CLAIMS

1. A prognostic signature for determining the risk of progression of melanoma, comprising two or more melanoma prognostic markers (MPMs).

2. The signature of claim 1, wherein the MPMs are selected from table 1.

3. A device for determining prognosis of melanoma, comprising:

a substrate having one or more locations thereon, each location having two or more oligonucleotides thereon, each oligonucleotide selected from the one or more MPMs.

4. The device of claim 3, wherein said the two or more oligonucleotides are MPMs selected from table 1.

5. A method for determining the prognosis of melanoma in a patient, comprising the steps of;

(i) determining the expression level of an MPM, or of a prognostic signature comprising two or more MPMs, in a melanoma tumour sample from the patient,

(ii) applying a predictive model, established by applying a predictive method to expressions levels of the MPM or of the prognostic signature in prognostically good and poor tumour samples,

(iii) establishing a prognosis.

6. A method for determining the suitability of a melanoma patient for a drug trial, comprising the steps of;

(i) determining the expression level of an MPM, or of a prognostic signature comprising two or more MPMs, in a melanoma tumour sample from the patient,

(ii) applying a predictive model, established by applying a predictive method to expression levels of the MPM or of the prognostic signature in prognostically good and poor tumour samples,

(iii) establishing the suitability of the patient to the trial.

7. The method of claim 5 or claim 6, wherein the MPMs are selected from table 1.

8. The method of claim 5, wherein said predictive method 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, independent components analysis.

9. The method of any one of claims 5 to 8, wherein the step of determining the expression level of an MPM or a prognostic signature is carried out by detecting the expression level of mRNA of each gene.

10. The method of any one of claims 5 to 8, wherein the step of determining the expression level of an MPM or of a prognostic signature is carried out by detecting the expression level of cDNA of each gene.

11. The method of claim 10, wherein the step of determining the expression level of an MPM or of a prognostic signature is carried out using a nucleotide complementary to at least a portion of said cDNA.

12. The method of claim 9, wherein the step of determining the expression level of an MPM or of a prognostic signature is carried out using qPCR method using a forward primer and a reverse primer.

13. The method of claim 8, wherein the step of determining the expression level of an MPM or of a prognostic signature is carried out using a device according to claim 3 or claim 4.

14. The method of any one of claims 5 to 8, wherein the step of determining the expression level of an MPM or of a prognostic signature is carried out by detecting the expression level of the protein of each marker.

15. The method of any one of claims 5 to 8, wherein the step of determining the expression level of an MPM or of a prognostic signature is carried out by detecting the expression level of the peptide of each marker.

16. The method of claim 13 or claim 14, wherein said step of detecting is carried out using an antibody directed against each marker.

17. The method of any one of claims 13 to 15, wherein said step of detecting is carried out using a sandwich-type immunoassay method.

18. The method of any one of claims 13 to 16, wherein said antibody is a monoclonal antibody.

19. The method of any one of claims 13 to 16, wherein said antibody is a polyclonal antiserum.

CLAIMS

1. A method for determining the prognosis of melanoma in a patient, comprising the steps of;

(i) determining the expression level of an MPM, which is milk fat globule GGF Factor 8 (MFGE8) or of a prognostic signature comprising two or more MPMs which is milk fat globule GGF Factor 8 (MFGE8) in a melanoma tumour sample from the patient,

(ii) applying a predictive model, established by applying a predictive method to expressions levels of the MPM or of the predictive signature in prognostically good and poor tumour samples,

(iii) establishing a prognosis.

2. A method for determining the suitability of a melanoma patient for a drug trial, comprising the steps of;

(i) determining the expression level of an MPM, which is milk fat globule GGF Factor 8 (MFGE8) or of a prognostic signature comprising two or more MPMs which is milk fat globule GGF Factor 8 (MFGE8) in a melanoma tumour sample from the patient,

(ii) applying a predictive model, established by applying a predictive method to expressions levels of the MPM or of the predictive signature in prognostically good and poor tumour samples,

(iii) establishing the suitability of the patient to the trial.

3. The method of claim 1 or claim 2, wherein the MPMs are selected from table 1.

4. The method of claim 3, wherein said predictive method 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, independent components analysis.

5. The method of any one of claims 1 to 4, wherein the step of determining the expression level of an MPM or of a prognostic signature is carried out by detecting the expression level of mRNA of each gene.

6. The method of any one of claims 1 to 4, wherein the step of determining the expression level of an MPM or of a prognostic signature is carried out by detecting the expression level of cDNA of each gene.

7. The method of claim 6, wherein the step of determining the expression level of an MPM or of a prognostic signature is carried out using a nucleotide complementary to at least a portion of said cDNA.

8. The method of claim 5, wherein the step of determining the expression level of an MPM or of a prognostic signature is carried out using qPCR method using a forward primer and a reverse primer.

9. The method of any one of claims 1 to 4, wherein the step of determining the expression level of an MPM or of a prognostic signature is carried out by detecting the expression level of the protein of each marker.

10. The method of any one of claims 1 to 4, wherein the step of determining the expression level of an MPM or of a prognostic signature is carried out by detecting the expression level of the peptide of each marker.

11. The method of claim 9, wherein said step of detecting is carried out using an antibody directed against each marker.

12. The method of any one of claims 9 or claim 10, wherein said step of detecting is carried out using a sandwich-type immunoassay method.

13. The method of claim 11, wherein said antibody is a monoclonal antibody.

14. The method of claim 11, wherein said antibody is a polyclonal antiserum.