

We claim:

1. A method for diagnosing colon cancer in a sample obtained from a subject, comprising:

5 detecting an expression level of at least ~~2~~70 colon cancer-related nucleic acid molecules listed in Table 6 in a sample comprising nucleic acids obtained from a subject; and

10 comparing the expression level of the at least ~~2~~70 colon cancer-related nucleic acid molecules, or a decision score derived therefrom to a control threshold indicative of a diagnosis of colon cancer, wherein the expression level, or a decision score derived therefrom, on the same side of the threshold indicates a diagnosis of colon cancer, thereby diagnosing colon cancer in the sample obtained from the subject.

15 2. The method of claim 1, wherein the control threshold comprises:
a threshold derived from corresponding transcripts from colon cancer-related nucleic acid molecules listed in Table 6 in a known colon cancer sample (or samples), wherein the expression level, or a decision score derived therefrom, on the same side of the threshold as a known colon cancer group indicates a diagnosis of colon cancer.

20 3. A method for classifying a colon cancer sample, comprising:
detecting an expression level of at least ~~2~~70 colon cancer-related nucleic acid molecules listed in Table 6 in a sample comprising nucleic acids obtained from a subject; and

25 comparing the expression level of the at least ~~2~~70 colon cancer-related nucleic acid molecules, or a decision score derived therefrom to a control threshold indicative of known classification, wherein the expression level, or a decision score derived therefrom, on the same side of the threshold permits classification of the colon cancer sample.

30 4. The method of claim 3, wherein the control threshold comprises:
a threshold derived from corresponding transcripts from colon cancer-related nucleic acid molecules listed in Table 6 in a colon cancer sample (or samples) of known classification, wherein the expression level, or a decision score derived
35 therefrom, on the same side of the threshold as a colon cancer sample (or samples) of

known classification permits classification of the colon cancer sample.

5. The method of any one of claims 3 or 4, wherein the colon cancer sample is classified as stage I, stage II, stage III and stage IV.

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6. The method of any one of claims 3-5, further comprising choosing a treatment plan that will be effective for the classified colon cancer.

7. The method of claim 6, wherein the treatment is surgical resection, chemotherapy, radiation or any combination thereof.

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8. A method for predicting a response to a treatment for colon cancer, comprising:

15 detecting an expression level of at least 2-70 colon cancer-related nucleic acid molecules listed in Table 6 in a sample comprising nucleic acids obtained from a subject; and

20 comparing the expression level of the at least 2-70 colon cancer-related nucleic acid molecules, or a decision score derived therefrom to a control threshold indicative of a known response to treatment, wherein the expression level, or a decision score derived therefrom, on the same side of the threshold indicates a similar response to treatment, thereby predicting response to treatment.

9. The method of claim 8, wherein the control threshold comprises:
a threshold derived from corresponding transcripts from colon cancer-related nucleic acid molecules listed in Table 6 in a colon cancer sample (or samples) having a known response to treatment, wherein the expression level, or a decision score derived therefrom, on the same side of the threshold as a colon cancer sample (or samples) having a known response to treatment indicates a similar response to treatment, thereby predicting response to treatment.

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10. The method of any one of claims 8 or 9, wherein the treatment is surgical resection.

11. The method of any one of claims 8-10, wherein the treatment is

chemotherapy and/or radiation.

12. A method for predicting long term survival of a subject with colon cancer, comprising:

- 5 | detecting an expression level of at least 2-70 colon cancer-related nucleic acid molecules listed in Table 6 in a sample comprising nucleic acids obtained from a subject; and
- | comparing the expression level of the at least 2-70 colon cancer-related nucleic acid molecules, or a decision score derived therefrom to a control threshold
- 10 | indicative of having a history of long term survival, wherein the expression level, or a decision score derived therefrom, on the same side of the threshold indicates long term survival of the subject, thereby predicting long term survival of a subject.

13. The method of claim 12, wherein the control threshold comprises:

- 15 | a threshold derived from corresponding transcripts from colon cancer-related nucleic acid molecules listed in Table 6 in a colon cancer sample (or samples) obtained from a subject (or subjects) having a history of long term survival, wherein the expression level, or a decision score derived therefrom, on the same side of the threshold as a colon cancer sample (or samples) obtained from a subject (or subjects)
- 20 | having a history of long term survival indicates long term survival of the subject, thereby predicting long term survival of a subject.

14. The method of claim 13, wherein long term survival comprises at least 5 year survival.

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15. A method for predicting of recurrence of colon cancer in a subject, comprising:

- | detecting an expression level of at least 2-70 colon cancer-related nucleic acid molecules listed in Table 6 in a sample comprising nucleic acids obtained from a
- 30 | subject; and
- | comparing the expression level of the at least 2-70 colon cancer-related nucleic acid molecules, or a decision score derived therefrom to a control threshold indicative of a history of recurrence, wherein the expression level, or a decision score derived therefrom, on the same side of the threshold indicates a recurrence in the subject.

16. The method of claim 15, wherein the control threshold comprises:
a threshold derived from corresponding transcripts from colon cancer-related
nucleic acid molecules listed in Table 6 in a colon cancer sample (or samples) having
5 a history of recurrence, wherein the expression level, or a decision score derived
therefrom, on the same side of the threshold as a colon cancer sample (or samples) of
known history of recurrence, indicates a recurrence in the subject.

17. A method of preparing a personalized colon cancer genomics profile
10 for a subject, comprising:
detecting an expression level of at least 2-70 colon cancer-related nucleic acid
molecules listed in Table 6 in a sample comprising nucleic acids obtained from a
subject; and
creating a report summarizing the data obtained by the gene expression
15 analysis.

18. The method of any one of claims 1-17, wherein the nucleic acids
obtained from the subject comprise RNA and/or cDNA transcribed from RNA
extracted from a sample of colorectal tissue obtained from the subject.

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19. The method of claim 18, wherein the sample is a biopsy sample.

20. The method of any one of claims 18 or 19, wherein the sample is a
fixed and/or paraffin embedded sample.

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21. The method of any one of claims 1-20, wherein the expression level is
normalized against a control gene or genes.

22. The method of any one of claims 1-21, wherein the level of expression
30 is determined with PCR and/or or microarray-based methods.

23. The method of any one of claims 1-22, wherein detecting the
expression level of at least 2-70 colon cancer-related nucleic acid molecules listed in
Table 6 comprises detecting the expression levels for MUM1 and SIGMAR1

transcripts.

24. The method of any one of claims 1-23, wherein detecting the expression level of at least 2-70 colon cancer-related nucleic acid molecules listed in Table 6 comprises detecting the expression levels for MUM1, SIGMAR1, ARSD, SULT1C2 and PPFIBP1 transcripts.

25. The method of any one of claims 1-24, wherein detecting the expression level of at least 2-70 colon cancer-related nucleic acid molecules listed in Table 6 comprises detecting the expression levels for ARSD, CXCL9, PCLO, SLC2A3, FCGBP, SLC2A14, SLC2A3, BCL9L and antisense sequences of MUC3A, OLFM4 and RNF39 transcripts.

26. The method of any one of claims 1-25, wherein detecting the expression level of at least 2-70 colon cancer-related nucleic acid molecules listed in Table 6 comprises detecting the expression levels for the transcripts listed in Table 1.

27. The method of any one of claims 1-26, wherein detecting the expression level of at least 2-70 colon cancer-related nucleic acid molecules listed in Table 6 comprises detecting the expression levels for the transcripts listed in Table 2.

28. A nucleic acid probe for detecting a gene expression signature for colon cancer, comprising or consisting substantially of a nucleic acid molecule between 20 and 40 nucleotides in length, capable of specifically hybridizing to one of the nucleic acid sequences set forth as SEQ ID NOs: 1-636 or its complement.

29. The nucleic acid probe according to claim 28, wherein the probe is labeled.

30. The nucleic acid probe according to claim 29, wherein the probe is radiolabeled, fluorescently-labeled, biotin-labeled, enzymatically-labeled, or chemically-labeled.

31. A set of probes, for detecting a gene expression signature for colon