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.

The two or more oligonucleotides can be MPMs selected from table 1.

The present invention also provides for the use of a reagent for detecting the expression of a MPM, or of a prognostic signature comprising two or more MPMs, in the manufacture of a kit for predicting the prognosis of melanoma in a patient. The MPMs can be selected from table 1.

The reagent can detect the level of expression of the one or more MPMs by detecting expression of MPM mRNA or MPM cDNA. The reagent can be an oligonucleotide complementary to at least a portion of the MPM mRNA or cDNA. Alternatively the reagent can detect the level of expression of the one or more MPMs by detecting expression of a MPM protein or peptide. The reagent can be an antibody, such as a monoclonal antibody of polyclonal antiserum.

The kit may be suitable for undertaking a sandwich-type immunoassay or an ELISA assay.

BRIEF DESCRIPTION OF THE FIGURES

This invention is described with reference to specific embodiments thereof and with reference to the figures, in which:

Figure 1 depicts the 22 genes used to build predictive scores ("melanoma markers"). Genes were selected using a Mann-Whitney test.

Figure 2 depicts the Gene Ontology groupings of the differentially expressed genes and associated significance. The most significant ontologies are determined by the number of genes which overlap between categories i.e the likelihood that it is a co-incidence that this many genes were in both the gene list and the category.

Figure 3 Experimental schema comprising a training set and two independent applied to Validation Set A using the qPS and Set B using the aPS. The training set was used to develop predictive genes which were then applied to Validation Set A using the qPS and Set B using the aPS.

CLAIMS

1. A method for determining the prognosis of melanoma in a patient with stage IIIB or stage III C melanoma, comprising the steps of:

(i) determining the expression level of Melanoma Prognostic Markers (MPMs), in a melanoma tumour sample from the patient, the MPMs comprising each of the five markers: milk fat globule-EGF factor 8 protein (MFGE8); isocitrate dehydrogenase 1 ($NADP^+$) soluble (IDH1); paired immunoglobin-like type 2 receptor alpha (PILRA); major histocompatibility complex, class 1, E (HLA-E); and thioredoxin domain containing 5 (TXNDCS); and

(ii) applying a predictive model established by applying a predictive method to expressions levels of each of said MPMs in prognostically good and poor tumour samples; and

(iii) establishing a prognosis.

2. The method of claim 1, wherein the predictive model is established by the formula:

qPS=[1328.15-187.42(IDH1)+137.10(MFGE8)+73.61(PILRA)+211.22(HLA-E)+143.94(TXNDC5)]x-1

wherein a qPS score of less than zero indicates poor prognosis and a qPS score of greater than zero indicates good prognosis.

3. The method of claim 1 or 2, wherein the step of determining the expression level of MPMs is carried out by detecting the expression level of mRNA of each gene.

4. The method of claim 1 or 2, wherein the step of determining the expression level of MPMs is carried out by detecting the expression level of cDNA of each gene.

5. The method of claim 4, wherein the step of determining the expression level of MPMs is carried out using a nucleotide complementary to at least a portion of said cDNA.

6. The method of claim 3, wherein the step of determining the expression level of MPMs is carried out using qPCR method using a forward primer and a reverse primer.

7. The method of claim 1 or 2, wherein the step of determining the expression level of MPMs is carried out by detecting the expression level of the protein of each marker.

8. The method of claim 1 or 2, wherein the step of determining the expression level of MPMs is carried out by detecting the expression level of the peptide of each marker.

9. The method of claim 7 or 8, wherein said step of detecting is carried out using an antibody directed against each marker.

10. The method of claim 7 or 8, wherein said step of detecting is carried out using a sandwich-type immunoassay method.

11. The method of claim 9 or 10, wherein said antibody is a monoclonal antibody.

12. The method of claim 9 or 10, wherein said antibody is a polyclonal antiserum.