

CLAIMS

1. A method of predicting the likelihood of long-term survival of a colorectal cancer patient without the recurrence of colorectal cancer, comprising determining the expression level of a combination of prognostic RNA transcripts or their expression products in a colorectal sample obtained from the patient, normalized against the expression level of all RNA transcripts or their expression products in the colorectal cancer tissue sample or normalized against a reference set of RNA transcripts or their expression products;
wherein the combination of prognostic RNA transcripts or their expression products comprises all of the transcripts in Table C; and
establishing the likelihood of long-term survival without colorectal cancer recurrence, wherein increased expression of each of the prognostic RNA transcripts or their expression products in Table C, compared to a colorectal cancer patient known to have recurrence, indicates an increased likelihood of long-term survival without colorectal cancer recurrence.
2. The method according to claim 1, wherein a predictive model is applied to establish the likelihood of long-term survival without colorectal cancer recurrence, said predictive model being established by applying a predictive method to expression levels of the predictive model in recurrent and non-recurrent tumour samples.
3. The method of claim 2, wherein said predictive model is selected from the group consisting of linear models, support vector machines, neural networks, classification and regression trees, ensemble learning methods, discriminant analysis, nearest neighbor method, bayesian networks, and independent components analysis.
4. The method of any one of claims 1 to 3 wherein the expression level of each of the RNA transcripts is determined.
5. The method of any one of claims 1 to 4 wherein RNA is isolated from a fixed, wax-embedded colorectal cancer tissue specimen of the patient.
6. The method of any one of claims 1 to 4 wherein RNA is isolated from core biopsy

tissue or fine needle aspirate cells.

7. The method of any one of claims 1 to 3 wherein the expression level of the expression products of each of the RNA transcripts is determined.

8. A method of predicting the likelihood of long-term survival of a patient diagnosed with colorectal cancer, without the recurrence of colorectal cancer, comprising the steps of:

(a) determining the expression levels of the combination of RNA transcripts or their expression products in Table C in a colorectal cancer tissue sample obtained from the patient, normalized against the expression levels of all RNA transcripts or their expression products in the colorectal cancer tissue sample, or normalized against a reference set of RNA transcripts or their expression products;

(b) subjecting data obtained in step (a) to statistical analysis; and

(c) establishing the likelihood of long-term survival without colorectal cancer recurrence, wherein increased expression of the combination of all of said RNA transcripts or their expression products in Table C, compared to a colorectal cancer patient known to have recurrence, indicates an increased likelihood of long-term survival without colorectal cancer recurrence.

9. The method of claim 8, wherein the statistical analysis is performed by using the Cox Proportional Hazards model.

10. A prognostic method for colorectal cancer in a patient, the method comprising: (a) subjecting a sample comprising colorectal cancer cells obtained from the patient to quantitative analysis of the levels of the combination of RNA transcripts or their expression products in Table C, and (b) identifying the patient as likely to have an increased likelihood of long-term survival without colorectal cancer recurrence if normalized expression levels of said RNA transcripts or their expression products are elevated above a defined expression threshold.

11. The method of claim 10, wherein the levels of the combination of RNA transcripts or their expression products in Table C are normalized relative to the mean level of the RNA transcript or the product of two or more housekeeping genes.

12. The method of claim 11 wherein the housekeeping genes are selected from the group consisting of glyceraldehyde-3-phosphate dehydrogenase (GAPDH), actins and mixtures thereof.
- 5 13. The method of any one of claims 10 to 12, wherein the levels of the combination of RNA transcripts or their expression products in Table C are normalized relative to the mean level of the RNA transcripts or the products of all assayed genes or a subset thereof.
- 10 14. The method of any one of claims 10 to 13, wherein the levels of the combination of RNA transcripts or their expression products in Table C are determined by quantitative RT-PCR.
- 15 15. The method of any one of claims 10 to 14, wherein the patient is human.
16. The method of any one of claims 10 to 15, wherein the sample is a fixed, paraffin-embedded tissue (FPET) sample, or a fresh or frozen tissue sample.
- 15 17. The method of any one of claims 10 to 15, wherein the sample is a tissue sample from fine needle, core, or other types of biopsy.
18. The method of any one of claims 10 to 17, wherein the quantitative analysis is performed by quantifying the products of the transcripts.
19. The method of any one of claims 10 to 18, wherein the products are quantified by immunohistochemistry or by proteomics technology.
- 20 20. The method of any one of claims 10 to 19, further comprising the step of preparing a report indicating that the patient has an increased likelihood of long-term survival without colorectal cancer recurrence.

25