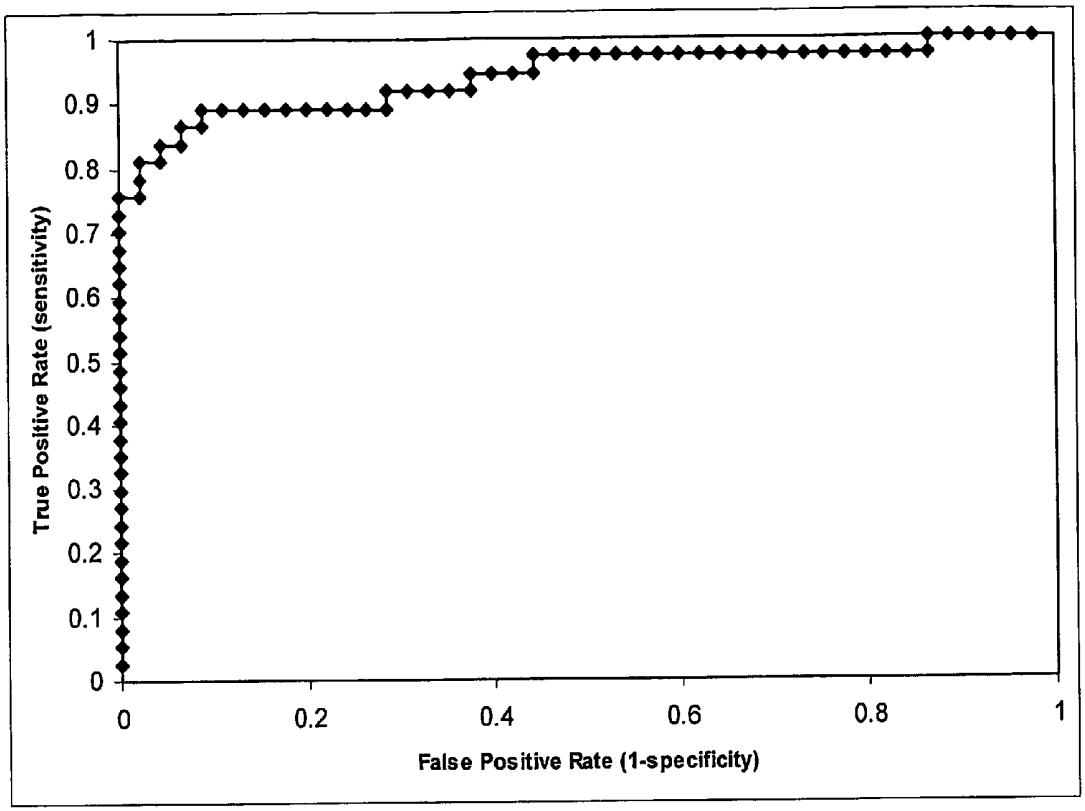

True Positive Rate (sensitivity)
False Positive Rate (1-specificity)
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1
0
0.2
0.4
0.6
0.8
1

FIGURE 17

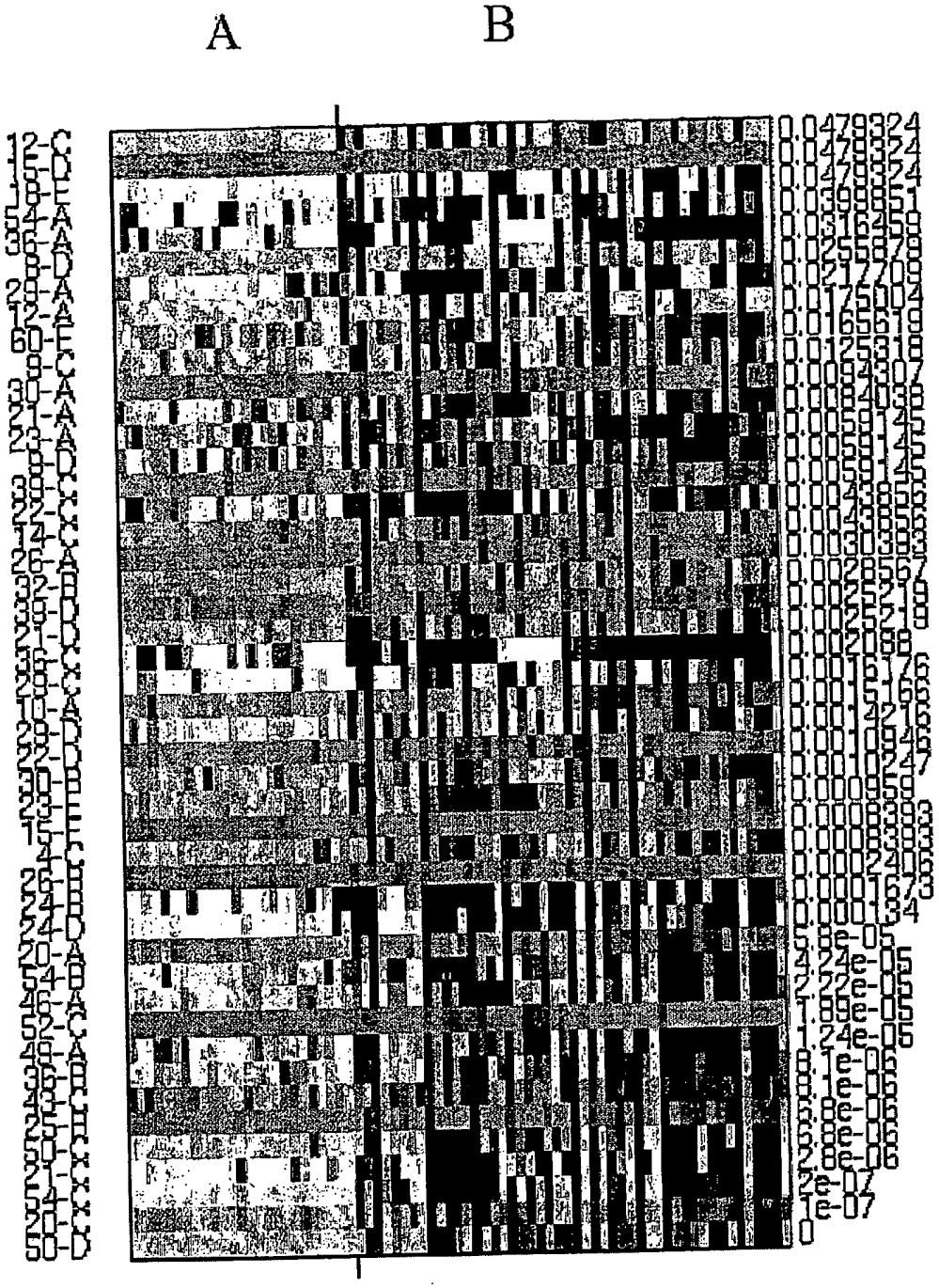


FIGURE 18

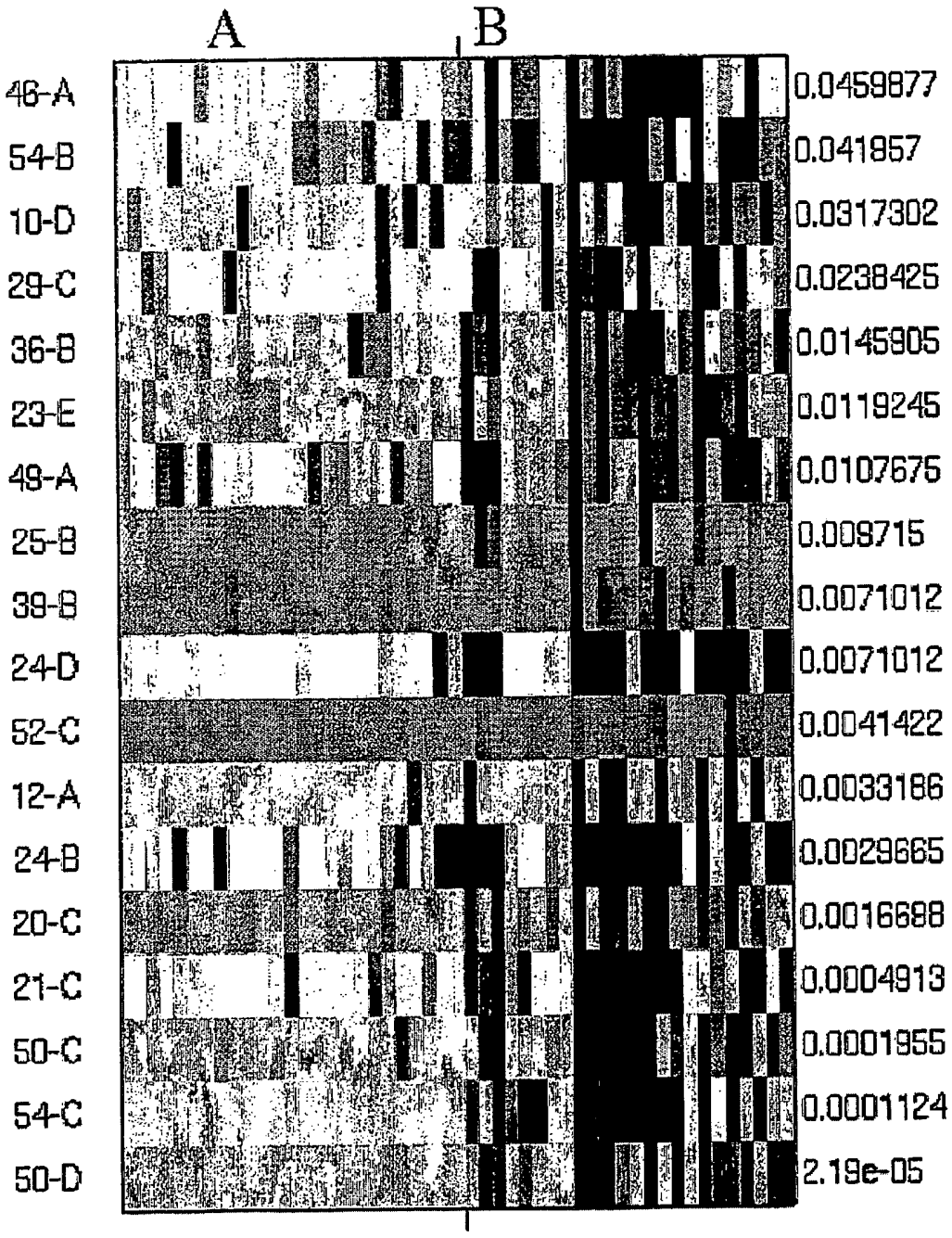

A
B
46-A
54-B
10-D
29-C
36-B
23-E
49-A
25-B
39-B
24-D
52-C
12-A
24-B
20-C
21-C
50-C
54-C
50-D
0.0459877
0.041857
0.0317302
0.0238425
0.0145905
0.0119245
0.0107675
0.009715
0.0071012
0.0071012
0.0041422
0.0033186
0.0029665
0.0016688
0.0004913
0.0001955
0.0001124
2.19e-05

FIGURE 19

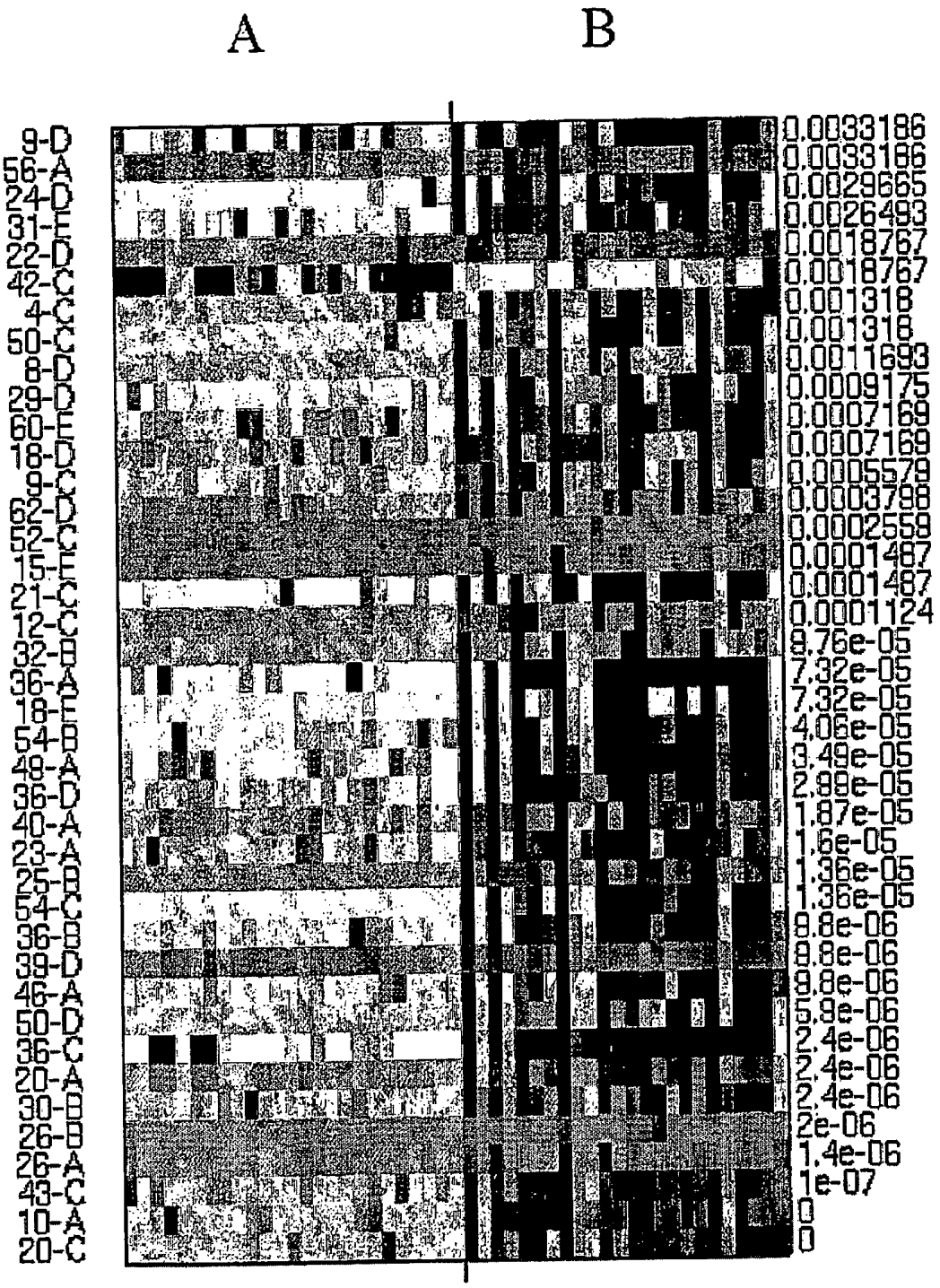

A
B
9-D
56-A
24-D
31-E
22-D
42-C
4-C
50-C
8-D
29-D
60-E
18-D
9-C
62-D
52-C
15-E
21-C
12-C
32-B
36-A
18-E
54-B
48-A
36-D
40-A
23-A
25-B
54-C
36-B
39-D
46-A
50-D
36-C
20-A
30-B
26-B
26-A
43-C
10-A
20-C
0.0033186
0.0033186
0.0029665
0.0026493
0.0018767
0.0018767
0.001318
0.001318
0.0011693
0.0009175
0.0007169
0.0007169
0.0005579
0.0003798
0.0002558
0.0001487
0.0001487
0.0001124
8.76e-05
7.32e-05
7.32e-05
4.06e-05
3.49e-05
2.98e-05
1.87e-05
1.6e-05
1.36e-05
1.36e-05
9.8e-06
9.8e-06
9.8e-06
5.9e-06
2.4e-06
2.4e-06
2.4e-06
2e-06
1.4e-06
1e-07
0
0

FIGURE 20

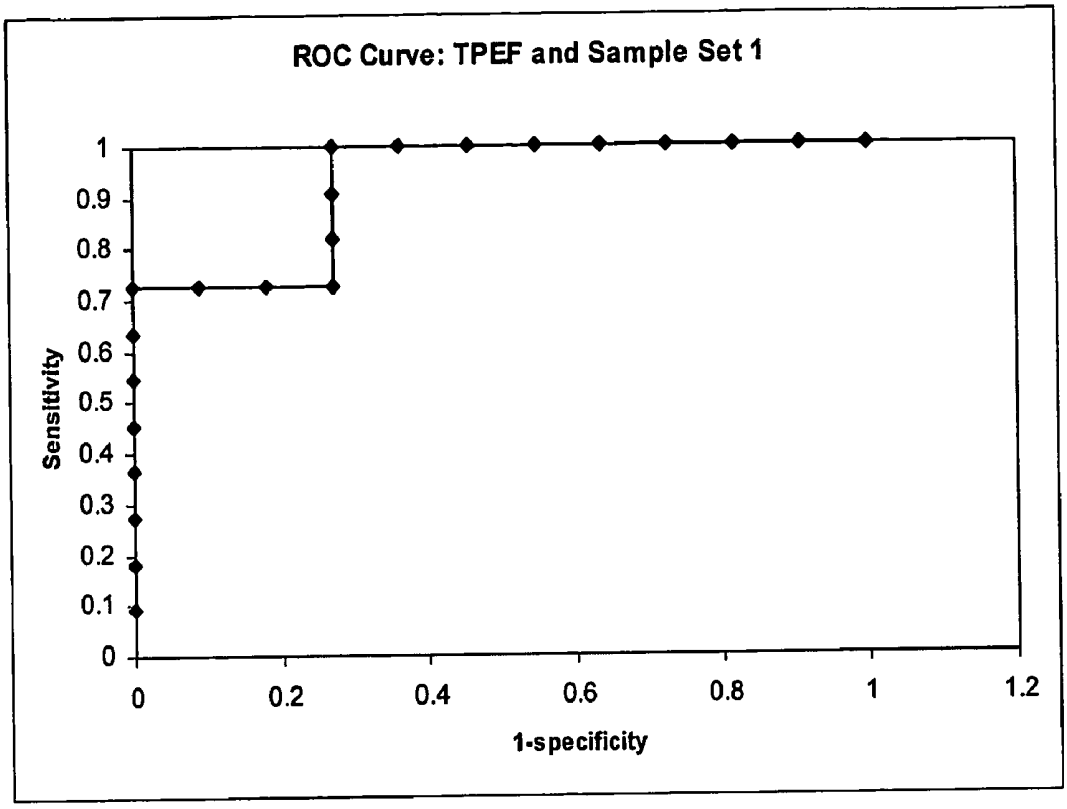

ROC Curve: TPEF and Sample Set 1
Sensitivity
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0
0.2
0.4
0.6
0.8
1
1.2
1-specificity

FIGURE 21

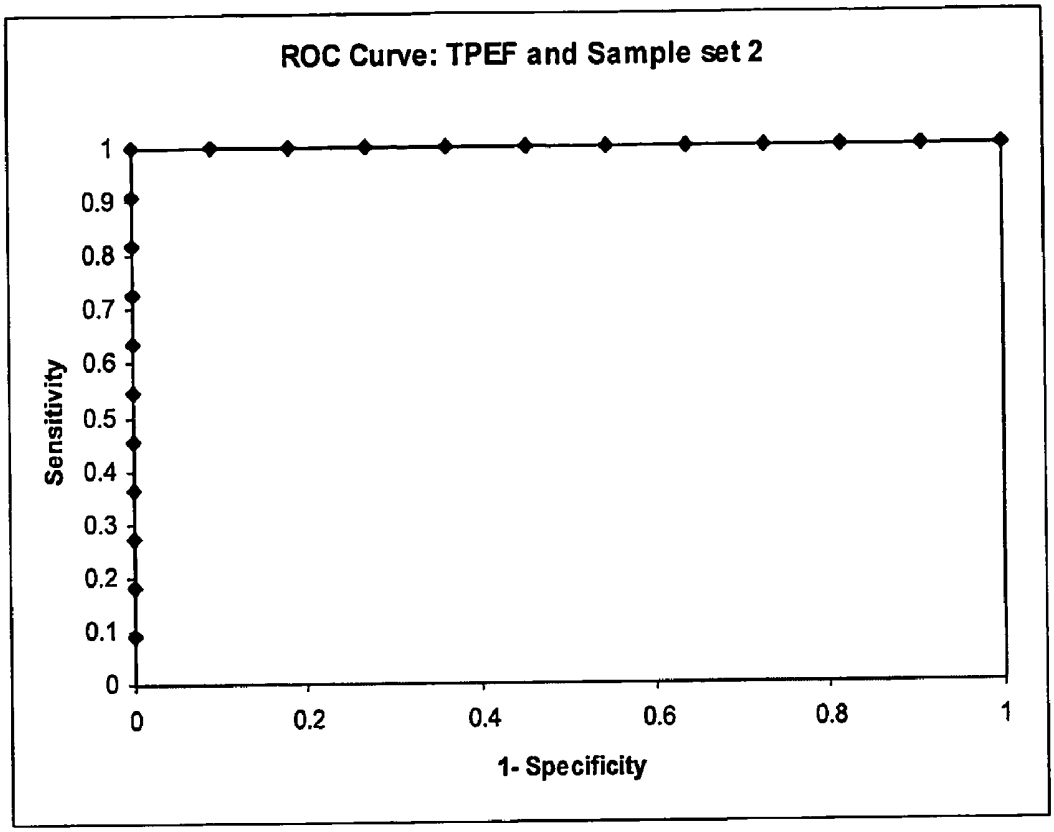

ROC Curve: TPEF and Sample set 2
Sensitivity
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0
0.2
0.4
0.6
0.8
1
1- Specificity

Figure 22

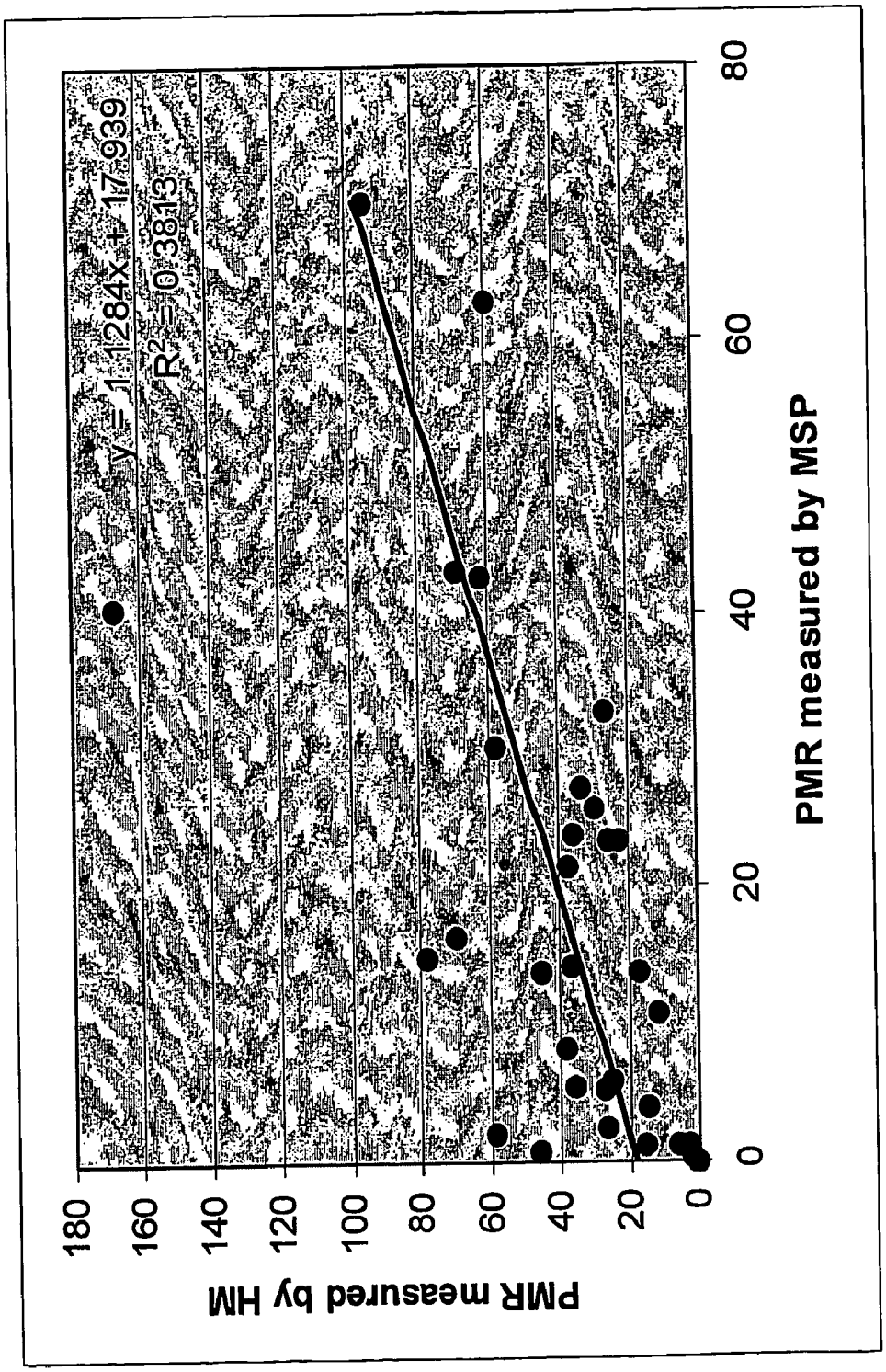
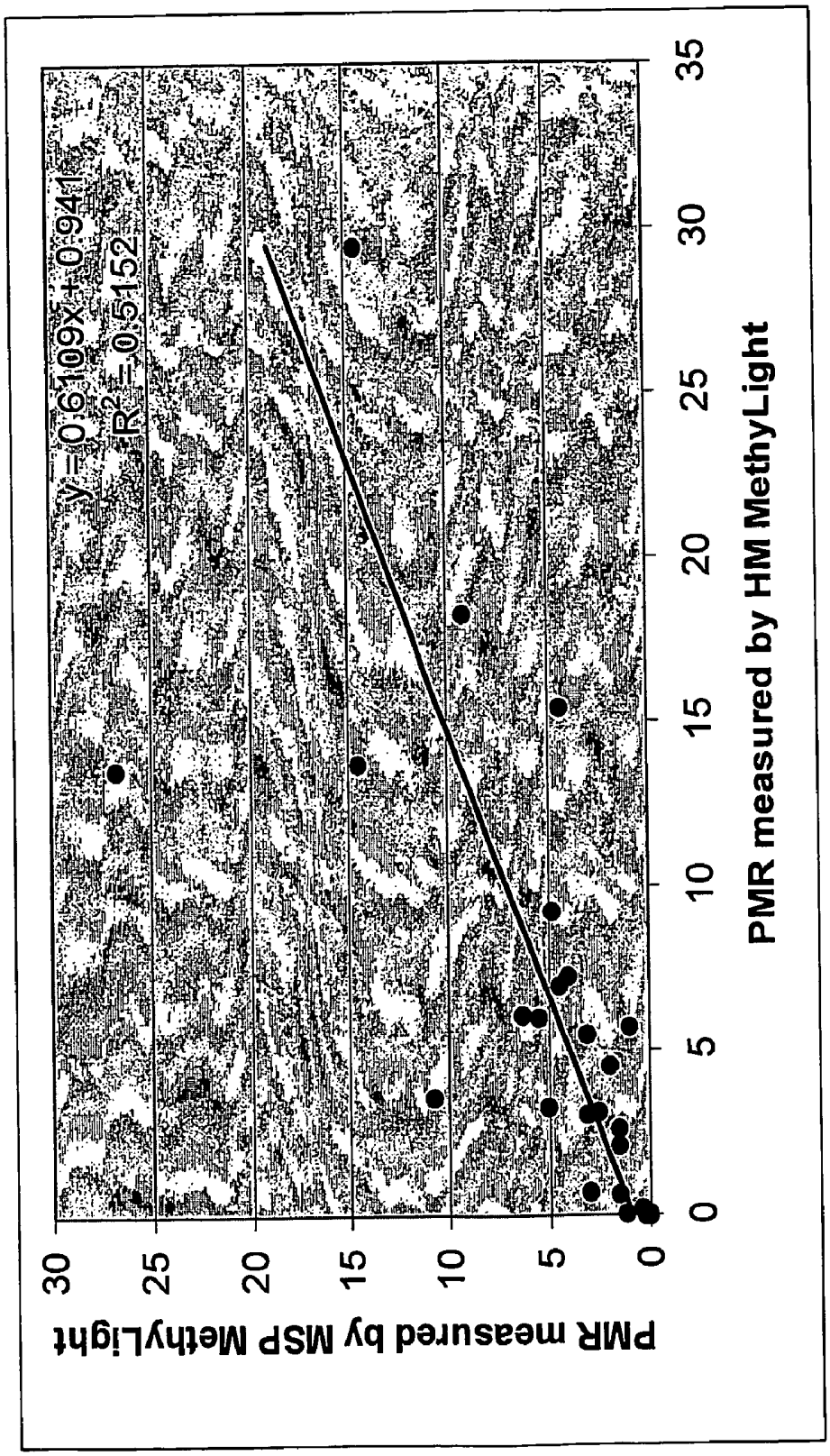

y = 1.1284x + 17.939
R² = 0.3813
PMR measured by HM
PMR measured by MSP
0
20
40
60
80
100
120
140
160
180

Figure 23


y = 0.6109x + 0.941
R² = 0.5152
PMR measured by MSP MethyLight
PMR measured by HM MethyLight
0
5
10
15
20
25
30
35

METHOD AND NUCLEIC ACIDS FOR THE ANALYSIS OF COLON CELL PROLIFERATIVE DISORDERS

FIELD OF THE INVENTION

[0001] Colon cancer is the fourth leading cause of cancer mortality in men and women. The 5-year survival rate is 61% over all stages with early detection being a prerequisite for curative therapy of the disease. Up to 95% of all colorectal cancers are adenocarcinomas of varying differentiation grades.

[0002] Sporadic colon cancer develops in a multistep process starting with the pathological transformation of normal colonic epithelium to an adenoma which consecutively progresses to invasive cancer. The progression rate of colonic adenomas is currently predicted based on their histological appearance, location, degree of spread and extent of bowel involvement. For example, tubular-type benign adenomas rarely progress to malignant tumours, whereas villous benign adenomas, particularly if larger than 2 cm in diameter, have a significant malignant potential.

[0003] During progression from benign proliferative lesions to malignant neoplasms several genetic and epigenetic alterations are known to occur. Somatic mutation of the APC gene seems to be one of the earliest events in 75 to 80% of colorectal adenomas and carcinomas. Activation of K-RAS is thought to be a critical step in the progression towards a malignant phenotype. Consecutively, mutations in other oncogenes as well as alterations leading to inactivation of tumor suppressor genes accumulate.

[0004] Aberrant DNA methylation within CpG islands is among the earliest and most common alterations in human cancers leading to abrogation or overexpression of a broad spectrum of genes. In addition, abnormal methylation has been shown to occur in CpG rich regulatory elements in intronic and coding parts of genes for certain tumours. In contrast to the specific hypermethylation of tumour suppressor genes, an overall hypomethylation of DNA can be observed in tumour cells. This decrease in global methylation can be detected early, far before the development of frank tumour formation. Also, correlation between hypomethylation and increased gene expression was reported for many oncogenes. In colon cancer, aberrant DNA methylation constitutes one of the most prominent alterations and inactivates many tumour suppressor genes such as p14ARF, p16INK4a, THBS1, MINT2, and MINT31 and DNA mismatch repair genes such as hMLH1.

[0005] In the molecular evolution of colorectal cancer, DNA methylation errors have been suggested to play two distinct roles. In normal colonic mucosa cells, methylation errors accumulate as a function of age or as time-dependent events predisposing these cells to neoplastic transformation. For example, hypermethylation of several loci could be shown to be already present in adenomas, particularly in the tubulovillous and villous subtype. At later stages, increased DNA methylation of CpG islands plays an important role in a subset of tumours affected by the so called CpG island methylator phenotype (CIMP). Most CIMP+ tumours, which constitute about 15% of all sporadic colorectal cancers, are characterized by microsatellite instability (MIN) due to hypermethylation of the hMLH1 promoter and other DNA mismatch repair genes. By contrast, CIMP-colon cancers evolve along a more classic genetic instability pathway (CIN), with a high rate of p53 mutations and chromosomal changes.

[0006] However, the molecular subtypes do not only show varying frequencies regarding molecular alterations. According to the presence of either micro satellite instability or chromosomal aberrations, colon cancer can be subclassified into two classes, which also exhibit significant clinical differences. Almost all MIN tumours originate in the proximal colon (ascending and transversum), whereas 70% of CIN tumours are located in the distal colon and rectum. This has been attributed to the varying prevalence of different carcinogens in different sections of the colon. Methylating carcinogens, which constitute the prevailing carcinogen in the proximal colon have been suggested to play a role in the pathogenesis of MIN cancers, whereas CIN tumours are thought to be more frequently caused by adduct-forming carcinogens, which occur more frequently in distal parts of the colon and rectum. Moreover, MIN tumours have a better prognosis than do tumours with a CIN phenotype and respond better to adjuvant chemotherapy.

[0007] The identification of markers for the differentiation of colon carcinoma as well as for early detection are main goals of current research.

[0008] The alpha-calcitonin gene encodes a small family of peptides: calcitonin, katacalcin, and calcitonin gene-related peptide (CGRP). Calcitonin is concerned with skeletal integrity, the secretion of calcitonin is, in part, oestrogen dependent, and it appears likely that a postmenopausal decline in calcitonin secretion is a factor in the development of postmenopausal osteoporosis.

[0009] Investigation of the Calcitonin gene has revealed that hypermethylation of the promoter region of the gene is present in neoplastic cells of several cancer types, particularly acute leukemias. The major part of said research was carried out using methylation sensitive enzyme based methods, this identified the general phenomenon of hypermethylation within the promoter and first exon regions of the gene in multiple types of cancers. However said methods do not allow for a targeted analysis of selected CpG positions. The observations of hypermethylation were enabled only by the assumption of comethylation within the region. Comethylation is a phenomenon whereby methylation of one CpG position is taken as indicative of methylation of all CpG positions within the region. Examples of research carried out using restriction enzyme based methods include the following:

[0010] Hiltunen M O, Koistinaho J, Alhonen L, Myohanen S, Marin S, Kosma V M, Paakkonen M, Janne J. Hypermethylation of the WT1 and calcitonin gene promoter regions at chromosome 11p in human colorectal cancer. Br J Cancer. 1997; 76(9):1124-30.

[0011] Silverman A L, Park J G, Hamilton S R, Gazdar A F, Luk G D, Baylin S B. Abnormal methylation of the calcitonin gene in human colonic neoplasms. Cancer Res. 1989 Jul. 1; 49(13):3468-73

[0012] The gene 'Versican', (NM_004385) also known as CSPG2 encodes a large chondroitin sulfate proteoglycan. This gene is known to exhibit aberrant methylation patterns and conflicting opinions on this matter have been published. For instance Adany R and lozzo R V. ('Altered methylation

of versican proteoglycan gene in human colon carcinoma.' Biochem Biophys Res Commun 1990 Sep. 28; 171(3):1402-13) observed a correlation between hypomethylation and colonic neoplasms. However, more recently Issa et. al. ('Accelerated Age-related CpG Island Methylation in Ulcerative Colitis' Cancer Research 61, 3573-3577, May 1, 2001) described an observed hypermethylation of dysplastic mucosa as compared to non-UC control mucosa (58% versus 31%, P=0.01) or compared with adjacent uninvolved mucosa (58% versus 35%, P=0.06). Therefore it would seem that although aberrant methylation of this gene has been observed in colorectal cell proliferative disorders, the characterisation of this aberrant methylation is as yet not obvious and it would appear that the commonly held assumption of comethylation does not hold in the case of this gene.

[0013] The gene TPEF (also known as TMEFF2) NM_016192 encodes a transmembrane protein containing EGF and follistatin domains. It was initially identified on the basis of its methylation properties by Jones et. al. ('The Gene for a Novel Transmembrane Protein Containing Epidermal Growth Factor and Follistatin Domains Is Frequently Hypermethylated in Human Tumor Cells' Cancer Research 60, 4907-4912, Sep. 1, 2000). It was therein shown that the 5' region of the gene contained a CpG island, a 3' region of which was shown to exhibit significant hypermethylation in tumor cell lines. Although significant said onbservation was carried out by means of arbitrarily primed PCR, a methodology that is not suitable for application in a clinical or diagnostic setting.

[0014] EYA4 is the most recently identified member of the vertebrate Eya (eyes-absent) gene family, a group of four transcriptional activators that interact with other proteins in a conserved regulatory hierarchy to ensure normal embryologic development. The EYA4 gene is mapped to 6q22.3 and encodes a 640 amino acid protein. The structure of EYA4 conforms to the basic pattern established by EYA1-3, and includes a highly conserved 271 amino acid C-terminus called the eya-homologous region (eyaHR; alternatively referred to as the eya domain or eya homology domain 1) and a more divergent proline-serine-threonine (PST)-rich (34-41%) transactivation domain at the N-terminus. EYA proteins interact with members of the SIX and DACH protein families during early embryonic development. Mutations in the EYA4 gene are responsible for postlingual, progressive, autosomal dominant hearing loss at the DFNA10 locus (Wayne S, Robertson N G, DeClau F, Chen N, Verhoeven K, Prasad S, Tranebjarg L, Morton C C, Ryan A F, Van Camp G, Smith R J: Mutations in the transcriptional activator EYA4 cause late-onset deafness at the DFNA10 locus. Hum Mol Genet 2001 Feb. 1; 10(3):195-200 with further references). A link between the Methylation of Cytosine positions in the EYA 4 gene and cancer has not yet been established.

[0015] The cadherins are a family of cell surface glycoproteins responsible for selective cell recognition and adhesion. Several family members, including CDH1 (E-cadherin) and CDH13 (H-cadherin, NM_001257) are located on the long arm of chromosome 16, while another gene cluster resides on the short arm of chromosome 5. The chromosomal locations of several of the cadherins are sites of frequent loss of heterozygosity in many tumor types. Deletions of 16q are frequent in breast, lung, and other carcinomas. Loss of expression of cadherins has been described in many epithelial cancers, and it may play a role in tumour cell invasion and metastasis CDH13 expression is diminished in breast and lung cancers. In ovarian tumours, the combination of deletion and aberrant methylation has been reported to inactivate CDH13. Aberrant methylation of CDH13 has also been reported in lung cancers.

[0016] 5-methylcytosine is the most frequent covalent base modification in the DNA of eukaryotic cells. It plays a role, for example, in the regulation of the transcription, in genetic imprinting, and in tumorigenesis. Therefore, the identification of 5-methylcytosine as a component of genetic information is of considerable interest. However, 5-methylcytosine positions cannot be identified by sequencing since 5-methylcytosine has the same base pairing behaviour as cytosine. Moreover, the epigenetic information carried by 5-methylcytosine is completely lost during PCR amplification.

[0017] A relatively new and currently the most frequently used method for analysing DNA for 5-methylcytosine is based upon the specific reaction of bisulfite with cytosine which, upon subsequent alkaline hydrolysis, is converted to uracil which corresponds to thymidine in its base pairing behaviour. However, 5-methylcytosine remains unmodified under these conditions. Consequently, the original DNA is converted in such a manner that methylcytosine, which originally could not be distinguished from cytosine by its hybridisation behaviour, can now be detected as the only remaining cytosine using "normal" molecular biological techniques, for example, by amplification and hybridisation or sequencing. All of these techniques are based on base pairing which can now be fully exploited. In terms of sensitivity, the prior art is defined by a method which encloses the DNA to be analysed in an agarose matrix, thus preventing the diffusion and renaturation of the DNA (bisulfite only reacts with single-stranded DNA), and which replaces all precipitation and purification steps with fast dialysis (Olek A, Oswald J, Walter J. A modified and improved method for bisulphite based cytosine methylation analysis. Nucleic Acids Res. 1996 Dec. 15; 24(24):5064-6). Using this method, it is possible to analyse individual cells, which illustrates the potential of the method. However, currently only individual regions of a length of up to approximately 3000 base pairs are analysed, a global analysis of cells for thousands of possible methylation events is not possible. However, this method cannot reliably analyse very small fragments from small sample quantities either. These are lost through the matrix in spite of the diffusion protection.

[0018] An overview of the further known methods of detecting 5-methylcytosine may be gathered from the following review article: Rein, T., DePamphilis, M. L., Zorbas, H., Nucleic Acids Res. 1998, 26, 2255.

[0019] To date, barring few exceptions (e.g., Zeschnigk M, Lich C, Buiting K, Doerfler W, Horsthemke B. A single-tube PCR test for the diagnosis of Angelman and Prader-Willi syndrome based on allelic methylation differences at the SNRPN locus. Eur J Hum Genet. 1997 March-April; 5(2):94-8) the bisulfite technique is only used in research. Always, however, short, specific fragments of a known gene are amplified subsequent to a bisulfite treatment and either completely sequenced (Olek A, Walter J. The pre-implantation ontogeny of the H19 methylation imprint.

Nat Genet. 1997 November; 17(3):275-6) or individual cytosine positions are detected by a primer extension reaction (Gonzalgo M L, Jones P A. Rapid quantitation of methylation differences at specific sites using methylation-sensitive single nucleotide primer extension (Ms-SNuPE). Nucleic Acids Res. 1997 Jun. 15; 25(12):2529-31, WO 95/00669) or by enzymatic digestion (Xiong Z, Laird P W. COBRA: a sensitive and quantitative DNA methylation assay. Nucleic Acids Res. 1997 Jun. 15; 25(12):2532-4). In addition, detection by hybridization has also been described (Olek et al., WO 99/28498).

[0020] Further publications dealing with the use of the bisulfite technique for methylation detection in individual genes are: Grigg G, Clark S. Sequencing 5-methylcytosine residues in genomic DNA. Bioessays. 1994 June; 16(6):431-6, 431; Zeschnigk M, Schmitz B, Dittrich B, Buiting K, Horsthemke B, Doerfler W. Imprinted segments in the human genome: different DNA methylation patterns in the Prader-Willi/Angelman syndrome region as determined by the genomic sequencing method. Hum Mol Genet. 1997 March; 6(3):387-95; Feil R, Charlton J, Bird A P, Walter J, Reik W. Methylation analysis on individual chromosomes: improved protocol for bisulphite genomic sequencing. Nucleic Acids Res. 1994 Feb. 25; 22(4):695-6; Martin V, Ribieras S, Song-Wang X, Rio M C, Dante R. Genomic sequencing indicates a correlation between DNA hypomethylation in the 5' region of the pS2 gene and its expression in human breast cancer cell lines. Gene. 1995 May 19; 157(1-2):261-4; WO 97/46705 and WO 95/15373.

[0021] An overview of the Prior Art in oligomer array manufacturing can be gathered from a special edition of Nature Genetics (Nature Genetics Supplement, Volume 21, January 1999), published in January 1999, and from the literature cited therein.

[0022] Fluorescently labeled probes are often used for the scanning of immobilized DNA arrays. The simple attachment of Cy3 and Cy5 dyes to the 5'-OH of the specific probe are particularly suitable for fluorescence labels. The detection of the fluorescence of the hybridized probes may be carried out, for example via a confocal microscope. Cy3 and Cy5 dyes, besides many others, are commercially available.

[0023] Matrix Assisted Laser Desorption Ionisation Mass Spectrometry (MALDI-TOF) is a very efficient development for the analysis of biomolecules (Karas M, Hillenkamp F. Laser desorption ionisation of proteins with molecular masses exceeding 10,000 daltons. Anal Chem. 1988 Oct. 15; 60(20):2299-301). An analyte is embedded in a light-absorbing matrix. The matrix is evaporated by a short laser pulse thus transporting the analyte molecule into the vapor phase in an unfragmented manner. The analyte is ionised by collisions with matrix molecules. An applied voltage accelerates the ions into a field-free flight tube. Due to their different masses, the ions are accelerated at different rates. Smaller ions reach the detector sooner than bigger ones.

[0024] MALDI-TOF spectrometry is excellently suited to the analysis of peptides and proteins. The analysis of nucleic acids is somewhat more difficult (Gut I G, Beck S. DNA and Matrix Assisted Laser Desorption Ionisation Mass Spectrometry. Current Innovations and Future Trends. 1995, 1; 147-57). The sensitivity to nucleic acids is approximately 100 times worse than to peptides and decreases disproportionally with increasing fragment size. For nucleic acids having a multiply negatively charged backbone, the ionisation process via the matrix is considerably less efficient. In MALDI-TOF spectrometry, the selection of the matrix plays an eminently important role. For the desorption of peptides, several very efficient matrixes have been found which produce a very fine crystallisation. There are now several responsive matrixes for DNA, however, the difference in sensitivity has not been reduced. The difference in sensitivity can be reduced by chemically modifying the DNA in such a manner that it becomes more similar to a peptide. Phosphorothioate nucleic acids in which the usual phosphates of the backbone are substituted with thiophosphates can be converted into a charge-neutral DNA using simple alkylation chemistry (Gut I G, Beck S. A procedure for selective DNA alkylation and detection by mass spectrometry. Nucleic Acids Res. 1995 Apr. 25; 23(8):1367-73). The coupling of a charge tag to this modified DNA results in an increase in sensitivity to the same level as that found for peptides. A further advantage of charge tagging is the increased stability of the analysis against impurities which make the detection of unmodified substrates considerably more difficult.

[0025] Genomic DNA is obtained from DNA of cell, tissue or other test samples using standard methods. This standard methodology is found in references such as Sambrook, Fritsch and Maniatis eds., Molecular Cloning: A Laboratory Manual, 1989.

DESCRIPTION

[0026] The invention provide a method for the analysis of biological samples for features associated with the development of colon cell proliferative disorders, characterised in that the nucleic acid of at least one member of the group comprising Versican, TPEF, H-Cadherin, Calcitonin and EYA4 is/are contacted with a reagent or series of reagents capable of distinguishing between methylated and non methylated CpG dinucleotides within the genomic sequence of interest.

[0027] The genes that form the basis of the present invention may also be used to form a "gene panel", i.e. a collection comprising the particular genetic sequences of the present invention and/or their respective informative methylation sites. The formation of gene panels allows for a quick and specific analysis of specific aspects of breast cancer treatment. The gene panel(s) as described and employed in this invention can be used with surprisingly high efficiency for the the improved diagnosis, treatment and monitoring of colon cell proliferative disorders.

[0028] The invention provides significant improvements over the state of the art in that there are currently no markers used to detect colorectal cancer from body fluid samples. Current methods used to detect and diagnose colon cell proliferative disorders include colonoscopy, sigmoidoscopy, and fecal occult blood colon cancer. In comparison to these methods, the disclosed invention is much less invasive than colonoscopy, and as, if not more sensitive than sigmoidoscopy and FOBT. Compared to the previous descriptions of these markers in the literature, the described invention provides significant advantages in terms of sensitivity and specificity due to the advantageous combination of using a gene panel and highly sensitive assay techniques.

[0029] The present invention makes available a method for ascertaining genetic and/or epigenetic parameters of

genomic DNA. The method is for use in the improved diagnosis, treatment and monitoring of colon cell proliferative disorders, more specifically by enabling the improved identification of and differentiation between subclasses of said disorder and the genetic predisposition to said disorders. The invention presents improvements over the state of the art in that it enables a highly specific classification of colon carcinomas, thereby allowing for improved and informed treatment of patients.

[0030] In one aspect of the invention, the disclosed matters provides novel nucleic acid sequences useful for the analysis of methylation within said gene, other aspects provide novel uses of the gene and the gene product as well as methods, assays and kits directed to detecting, differentiating and distinguishing colon cell proliferative disorders. The method and nucleic acids according to the invention may be used for the analysis of colon cell proliferative disorders taken form the group comprising adenocarcinomas, polyps, squamous cell cancers, carcinoid tumours, sarcomas and lymphomas.

[0031] In one embodiment the method discloses the use of one or more genes selected from the group comprising Versican, TPEF, H-Cadherin, Calcitonin and EYA4 as markers for the differentiation, detection and distinguishing of colon cell proliferative disorders. Said use of the gene may be enabled by means of analysis of the methylation status of one or more genes selected from the group comprising Versican, TPEF, H-Cadherin, Calcitonin and EYA4 and their promoter or regulatory elements.

[0032] The objective of the invention may be achieved by analysis of the methylation state of the CpG dinucleotides within one or more of the genomic sequence according to SEQ ID NO 1 to SEQ ID NO 5 and sequences complementary thereto. SEQ ID NO 1 to SEQ ID NO 5 disclose the nucleic acid sequences of the genes from the group consisting of Versican, TPEF, H-Cadherin, Calcitonin and EYA4 and their promoter and regulatory elements, wherein said fragment comprises CpG dinucleotides exhibiting a disease specific methylation pattern. Due to the degeneracy of the genetic code, the sequence as identified in SEQ ID NO 1 to SEQ ID NO 5 should be interpreted so as to include all substantially similar and equivalent sequences upstream of the promoter region of a gene which encodes a polypeptide with the biological activity of that encoded by the genes Versican, TPEF, H-Cadherin, Calcitonin and EYA4.

[0033] In a preferred embodiment of the method, the objective of the invention is achieved by analysis of a nucleic acid comprising a sequence of at least 18 bases in length according to one of SEQ ID NO 6 to SEQ ID NO 25 and sequences complementary thereto.

[0034] The sequences of SEQ ID NO 6 to SEQ ID NO 25 provide modified versions of the nucleic acid according to SEQ ID NO 1 to SEQ ID NO 5, wherein the conversion of said sequence results in the synthesis of a nucleic acid having a sequence that is unique and distinct from SEQ ID NO 1 to SEQ ID NO 5 as follows. (see also the following TABLE 1): SEQ ID NO 1 to SEQ ID NO 5, sense DNA strand of Versican, TPEF, H-Cadherin, Calcitonin and EYA4 and their promoter and regulatory elements; SEQ ID NO 6 to SEQ ID NO 15, converted SEQ ID NO 1 to SEQ ID NO 5 and complementary sequences, wherein "C" or "T," but "CpG" remains "CpG" (i.e., corresponds to case where all "C" residues of CpG dinucleotide sequences are methylated and are thus not converted); SEQ ID NO 16 to SEQ ID NO 25, converted SEQ ID NO 1 to SEQ ID NO 5 and complementary sequences, wherein "C" converted to "T" for all "C" residues, including those of "CpG" dinucleotide sequences (i.e., corresponds to case where, for SEQ ID NO 1 to SEQ ID NO 5, all "C" residues of CpG dinucleotide sequences are unmethylated);

TABLE 1

Description of SEQ ID NO 1 to SEQ ID NO 25

SEQ ID NO	Relationship to SEQ ID NO 1 to SEQ ID NO 5	Nature of cytosine base conversion
SEQ ID NO 1 to SEQ ID NO 5	Sense strand (Versican, TPEF, H-Cadherin, Calcitonin and EYA4 including promoter and regulatory elements)	None; untreated sequence
SEQ ID NO 6 to 15	Converted methylated strand	"C"to"T," but "CpG" remains "CpG" (all "C" residues of CpGs are methylated)
SEQ ID NO 16 to 25	Converted sense strand	"C" to "T" for all "C" residues (all "C" residues of CpGs are unmethylated)

[0035] Significantly, heretofore, the nucleic acid sequences and molecules according to SEQ ID NO 6 to SEQ ID NO 25 were not implicated in or connected with the ascertainment of colon cell proliferative disorders.

[0036] The described invention further disclose an oligonucleotide or oligomer for detecting the cytosine methylation state within pretreated DNA, according to SEQ ID NO 6 to SEQ ID NO 25. Said oligonucleotide or oligomer comprising a nucleic acid sequence having a length of at least nine (9) nucleotides which hybridizes, under moderately stringent or stringent conditions (as defined herein above), to a pretreated nucleic acid sequence according to SEQ ID NO 6 to SEQ ID NO 25 and/or sequences complementary thereto.

[0037] Thus, the present invention includes nucleic acid molecules (e.g., oligonucleotides and peptide nucleic acid (PNA) molecules (PNA-oligomers)) that hybridise under moderately stringent and/or stringent hybridisation conditions to all or a portion of the sequences of SEQ ID NO 6 to SEQ ID NO 25, or to the complements thereof. The hybridising portion of the hybridising nucleic acids is typically at least 9, 15, 20, 25, 30 or 35 nucleotides in length. However, longer molecules have inventive utility, and are thus within the scope of the present invention.

[0038] Preferably, the hybridising portion of the inventive hybridising nucleic acids is at least 95%, or at least 98%, or 100% identical to the sequence, or to a portion thereof of SEQ ID NO 6 to SEQ ID NO 25, or to the complements thereof.

[0039] Hybridising nucleic acids of the type described herein can be used, for example, as a primer (e.g., a PCR primer), or a diagnostic and/or prognostic probe or primer. Preferably, hybridisation of the oligonucleotide probe to a nucleic acid sample is performed under stringent conditions and the probe is 100% identical to the target sequence.

Nucleic acid duplex or hybrid stability is expressed as the melting temperature or Tm, which is the temperature at which a probe dissociates from a target DNA. This melting temperature is used to define the required stringency conditions.

[0040] For target sequences that are related and substantially identical to the corresponding sequence of SEQ ID NO 1 to SEQ ID NO 5 (such as allelic variants and SNPs), rather than identical, it is useful to first establish the lowest temperature at which only homologous hybridisation occurs with a particular concentration of salt (e.g., SSC or SSPE). Then, assuming that 1% mismatching results in a 1° C. decrease in the Tm, the temperature of the final wash in the hybridisation reaction is reduced accordingly (for example, if sequences having >95% identity with the probe are sought, the final wash temperature is decreased by 5° C.). In practice, the change in Tm can be between 0.5° C. and 1.5° C. per 1% mismatch.

[0041] Examples of inventive oligonucleotides of length X (in nucleotides), as indicated by polynucleotide positions with reference to, e.g., SEQ ID NO 1 to SEQ ID NO 5, include those corresponding to sets of consecutively overlapping oligonucleotides of length X, where the oligonucleotides within each consecutively overlapping set (corresponding to a given X value) are defined as the finite set of Z oligonucleotides from nucleotide positions:

[0042] n to (n+(X−1));

[0043] where n=1, 2, 3, . . . (Y−(X−1));

[0044] where Y equals the length (nucleotides or base pairs) of SEQ ID NO 1 to SEQ ID NO 5;

[0045] where X equals the common length (in nucleotides) of each oligonucleotide in the set (e.g., X=20 for a set of consecutively overlapping 20-mers); and

[0046] where the number (Z) of consecutively overlapping oligomers of length X for a given SEQ ID NO of length Y is equal to Y−(X−1). For example Z=2,785−19=2,766 for either sense or antisense sets of SEQ ID NO 1 to SEQ ID NO 5, where X=20.

[0047] Preferably, the set is limited to those oligomers that comprise at least one CpG, TpG or CpA dinucleotide.

[0048] The present invention encompasses, for each of SEQ ID NO 6 to SEQ ID NO 25 (sense and antisense), multiple consecutively overlapping sets of oligonucleotides or modified oligonucleotides of length X, where, e.g., X=9, 10, 17, 20, 22, 23, 25, 27, 30 or 35 nucleotides.

[0049] The oligonucleotides or oligomers according to the present invention constitute effective tools useful to ascertain genetic and epigenetic parameters of the genomic sequence corresponding to SEQ ID NO 1 to SEQ ID NO 5. Preferred sets of such oligonucleotides or modified oligonucleotides of length X are those consecutively overlapping sets of oligomers corresponding to SEQ ID NO 1 to SEQ ID NO 25 (and to the complements thereof). Preferably, said oligomers comprise at least one CpG, TpG or CpA dinucleotide. Included in these preferred sets are the preferred oligomers corresponding to SEQ ID NO 11 to SEQ ID NO 15.

[0050] Particularly preferred oligonucleotides or oligomers according to the present invention are those in which the cytosine of the CpG dinucleotide (or the thymine of the TpG or the adenosine of the CpA dinucleotide) sequences is within the middle third of the oligonucleotide; that is, where the oligonucleotide is, for example, 13 bases in length, the CpG, TpG or CpA dinucleotide is positioned within the fifth to ninth nucleotide from the 5'-end.

[0051] The oligonucleotides of the invention can also be modified by chemically linking the oligonucleotide to one or more moieties or conjugates to enhance the activity, stability or detection of the oligonucleotide. Such moieties or conjugates include chromophores, fluorophors, lipids such as cholesterol, cholic acid, thioether, aliphatic chains, phospholipids, polyamines, polyethylene glycol (PEG), palmityl moieties, and others as disclosed in, for example, U.S. Pat. Nos. 5,514,758, 5,565,552, 5,567,810, 5,574,142, 5,585,481, 5,587,371, 5,597,696 and 5,958,773. The probes may also exist in the form of a PNA (peptide nucleic acid) which has particularly preferred pairing properties. Thus, the oligonucleotide may include other appended groups such as peptides, and may include hybridization-triggered cleavage agents (Krol et al., *BioTechniques* 6:958-976, 1988) or intercalating agents (Zon, *Pharm. Res.* 5:539-549, 1988). To this end, the oligonucleotide may be conjugated to another molecule, e.g., a chromophore, fluorophor, peptide, hybridisation-triggered cross-linking agent, transport agent, hybridisation-triggered cleavage agent, etc.

[0052] The oligonucleotide may also comprise at least one art-recognised modified sugar and/or base moiety, or may comprise a modified backbone or non-natural internucleoside linkage.

[0053] The oligomers according to the present invention are normally used in so called "sets" which in one embodiment contain at least one oligomer for analysis of each of the CpG dinucleotides of a genomic sequence comprising SEQ ID NO 1 to SEQ ID NO 5 and sequences complementary thereto or to their corresponding CG, TG or CA dinucleotide within the pretreated nucleic acids according to SEQ ID NO 6 to SEQ ID NO 25 and sequences complementary thereto. Preferred is a set which contains at least one oligomer for each of the CpG dinucleotides within one or more genes selected from the group comprising Versican, TPEF, H-Cadherin, Calcitonin and EYA4 and their promoter and regulatory elements in both the pretreated and genomic versions of each gene, SEQ ID NO 1 to SEQ ID NO 25 respectively. However, it is anticipated that for economic or other factors it may be preferable to analyse a limited selection of the CpG dinucleotides within said sequences and the contents of the set of oligonucleotides should be altered accordingly. Therefore, the present invention moreover relates to a set of at least 4 oligonucleotides and/or PNA-oligomers used for detecting the cytosine methylation state in pretreated genomic DNA (SEQ ID NO 6 to SEQ ID NO 25 and sequences complementary thereto) and genomic DNA (SEQ ID NO 1 to SEQ ID NO 5 and sequences complementary thereto). These probes enable diagnosis and/or therapy of genetic and epigenetic parameters of cell proliferative disorders. The set of oligomers may also be used for detecting single nucleotide polymorphisms (SNPs) in pretreated genomic DNA (SEQ ID NO 6 to SEQ ID NO 25, and sequences complementary thereto) and genomic DNA (SEQ ID NO 1 to SEQ ID NO 5, and sequences complementary thereto).

[0054] Moreover, the present invention makes available a set of at least two oligonucleotides which can be used as so-called "primer oligonucleotides" for amplifying DNA sequences of one of SEQ ID NO 6 to SEQ ID NO 25 and sequences complementary thereto, or segments thereof.

[0055] In the case of the sets of oligonucleotides according to the present invention, it is preferred that at least one and more preferably all members of the set of oligonucleotides is bound to a solid phase.

[0056] According to the present invention, it is preferred that an arrangement of different oligonucleotides and/or PNA-oligomers (a so-called "array") made available by the present invention is present in a manner that it is likewise bound to a solid phase. This array of different oligonucleotide- and/or PNA-oligomer sequences can be characterized in that it is arranged on the solid phase in the form of a rectangular or hexagonal lattice. The solid phase surface is preferably composed of silicon, glass, polystyrene, aluminium, steel, iron, copper, nickel, silver, or gold. However, nitrocellulose as well as plastics such as nylon which can exist in the form of pellets or also as resin matrices may also be used.

[0057] Therefore, a further subject matter of the present invention is a method for manufacturing an array fixed to a carrier material for analysis in connection with cell proliferative disorders, in which method at least one oligomer according to the present invention is coupled to a solid phase. Methods for manufacturing such arrays are known, for example, from U.S. Pat. No. 5,744,305 by means of solid-phase chemistry and photolabile protecting groups.

[0058] A further subject matter of the present invention relates to a DNA chip for the analysis of cell proliferative disorders. DNA chips are known, for example, in U.S. Pat. No. 5,837,832.

[0059] The present invention further provides a method for conducting an assay in order to ascertain genetic and/or epigenetic parameters of one or more genes selected from the group comprising Versican, TPEF, H-Cadherin, Calcitonin and EYA4 and their promoter and regulatory elements. Most preferably the assays according to the following method are used in order to detect methylation within one or more genes selected from the group comprising Versican, TPEF, H-Cadherin, Calcitonin and EYA4 wherein said methylated nucleic acids are present in a solution further comprising an excess of background DNA, wherein the background DNA is present in between 100 to 1000 times the concentration of the DNA to be detected. Said method comprises contacting a nucleic acid sample obtained from a subject with at least one reagent or a series of reagents, wherein said reagent or series of reagents, distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid.

[0060] Preferably, said method comprises the following steps: In the first step, a sample of the tissue to be analysed is obtained. The source may be any suitable source, preferably, the source of the sample is selected from the group consisting of histological slides, biopsies, paraffin-embedded tissue, bodily fluids, stool, blood, serum, plasma, urine, sputum and combinations thereof. Preferably, the source is biopsies, bodily fluids, urine, or blood.

[0061] The DNA is then isolated from the sample. Extraction may be by means that are standard to one skilled in the art, including the use of detergent lysates, sonification and vortexing with glass beads. Once the nucleic acids have been extracted, the genomic double stranded DNA is used in the analysis.

[0062] In the second step of the method, the genomic DNA sample is treated in such a manner that cytosine bases which are unmethylated at the 5'-position are converted to uracil, thymine, or another base which is dissimilar to cytosine in terms of hybridisation behavior. This will be understood as 'pretreatment' herein.

[0063] The above described treatment of genomic DNA is preferably carried out with bisulfite (hydrogen sulfite, disulfite) and subsequent alkaline hydrolysis which results in a conversion of non-methylated cytosine nucleobases to uracil or to another base which is dissimilar to cytosine in terms of base pairing behaviour. Enclosing the DNA to be analysed in an agarose matrix, thereby preventing the diffusion and renaturation of the DNA (bisulfite only reacts with single-stranded DNA), and replacing all precipitation and purification steps with fast dialysis (Olek A, et al., A modified and improved method for bisulfite based cytosine methylation analysis, *Nucleic Acids Res.* 24:5064-6, 1996). It is further preferred that the bisulfite treatment is carried out in the presence of a radical trap or DNA denaturing agent.

[0064] In the third step of the method, fragments of the pretreated DNA are amplified. Wherein the source of the DNA is free DNA from serum, or DNA extracted from paraffin it is particularly preferred that the size of the amplificate fragment is between 100 and 200 base pairs in length, and wherein said DNA source is extracted from cellular sources (e.g. tissues, biopsies, cell lines) it is preferred that the amplificate is between 100 and 350 base pairs in length. It is particularly preferred that said amplificates comprise at least one 20 base pair sequence comprising at least three CpG dinucleotides. Said amplification is carried out using sets of primer oligonucleotides according to the present invention, and a preferably heat-stable polymerase. The amplification of several DNA segments can be carried out simultaneously in one and the same reaction vessel, in one embodiment of the method preferably two or more fragments are amplified simultaneously. Typically, the amplification is carried out using a polymerase chain reaction (PCR). The set of primer oligonucleotides includes at least two oligonucleotides whose sequences are each reverse complementary, identical, or hybridise under stringent or highly stringent conditions to an at least 18-base-pair long segment of the base sequences of SEQ ID NO 6 to SEQ ID NO 25 and sequences complementary thereto.

[0065] In an alternate embodiment of the method, the methylation status of preselected CpG positions within the nucleic acid sequences comprising SEQ ID NO 6 to SEQ ID NO 25 may be detected by use of methylation-specific primer oligonucleotides. This technique (MSP) has been described in U.S. Pat. No. 6,265,171 to Herman. The use of methylation status specific primers for the amplification of bisulfite treated DNA allows the differentiation between methylated and unmethylated nucleic acids. MSP primers pairs contain at least one primer which hybridizes to a bisulfite treated CpG dinucleotide. Therefore, the sequence of said primers comprises at least one CpG, TpG or CpA dinucleotide. MSP primers specific for non-methylated DNA contain a "T' at the 3' position of the C position in the

CpG. Preferably, therefore, the base sequence of said primers is required to comprise a sequence having a length of at least 18 nucleotides which hybridizes to a pretreated nucleic acid sequence according to SEQ ID NO 6 to SEQ ID NO 25 and sequences complementary thereto, wherein the base sequence of said oligomers comprises at least one CpG, TpG or CpA dinucleotide. In this embodiment of the method according to the invention it is particularly preferred that the MSP primers comprise between 2 and 5 CpG, TpG or CpA dinucleotides. It is further preferred that said dinucleotides are located within the 3' half of the primer e.g. wherein a primer is 18 bases in length the specified dinucleotides are located within the first 9 bases form the 3' end of the molecule. In addition to the CpG, TpG or CpA dinucleotides it is further preferred that said primers should further comprise several bisulfite converted bases (i.e. cytosine converted to thymine, or on the hybridizing strand, guanine converted to adenosine). In a further preferred embodiment said primers are designed so as to comprise no more than 2 cytosine or guanine bases.

[0066] In one embodiment of the method the primers may be selected from the group consisting of SEQ ID NO 34 to SEQ ID NO 49, 96, 97, 101, 102, 106 and 107.

[0067] The fragments obtained by means of the amplification can carry a directly or indirectly detectable label. Preferred are labels in the form of fluorescence labels, radionuclides, or detachable molecule fragments having a typical mass which can be detected in a mass spectrometer. Where said labels are mass labels, it is preferred that the labelled amplificates have a single positive or negative net charge, allowing for better detectability in the mass spectrometer. The detection may be carried out and visualised by means of, e.g., matrix assisted laser desorption/ionisation mass spectrometry (MALDI) or using electron spray mass spectrometry (ESI).

[0068] Matrix Assisted Laser Desorption/Ionization Mass Spectrometry (MALDI-TOF) is a very efficient development for the analysis of biomolecules (Karas & Hillenkamp, *Anal Chem.,* 60:2299-301, 1988). An analyte is embedded in a light-absorbing matrix. The matrix is evaporated by a short laser pulse thus transporting the analyte molecule into the vapour phase in an unfragmented manner. The analyte is ionised by collisions with matrix molecules. An applied voltage accelerates the ions into a field-free flight tube. Due to their different masses, the ions are accelerated at different rates. Smaller ions reach the detector sooner than bigger ones. MALDI-TOF spectrometry is well suited to the analysis of peptides and proteins. The analysis of nucleic acids is somewhat more difficult (Gut & Beck, *Current Innovations and Future Trends,* 1:147-57, 1995). The sensitivity with respect to nucleic acid analysis is approximately 100-times less than for peptides, and decreases disproportionally with increasing fragment size. Moreover, for nucleic acids having a multiply negatively charged backbone, the ionisation process via the matrix is considerably less efficient. In MALDI-TOF spectrometry, the selection of the matrix plays an eminently important role. For the desorption of peptides, several very efficient matrixes have been found which produce a very fine crystallisation. There are now several responsive matrixes for DNA, however, the difference in sensitivity between peptides and nucleic acids has not been reduced. This difference in sensitivity can be reduced, however, by chemically modifying the DNA in such a manner that it becomes more similar to a peptide. For example, phosphorothioate nucleic acids, in which the usual phosphates of the backbone are substituted with thiophosphates, can be converted into a charge-neutral DNA using simple alkylation chemistry (Gut & Beck, *Nucleic Acids Res.* 23: 1367-73, 1995). The coupling of a charge tag to this modified DNA results in an increase in MALDI-TOF sensitivity to the same level as that found for peptides. A further advantage of charge tagging is the increased stability of the analysis against impurities, which makes the detection of unmodified substrates considerably more difficult.

[0069] In a particularly preferred embodiment of the method the amplification of step three is carried out in the presence of at least one species of blocker oligonucleotides. The use of such blocker oligonucleotides has been described by Yu et al., *BioTechniques* 23:714-720, 1997. The use of blocking oligonucleotides enables the improved specificity of the amplification of a sub-population of nucleic acids. Blocking probes hybridised to a nucleic acid suppress, or hinder the polymerase mediated amplification of said nucleic acid. In one embodiment of the method blocking oligonucleotides are designed so as to hybridise to background DNA. In a further embodiment of the method said oligonucleotides are designed so as to hinder or suppress the amplification of unmethylated nucleic acids as opposed to methylated nucleic acids or vice versa.

[0070] Blocking probe oligonucleotides are hybridised to the bisulfite treated nucleic acid concurrently with the PCR primers. PCR amplification of the nucleic acid is terminated at the 5' position of the blocking probe, such that amplification of a nucleic acid is suppressed where the complementary sequence to the blocking probe is present. The probes may be designed to hybridize to the bisulfite treated nucleic acid in a methylation status specific manner. For example, for detection of methylated nucleic acids within a population of unmethylated nucleic acids, suppression of the amplification of nucleic acids which are unmethylated at the position in question would be carried out by the use of blocking probes comprising a 'TpG' at the position in question, as opposed to a 'CpG.' In one embodiment of the method the sequence of said blocking oligonucleotides should be identical or complementary to molecule is complementary or identical to a sequence at least 18 base pairs in length selected from the group consisting of SEQ ID NO 6 to SEQ ID NO 25, preferably comprising one or more CpG, TpG or CpA dinucleotides. In one embodiment of the method the sequence of said oligonucleotides is selected from the group consisting SEQ ID NO 85 to SEQ ID NO 87, 98, 103 and 108 and sequences complementary thereto.

[0071] For PCR methods using blocker oligonucleotides, efficient disruption of polymerase-mediated amplification requires that blocker oligonucleotides not be elongated by the polymerase. Preferably, this is achieved through the use of blockers that are 3'-deoxyoligonucleotides, or oligonucleotides derivitized at the 3' position with other than a "free" hydroxyl group. For example, 3'-O-acetyl oligonucleotides are representative of a preferred class of blocker molecule.

[0072] Additionally, polymerase-mediated decomposition of the blocker oligonucleotides should be precluded. Preferably, such preclusion comprises either use of a polymerase lacking 5'-3' exonuclease activity, or use of modified blocker oligonucleotides having, for example, thioate bridges at the

5'-terminii thereof that render the blocker molecule nuclease-resistant. Particular applications may not require such 5' modifications of the blocker. For example, if the blocker- and primer-binding sites overlap, thereby precluding binding of the primer (e.g., with excess blocker), degradation of the blocker oligonucleotide will be substantially precluded. This is because the polymerase will not extend the primer toward, and through (in the 5'-3' direction) the blocker—a process that normally results in degradation of the hybridized blocker oligonucleotide.

[0073] A particularly preferred blocker/PCR embodiment, for purposes of the present invention and as implemented herein, comprises the use of peptide nucleic acid (PNA) oligomers as blocking oligonucleotides. Such PNA blocker oligomers are ideally suited, because they are neither decomposed nor extended by the polymerase.

[0074] In one embodiment of the method, the binding site of the blocking oligonucleotide is identical to, or overlaps with that of the primer and thereby hinders the hybridisation of the primer to its binding site. In a further preferred embodiment of the method, two or more such blocking oligonucleotides are used. In a particularly preferred embodiment, the hybridisation of one of the blocking oligonucleotides hinders the hybridisation of a forward primer, and the hybridisation of another of the probe (blocker) oligonucleotides hinders the hybridisation of a reverse primer that binds to the amplificate product of said forward primer.

[0075] In an alternative embodiment of the method, the blocking oligonucleotide hybridises to a location between the reverse and forward primer positions of the treated background DNA, thereby hindering the elongation of the primer oligonucleotides.

[0076] It is particularly preferred that the blocking oligonucleotides are present in at least 5 times the concentration of the primers.

[0077] In the fourth step of the method, the amplificates obtained during the third step of the method are analysed in order to ascertain the methylation status of the CpG dinucleotides prior to the treatment.

[0078] In embodiments where the amplificates were obtained by means of MSP amplification and/or blocking oligonucleotides, the presence or absence of an amplificate is in itself indicative of the methylation state of the CpG positions covered by the primers and or blocking oligonucleotide, according to the base sequences thereof. All possible known molecular biological methods may be used for this detection, including, but not limited to gel electrophoresis, sequencing, liquid chromatography, hybridisations, real time PCR analysis or combinations thereof. This step of the method further acts as a qualitative control of the preceding steps.

[0079] In the fourth step of the method amplificates obtained by means of both standard and methylation specific PCR are further analysed in order to determine the CpG methylation status of the genomic DNA isolated in the first step of the method. This may be carried out by means of based-based methods such as, but not limited to, array technology and probe based technologies as well as by means of techniques such as sequencing and template directed extension.

[0080] In one embodiment of the method, the amplificates synthesised in step three are subsequently hybridised to an array or a set of oligonucleotides and/or PNA probes. In this context, the hybridisation takes place in the following manner: the set of probes used during the hybridisation is preferably composed of at least 2 oligonucleotides or PNA-oligomers; in the process, the amplificates serve as probes which hybridise to oligonucleotides previously bonded to a solid phase; the non-hybridised fragments are subsequently removed; said oligonucleotides contain at least one base sequence having a length of at least 9 nucleotides which is reverse complementary or identical to a segment of the base sequences specified in the SEQ ID NO 2 to SEQ ID NO 5; and the segment comprises at least one CpG, TpG or CpA dinucleotide.

[0081] In a preferred embodiment, said dinucleotide is present in the central third of the oligomer. For example, wherein the oligomer comprises one CpG dinucleotide, said dinucleotide is preferably the fifth to ninth nucleotide from the 5'-end of a 13-mer. One oligonucleotide exists for the analysis of each CpG dinucleotide within the sequence according to SEQ ID NO 1 to SEQ ID NO 5, and the equivalent positions within SEQ ID NO 6 to SEQ ID NO 25. Said oligonucleotides may also be in the form of peptide nucleic acids. The non-hybridised amplificates are then removed. The hybridised amplificates are detected. In this context, it is preferred that labels attached to the amplificates are identifiable at each position of the solid phase at which an oligonucleotide sequence is located. In one embodiment of the method said oligonucleotides may be selected from the group comprising SEQ ID NOS 50-77, 88 and 89.

[0082] In yet a further embodiment of the method, the genomic methylation status of the CpG positions may be ascertained by means of oligonucleotide probes that are hybridised to the bisulfite treated DNA concurrently with the PCR amplification primers (wherein said primers may either be methylation specific or standard).

[0083] A particularly preferred embodiment of this method is the use of fluorescence-based Real Time Quantitative PCR (Heid et al., *Genome Res.* 6:986-994, 1996; also see U.S. Pat. No. 6,331,393). There are two preferred embodiments of utilising this method. One embodiment, known as the TaqMan™ assay employs a dual-labelled fluorescent oligonucleotide probe. The TaqMan™ PCR reaction employs the use of a nonextendible interrogating oligonucleotide, called a TaqMan™ probe, which is designed to hybridise to a GpC-rich sequence located between the forward and reverse amplification primers. The TaqMan™ probe further comprises a fluorescent "reporter moiety" and a "quencher moiety" covalently bound to linker moieties (e.g., phosphoramidites) attached to the nucleotides of the TaqMan™ oligonucleotide. Hybridised probes are displaced and broken down by the polymerase of the amplification reaction thereby leading to an increase in fluorescence. For analysis of methylation within nucleic acids subsequent to bisulfite treatment, it is required that the probe be methylation specific, as described in U.S. Pat. No. 6,331,393, (hereby incorporated by reference in its entirety) also known as the MethylLight™ assay. The second preferred embodiment of this technology is the use of dual-probe technology (Lightcycler™), each carrying donor or recipient fluorescent moieties, hybridisation of two probes in proximity to each other is indicated by an increase or

fluorescent amplification primers. Both these techniques may be adapted in a manner suitable for use with bisulfite treated DNA, and moreover for methylation analysis within CpG dinucleotides. In one embodiment of the method the sequence of said probe oligonucleotides may be selected from the group comprising SEQ ID NO 78-84, 90, 99, 100, 104, 105, 109 and 110.

[0084] In a further preferred embodiment of the method, the fourth step of the method comprises the use of template-directed oligonucleotide extension, such as MS-SNuPE as described by Gonzalgo & Jones, *Nucleic Acids Res.* 25:2529-2531, 1997. In said embodiment it is preferred that the Ms-SNuPE primer is identical or complementary to a sequence at least nine but preferably no more than twenty five nucleotides in length of one or more of the sequences taken from the group of SEQ ID NO 2 to SEQ ID NO 5.

[0085] In yet a further embodiment of the method, the fourth step of the method comprises sequencing and subsequent sequence analysis of the amplificate generated in the third step of the method (Sanger F., et al., *Proc Natl Acad Sci USA* 74:5463-5467, 1977).

[0086] Additional embodiments of the invention provide a method for the analysis of the methylation status of genomic DNA according to the invention (SEQ ID NO 1 to SEQ ID NO 5) without the need for pretreatment.

[0087] In the first step of such additional embodiments, the genomic DNA sample is isolated from tissue or cellular sources. Preferably, such sources include cell lines, histological slides, body fluids, or tissue embedded in paraffin. Extraction may be by means that are standard to one skilled in the art, including but not limited to the use of detergent lysates, sonification and vortexing with glass beads. Once the nucleic acids have been extracted, the genomic double-stranded DNA is used in the analysis.

[0088] In a preferred embodiment, the DNA may be cleaved prior to the treatment, and this may be by any means standard in the state of the art, in particular with methylation-sensitive restriction endonucleases.

[0089] In the second step, the DNA is then digested with one or more methylation sensitive restriction enzymes. The digestion is carried out such that hydrolysis of the DNA at the restriction site is informative of the methylation status of a specific CpG dinucleotide.

[0090] In the third step, which is optional but a preferred embodiment, the restriction fragments are amplified. This is preferably carried out using a polymerase chain reaction, and said amplificates may carry suitable detectable labels as discussed above, namely fluorophore labels, radionuclides and mass labels.

[0091] In the final step the amplificates are detected. The detection may be by any means standard in the art, for example, but not limited to, gel electrophoresis analysis, hybridisation analysis, incorporation of detectable tags within the PCR products, DNA array analysis, MALDI or ESI analysis.

[0092] The present invention enables diagnosis and/or prognosis of events which are disadvantageous to patients or individuals in which important genetic and/or epigenetic parameters within the Versican, TPEF, H-Cadherin, Calcitonin and EYA4 and their promoter or regulatory elements may be used as markers. Said parameters obtained by means of the present invention may be compared to another set of genetic and/or epigenetic parameters, the differences serving as the basis for a diagnosis and/or prognosis of events which are disadvantageous to patients or individuals.

[0093] Specifically, the present invention provides for diagnostic and/or prognostic cancer assays based on measurement of differential methylation of Versican, TPEF, H-Cadherin, Calcitonin and/or EYA4 CpG dinucleotide sequences. Preferred gene sequences useful to measure such differential methylation are represented herein by SEQ ID NO 1 to SEQ ID NO 25. Typically, such assays involve obtaining a tissue sample from a test tissue, performing an assay to measure the methylation status of at least one of the inventive Versican, TPEF, H-Cadherin, Calcitonin and/or EYA4 specific CpG dinucleotide sequences derived from the tissue sample, relative to a control sample, and making a diagnosis or prognosis based thereon.

[0094] In particular preferred embodiments, inventive oligomers are used to assess Versican, TPEF, H-Cadherin, Calcitonin and/or EYA4 specific CpG dinucleotide methylation status, such as those based on SEQ ID NO 1 to SEQ ID NO 25, including the representative preferred oligomers corresponding to SEQ ID NOS: ALL OLIGOS, or arrays thereof, as well as a kit based thereon are useful for the diagnosis and/or prognosis of cancer and/or other prostate cell proliferative disorders.

[0095] The present invention moreover relates to a diagnostic agent and/or therapeutic agent for the diagnosis and/or therapy colon cell proliferative disorders, the diagnostic agent and/or therapeutic agent being characterised in that at least one primer or probe based on SEQ ID NO 1 to SEQ ID NO 25 is used for manufacturing it, possibly together with suitable additives and ancillary agents.

[0096] Moreover, an additional aspect of the present invention is a kit comprising, for example: a bisulfite-containing reagent as well as at least one oligonucleotide whose sequences in each case correspond, are complementary, or hybridise under stringent or highly stringent conditions to a 18-base long segment of the sequences SEQ ID NO 1 to SEQ ID NO 5. Said kit may further comprise instructions for carrying out and evaluating the described method. In a further preferred embodiment, said kit may further comprise standard reagents for performing a CpG position-specific methylation analysis, wherein said analysis comprises one or more of the following techniques: MS-SNuPE, MSP, MethyLight, HeavyMethyl™ COBRA, and nucleic acid sequencing. However, a kit along the lines of the present invention can also contain only part of the aforementioned components.

[0097] Typical reagents (e.g., as might be found in a typical COBRA-based kit) for COBRA analysis may include, but are not limited to: PCR primers for specific gene (or methylation-altered DNA sequence or CpG island); restriction enzyme and appropriate buffer; gene-hybridisation oligo; control hybridisation oligo; kinase labelling kit for oligo probe; and radioactive nucleotides. Additionally, bisulfite conversion reagents may include: DNA denaturation buffer; sulfonation buffer; DNA recovery reagents or kits (e.g., precipitation, ultrafiltration, affinity column); desulfonation buffer; and DNA recovery components.

[0098] Typical reagents (e.g., as might be found in a typical MethyLight-based kit) for MethyLight analysis may

include, but are not limited to: PCR primers for specific gene (or methylation-altered DNA sequence or CpG island); TaqMan® probes; optimized PCR buffers and deoxynucleotides; and Taq polymerase.

[0099] Typical reagents (e.g., as might be found in a typical Ms-SNuPE-based kit) for Ms-SNuPE analysis may include, but are not limited to: PCR primers for specific gene (or methylation-altered DNA sequence or CpG island); optimised PCR buffers and deoxynucleotides; gel extraction kit; positive control primers; Ms-SNuPE primers for specific gene; reaction buffer (for the Ms-SNuPE reaction); and radioactive nucleotides. Additionally, bisulfite conversion reagents may include: DNA denaturation buffer; sulfonation buffer; DNA recovery regents or kit (e.g., precipitation, ultrafiltration, affinity column); desulfonation buffer; and DNA recovery components.

[0100] Typical reagents (e.g., as might be found in a typical MSP-based kit) for MSP analysis may include, but are not limited to: methylated and unmethylated PCR primers for specific gene (or methylation-altered DNA sequence or CpG island), optimized PCR buffers and deoxynucleotides, and specific probes.

Definitions:

[0101] The term "CpG island" refers to a contiguous region of genomic DNA that satisfies the criteria of (1) having a frequency of CpG dinucleotides corresponding to an "Observed/Expected Ratio">0.6, and (2) having a "GC Content">0.5. CpG islands are typically, but not always, between about 0.2 to about 1 kb in length.

[0102] The term "methylation state" or "methylation status" refers to the presence or absence of 5-methylcytosine ("5-mCyt") at one or a plurality of CpG dinucleotides within a DNA sequence. Methylation states at one or more particular palindromic CpG methylation sites (each having two CpG CpG dinucleotide sequences) within a DNA sequence include "unmethylated,""fully-methylated" and "hemi-methylated."

[0103] The term "hemi-methylation" or "hemimethylation" refers to the methylation state of a palindromic CpG methylation site, where only a single cytosine in one of the two CpG dinucleotide sequences of the palindromic CpG methylation site is methylated (e.g., 5'-CC^{M}GG-3' (top strand): 3'-GGCC-5' (bottom strand)).

[0104] The term "hypermethylation" refers to the average methylation state corresponding to an increased presence of 5-mCyt at one or a plurality of CpG dinucleotides within a DNA sequence of a test DNA sample, relative to the amount of 5-mCyt found at corresponding CpG dinucleotides within a normal control DNA sample.

[0105] The term "hypomethylation" refers to the average methylation state corresponding to a decreased presence of 5-mCyt at one or a plurality of CpG dinucleotides within a DNA sequence of a test DNA sample, relative to the amount of 5-mCyt found at corresponding CpG dinucleotides within a normal control DNA sample.

[0106] The term "microarray" refers broadly to both "DNA microarrays," and 'DNA chip(s),' as recognised in the art, encompasses all art-recognized solid supports, and encompasses all methods for affixing nucleic acid molecules thereto or synthesis of nucleic acids thereon.

[0107] "Genetic parameters" are mutations and polymorphisms of genes and sequences further required for their regulation. To be designated as mutations are, in particular, insertions, deletions, point mutations, inversions and polymorphisms and, particularly preferred, SNPs (single nucleotide polymorphisms).

[0108] "Epigenetic parameters" are, in particular, cytosine methylations. Further epigenetic parameters include, for example, the acetylation of histones which, however, cannot be directly analysed using the described method but which, in turn, correlate with the DNA methylation.

[0109] The term "bisulfite reagent" refers to a reagent comprising bisulfite, disulfite, hydrogen sulfite or combinations thereof, useful as disclosed herein to distinguish between methylated and unmethylated CpG dinucleotide sequences.

[0110] The term "Methylation assay" refers to any assay for determining the methylation state of one or more CpG dinucleotide sequences within a sequence of DNA.

[0111] The term "MS.AP-PCR" (Methylation-Sensitive Arbitrarily-Primed Polymerase Chain Reaction) refers to the art-recognised technology that allows for a global scan of the genome using CG-rich primers to focus on the regions most likely to contain CpG dinucleotides, and described by Gonzalgo et al., *Cancer Research* 57:594-599, 1997.

[0112] The term "MethyLight" refers to the art-recognised fluorescence-based real-time PCR technique described by Eads et al., *Cancer Res.* 59:2302-2306, 1999.

[0113] The term "HeavyMethyl" assay, in the embodiment thereof implemented herein, refers to a HeavyMethyl™ MethylLight assay, which is a variation of the MethylLight□ assay, wherein the MethylLight assay is combined with methylation specific blocking probes covering CpG positions between the amplification primers.

[0114] The term "Ms-SNuPE" (Methylation-sensitive Single Nucleotide Primer Extension) refers to the art-recognised assay described by Gonzalgo & Jones, *Nucleic Acids Res.* 25:2529-2531, 1997.

[0115] The term "MSP" (Methylation-specific PCR) refers to the art-recognized methylation assay described by Herman et al. *Proc. Natl. Acad. Sci. USA* 93:9821-9826, 1996, and by U.S. Pat. No. 5,786,146.

[0116] The term "COBRA" (Combined Bisulfite Restriction Analysis) refers to the art-recognized methylation assay described by Xiong & Laird, *Nucleic Acids Res.* 25:2532-2534, 1997.

[0117] The term "hybridisation" is to be understood as a bond of an oligonucleotide to a complementary sequence along the lines of the Watson-Crick base pairings in the sample DNA, forming a duplex structure.

[0118] "Stringent hybridisation conditions," as defined herein, involve hybridising at 68° C. in 5×SSC/5× Denhardt's solution/1.0% SDS, and washing in 0.2×SSC/0.1% SDS at room temperature, or involve the art-recognised equivalent thereof (e.g., conditions in which a hybridisation is carried out at 60° C. in 2.5×SSC buffer, followed by several washing steps at 37° C. in a low buffer concentration, and remains stable). Moderately stringent conditions, as defined herein, involve including washing in 3×SSC at 42°

C., or the art-recognised equivalent thereof. The parameters of salt concentration and temperature can be varied to achieve the optimal level of identity between the probe and the target nucleic acid. Guidance regarding such conditions is available in the art, for example, by Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, N.Y.; and Ausubel et al. (eds.), 1995, Current Protocols in Molecular Biology, (John Wiley & Sons, N.Y.) at Unit 2.10.

[0119] "Background DNA" as used herein refers to any nucleic acids which originate from sources other than colon cells.

LEGENDS TO FIGURES

[0120] **FIG. 1** shows the level of methylation determined by different MSP MethyLight assays and HeavyMethyl MethyLight assays. The Y-axis shows the degree of methylation. Tumor samples are represented by white points, and normal colon tissue samples by black points. A significantly higher degree of methylation was observed in tumor samples than in healthy tissue samples.

[0121] **FIG. 2** shows the Receiver Operating Characteristic curve (ROC curve) of the EYA4-MSP-Methyl-Light-Assay for adenocarcinomas according to Example 1. The AUC for the MSP-Methyl-Light-Assay is: 0.94.

[0122] **FIG. 3** shows the Receiver Operating Characteristic curve (ROC curve) of the EYA4-HM-Methyl-Light-Assay for Adenocarcinoma according to Example 2. The AUC for the HM-Methyl-Light-Assay is: 0.91.

[0123] **FIG. 4** shows the level of methylation determined by a EYA4-HeavyMethyl MethyLight™ assay according to example 2, testing an additional set of colon samples (25 adenocarcinoma, 33 normals, and 13 adenomas). The Y-axis shows the degree of methylation within the region of the EYA4 gene investigated. Adenocarcinoma samples are represented by white squares, and normal colon tissue samples by black diamonds. A significantly higher degree of methylation was observed in tumor samples than in healthy tissue samples. The level of significance as measured using a t-test was 0.00424.

[0124] **FIG. 5** shows the Receiver Operating Characteristic curve (ROC curve) of the EYA4-HM-Methyl-Light-Assay for Adenocarcinoma and Adenoma according to Example 2 (additional sets of samples). The area under an ROC curve (AUC) is a measure for the accuracy of a diagnostic test. The AUC for the HM-Methyl-Light-Assay is 0.81.

[0125] **FIG. 6** shows the Receiver Operating Characteristic curve (ROC curve) of the EYA4-HM-Methyl-Light-Assay for Adenocarcinoma only according to Example 2 (additional sets of samples). The area under an ROC curve (AUC) is a measure for the accuracy of a diagnostic test. The AUC for the HM-Methyl-Light-Assay is: 0.844.

[0126] **FIG. 7** shows the Receiver Operating Characteristic curve (ROC curve) of the EYA4-HM-Methyl-Light-Assay for Adenenomas according to Example 2 (additional sets of samples). The area under an ROC curve (AUC) is a measure for the accuracy of a diagnostic test. The AUC for the HM-Methyl-Light-Assay is: 0.748.

[0127] **FIG. 8** shows the level of methylation in different tumor and healthy tissues determined by a EYA4-HeavyMethyl MethyLight™ assay according to example 3. The Y-axis shows the degree of methylation within the region of the EYA4 gene investigated. Besides the colon cancer samples only one of the two breast cancer tissues were methylated.

[0128] **FIG. 9** shows the level of methylation in different breast cancer tissues determined by a EYA4-HeavyMethyl MethyLight™ assay according to example 3. Only one was methylated.

[0129] **FIG. 10** shows the level of methylation in serum samples determined by a EYA4-HeavyMethyl MethyLight™ assay according to example 4. The Y-axis shows the degree of methylation within the region of the EYA4 gene investigated.

[0130] **FIG. 11** shows the Receiver Operating Characteristic curve (ROC curve) of the Calcitonin-MSP-Methyl-Light-Assay according to Example 5. The area under an ROC curve (AUC) is a measure for the accuracy of a diagnostic test. The AUC for the HM-Methyl-Light-Assay is: 0.85.

[0131] **FIG. 12** shows the ROC curve of the Calcitonin-HM-Methyl-Light-Assay according to Example 6. The AUC is: 0.81.

[0132] **FIG. 13** shows the ROC curve of the Versican-MSP-Methyl-Light-Assay according to Example 9. The AUC is: 0.84.

[0133] **FIG. 14** shows the ROC curve of the TBEF-MSP-Methyl-Light-Assay according to Example 10. The AUC is: 0.80.

[0134] **FIG. 15** shows the ROC curve of the Cadherin-MSP-Methyl-Light-Assay according to Example 12. The AUC is: 0.94.

[0135] **FIG. 16** shows the differentiation of healthy tissue from non healthy tissue wherein the non healthy specimens are obtained from either colon adenoma or colon carcinoma tissue (Example 13). The evaluation is carried out using informative CpG positions from 27 genes. Informative CpG positions from the genes Versican, TPEF, EYA4 and H-Cadherin are further described in Table 3.

[0136] **FIG. 17** shows the differentiation of healthy tissue from carcinoma tissue using informative CpG positions from 15 genes (Example 13). Informative CpG positions from the genes Versican, TPEF, EYA4 and H-Cadherin are further described in Table 4.

[0137] **FIG. 18** shows the differentiation of healthy tissue from adenoma tissue using informative CpG positions from 40 genes (Example 13). Informative CpG positions from the genes Versican, TPEF, EYA4 and H-Cadherin are further described in Table 5.

[0138] **FIG. 19** shows the ROC curve of the TPEF-MSP-Methyl-Light-Assay according to Example 11 (first sample set). The AUC is: 0.93.

[0139] **FIG. 20** shows the ROC curve of the TPEF-MSP-Methyl-Light-Assay according to Example 11 (second sample set). The AUC is: 1.

[0140] **FIG. 21** shows the ROC curve of a combined EYA4-Calcitonin-Heavymethyl-Methyl-Light-Assay according to Example 6. The AUC is: 0.97.

[0141] **FIG. 22** shows the regression plot of the percentage methylation within the EYA 4 gene calculated in each sample using the MSP and HeavyMethyl variants of the MethyLight assay.

[0142] **FIG. 23** shows the regression plot of the percentage methylation within the Calcitonin gene calculated in each sample using the MSP and HeavyMethyl variants of the MethyLight assay.

EXAMPLES

[0143] The following examples describe the analysis of the methylation status of the genes EYA 4, Calcitonin, TPEF, H-Cadherin and Versican in healthy and sick colon cell proliferative disorder samples. The initial link between said genes and colon cell proliferative disorders was initially carried by means of hybridisation analysis as described in examples 13 onwards. The genes EYA 4, Calcitonin, TPEF, H-Cadherin and Versican were then selected from the larger set of genes analysed in said examples, and the correlation between methylation status and colon cell proliferative disorder states was validated by analysis of samples using other methylation analysis techniques, namely the MSP-MethyLight and HeavyMethyl MethyLight assays. Please not that the term 'MethyLight' is used to describe real time PCR analysis of bisulfite treated DNA using probes of both the Taqman ingle sprobe) and Lightcycler (dual probe) technologies.

Example 1

[0144] Analysis of methylation within colon cancer using an MSP-MethyLight assay (EYA4) DNA was extracted from 33 colon adenocarcinoma samples and 43 colon normal adjacent tissues using a Qiagen extraction kit. The DNA from each sample was treated using a bisulfite solution (hydrogen sulfite, disulfite) according to the agarose-bead method (Olek et al 1996). The treatment is such that all non methylated cytosines within the sample are converted to thymidine. Conversely, 5-methylated cytosines within the sample remain unmodified.

[0145] The methylation status was determined with a MSP-MethyLight assay designed for the CpG island of interest and a control fragment from the beta actin gene (Eads et al., 2001). The CpG island assay covers CpG sites in both the primers and the Taqman style probe, while the control gene does not. The control gene is used as a measure of total DNA concentration, and the CpG island assay (methylation assay) determines the methylation levels at that site.

[0146] Methods: The EYA4 gene CpG island assay was performed using the following primers and probes: Forward Primer: CGGAGGGTACGGAGATTACG (SEQ ID NO:40); Reverse Primer: CGACGACGCGCGAAA (SEQ ID NO:41); and Probe: CGAAACCCTAAATATCCCGAATAACGCCG (SEQ ID NO:81). The corresponding control assay was performed using the following primers and probes: Primer: TGGTGATGGAGGAGGTTTAGTAAGT (SEQ ID NO:91); Primer: AACCAATAAAACCTACTCCTCCCTTAA (SEQ ID NO:92); and Probe: ACCACCACCCAACACACAATAACAAACACA (SEQ ID NO:93) The reactions were run in triplicate on each DNA sample with the following assay conditions: Reaction solution: (900 nM primers; 300 nM probe; 3.5 mM Magnesium Chloride; 1 unit of taq polymerase; 200 μM dNTPs; 7 μl of DNA, in a final reaction volume of 20 μl); Cycling conditions: (95° C. for 10 minutes; then 50 cycles of: 95° C. for 15 seconds; 60° C. for 1 minute).

[0147] The data was analysed using a PMR calculation previously described in the literature (Eads et al 2001). Results. The mean PMR for normal samples was 0.15, with a standard deviation of 0.18. The mean PMR for tumour samples was 17.98, with a standard deviation of 18.18. The overall difference in methylation levels between tumour and normal samples is significant in a t-test (p=0.00000312). The results are shown in **FIG. 1**. A Receiver Operating Characteristic curve (ROC curve) of the assay was also determined. A ROC is a plot of the true positive rate against the false positive rate for the different possible cutpoints of a diagnostic test. It shows the tradeoff between sensitivity and specificity depending on the selected cutpoint (any increase in sensitivity will be accompanied by a decrease in specificity). The area under an ROC curve (AUC) is a measure for the accuracy of a diagnostic test (the larger the area the better, optimum is 1, a random test would have a ROC curve lying on the diagonal with an area of 0.5; for reference: J. P. Egan. Signal Detection Theory and ROC Analysis, Academic Press, New York, 1975). The AUC for the MSP-Methyl-Light-Assay is: 0.94 (**FIG. 2**)

Example 2

[0148] Methylation within colon cancer was analysed using a EYA4-HeavyMethyl MethyLight assay. The same DNA samples were also used to analyse methylation of the CpG island with a HeavyMethyl MethyLight (or HM MethyLight) assay, also referred to as the HeavyMethyl assay. The methylation status was determined with a HM MethyLight assay designed for the CpG island of interest and the same control gene assay described above. The CpG island assay covers CpG sites in both the blockers and the Taqman style probe, while the control gene does not.

[0149] Methods. The CpG island assay (methylation assay) was performed using the following primers and probes:

```
Forward Primer:
GGTGATTGTTTATTGTTATGGTTTG      (SEQ ID NO:44)

Reverse Primer:
CCCCTCAACCTAAAAACTACAAC        (SEQ ID NO:45)

Forward Blocker:
GTTATGGTTTGTGATTTTGTGTGGG      (SEQ ID NO:87)

Reverse Blocker:
AAACTACAACCACTCAAATCAACCCA     (SEQ ID NO:86)

Probe:
AAAATTACGACGACGCCACCCGAAA      (SEQ ID NO:84)
```

[0150] The reactions were each run in triplicate on each DNA sample with the following assay conditions:

[0151] Reaction solution: (400 nM primers; 400 nM probe; 10 μM both blockers; 3.5 mM magnesium chloride;

1×ABI Taqman buffer; 1 unit of ABI TaqGold polymerase; 200 μM dNTPs; and 7 μl of DNA, in a final reaction volume of 20 μl);

[0152] Cycling conditions: (95□C for 10 minutes); (95°□C. for 15 seconds, 64° C. for 1 minute (2 cycles)); (95° C. for 15 seconds, 62° C. for 1 minute (2 cycles); (95° C. for 15 seconds, 60° C. for 1 minute (2 cycles)); and (95° C. for 15 seconds, 58° C. for 1 minute, 60° C. for 40 seconds (41 cycles)).

[0153] Results. The mean PMR for normal samples was 1.12 with a standard deviation of 1.45. The mean PMR for tumour samples was 38.23 with a standard deviation of 33.22. The overall difference in methylation levels between tumour and normal samples is significant in a t-test (p=0.000000326). The results are shown in **FIG. 1**.

[0154] A ROC curve of the assay was also determined. The AUC for the MSP-Methyl-Light-Assay is 0.91 (**FIG. 3**)

[0155] The assay was tested on an additional set of colon samples (25 adenocarcinoma, 33 normals, and 13 adenomas). The results showed a significant difference again (**FIG. 4**). The ROC are shown in **FIG. 5-7**.

[0156] The MSP and HeavyMethyl variants of the MethyLight assay were determined to be equivalent for the analysis of methylation in the gene EYA4, **FIG. 22** shows the regression plot of the percentage methylation detected in each sample using the two methods.

Example 3

[0157] The EYA4-HeavyMethyl-MethyLight-assay was also tested against a panel of other tissues (**FIG. 8**). Besides the colon cancer samples only one of the two breast cancer tissues were methylated. However, on a panel of 21 additional breast tumours (different stages), only one was methylated (**FIG. 9**). So the marker is specific for colon tumour samples. All primers, probes, blockers and reaction conditions were identical to those used in the analysis of the colon cancer samples (Example 2).

Example 4

[0158] Twelve of the colon tissues analysed by real-time PCR also had paired serum taken before surgery. We extracted DNA from 1 ml of that serum using a Qiagen UltraSens□ DNA extraction kit, bisulfite treated the DNA sample, and ran the EYA4-HeavyMethyl-MethyLight-assay on those samples. The control gene did not amplify for three of the cancer serum samples and three of the normal serum samples, so we can conclude that the sample preparation did not work in these cases. In the other cases, there was evidence of higher methylation in the cancer samples than the normal samples (**FIG. 10**).

Example 5

[0159] Analysis of methylation within colon cancer using a Calcitonin-MSP-MethyLight Assay The colon cancer samples described in Example 1 were also analysed using a Calcitonin-MSP-MethyLight Assay, with a Taqman® style probe. The sample preparation was carried out as described above (Example 1) The assay was performed using the following primers and probes:

```
Primer:
AGGTTATCGTCGTGCGAGTGT;          (SEQ ID NO:34)

Primer:
TCACTCAAACGTATCCCAAACCTA;       (SEQ ID NO:35)
and

Probe:
CGAATCTCTCGAACGATCGCATCCA.      (SEQ ID NO:78)
```

[0160] The corresponding control assay was performed as described above (Example 1)

[0161] The reactions were run in triplicate on each DNA sample with the following assay conditions:

[0162] Reaction solution: (900 nM primers; 300 nM probe; 3.5 mM Magnesium Chloride; 1 unit of taq polymerase; 200 μM dNTPs; 7 μl of DNA, in a final reaction volume of 20 μl);

[0163] Cycling conditions: (95° C. for 10 minutes; 95□C for 15 seconds; 67° C. for 1 minute (3 cycles)); (95° C. for 15 seconds, 64° C. for 1 minute (3 cycles)); (95° C. for 15 seconds, 62° C. for 1 minute (3 cycles)); and (95° C. for 15 seconds, 60° C. for 1 minute (40 cycles)).

[0164] The data was analysed using a PMR calculation previously described in the literature (Eads et al 2001).

[0165] Results. The mean PMR for normal samples was 0.19, with a standard deviation of 0.79. None of the normal samples was greater than 2 standard deviations about the normal mean, while 18 of 33 tumour samples reached this level of methylation. The overall difference in methylation levels between tumour and normal samples is significant in a t-test (p=0.002). The results are shown in **FIG. 1**. Significantly, the tumour samples are substantially hypermethylated relative to normal control tissue. A ROC curve of the assay was also determined. The AUC for the MSP-Methyl-Light-Assay is 0.80 (**FIG. 11**)

Example 6

[0166] Methylation within colon cancer was analysed using a Calcitonin-HeavyMethyl MethyLight assay. The same DNA samples were also used to analyse methylation of the Calcitonin-CpG island with a HeavyMethyl MethyLight assay using a Taqman® style probe (see Example 2).

[0167] The CpG island assay (methylation assay) was performed using the following primers and probes:

```
Primer:
GGATGTGAGAGTTGTTGAGGTTA;        (SEQ ID NO: 46)

Primer:
ACACACCCAAACCCATTACTATCT;       (SEQ ID NO: 47)

Probe:
ACCTCCGAATCTCTCGAACGATCGC;      (SEQ ID NO: 83)
and

Blocker:
TGTTGAGGTTATGTGTAATTGGGTGTGA.   (SEQ ID NO: 85)
```

[0168] The reactions were each run in triplicate on each DNA sample with the following assay conditions:

[0169] Reaction solution: (300 nM primers; 450 nM probe; 3.5 mM magnesium chloride; 2 units of taq polymerase; 400 μM dNTPs, 5 μM blocker; and 7 μl of DNA, in a final reaction volume of 20 μl);

[0170] Cycling conditions: (95° C. for 10 minutes); (95° C. for 15 seconds, 67° C. for 1 minute (3 cycles)); (95° C. for 15 seconds, 64° C. for 1 minute (3 cycles); (95° C. for 15 seconds, 62° C. for 1 minute (3 cycles)); and (95° C. for 15 seconds, 60° C. for 1 minute (40 cycles)).

[0171] The corresponding control assay was performed as described above (Example 2)

[0172] Results. The mean PMR for normal samples was 0.13 with a standard deviation of 0.58. None of the normal samples was greater than 2 standard deviations about the normal mean, while 19 of 33 tumour samples reached this level of methylation. The overall difference in methylation levels between tumour and normal samples is significant in a t-test (p=0.0004). The results are shown in **FIG. 1**. A ROC curve of the assay was also determined. The AUC for the HM-Methyl-Light-Assay is 0.84 (**FIG. 12**)

[0173] In order to estimate the sensitivity and specificity of a real time assay analysing a gene panel comprising the genes Calcitonin and EYA 4, the ROC of said assay was in sillico determined by combining the ROCs of the 2 genes (as described above) using a logistics model. The AUC of said curve (**FIG. 21**) is 0.97.

[0174] The MSP and HeavyMethyl variants of the MethyLight assay were determined to be equivalent for the analysis of methylation in the gene Calcitonin, **FIG. 23** shows the regression plot of the percentage methylation detected in each sample using the two methods.

Example 7

[0175] Serum analysis with Calcitonin-HM MethyLight assay. Twelve of the colon tissues analysed by real-time PCR also had paired serum taken before surgery. We extracted DNA from 1 ml of that serum using a Qiagen UltraSens® DNA extraction kit, bisulfite treated the DNA sample, and ran the HeavyMethyl-MethyLight-assay on those samples (see Example 3). Calcitonin was not methylated in all tumours, but of the five patients with the highest levels of methylation in the tumours, we were able to detect methylation in the serum of four of them. In contrast, we did not detect methylation in any of the 11 serum samples taken from healthy donors.

Example 8

[0176] Identification of the methylation status of a CpG site within the Calcitonin Gene. A fragment of the upstream region of the calcitonin gene (SEQ ID NO: 1) was amplified by PCR using the primers CCTTAGTCCCTACCTCTGCT (SEQ ID NO:94) and CTCATTTACACACACCCAAAC (SEQ ID NO:95). The resultant amplificate, 378 bp in length, contained an informative CpG at position 165. The amplificate DNA was digested with the methylation sensitive restriction endonuclease Nar I; recognition motif GGCGCC. Hydrolysis by said endonuclease is blocked by methylation of the CpG at position 165 of the amplificate. The digest was used as a control.

[0177] Genomic DNA was isolated from the samples using the DNA wizzard® DNA isolation kit (Promega□). Each sample was digested using Nar I according to manufacturer's recommendations (New England Biolabs).

[0178] About 10 ng of each genomic digest was then amplified using PCR primers CCTTAGTCCCTACCTCTGCT (SEQ ID NO: 94) and CTCATTTACACACACCCAAAC (SEQ ID NO: 95). The PCR reactions were performed using a thermocycler (Eppendorf GmbH) using 10 ng of DNA, 6 pmole of each primer, 200 μM of each dNTP, 1.5 mM $MgCl_2$ and 1 U of Hotstart®Taq (Qiagen AG). The other conditions were as recommended by the Taq polymerase manufacturer.

[0179] Using the above mentioned primers, gene fragments were amplified by PCR performing a first denaturation step for 14 min at 96° C., followed by 30-45 cycles (step 2: 60 sec at 96° C., step 3: 45 sec at 52° C., step 4: 75 sec at 72° C.) and a subsequent final elongation of 10 min at 72° C. The presence of PCR products was analysed by agarose gel electrophoresis.

[0180] PCR products were detectable, with Nar I-hydrolyzed DNA isolated wherein the tissue in question contained upmethylated DNA, when step 2 to step 4 of the cycle program were repeated 34, 37, 39, 42 and 45 fold. In contrast, PCR products were only detectable with Nar I-hydrolysed DNA isolated from downmethylated tissue when steps 2 to step 4 of the cycle program were repeated 42- and 45-fold.

Example 9

[0181] Analysis of methylation within colon cancer using a Versican-MSP-MethyLight Assay. The colon cancer samples described in Example 1 were also analysed using a Versican-MSP-MethyLight Assay with a Taqman® style probe. The sample preparation was carried out as described above (Example 1) The assay was performed using the following primers and probes:

```
Forward Primer:
TGGGATTAAGATTTTCGGTTAGTTTC          (SEQ ID No 36)

Reverse Primer:
CACTACAACGCTACGCGACTAAA             (SEQ ID No 37)

Probe:
TCGACGTTACCCAAACGAATCACATAAAAAAC    (SEQ ID No 79)
```

[0182] The corresponding control assay was performed as described above (Example 1)

[0183] The reactions were run in triplicate on each DNA sample with the following assay conditions:

[0184] Reaction solution: (900 nM primers; 300 nM probe; 3.5 mM magnesium chloride; 1 units of taq polymerase; 200 μM dNTPs, 5 μM blocker; and 7 μl of DNA, in a final reaction volume of 20 μl);

[0185] Cycling conditions: 95° C. for 10 minutes; (95° C. for 15 seconds, 60° C. for 1 minute) 50 cycles

[0186] The data was analysed using a PMR calculation previously described in the literature (Eads et al 2001).

[0187] Results. The results are shown in **FIG. 1**. The mean PMR for normal samples was 3.93, with a standard deviation of 3.57. The mean PMR for tumour samples was 23.06, with a standard deviation of 20.23 The overall difference in methylation levels between tumour and normal samples is significant in a t-test (p=0.000003063). The ROC curve of the assay is shown in **FIG. 13**. The AUC is 0.84.

[0188] This was further confirmed using a Versican-HeavyMethyl MethyLight assay, using dual Lightcycler probes.

[0189] Methods. The CpG island assay (methylation assay) was performed using the following primers and probes:

```
Forward Primer:
TGGATAGGAGTTGGGATTAAGATTTT          (SEQ ID NO:96)

Reverse Primer:
CTTATTACAATTTAAAAAAAAAATTCACTACAA  (SEQ ID NO:97)

Blocker:
AAATTCACTACAACACTACACAACTAAATTCAAC (SEQ ID NO:98)
ATTAC

Probe:
TTTTCGTATTTTTTTTCGGGTTATTACGTTTT-  (SEQ ID NO:99)
Fluor

Probe:
LC640-ATGTGATTCGTTTGGGTAACGTCGA-   (SEQ ID NO:100)
Phos
```

[0190] The reactions were each run in triplicate on each DNA sample with the following assay conditions:

[0191] Reaction conditions:

[0192] 500 nM primers

[0193] 10 uM blocker

[0194] 250 nM probes

LightCycler FastStart Hybridization Probes Mix

[0195] 4 mM Magnesium Chloride

[0196] Cycling profile:

[0197] 95 degree denaturation for 10 minutes

[0198] 50 cycles: 95 degrees 10 seconds, 57 degrees 30 seconds, 72 degrees 20 seconds

Example 10

[0199] Analysis of methylation within colon cancer using a TPEF-MSP-MethyLight Assay. The colon cancer samples described in Example 1 were also analysed using a TPEF-MSP-MethyLight Assay with a Taqman® style probe. The sample preparation was carried out as described above (Example 1) The assay was performed using the following primers and probes:

```
Forward Primer:
TTTTTTTTTCGGACGTCGTTG      (SEQ ID No 38)

Reverse Primer:
CCTCTACATACGCCGCGAAT       (SEQ ID No 39)
```

-continued

```
Probe:
AATTACCGAAAACATCGACCGA     (SEQ ID No 80)
```

[0200] The reactions were run in triplicate on each DNA sample with the following assay conditions:

[0201] Reaction solution: (900 nM primers; 300 nM probe; 3.5 mM magnesium chloride; 1 units of taq polymerase; 200 μM dNTPs, 5 μM blocker; and 7 μl of DNA, in a final reaction volume of 20 μl);

[0202] Cycling conditions: 95° C. for 10 minutes; (95° C. for 15 seconds, 60° C. for 1 minute) 50 cycles

[0203] The corresponding control assay was performed as described above (Example 1)

[0204] The data was analysed using a PMR calculation previously described in the literature (Eads et al 2001).

[0205] Results. The results are shown in **FIG. 1**. The mean PMR for normal samples was 3.04, with a standard deviation of 4.21. The mean PMR for tumour samples was 21.38, with a standard deviation of 24.08 The overall difference in methylation levels between tumour and normal samples is significant in a t-test (p=0.0000101973). The ROC curve of the assay is shown in **FIG. 14**. The AUC is 0.80.

[0206] This was further confirmed using a TPEF-HeavyMethyl MethyLight assay (using dual labeled Lightcycler probes.

[0207] Methods. The CpG island assay (methylation assay) was performed using the following primers and probes:

```
Forward Primer:
GTAGGGTTATTGTTTGGGTTAATAAAT        (SEQ ID NO:101)

Reverse Primer:
TAAAAAAAAAAAAAAAACTCCTCTACATAC     (SEQ ID NO:102)

Blocker:
AACTCCTCTACATACACCACAAATAAATT       (SEQ ID NO:103)

Probe:
CGAAAACATCGACCGAACAACG-Fluor        (SEQ ID NO:104)

Probe:
LC640-GTCCGAAAAAAAAAAAACGAACTCC-   (SEQ ID NO:105)
Phos
```

[0208] The reactions were each run in triplicate on each DNA sample with the following assay conditions:

[0209] Reaction conditions:

Forward primer:	600 nM
Reverse primer:	300 nM
Blocker:	10 uM
Probes:	500 nM
Taq polymerase:	0.1 U/ul
dNTPs:	0.2 mM each
Magnesium Chloride:	4 mM
BSA:	0.25 mg/ml
Roche buffer with no MgCl:	1x

[0210] Cycling conditions:

[0211] 95-degree denaturation for 10 minutes

[0212] 50 cycles: 95-degrees for 10 seconds, 57-degrees for 25 seconds, 72 degrees for 10 seconds

Example 11

[0213] Analysis of methylation within colon cancer using a TPEF-MSP-MethyLight Assay. An additional assay for TPEF was tested on colon samples. The assay was tested on two sets of tissues, each with 12 colon adenocarcinomas and 12 normal adjacent tissue samples.

[0214] The sample preparation was carried out as described above (Example 1) The assay was performed using the following primers and probes:

```
Forward Primer:
GGACGTTTTTTATCGAAGGCG      (SEQ ID No 48)

Reverse Primer:
GCCACCCAACCGCGA            (SEQ ID No 49)

Probe:
ACCCGAAATCACGCGCGAAAAA      (SEQ ID No 90)
```

[0215] The reactions were run in triplicate on each DNA sample with the following assay conditions:

[0216] Reaction solution: (900 nM primers; 300 nM probe; 3.5 mM magnesium chloride; 1 units of taq polymerase; 200 μM dNTPs, 5 μM blocker; and 7 μl of DNA, in a final reaction volume of 20 μl);

[0217] Cycling conditions: 95° C. for 10 minutes; (95° C. for 15 seconds, 60° C. for 1 minute) 50 cycles

[0218] The corresponding control assay was performed as described above (Example 1)

[0219] The data was analysed using a PMR calculation previously described in the literature (Eads et al 2001). In both cases, TPEF was significantly more methylated in the cancer samples The ROC curves of the assays are shown in **FIG. 19-20**. The AUC are 0.93 and 1.

Example 12

[0220] Analysis of methylation within colon cancer using a H Cadherin-MSP-MethyLight Assay The colon cancer samples described in Example 1 were also analysed using a H Cadherin-MSP-MethyLight Assay. The sample preparation was carried out as described above (Example 1) The assay was performed using the following primers and probes:

```
Forward Primer:
GACGGATTTTTTTTAACGTTTTTTC     (SEQ ID No 42)

Reverse Primer:
AAATAAAATACCACCTCCGCGA         (SEQ ID No 43)

Probe:
GCTCCTCGCGAAATACTCACCCCG       (SEQ ID No 82)
```

[0221] The reactions were run in triplicate on each DNA sample with the following assay conditions:

[0222] Reaction solution: (900 nM primers; 300 nM probe; 3.5 mM magnesium chloride; 1 units of taq polymerase; 200 μM dNTPs, 5 μM blocker; and 7 μl of DNA, in a final reaction volume of 20 μl);

[0223] Cycling conditions: 95° C. for 10 minutes; (95° C. for 15 seconds, 60° C. for 1 minute) 50 cycles

[0224] The corresponding control assay was performed as described above (Example 1)

[0225] The data was analysed using a PMR calculation previously described in the literature (Eads et al 2001).

[0226] Results. The results are shown in **FIG. 1**. The mean PMR for normal samples was 2.25, with a standard deviation of 2.42. The mean PMR for tumour samples was 25.67, with a standard deviation of 17.57 The overall difference in methylation levels between tumour and normal samples is significant in a t-test (p=0.00000000118). The ROC curve of the assay is shown in **FIG. 15**. The AUC is 0.94

[0227] This was further confirmed using a H Cadherin-HeavyMethyl MethyLight assay, using dual Lightcycler probes using Lightcycler style dual probe technology.

[0228] Methods. The CpG island assay (methylation assay) was performed using the following primers and probes:

```
Forward Primer:
GTTAGTTAGTTAATTTTTTAAATAGATTAGTAG  (SEQ ID NO:106)

Reverse Primer:
CAAAAAAACAAATAAAATACCACCTCC        (SEQ ID NO:107)

Blocker:
CCTCCACAAAACTCACTCCTCACAAAATAC     (SEQ ID NO:108)

Probe: red640
TTTCGTTTTGTATGGTAGATACGGGGTGA-     (SEQ ID NO:109)
phosphate

Probe:
ATTAATGGTTTTATAAGACGGATTTTTTTTTAAC (SEQ ID NO:110)
GT-fluorescine
```

[0229] The reactions were each run in triplicate on each DNA sample with the following assay conditions:

[0230] Reaction conditions:

Forward primer:	600 nM
Reverse primer:	300 nM
Blocker:	10 uM
Probes:	500 nM
Taq polymerase:	0.1 U/ul
dNTPs:	0.2 mM each
Magnesium Chloride:	4 mM
BSA:	0.25 mg/ml
Roche buffer with no MgCl:	1x

[0231] Cycling conditions:

[0232] 95-degree denaturation for 10 minutes

[0233] 50 cycles: 95-degrees for 10 seconds, 57-degrees for 25 seconds, 72 degrees for 10 seconds

Example 13

[0234] Multiplex-PCR of colon cancer samples. In the first step the genomic DNA was isolated from the cell samples using the Wizzard kit from (Promega). The isolated genomic DNA from the samples are treated using a bisulfite solution (hydrogen sulfite, disulfite). The treatment is such that all non methylated cytosines within the sample are converted to thiamine, conversely 5-methylated cytosines within the sample remain unmodified. The treated nucleic acids were then amplified using multiplex PCRs, amplifying 8 fragments per reaction with Cy5 fluorescently labelled primers. PCR primers used are described in Table 1. PCR conditions were as follows.

[0235] Reaction solution:

[0236] 10 ng bisulfite treated DNA

[0237] 3.5 mM MgCl2

[0238] 400 μM dNTPs

[0239] 2 pmol each primer

[0240] 1 U Hot Star Taq (Qiagen)

[0241] Forty cycles were carried out as follows. Denaturation at 95° C. for 15 min, followed by annealing at 55° C. for 45 sec., primer elongation at 65° C. for 2 min. A final elongation at 65° C. was carried out for 10 min.

[0242] All PCR products from each individual sample were then hybridised to glass slides carrying a pair of immobilised oligonucleotides for each CpG position under analysis. Each of these detection oligonucleotides was designed to hybridise to the bisulphite converted sequence around one CpG site which was either originally unmethylated (TG) or methylated (CG). See Table 2 for further details of all hybridisation oligonucleotides used (both informative and non-informative) Hybridisation conditions were selected to allow the detection of the single nucleotide differences between the TG and CG variants.

[0243] 5 μl volume of each multiplex PCR product was diluted in 10×Ssarc buffer (10×Ssarc: 230 ml 20×SSC, 180 ml sodium lauroyl sarcosinate solution 20%, dilute to 1000 ml with dH2O). The reaction mixture was then hybridised to the detection oligonucleotides as follows. Denaturation at 95° C., cooling down to 10° C., hybridisation at 42° C. overnight followed by washing with 10×Ssarc and dH2O at 42° C.

[0244] Fluorescent signals from each hybridised oligonucleotide were detected using genepix scanner and software. Ratios for the two signals (from the CG oligonucleotide and the TG oligonucleotide used to analyse each CpG position) were calculated based on comparison of intensity of the fluorescent signals.

[0245] The data was then sorted into a ranked matrix (as shown in FIGS. **16** to **18**) according to CpG methylation differences between the two classes of tissues, using an algorithm. The most significant CpG positions are at the bottom of the matrix with significance decreasing towards the top. Black indicates total methylation at a given CpG position, white represents no methylation at the particular position, with degrees of methylation represented in gray, from light (low proportion of methylation) to dark (high proportion of methylation). Each row represents one specific CpG position within a gene and each column shows the methylation profile for the different CpGs for one sample. On the left side a CpG and gene identifier is shown this may be cross referenced with the accompanying tables (Table 1 to 6) in order to ascertain the gene in question and the detection oligomer used. On the right side p values for the individual CpG positions are shown. The p values are the probabilities that the observed distribution occurred by chance in the data set.

[0246] For selected distinctions, we trained a learning algorithm (support vector machine, SVM). The SVM (as discussed by F. Model, P. Adorjan, A. Olek, C. Piepenbrock, Feature selection for DNA methylation based cancer classification. Bioinformatics. 2001 June; 17 Suppl 1:S157-64) constructs an optimal discriminant between two classes of given training samples. In this case each sample is described by the methylation patterns (CG/TG ratios) at the investigated CpG sites. The SVM was trained on a subset of samples of each class, which were presented with the diagnosis attached. Independent test samples, which were not shown to the SVM before were then presented to evaluate, if the diagnosis can be predicted correctly based on the predictor created in the training round. This procedure was repeated several times using different partitions of the samples, a method called crossvalidation. Please note that all rounds are performed without using any knowledge obtained in the previous runs. The number of correct classifications was averaged over all runs, which gives a good estimate of our test accuracy (percent of correct classified samples over all rounds).

TABLES

Table 1: PCR primers and products

Gene	Primers	Amplificate length
Versican (SEQ ID NO 2)	GGATAGGAGTTGGGATTA AGAT AAATCTTTTTCAACACCA AAAT	414
EYA4 (SEQ ID NO 3)	GGAAGAGGTGATTAAATG GAT CCCAAAAATCAAACAACA A	226
H-Cadherin (SEQ ID NO 4)	TTTGTATTAGGTTGGAAGT GGT CCCAAATAAATCAACAAC AACA	286
TPEF (SEQ ID NO 5)	TTGTTTGGGTTAATAAATG GA CTTCTCTCTTCTCCCCTCT C	295

[0247]

Table 2: Hybridisation oligonucleotides

Gene	Oligomer sequence
Versican (SEQ ID NO 2)	AAGATTTTCGGTTAGTTT (SEQ ID NO 88)

-continued

Table 2: Hybridisation oligonucleotides

Gene	Oligomer sequence
Versican (SEQ ID NO 2)	AAGATTTTTGGTTAGTTT (SEQ ID NO 89)
Versican (SEQ ID NO 2)	ATGTGATTCGTTTGGGTA (SEQ ID NO 50)
Versican (SEQ ID NO 2)	ATGTGATTTGTTTGGGTA (SEQ ID NO 51)
Versican (SEQ ID NO 2)	GGGTAACGTCGAATTTAG (SEQ ID NO 52)
Versican (SEQ ID NO 2)	GGGTAATGTTGAATTTAG (SEQ ID NO 53)
Versican (SEQ ID NO 2)	AAAAATTCGCGAGTTTAG (SEQ ID NO 54)
Versican (SEQ ID NO 2)	AAAAATTTGTGAGTTTAG (SEQ ID NO 55)
EYA4 (SEQ ID NO 3)	TATATATACGTGTGGGTA (SEQ ID NO 56)
EYA4 (SEQ ID NO 3)	TATATATATGTGTGGGTA (SEQ ID NO 57)
EYA4 (SEQ ID NO 3)	AGTGTATGCGTAGAAGGT (SEQ ID NO 58)
EYA4 (SEQ ID NO 3)	AGTGTATGTGTAGAAGGT (SEQ ID NO 59)
EYA4 (SEQ ID NO 3)	TTTAGATACGAAATGTTA (SEQ ID NO 60)
EYA4 (SEQ ID NO 3)	TTTAGATATGAAATGTTA (SEQ ID NO 61)
EYA4 (SEQ ID NO 3)	AAGTAAGTCGTTGTTGTT (SEQ ID NO 62)
EYA4 (SEQ ID NO 3)	AAGTAAGTTGTTGTTGTT (SEQ ID NO 63)
H-Cadherin (SEQ ID NO 4)	GAAGTGGTCGTTAGTTTT (SEQ ID NO 64)
H-Cadherin (SEQ ID NO 4)	GAAGTGGTTGTTAGTTTTT (SEQ ID NO 65)
H-Cadherin (SEQ ID NO 4)	TTGTTTAGCGTGATTTGT (SEQ ID NO 66)
H-Cadherin (SEQ ID NO 4)	TTGTTTAGTGTGATTTGT (SEQ ID NO 67)
H-Cadherin (SEQ ID NO 4)	AAGGAATTCGTTTTGTAA (SEQ ID NO 68)
H-Cadherin (SEQ ID NO 4)	AAGGAATTTGTTTTGTAA (SEQ ID NO 69)
H-Cadherin (SEQ ID NO 4)	AATGTTTTCGTGATGTTG (SEQ ID NO 70)
H-Cadherin (SEQ ID NO 4)	AATGTTTTTGTGATGTTG (SEQ ID NO 71)
TPEF (SEQ ID NO 5)	ATTTGTTTCGATTAATTT (SEQ ID NO 72)

-continued

Table 2: Hybridisation oligonucleotides

Gene	Oligomer sequence
TPEF (SEQ ID NO 5)	ATTTGTTTTGATTAATTT (SEQ ID NO 73)
TPEF (SEQ ID NO 5)	ATAGGTTACGGGTTGGAG (SEQ ID NO 74)
TPEF (SEQ ID NO 5)	ATAGGTTATGGGTTGGAG (SEQ ID NO 75)
TPEF (SEQ ID NO 5)	AATTTGCGAACGTTTGGG
TPEF (SEQ ID NO 5)	AATTTGTGAATGTTTGGG

[0248]

Table 3: Oligonucleotides used in differentiation between colon adenomas or carcinoma tissue and healthy colon tissue.

Gene	Oligo:
H-Cadherin (SEQ ID NO 4)	AATGTTTTCGTGATGTTG (SEQ ID NO: 70)
H-Cadherin (SEQ ID NO 4)	AATGTTTTTGTGATGTTG (SEQ ID NO: 71)
TPEF (SEQ ID NO 5)	AATTTGCGAACGTTTGGG (SEQ ID NO 76)
TPEF (SEQ ID NO 5)	AATTTGTGAATGTTTGGG (SEQ ID NO 77)
Versican (SEQ ID NO 2)	GGGTAACGTCGAATTTAG (SEQ ID NO: 52)
Versican (SEQ ID NO 2)	GGGTAATGTTGAATTTAG (SEQ ID NO: 53)
H-Cadherin (SEQ ID NO 4)	AAGGAATTCGTTTTGTAA (SEQ ID NO 68)
H-Cadherin (SEQ ID NO 4)	AAGGAATTTGTTTTGTAA (SEQ ID NO 69)
TPEF (SEQ ID NO 5)	ATAGGTTACGGGTTGGAG (SEQ ID NO 74)
TPEF (SEQ ID NO 5)	ATAGGTTATGGGTTGGAG (SEQ ID NO 75)
EYA4 (SEQ ID NO 3)	AAGTAAGTCGTTGTTGTT (SEQ ID NO 62)
EYA4 (SEQ ID NO 3)	AAGTAAGTTGTTGTTGTT (SEQ ID NO 63)
EYA4 (SEQ ID NO 3)	AGTGTATGCGTAGAAGGT (SEQ ID NO 58)
EYA4 (SEQ ID NO 3)	AGTGTATGTGTAGAAGGT (SEQ ID NO 59)
Versican (SEQ ID NO 2)	AAAAATTCGCGAGTTTAG (SEQ ID NO 54)

-continued

Table 3: Oligonucleotides used in differentiation between colon adenomas or carcinoma tissue and healthy colon tissue.

Gene	Oligo:
Versican (SEQ ID NO 2)	AAAAATTTGTGAGTTTAG (SEQ ID NO 55)
Versican (SEQ ID NO 2)	AAGATTTTCGGTTAGTTT (SEQ ID NO 88)
Versican (SEQ ID NO 2)	AAGATTTTTGGTTAGTTT (SEQ ID NO 89)
TPEF (SEQ ID NO 5)	ATTTGTTTCGATTAATTT (SEQ ID NO 72)
TPEF (SEQ ID NO 5)	ATTTGTTTTGATTAATTT (SEQ ID NO 73)

[0249]

TABLE 4: OLIGONUCLEOTIDES USED IN DIFFERENTIATION BETWEEN COLON CARCINOMA TISSUE AND HEALTHY COLON TISSUE.

Gene	Oligo:
H-Cadherin (SEQ ID NO 4)	AATGTTTTCGTGATGTTG (SEQ ID NO 70)
H-Cadherin (SEQ ID NO 4)	AATGTTTTTGTGATGTTG (SEQ ID NO 71)
TPEF (SEQ ID NO 5)	AATTTGCGAACGTTTGGG (SEQ ID NO 76)
TPEF (SEQ ID NO 5)	AATTTGTGAATGTTTGGG (SEQ ID NO 77)
H-Cadherin (SEQ ID NO 4)	AAGGAATTCGTTTTGTAA (SEQ ID NO 68)
H-Cadherin (SEQ ID NO 4)	AAGGAATTTGTTTTGTAA (SEQ ID NO 69)
Versican (SEQ ID NO 2)	GGGTAACGTCGAATTTAG (SEQ ID NO: 52)
Versican (SEQ ID NO 2)	GGGTAATGTTGAATTTAG (SEQ ID NO: 53)
EYA4 (SEQ ID NO 3)	AGTGTATGCGTAGAAGGT (SEQ ID NO 58)
EYA4 (SEQ ID NO 3)	AGTGTATGTGTAGAAGGT (SEQ ID NO 59)
EYA4 (SEQ ID NO 3)	AAGTAAGTCGTTGTTGTT (SEQ ID NO 62)
EYA4 (SEQ ID NO 3)	AAGTAAGTTGTTGTTGTT (SEQ ID NO 63)
TPEF (SEQ ID NO 5)	ATAGGTTACGGGTTGGAG (SEQ ID NO 74)

-continued

TABLE 4: OLIGONUCLEOTIDES USED IN DIFFERENTIATION BETWEEN COLON CARCINOMA TISSUE AND HEALTHY COLON TISSUE.

Gene	Oligo:
TPEF (SEQ ID NO 5)	ATAGGTTATGGGTTGGAG (SEQ ID NO 75)

[0250]

Table 5: Oligonucleotides used in differentiation between colon adenoma tissue and healthy colon tissue.

H-Cadherin (SEQ ID NO 4)	AATGTTTTCGTGATGTTG (SEQ ID NO: 70)
H-Cadherin (SEQ ID NO 4)	AATGTTTTTGTGATGTTG (SEQ ID NO: 71)
TPEF (SEQ ID NO 5)	AATTTGCGAACGTTTGGG (SEQ ID NO 76)
TPEF (SEQ ID NO 5)	AATTTGTGAATGTTTGGG (SEQ ID NO 77)
TPEF (SEQ ID NO 5)	ATAGGTTACGGGTTGGAG (SEQ ID NO 74)
TPEF (SEQ ID NO 5)	ATAGGTTATGGGTTGGAG (SEQ ID NO 75)
Versican (SEQ ID NO 2)	GGGTAACGTCGAATTTAG (SEQ ID NO: 52)
Versican (SEQ ID NO 2)	GGGTAATGTTGAATTTAG (SEQ ID NO: 53)
H-Cadherin (SEQ ID NO 4)	AAGGAATTCGTTTTGTAA (SEQ ID NO 68)
H-Cadherin (SEQ ID NO 3)	AAGGAATTTGTTTTGTAA (SEQ ID NO 69)
EYA4 (SEQ ID NO 3)	AAGTAAGTCGTTGTTGTT (SEQ ID NO 62)
EYA4 (SEQ ID NO 3)	AAGTAAGTTGTTGTTGTT (SEQ ID NO 63)
EYA4 (SEQ ID NO 3)	AGTGTATGCGTAGAAGGT (SEQ ID NO 58)
EYA4 (SEQ ID NO 3)	AGTGTATGTGTAGAAGGT (SEQ ID NO 59)
Versican (SEQ ID NO 2)	AAAAATTCGCGAGTTTAG (SEQ ID NO 54)
Versican (SEQ ID NO 2)	AAAAATTTGTGAGTTTAG (SEQ ID NO 55)

[0251]

TABLE 6

Genes analysed according to FIGS. 16 to 18

Number in Figures	Gene name
	Healthy vs Non-Healthy
50-D	H-CADHERIN
20-C	CD44
54-C	TPEF (=TMEFF2; =HPP1)
21-C	VERSICAN
50-C	H-CADHERIN
25-B	GSTP1
43-C	TGFBR2
36-B	N33
49-A	CAV1
52-C	PTGS2
46-A	TP73
54-B	TPEF (=TMEFF2; =HPP1)
20-A	CD44
24-D	EYA4
24-B	EYA4
26-B	GTBP/MSH6
4-C	EGR4
15-E	CDH1
23-E	EGFR
30-B	LKB1
22-D	DAPK1
29-D	IGF2
10-A	HLA-F
29-C	IGF2
36-C	N33
21-D	VERSICAN
39-D	PTEN
32-B	MLH1
26-A	GTBP/MSH6
14-C	CALCA
22-C	DAPK1
39-C	PTEN
9-D	WT1
23-A	EGFR
21-A	VERSICAN
30-A	LKB1
9-C	WT1
60-E	ESR1
12-A	APC
29-A	IGF2
8-D	MYOD1
36-A	N33
54-A	TPEF (=TMEFF2; =HPP1)
18-E	CDKN2a
15-D	CDH1
12-C	APC
	Healthy vs Carcinoma
50-D	H-CADHERIN
54-C	TPEF (=TMEFF2; =HPP1)
50-C	H-CADHERIN
21-C	VERSICAN
20-C	CD44
24-B	EYA4
12-A	APC
52-C	PTGS2
24-D	EYA4
39-B	PGR
25-B	GSTP1
49-A	CAV1
23-E	EGFR
36-B	N33
29-C	IGF2
10-D	HLA-F
54-B	TPEF (=TMEFF2; =HPP1)
46-A	TP73

TABLE 6-continued

Genes analysed according to FIGS. 16 to 18

Number in Figures	Gene name
	Healthy vs Adenoma
20-C	CD44
10-A	HLA-F
43-C	TGFBR2
26-A	GTBP/MSH6
26-B	GTBP/MSH6
30-B	LKB1
20-A	CD44
36-C	N33
50-D	H-CADHERIN
46-A	TP73
39-D	PTEN
36-B	N33
54-C	TPEF (=TMEFF2; =HPP1)
25-B	GSTP1
23-A	EGFR
40-A	RARB
36-D	N33
49-A	CAV1
54-B	TPEF (=TMEFF2; =HPP1)
18-E	CDKN2a
36-A	N33
32-B	MLH1
12-C	APC
21-C	VERSICAN
15-E	CDH1
52-C	PTGS2
62-D	RASSF1
9-C	WT1
18-D	CDKN2a
60-E	ESR1
29-D	IGF2
8-D	MYOD1
50-C	H-CADHERIN
4-C	EGR4
42-C	S100A2
22-D	DAPK1
31-E	MGMT
24-D	EYA4
56-A	CEA
9-D	WT1
7-E	GPIb beta
14-C	CALCA
52-D	PTGS2
8-B	MYOD1
24-B	EYA4
21-D	VERSICAN
38-C	PGR
58-A	PCNA
34-D	MSH3
9-B	WT1
35-B	MYC
27-C	HIC-1
52-B	PTGS2
23-E	EGFR
30-A	LKB1
29-C	IGF2
39-C	PTEN
13-D	BCL2
5-B	AR
15-D	CDH1
	Carcinoma vs Adenoma
18-B	CDKN2a
7-E	GPIb beta

[0252]

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tttaatgtta atagatttta taatatttga ttaaatattt ttataggata aaggtatttt 13980

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taaaattatt agaagttttt gaatgggaaa atatatattt tttaggtttt ataattaaaa 14400

ttgtatttat ttgtttatta tatttaagta tgaattaaat agtaattaaa atattatttt 14460

gtgagttttt ttttaaatta tatttttgta ttggggatat tttttgtgaa aattttaaga 14520

ttttaggtat aaataaagta agatttttat ttataatgtt tgtgtttaaa agaaattata 14580

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gatttgattg gttttaggta taattaagta aattattttt attggatgat atagtaatgt 14940

tatagattaa aaatgtattt ttaattttta aagattttgg aaaaaggaag tttatttttt 15000

aagattgtgt tataattttt tttttaaata aaatattgta aattagggat agatatttta 15060

tttagtattt tgaatttttt ttggtttttt aggaaaggta gaaatataag gtttttattg 15120

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tagaaagtta taaaatatta gatttttttt agatattaga tattgagttt ttgtttttta 15300

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gttgtaaatg ttttgtttat ggttgagtag atttttttag aatttaattg aaagattatt 15420

tatattacga tagaattatg taagttaaag ttaagtttta atatggagtg atgggagagg 15480

tcgggttgtc gagaggagat gattttatta gtgagaagag aggttttttg agtcggtttt 15540

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tattaaaaac gttatttttt ttataaagaa aaagatgaag gtataaagaa tatagtttaa 15660

ttaaattgaa ttaaagattg tattattttt attttttttt tagttatttt tttaaagttt 15720

ttttttttt tttttatagt ttgaaaaata taggttattt ttataaagta tttgtttgat 15780

tgaagtaaga taaattgaag agtttggttt ttgaatataa ggaagcggta gagattttag 15840

aattaatgag gtagggcgga atataatgta gaaggttttt taagaggtaa aatttttgta 15900

gttgttgttt atttttagtg attattcgtt tttatttatt taattagatt atagtgggat 15960

cgagataagg agtataatga aagttgttgt attgatggtg taaaaagata tatggtatta 16020

ttaatgtttt tgtggtgagt aaaggtagaa cgtaagatag aaaataagga aatttttgcg 16080

ttgtaagaaa agtgtttagt atgggtatta atcggtatgt agaagtagta agtatatatt 16140

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gagaaattat attttaattt tataaattaa aggttaaata tttgttgtaa taattttaaa 16260

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aaaaagagaa gatttgtaag atttagtaaa tatttattat aaatagattg tttttaattt 16320

tttatatttt tttttaattt aataaaagtt tattgagtag tttttatgtg tattgtttta 16380

gatagtaggt attatttaaa aaagtaataa ttatttttta tttttaagga gtttataatg 16440

tttttagaaa gaaattaatt tattggagta gttaaagtta taattgattt ataaaatgat 16500

tagtgaattt agaggaaaat tatatataaa tatttttgtt tttattggtt ggtttagtta 16560

gatattattt taaaaaata 16579

<210> SEQ ID NO 10
<211> LENGTH: 3000
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)

<400> SEQUENCE: 10

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ttgaatatta ttaatattaa taatagtatt atagtgatta agagtggatt taaataaagg 120

ttggtttgaa atttaggttt gttatttatt agtaagtttt taaaaatttt gagtttttag 180

ttttttttata tgtgaaatgg agaaaataaa tttgtaaaat taattaaatt tgtttattta 240

tatttttttt tttagtgtat attaattggt atttttcgtt aggttagaat gtgtttttaa 300

ttatgtttta aattcgtttt gtgttaattt tattgttaga atttttttta ttttgagaat 360

tagaaaagga aatattatgt ttggtaatgt ttatattttt taaaataaat ttgtaggaaa 420

gaatatttag taagtgatga gagtagtaac gattgttttt attattttaa atttataata 480

ttatttttttt tagagttttt taagtattgt agataatttt ttatttatta aaaaataaat 540

tgtaattata agtatttagg gttgatattg tttttgaatt agatagtgtt tatattagtt 600

gtataagatt aatttaaagt agaggatgaa attttttttt tgaatttttt ttagaacgta 660

atttagtgaa tatattaaaa ttaaattttt tttgaatggg agtaattttt acggattaat 720

ttgtaatttt ttagattata tttaaggtaa tgtagaggtt gttgtattat aggttttgtg 780

attagagatt attggatttg tttttggaaa agttatttat gatttttgg gttttggttt 840

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atttatgtat tataagtgat taatataatg attgatattt agtgatttat taataaatta 960

aaatatttat tattaatatg atagagaagg tgtcgttaaa atagataata ggtttttgga 1020

agaggtgatt aaatggatgt aaaatttatg gattgtttat ttcgtttatt tttgttgtgt 1080

tttttggttg tggtatatat acgtgtgggt ataaaatcgt aaattttatg tagtcgcgta 1140

gtgtatgcgt agaaggttta gatacgaaat gttattttag taatgtgttt agagaagttt 1200

tgacgtcgtt ttggaagtaa gtcgttgttg tttgattttt gggcgtttgg gacggatgtt 1260

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aagtaggtgg ggatcgatag tggtttttcg gtttagggag gagagcgcgg tcgcgggttt 1620

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ggttttcggc ggttttacga gttcgtagta gtcggtggcg acgtcgtttt cgttttattt 1920

ttttgcgtaa gtgcgaggtt gtcggtagcg cggcgtacgt ttcggtcgtt ttcggttttc 1980

gcgtaaaatt tttattttgt ttacgtgaag ttgtcgttgt tttagagagg gggaaagagt 2040

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gggtggtcga aggggatgtt ttgtttttat tagaggtata gcgcgaaggg gaaatttcga 2280

tattggaagg aacgagaata aatatttaat tacggacgta ttgaatcgcg gttgggatag 2340

atatttcggg aattcgaggc ggatcgggcg acgaggtgag tgatttttt ttttaatttt 2400

cgttttaggg ttttcggggg agtttgagtt gagagaattt ttaaattttt cgggaaagtg 2460

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gggtttttta attgcggcga ttttatttta atagttttta tgtggcgtgg attgaatgtt 3000

<210> SEQ ID NO 11
<211> LENGTH: 3000
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)

<400> SEQUENCE: 11

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aagtttaggc gtttgtgatt tttcgaagga ttttgggtta gtattttcgc gtttggatta 180

tttagggggt tattagaaag taatatacgt tataagaaag atgtggggga gatttcgatg 240

ttcgcgtttt tgttaggtgg aggcggggtg taggtagaag tcgcgcgttg gattgttgga 300

tgaatttcgt tacgcgtagg tttcgcgtcg atttcggaag ggataggtag gttcggaagg 360

gatttttggg gtttggggac gtttttttagg gtagagagta tcgttgcggt tcgagcggtt 420

cgggtttttа ggcgtggggt attcggtttt taagcgtttt tcggggacgt aggcgtttac 480

gtatcgttta gttgcgcgtt tttagtattt agcgttcggc gttttcggcg gagtttcgcg 540

tatttttttcg gaaagtttgg gggttttttt aatttaggtt ttttcgggag ttttggggcg 600

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ggggttggaa gaaggggtta tttatttcgt cgttcggttc gtttcgggtt ttcgaagtgt 660

ttgttttagt cgcggtttag tgcgttcgta attaagtatt tattttcgtt ttttttagtg 720

tcgaagtttt tttttcgcgt tgtgtttttg gtgaaaatag gatatttttt tcggttattt 780

tataataaat agcgtatata agcgggggag aagcggggcg gagggagaag tcggtttcga 840

gggggaggag gaaaggagag gagttaaaat ttcggattgc gatagggggg aaaggagaag 900

aaaagaaaat gagagagcgc gtttagtcgt cgtagtcgtt atttttcggt ttttttcgta 960

gttttttttt tttttttaag gtagcgataa ttttacgtgg ataggatgga agttttgcgc 1020

ggaagtcggg aacggtcgga gcgtgcgtcg cgttgtcggt agtttcgtat ttgcgtaggg 1080

aggtggggcg ggggcgacgt cgttatcggt tattgcgggt tcgtgaggtc gtcgggggtt 1140

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tacgcgatta tataggattt acgattttat atttatacgt gtgtatgtta taattagggg 1920

atatagtaaa ggtagacgga ataaataatt tataaatttt gtatttattt aattattttt 1980

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aaattaaagt ttaaagaatt atgagtgatt tttttaaaga taaatttagt ggtttttaat 2220

tataaagttt atgatataat aatttttata ttattttagg tgtggtttaa gagattatag 2280

attaattcgt agaaattatt tttatttaaa gaaagtttag ttttaatata tttattaagt 2340

tacgttttga aaaaggttta gaaaaaagat tttatttttt attttaggtt ggttttatgt 2400

aattgatatg agtattgttt aatttaaaag tagtattaat tttgaatatt tatggttata 2460

atttatttttt taatgagtgg ggaattattt ataatgttta agaggtttta gaaaaggtgg 2520

tgttgtaaat ttaaaatgat aaaggtagtc gttgttgttt ttattattta ttgggtgttt 2580

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gtttttaagg tagaaagggt tttggtagtg gggttggtat aaagcggatt tggagtatgg 2700

ttgagagtat attttggttt aacgaggaat gttagttaat atatattgga gagaaaaata 2760

tgaatggata gatttaatta attttgtaga tttatttttt ttattttata tgtgagaaaa 2820

ttaagggttt agaattttta gaagtttgtt aataaatggt agatttgagt tttaagttag 2880

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ttttttattta agtttatttt tagttattgt gatgttatta ttagtattaa tggtatttag 2940

aaaaatagta atttttttaa atatgtaata tattataagt taaatatgta atttaaatgt 3000

<210> SEQ ID NO 12
<211> LENGTH: 1984
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
<220> FEATURE:
<221> NAME/KEY: unsure
<222> LOCATION: (9, 17, 18, 33, 41, 49, 50, 52, 54, 62, 80, 84, 127, 157, 159)
<223> OTHER INFORMATION: unknown base
<220> FEATURE:
<221> NAME/KEY: unsure
<222> LOCATION: (175, 207..209, 214, 1181)
<223> OTHER INFORMATION: unknown base

<400> SEQUENCE: 12

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gnttaaatag tagttaatgn aggnatttta aaaggtatat tattttatat ttatttagtg 120

gttatgntat tatttaattt ttattataat tttgtgngnt tagtataatt tgtgntttta 180

ttttatttgt gaataaatgg aggtagnnnt ttgngtaatt tataagtaag tggtagattc 240

gggggttgtg tttagataat gtggttttag atttttttgtt ttttttgtt ttttgttgta 300

ttttgattga gtttagttat ttatttttt aatatatatt aattgttgtt tttatgtttt 360

aggttttgtg ttagatgtta gaaatatatt tttatttatt ggattttggt atggtttatt 420

gtttagtgtt ttgttatgtt acgtgttata taatgtattt atttcggtat ttagtttatg 480

gaaaataatg ttgaaagata ttgtatgtat gtttttataa taaaattatg taatttatgt 540

ttttttttatt gttttggtta ttaggaagtt tttatttaaa ttagagtaaa tatattagaa 600

tttgggtttg ttattttagt ttgttgaatt ttttttttg gtttagattt tttattttgg 660

tttataaatt ttattgtata aatgtttttt attgtaaaat attttaaatt ttttttaagg 720

gaaggttgta tggaaatgat atagtaaggt tttttttgta ttttttaga tttttattag 780

ggaaggtaga tttagatgtt ttttttattt ttagttttaa agtttttttat ttataaaatt 840

ttttaagtag tgattattgt tgttttgagt atttggaggt agtttagagt ttttgaaagg 900

taaaatttat atataaaaag aagtttttttt cgatttagat tttagttttg gtgttagatg 960

tatatttgag gagtaggtgg ttagttagat ttttatttga gtagttaata aaatttattg 1020

ttttttaatg gaatttttttt tgtaagttcg aattgatttg ttatttttgt gatttgtgag 1080

atggtaggga agtattaaat attattatga tttgggttat agtggtggga aaaaaggaaa 1140

aaagaaaaaa aaaatttatt gttaagtttt gttaggcgta naaagggttg gaattgttgg 1200

ggttatttta tttgatttat tggaaataga gtggatttta ttaatatttt aataaagaga 1260

atttttttgt attaggttgg aagtggtcgt tagtttttcg tgtaatttta ttttttggaa 1320

aagtggaatt agttggtatt gtttagcgtg atttgtgagg ttgagtttta atagtttaaa 1380

gaagtaaatg ggatgttatt ttcgcggggt tcgtttttcg cgaggtgttt atttcgtatt 1440

tgttatgtaa aacgagggag cgttaggaag gaattcgttt tgtaaagtta ttggttttgg 1500

ttattagttt ttatttaatg ttttcgtgat gttgttgttg atttatttgg gaagttggtt 1560

ggttggcgag gtagagtttt tttttaaagt ttggttttta cggaaaatat gtttagtgta 1620

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cgagtttaga gattttaggt atttttata tataggtttt tattttggcg tgcgtgcgtg 1920

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agga 1984

<210> SEQ ID NO 13
<211> LENGTH: 1984
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
<220> FEATURE:
<221> NAME/KEY: unsure
<222> LOCATION: (804, 1771, 1776..1778, 1810, 1826, 1828, 1858, 1901, 1905)
<223> OTHER INFORMATION: unknown base
<220> FEATURE:
<221> NAME/KEY: unsure
<222> LOCATION: (1923, 1931, 1933, 1935, 1936, 1944, 1952, 1967, 1968, 1976)
<223> OTHER INFORMATION: unknown base

<400> SEQUENCE: 13

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gagttttcgg ttgtattttg ttcgattaga agcgttcggc ggcgttttta tttatgtacg 360

cggttgtatt gagtatattt ttcgtgggag ttaggttttg aggagaggtt ttgtttcgtt 420

agttagttaa ttttttaaat agattagtag tagtattacg aaagtattgg gtagaggttg 480

atgattagga ttaatggttt tataagacgg attttttttt aacgtttttt cgttttgtat 540

ggtagatacg gggtgagtat ttcgcgagga gcgagtttcg cggaggtggt attttatttg 600

ttttttgga ttgttggggt ttagttttat aaattacgtt gggtaatgtt agttgatttt 660

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agatttttt tattaaaatg ttaataagat ttattttatt tttaataaat tagataaaat 780

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ttttttttt ttttttttat tattgtggtt taagttatga tggtgtttgg tgttttttg 900

ttattttata aattataaag atgatagatt aattcgagtt tgtagaaaaa attttattaa 960

ggggtaatag attttattaa ttgtttaggt gagagtttga ttagttattt atttttaaa 1020

tgtgtatttg gtattaaagt tgggatttgg atcggaagga attttttttt gtatatggat 1080

tttatttttt agaagttttg aattattttt aggtatttag aatagtagta gttattgttt 1140

aagggatttt ataaatgggg ggttttggga ttgagggtaa gagggatatt taggtttgtt 1200

ttttttaata ggaatttaag aaaatgtagg gaagatttta ttgtattatt tttatgtagt 1260

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tttttttag aaagaattta aggtgtttta taataaagga tatttgtgta atagaattta 1320

tgaattaaaa tagaaaattt gggttagaag gaaaagttta gtaaattgaa atgataagtt 1380

taaattttaa tgtatttgtt ttgatttgga taagagtttt ttgatagtta aagtaataaa 1440

agaaatataa gttatatagt tttgttgtag aaatatgtat ataatgtttt ttagtattat 1500

tttttatggg ttaaatatcg gaataaatgt attatgtaat acgtaatata gtaggatatt 1560

gagtaatgga ttatgttaag atttagtgga tggggatgta tttttagtat ttggtatagg 1620

gtttggaata tggagatagt aattagtgtg tgttaaagaa atagatggtt agatttaatt 1680

aagatgtagt agaaggtagg gaggggtaag gagtttggag ttatattgtt taggtatagt 1740

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taattattga ataaatataa agtgatgtgt tttttaagat ntttntattg gttgttgttt 1920

ggntagaagg ntntnntttg tggntttaag gntattgata aagatgnnag tgatgnttga 1980

agtt 1984

<210> SEQ ID NO 14
<211> LENGTH: 7833
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)

<400> SEQUENCE: 14

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 18

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<210> SEQ ID NO 22
<211> LENGTH: 1984
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
<220> FEATURE:
<221> NAME/KEY: unsure
<222> LOCATION: (9, 17, 18, 33, 41, 49, 50, 52, 54, 62, 80, 84, 127,
157, 159)
<223> OTHER INFORMATION: unknown base
<220> FEATURE:
<221> NAME/KEY: unsure
<222> LOCATION: (175, 207..209, 214, 1181)
<223> OTHER INFORMATION: unknown base

<400> SEQUENCE: 22

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<210> SEQ ID NO 23
<211> LENGTH: 1984
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
<220> FEATURE:
<221> NAME/KEY: unsure
<222> LOCATION: (804, 1771, 1776..1778, 1810, 1826, 1828, 1858, 1901, 1905)
<223> OTHER INFORMATION: unknown base
<220> FEATURE:
<221> NAME/KEY: unsure
<222> LOCATION: (1923, 1931, 1933, 1935, 1936, 1944, 1952, 1967, 1968, 1976)
<223> OTHER INFORMATION: unknown base

<400> SEQUENCE: 23

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<210> SEQ ID NO 24
<211> LENGTH: 7833
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)

<400> SEQUENCE: 24

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<400> SEQUENCE: 37

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<400> SEQUENCE: 42

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<400> SEQUENCE: 43

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<400> SEQUENCE: 46

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<400> SEQUENCE: 62

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<400> SEQUENCE: 63

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<400> SEQUENCE: 71

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<212> TYPE: DNA
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<400> SEQUENCE: 72

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<210> SEQ ID NO 74
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<220> FEATURE:
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<400> SEQUENCE: 74

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<220> FEATURE:
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<400> SEQUENCE: 75

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<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 76

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<223> OTHER INFORMATION: 0002393:1332B186

<400> SEQUENCE: 77

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Calcitonin ML probe

<400> SEQUENCE: 78

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<210> SEQ ID NO 79
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Versican ML probe

<400> SEQUENCE: 79

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<210> SEQ ID NO 80
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: TPEF ML probe

<400> SEQUENCE: 80

aattaccgaa aacatcgacc ga 22

<210> SEQ ID NO 81
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: EYA4 ML probe

<400> SEQUENCE: 81

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<210> SEQ ID NO 82
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: HCadherin ML probe

<400> SEQUENCE: 82

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<210> SEQ ID NO 83
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<212> TYPE: DNA
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<400> SEQUENCE: 83

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<210> SEQ ID NO 84
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: EYA4 HM probe

<400> SEQUENCE: 84

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<210> SEQ ID NO 85
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Calcitonin HM blocker

<400> SEQUENCE: 85

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<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 86

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<210> SEQ ID NO 87
<211> LENGTH: 25
<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 87

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<210> SEQ ID NO 88
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 88

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<220> FEATURE:
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<210> SEQ ID NO 90

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<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: TPEF ML PROBE

<400> SEQUENCE: 90

acccgaaatc acgcgcgaaa aa 22

<210> SEQ ID NO 91
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: control primer

<400> SEQUENCE: 91

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<210> SEQ ID NO 92
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: control primer

<400> SEQUENCE: 92

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<210> SEQ ID NO 93
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: control probe

<400> SEQUENCE: 93

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<400> SEQUENCE: 94

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<212> TYPE: DNA
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 95

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<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 96

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<223> OTHER INFORMATION: primer

<400> SEQUENCE: 97

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<210> SEQ ID NO 98
<211> LENGTH: 39
<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 98

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<210> SEQ ID NO 99
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Probe

<400> SEQUENCE: 99

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<210> SEQ ID NO 100
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 100

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<223> OTHER INFORMATION: primer

<400> SEQUENCE: 101

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<210> SEQ ID NO 102
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<400> SEQUENCE: 102

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<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: blocker

<400> SEQUENCE: 103

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<210> SEQ ID NO 104
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<212> TYPE: DNA
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<400> SEQUENCE: 104

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<212> TYPE: DNA
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<400> SEQUENCE: 105

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<210> SEQ ID NO 106
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Forward Primer

<400> SEQUENCE: 106

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<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Reverse Primer

<400> SEQUENCE: 107

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<210> SEQ ID NO 108
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 108

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<210> SEQ ID NO 109
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: LC Probe

<400> SEQUENCE: 109

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<210> SEQ ID NO 110
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: LC Probe

<400> SEQUENCE: 110

attaatggtt ttataagacg gatttttttt taacgt 36

1. A nucleic acid comprising a sequence at least 18 bases in length of a segment of the chemically pretreated genomic DNA according to one of the sequences taken from the group comprising SEQ ID NO 6 to SEQ ID NO 25 and sequences complementary thereto.

2. An oligomer, in particular an oligonucleotide or peptide nucleic acid (PNA)-oligomer, said oligomer comprising at least one base sequence having a length of at least 9 nucleotides which is complementary to, or hybridises under moderately stringent or stringent conditions to a pretreated genomic DNA according to one of the SEQ ID NO 6 to SEQ ID NO 25 or sequences complementary thereto.

3. The oligomer as recited in claim 2, wherein the base sequence includes at least one CpG, TpG or CpA dinucleotide.

4. The oligomer as recited in claim 3, characterised in that the cytosine of the CpG, or the thymine of the TpG or the adenosine of the CpA dinucleotide is located approximately in the middle third of the oligomer.

5. A set of oligomers, comprising at least two oligomers according to any of claims 2 to 4.

6. A set of at least two oligonucleotides as recited in claims 2 to 5, which can be used as primer oligonucleotides for the amplification of DNA sequences of one of SEQ ID NO 6 to SEQ ID NO 25 and sequences complementary thereto.

7. A set of oligonucleotides as recited in claims 2 to 5, characterised in that at least one oligonucleotide is bound to a solid phase.

8. Use of a set of oligomer probes comprising at least four of the oligomers according to any of claims **5** through **7** for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) within one of the sequences according to SEQ ID NO 1 to SEQ ID NO 5, or sequences complementary thereto.

9. A method for manufacturing an arrangement of different oligomers (array) fixed to a carrier material for analysing colon cell proliferative disorders associated with the methylation state of the CpG dinucleotides of one of SEQ ID NO 1 to SEQ ID NO 5, and sequences complementary thereto wherein at least one oligomer according to any of the claims **2** through **5** and **7** is coupled to a solid phase.

10. An arrangement of different oligomers (array) obtainable according to claim 7.

11. An array of different oligonucleotide- and/or PNA-oligomer sequences as recited in claim 10, characterised in that these are arranged on a solid phase in the form of a rectangular or hexagonal lattice.

12. The array as recited in any of the claims **10** or **11**, characterised in that the solid phase surface is composed of silicon, glass, polystyrene, aluminium, steel, iron, copper, nickel, silver, or gold.

13. A method for detecting, differentiating or distinguishing between colon cell proliferative disorders associated with at least one gene and/or their regulatory regions from the group comprising Versican, TPEF, H-Cadherin, Calcitonin and EYA4 in a subject, said method comprising contacting a target nucleic acid in a biological sample obtained from said subject with at least one reagent or a series of reagents, wherein said reagent or series of reagents, distinguishes between methylated and non methylated CpG dinucleotides within the target nucleic acid.

14. A method according to claim 13, comprising:

a) obtaining, from a subject, a biological sample having subject genomic DNA;

b) treating the genomic DNA, or a fragment thereof, with one or more reagents to convert 5-position unmethylated cytosine bases to uracil or to another base that is detectably dissimilar to cytosine in terms of hybridisation properties;

c) contacting the treated genomic DNA, or the treated fragment thereof, with an amplification enzyme and at least two primers comprising, in each case a contiguous sequence at least 16 nucleotides in length that is complementary to, or hybridises under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO 6 to SEQ ID NO 25, or complements thereof, wherein the treated DNA or a fragment thereof is either amplified to produce one or more amplificates, or is not amplified; and

d) determining, based on the presence or absence of, or on a property of said amplificate, the methylation state of at least one CpG dinucleotide sequence of SEQ ID NO 1 to SEQ ID NO 5, or an average, or a value reflecting an average methylation state of a plurality of CpG dinucleotide sequences of SEQ ID NO 1 to SEQ ID NO

5, whereby at least one of detecting or distinguishing between colon cell proliferative disorders is, at least in part, enabled.

15. A method according to claim 13 comprising the following steps of

a) obtaining, from a subject, a biological sample having subject genomic DNA;

b) treating the genomic DNA, or a fragment thereof, with one or more reagents to convert 5-position unmethylated cytosine bases to uracil or to another base that is detectably dissimilar to cytosine in terms of hybridization properties;

c) amplifying one or more fragments of the treated DNA such that only or preferentially DNA originating from colon or colon cell proliferative disorder cells are amplified;

d) detecting the amplificates or characteristics thereof and thereby deducing on the presence or absence of a colon cell proliferative disorder.

16. A method according to claims 13 to 15 wherein said colon cell proliferative disorders are taken from the group comprising adenocarcinomas, polyps, squamous cell cancers, carcinoid tumours, sarcomas and lymphomas.

17. The method of claims 14 to 16, wherein in step a) the biological sample obtained from the subject is selected form the group consisting of histological slides, biopsies, paraffin-embedded tissue, bodily fluid, stool, blood, serum, plasma, urine, sputum and combinations thereof.

18. The method of one of claims 14 to 17, wherein step b) treating the genomic DNA, or the fragment thereof, comprises use of a bisulfite solution.

19. The method of one of claims 14 to 16, wherein treating in b) is subsequent to embedding the DNA in agarose.

20. The method of one of claims 14 to 19, wherein step b) treating the genomic DNA, comprises treating in the presence of at least one of a DNA denaturing agent or a radical scavenger.

21. The method of one of claims 14 to 20, wherein contacting or amplifying in step c) comprises use of at least one method selected from the group consisting of: use of a heat-resistant DNA polymerase as the amplification enzyme; use of a polymerase lacking 5'-3' exonuclease activity; use of a polymerase chain reaction (PCR); generation of a amplificate nucleic acid molecule carrying a detectable labels; and combinations thereof.

22. The method of claim 21, wherein the detectable amplificate label is selected from the label group consisting of: fluorescent labels; radionuclides or radiolabels; amplificate mass labels detectable in a mass spectrometer; detachable amplificate fragment mass labels detectable in a mass spectrometer; amplificate, and detachable amplificate fragment mass labels having a single-positive or single-negative net charge detectable in a mass spectrometer; and combinations thereof.

23. The method of claim 22, comprising in step d) use of mass spectrometry for detecting the amplificate, or detachable amplificate fragment mass labels.

24. The method according to one of claims 14 to 23 wherein in step c) of the method 2 or more different fragments are amplified.

25. The method according to one of claims 14 to 24 wherein one or more of said primers comprise sequences taken from the group according to SEQ ID NO 34 to SEQ ID NO 49, 96, 97, 101, 102, 106 and 107.

26. The method according to one of claims 14 to 24 wherein one or more of said primers comprise one or more CpG, TpG or CpA dinucleotides.

27. The method of claim 26 wherein said primers comprise between 2 to 5 CpG, TpG or CpA dinucleotides.

28. The method according to one of claims **26** or **27** wherein said one or more CpG, TpG or CpA dinucleotides are located within the 3' half of the primer.

29. The method according to one of claims 26 to 28 wherein said primers comprise one or more bases which hybridise to positions that were converted in the treatment of step b) in claim 14, or of step c) in claim 15.

30. The method of claim 29 wherein at least one of said bases are located within the 3' half of the primer.

31. The method according to one of claims 14 to 30 wherein said amplificates obtained in step d) comprise at least one 20 base pair sequence that comprises 3 or more CpG, TpG or CpA dinucleotides.

32. The method according to one of claims 14 to 31, further comprising in step c) the use of at least one nucleic acid molecule or peptide nucleic acid molecule at least 18 base pairs in length comprising one or more CpG, TpG or CpA dinucleotides and wherein the sequence of said molecule is complementary or identical to a sequence selected from the group consisting of SEQ ID NO 6 to SEQ ID NO 25, and complements thereof, and wherein said nucleic acid molecule or peptide nucleic acid molecule suppresses amplification of the nucleic acid to which it is hybridised.

33. The method according to claim 32 wherein the sequence of said nucleic acid(s) or peptide nucleic acid(s) is selected from the group consisting SEQ ID NO 85 to SEQ ID NO 87, 98, 103 and 108 and sequences complementary thereto.

34. The method of claim 32, wherein amplification of DNA that was unmethylated prior to treatment of step b) is suppressed.

35. The method of one of claims 32 to 34, wherein said nucleic acid molecule or peptide nucleic acid molecule is in each case modified at the 5'-end thereof to preclude degradation by an enzyme having a 5'-3' exonuclease activity.

36. The method of one of claims 32 to 35, wherein said nucleic acid molecule or peptide nucleic acid molecule in each case lack a 3' hydroxyl group.

37. The method of one of claims 32 to 36, wherein the amplification enzyme is a polymerase lacking 5'-3' exonuclease activity.

38. The method of one of claims 32 to 37, wherein the binding site of the oligonucleotide or PNA oligomer is identical to, or overlaps with that of the primer and thereby hinders hybridisation of the primer to its binding site.

39. The method of one of claims 32 to 38, wherein the binding sites of at least two of the oligonucleotides or PNA oligomers are identical to, or overlap with those of at least two of the primers, and thereby hinder hybridisation of the primers to their binding site.

40. The method of claim 39, wherein hybridisation of at least one of the oligonucleotides or peptide nucleic acid oligomers hinders hybridisation of a forward primer, and the hybridisation of at least one of the oligonucleotides or

peptide nucleic acid oligomers hinders the hybridisation of a reverse primer that binds to the elongation product of said forward primer.

41. The method of one of claims 32 to 38, wherein said oligonucleotide or peptide nucleic acid oligomer hybridises between the binding sites of the forward and reverse primers.

42. The method of one of claims **14** or **15**, wherein determining in step d), comprises hybridisation of at least one nucleic acid molecule or peptide nucleic acid molecule in each case comprising a contiguous sequence at least 9 nucleotides in length comprising one or more CpG, TpG or CpA dinucleotides and wherein the sequence of said molecule that is complementary or identical to a sequence selected from the group consisting of SEQ ID NO 6 to SEQ ID NO 25.

43. The method of claim 42, wherein at least one such hybridising nucleic acid molecule or peptide nucleic acid molecule is bound to a solid phase.

44. The method of claim 43, wherein a plurality of such hybridising nucleic acid molecules or peptide nucleic acid molecules are bound to a solid phase in the form of a nucleic acid or peptide nucleic acid array selected from the array group consisting of linear, hexagonal, rectangular, and combinations thereof.

45. The method of one of claims **14** or **15**, wherein determining in step d), comprises sequencing of the amplificate.

46. The method of one of claims **14** or **15**, wherein determining in step d), comprises: hybridising at least one nucleic acid molecule comprising a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridises under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO 6 to SEQ ID NO 25, and complements thereof; and extending at least one such hybridised nucleic acid molecule by at least one nucleotide base.

47. The method according to claim 42 wherein the sequence of said nucleic acid(s) or peptide nucleic acid(s) is selected from the group consisting SEQ ID NO 50 to SEQ ID NO 84, SEQ ID NO 88 to SEQ ID NO 90, 99, 100, 104, 105, 109, 110 and sequences complementary thereto.

48. The method according to claim 42 wherein said oligonucleotides or PNA oligomers are fluorescently labelled, and wherein detection thereof is by either an increase or a decrease in fluorescence or fluorescence polarisation.

49. The method according to claim 42 wherein the hybridisation of the oligonucleotides or PNA oligomers is detectable by fluorescence resonance energy transfer, and wherein the detection is by either an increase or a decrease in fluorescence.

50. The method of one of claims **14** or **15**, wherein the background DNA concentration is at between 100 to 1000 fold excess of the concentration of the DNA to be investigated.

51. A method according to claim 13, comprising:

a) obtaining, from a subject, a biological sample having subject genomic DNA;

b) extracting the genomic DNA;

c) contacting the genomic DNA, or a fragment thereof, comprising SEQ ID NO 1 to SEQ ID NO 5 or a sequence that hybridises under stringent conditions to SEQ ID NO 1 to SEQ ID NO 5, with one or more methylation-sensitive restriction enzymes, wherein the genomic DNA is either digested thereby to produce digestion fragments, or is not digested thereby; and

d) determining, based on a presence or absence of, or on property of at least one such fragment, the methylation state of at least one CpG dinucleotide sequence of SEQ ID NO 1 to SEQ ID NO 5, or an average, or a value reflecting an average methylation state of a plurality of CpG dinucleotide sequences of SEQ ID NO 1 to SEQ ID NO 5, whereby at least one of detecting the prostate cell proliferative disorder, or distinguishing between a transitional and a peripheral zone of origin of the prostate cell proliferative disorder is, at least in part, afforded.

52. The method of claim 51, further comprising, prior to determining in step d), amplifying of the digested or undigested genomic DNA.

53. The method of claim 52, wherein amplifying comprises use of at least one method selected from the group consisting of: use of a heat resistant DNA polymerase as an amplification enzyme; generation of a amplificate nucleic acid carrying a detectable label; and combinations thereof.

54. The method of claim 53, wherein the detectable amplificate label is selected from the label group consisting of: fluorescent labels; radionuclides or radiolabels; amplificate mass labels detectable in a mass spectrometer; detachable amplificate fragment mass labels detectable in a mass spectrometer; amplificate, and detachable amplificate fragment mass labels having a single-positive or single-negative net charge detectable in a mass spectrometer; and combinations thereof.

55. The method of claim 54, comprising use of mass spectrometry for detecting amplificate, or detachable amplificate fragment mass labels.

56. The method of claim 55, wherein the mass spectrometry is selected from the group consisting of matrix assisted laser desorption/ionisation mass spectrometry (MALDI), electron spray mass spectrometry (ESI), and combinations thereof.

57. The method of claim 51, wherein the biological sample obtained from the subject is selected from the group consisting of histological slides, biopsies, paraffin-embedded tissue, bodily fluid, stool, blood, serum, plasma, urine, sputum and combinations thereof.

58. A kit useful for detecting, differentiating or distinguishing between colon cell proliferative disorders, comprising:

i) a bisulfite reagent; and

ii) at least one nucleic acid molecule or peptide nucleic acid molecule comprising, in each case a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridises under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO 1 to SEQ ID NO 25, and complements thereof.

59. The kit of claim 58, further comprising standard reagents for performing a methylation assay selected from the group consisting of MS-SNuPE, MSP, MethylLight, HeavyMethyl, COBRA, nucleic acid sequencing, and combinations thereof.

60. The use of a nucleic acid according to claim 1, of an oligonucleotide or PNA-oligomer according to one of the claims **2** through **7**, of a kit according to claims **58** or **59**, of an array according to one of the claims **11** through **12**, of a set of oligonucleotides according to one of claims **5** through **7**, or a method according to claims 13 to 57, for the classification, differentiation and/or diagnosis of colon cell proliferative disorders or the predisposition to colon cell proliferative disorders.

61. The use of a nucleic acid according to claim 1, of an oligonucleotide or PNA-oligomer according to one of the claims **2** through **7**, of a kit according to claims **58** or **59**, of an array according to one of the claims **11** through **12**, of a set of oligonucleotides according to one of claims **5** through **7**, or a method according to claims 13 to 57, for the therapy of colon cell proliferative disorders.

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专利名称(译)	用于分析结肠细胞增殖性疾病的方法和核酸		
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[标]发明人	ADORJAN PETER BURGER MATTHIAS MAIER SABINE LESCHE RALF COTTRELL SUSAN MOONEY SUZANNE		
发明人	ADORJAN, PETER BURGER, MATTHIAS MAIER, SABINE LESCHE, RALF COTTRELL, SUSAN MOONEY, SUZANNE		
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摘要(译)

本发明提供了通过分析Versican，TPEF，H-钙粘着蛋白，降钙素和EYA4中的一种或多种基因来检测，区分或区分结肠细胞增殖性疾病的方法和核酸。本发明还提供了可用于所述基因的细胞增殖性疾病特异性分析的新型核酸序列及其方法，测定和试剂盒。

FIGURE 1