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(54) Titre : MARQUEURS D'EXPRESSION GENIQUE POUR LE PRONOSTIC DU CANCER DU SEIN
(54) Title: GENE EXPRESSION MARKERS FOR BREAST CANCER PROGNOSIS

(57) Abrégé/Abstract:
The present invention provides gene sets the expression of which is important in the diagnosis and/or prognosis of breast cancer.

ABSTRACT

The present invention provides gene sets the expression of which is important in the diagnosis and/or prognosis of breast cancer.

Gene Expression Markers for Breast Cancer Prognosis

Background of the Invention

Field of the Invention

The present invention provides genes and gene sets the expression of which is important in the diagnosis and/or prognosis of breast cancer.

Description of the Related Art

Oncologists have a number of treatment options available to them, including different combinations of chemotherapeutic drugs that are characterized as "standard of care," and a number of drugs that do not carry a label claim for particular cancer, but for which there is evidence of efficacy in that cancer. Best likelihood of good treatment outcome requires that patients be assigned to optimal available cancer treatment, and that this assignment be made as quickly as possible following diagnosis.

Currently, diagnostic tests used in clinical practice are single analyte, and therefore do not capture the potential value of knowing relationships between dozens of different markers. Moreover, diagnostic tests are frequently not quantitative, relying on immunohistochemistry. This method often yields different results in different laboratories, in part because the reagents are not standardized, and in part because the interpretations are subjective and cannot be easily quantified. RNA-based tests have not often been used because of the problem of RNA degradation over time and the fact that it is difficult to obtain fresh tissue samples from patients for analysis. Fixed paraffin-embedded tissue is more readily available and methods have been established to detect RNA in fixed tissue. However, these methods typically do not allow for the study of large numbers of genes (DNA or RNA) from small amounts of material. Thus, traditionally fixed tissue has been rarely used other than for immunohistochemistry detection of proteins.

Recently, several groups have published studies concerning the classification of various cancer types by microarray gene expression analysis (see, e.g. Golub *et al., Science* 286:531-537 (1999); Bhattacharjae *et al., Proc. Natl. Acad. Sci. USA* 98:13790-13795 (2001); Chen-Hsiang *et al., Bioinformatics* 17 (Suppl. 1):S316-S322 (2001); Ramaswamy *et al., Proc. Natl. Acad. Sci. USA* 98:15149-15154 (2001)). Certain classifications of human breast

cancers based on gene expression patterns have also been reported (Martin *et al., Cancer Res.* 60:2232-2238 (2000); West *et al., Proc. Natl. Acad. Sci. USA* 98:11462-11467 (2001); Sorlie *et al., Proc. Natl. Acad. Sci. USA* 98:10869-10874 (2001); Yan *et al., Cancer Res.* 61:8375-8380 (2001)). However, these studies mostly focus on improving and refining the already established classification of various types of cancer, including breast cancer, and generally do not provide new insights into the relationships of the differentially expressed genes, and do not link the findings to treatment strategies in order to improve the clinical outcome of cancer therapy.

Although modern molecular biology and biochemistry have revealed hundreds of genes whose activities influence the behavior of tumor cells, state of their differentiation, and their sensitivity or resistance to certain therapeutic drugs, with a few exceptions, the status of these genes has not been exploited for the purpose of routinely making clinical decisions about drug treatments. One notable exception is the use of estrogen receptor (ER) protein expression in breast carcinomas to select patients to treatment with anti-estrogen drugs, such as tamoxifen. Another exceptional example is the use of ErbB2 (Her2) protein expression in breast carcinomas to select patients with the Her2 antagonist drug Herceptin® (Genentech, Inc., South San Francisco, CA).

Despite recent advances, the challenge of cancer treatment remains to target specific treatment regimens to pathogenically distinct tumor types, and ultimately personalize tumor treatment in order to maximize outcome. Hence, a need exists for tests that simultaneously provide predictive information about patient responses to the variety of treatment options. This is particularly true for breast cancer, the biology of which is poorly understood. It is clear that the classification of breast cancer into a few subgroups, such as $ErbB2^+$ subgroup, and subgroups characterized by low to absent gene expression of the estrogen receptor (ER) and a few additional transcriptional factors (Perou *et al., Nature* 406:747-752 (2000)) does not reflect the cellular and molecular heterogeneity of breast cancer, and does not allow the design of treatment strategies maximizing patient response.

Summary of the Invention

The present invention provides a set of genes, the expression of which has prognostic value, specifically with respect to disease-free survival.

Various embodiments of this invention provide a method of predicting the likelihood of long-term survival of a breast cancer patient without the recurrence of breast cancer, comprising: determining an expression level of an RNA transcript of MDM2 in a fixed, wax-embedded breast cancer tumor sample from the patient; normalizing said expression level to obtain a normalized expression level of MDM2; whercin incrcased normalized expression level of MDM2 indicates an increased likelihood of long-term survival without breast cancer recurrence.

Various embodiments of this invention provide a method of predicting the likelihood of long-term survival of a breast cancer patient without the recurrence of breast cancer, comprising: determining expression levels of RNA transcripts of a panel of genes comprising MDM2 and MYBL2 in a fixed, wax-embedded breast cancer tumor sample from the patient; normalizing said expression levels to obtain normalized expression levels of each gene; wherein increased normalized expression level of MDM2 indicates an increased likelihood of long-term survival without breast cancer recurrence, and wherein increased normalized expression level of MYBL2 indicates a decreased likelihood of long-term survival without breast cancer recurrence.

Various embodiments of this invention provide a method of preparing a personalized genomics profile for a breast cancer patient, comprising: (a) subjecting RNA extracted from a fixed, wax-embedded breast tissue sample of the patient to gene expression analysis; (b) determining an expression level of an RNA transcript of MDM2, wherein the expression level is normalized against the expression level of at least one reference gene to obtain normalized data, and optionally is compared to expression level of MDM2 in a breast cancer reference tissue set; and (c) creating a report summarizing the normalized data obtained by said gene expression analysis, wherein said report includes a prediction of the likelihood of long-term survival of the patient without recurrence of breast cancer, wherein increased normalized expression of MDM2 indicates an increased likelihood of long-term survival without breast cancer recurrence.

Various embodiments of this invention provide a method of preparing a personalized genomics profile for a breast cancer patient, comprising: (a) subjecting RNA extracted from a fixed, wax-embedded breast tissue sample of the patient to gene expression analysis; (b) determining expression levels of RNA transcripts of a panel of genes comprising MDM2 and MYBL2, wherein the expression levels are normalized against the expression level of at least one reference gene to obtain normalized data, and optionally are compared to expression levels of the genes in the panel in a breast cancer reference tissue set; and (c) creating a report summarizing the normalized data obtained by said gene expression analysis, wherein said report includes a prediction of the likelihood of long-term survival of the patient without recurrence of breast cancer, wherein increased normalized expression of MDM2

indicates an increased likelihood of long-term survival without breast cancer recurrence, and wherein increased normalized expression of MYBL2 indicates an reduced likelihood of long-term survival without breast cancer recurrence.

Various embodiments of this invention provide a method of predicting the likelihood of long-term survival of a breast cancer patient without the recurrence of breast cancer, comprising: isolating RNA from a fixed, wax-embedded tissue sample obtained from a breast tumor of the patient; reverse transcribing an RNA transcript of MDM2 to produce a cDNA of MDM2; amplifying the cDNA of MDM2 to produce an amplicon of the RNA transcript of MDM2; assaying a level of the amplicon of the RNA transcript of MDM2; normalizing said level against a level of an amplicon of at least one reference RNA transcript in said tissue sample to provide a normalized MDM2 amplicon level; comparing the normalized MDM2 amplicon level to a normalized MDM2 amplicon level in reference breast tumor samples; and predicting the likelihood of long-term survival without the recurrence of breast cancer, wherein increased normalized MDM2 amplicon level is indicative of an increased likelihood of long-term survival without recurrence of breast cancer.

Various embodiments of this invention provide a method of predicting the likelihood of long-term survival of a breast cancer patient without the recurrence of breast cancer, comprising: determining expression levels of RNA transcripts of a panel of genes comprising MDM2 and MYBL2 in a breast cancer tumor sample from the patient, wherein the expression level of the RNA transcript of MYBL2 is obtained by reverse transcription with at least one primer comprising the nucleotide sequence of SEQ ID NO: 18, SEQ ID NO: 24, and SEQ ID NO: 27; normalizing said expression levels to obtain normalized expression levels of each gene; wherein increased normalized expression level of MDM2 indicates an increased likelihood of long-term survival without breast cancer recurrence, and wherein increased normalized expression level of MYBL2 indicates a decreased likelihood of long-term survival without breast cancer recurrence

Various embodiments of this invention provide a method of preparing a personalized genomics profile for a breast cancer patient, comprising: (a) subjecting RNA extracted from a breast tissue sample of the patient to gene expression analysis; (b) determining expression levels of RNA transcripts of a panel of genes comprising MDM2 and MYBL2, wherein the expression level of the RNA transcript of MYBL2 is obtained by reverse transcription with at least one primer comprising the nucleotide sequence of SEQ ID NO: 18, SEQ ID NO: 24, and SEQ ID NO: 27, and wherein the expression levels are normalized against the expression level of at least one reference gene to obtain normalized data, and optionally are compared to expression levels of the genes in the panel in a breast cancer reference tissue set; and (c) creating a report summarizing the normalized data obtained by said gene expression

analysis, wherein said report includes a prediction of the likelihood of long-term survival of the patient without recurrence of breast cancer, wherein increased normalized expression of MDM2 indicates an increased likelihood of long-term survival without breast cancer recurrence, and wherein increased normalized expression of MYBL2 indicates an reduced likelihood of long-term survival without breast cancer recurrence.

Various embodiments of this invention provide a method of predicting the likelihood of long-term survival of a breast cancer patient without the recurrence of breast cancer, comprising: isolating RNA from a tissue sample obtained from a breast tumor of the patient; reverse transcribing RNA transcripts of a panel of genes comprising MDM2 and MYBL2 to produce a cDNAs of the panel of genes, wherein reverse transcribing the RNA transcript of MYBL2 is performed with at least one primer comprising the nucleotide sequence of SEQ ID NO: 18, SEQ ID NO: 24, and SEQ ID NO: 27; amplifying the cDNAs to produce amplicons of the RNA transcripts; assaying levels of the amplicons of the RNA transcripts; normalizing said levels against a level of an amplicon of at least one reference RNA transcript in said tissue sample to provide normalized amplicon levels of the panel of genes comprising MDM2 and MYBL2; comparing the normalized amplicon levels to a normalized amplicon levels of the same genes in reference breast tumor samples; and predicting the likelihood of long-term survival without the recurrence of breast cancer, wherein increased normalized MDM2 amplicon level is indicative of an increased likelihood of long-term survival without recurrence of breast cancer and increased normalized MYBL2 amplicon level is indicative of a reduced likelihood of long-term survival without recurrence of breast cancer.

The present invention accommodates the use of archived paraffin-embedded biopsy material for assay of all markers in the set, and therefore is compatible with the most widely

available type of biopsy material. It is also compatible with several different methods of tumor tissue harvest, for example, via core biopsy or fine needle aspiration. Further, for each member of the gene set, the invention specifies oligonucleotide sequences that can be used in the test.

In one aspect, the invention concerns a method of predicting the likelihood of long-term survival of a breast cancer patient without the recurrence of breast cancer, comprising determining the expression level of one or more prognostic RNA transcripts or their expression products in a breast cancer tissue sample obtained from the patient, normalized against the expression level of all RNA transcripts or their products in the breast cancer tissue sample, or of a reference set of RNA transcripts or their expression products, wherein the prognostic RNA transcript is the transcript of one or more genes selected from the group consisting of: TP53BP2, GRB7, PR, CD68, Bcl2, KRT14, IRS1, CTSL, EstR1, Chk1, IGFBP2, BAG1, CEGP1, STK15, GSTM1, FHIT, RIZ1, AIB1, SURV, BBC3, IGF1R, p27, GATA3, ZNF217, EGFR, CD9, MYBL2, HIF1α, pS2, ErbB3, TOP2B, MDM2, RAD51C, KRT19, TS, Her2, KLK10, β-Catenin, γ-Catenin, MCM2, PI3KC2A, IGF1, TBP, CCNB1, FBXO5, and DR5,

wherein expression of one or more of GRB7, CD68, CTSL, Chk1, AIB1, CCNB1, MCM2, FBXO5, Her2, STK15, SURV, EGFR, MYBL2, HIF1α, and TS indicates a decreased likelihood of long-term survival without breast cancer recurrence, and

the expression of one or more of TP53BP2, PR, Bcl2, KRT14, EstR1, IGFBP2, BAG1, CEGP1, KLK10, β-Catenin, γ-Catenin, DR5, PI3KCA2, RAD51C, GSTM1, FHIT, RIZ1, BBC3, TBP, p27, IRS1, IGF1R, GATA3, ZNF217, CD9, pS2, ErbB3, TOP2B, MDM2, IGF1, and KRT19 indicates an increased likelihood of long-term survival without breast cancer recurrence.

In a particular embodiment, the expression levels of at least two, or at least 5, or at least 10, or at least 15 of the prognostic RNA transcripts or their expression products are determined. In another embodiment, the method comprises the determination of the expression levels of all prognostic RNA transcripts or their expression products.

In another particular embodiment, the breast cancer is invasive breast carcinoma.

In a further embodiment, RNA is isolated from a fixed, wax-embedded breast cancer tissue specimen of the patient. Isolation may be performed by any technique known in the art, for example from core biopsy tissue or fine needle aspirate cells.

In another aspect, the invention concerns an array comprising polynucleotides hybridizing to two or more of the following genes: α-Catenin, AIB1, AKT1, AKT2, β-actin, BAG1, BBC3, Bcl2, CCNB1, CCND1, CD68, CD9, CDH1, CEGP1, Chk1, CIAP1, cMet.2, Contig 27882, CTSL, DR5, EGFR, EIF4E, EPHX1, ErbB3, EstR1, FBXO5, FHIT1 FRP1, GAPDH, GATA3, G-Catenin, GRB7, GRO1, GSTM1, GUS, HER2, HIF1A, HNF3A, IGF1R, IGFBP2, KLK10, KRT14, KRT17, KRT18, KRT19, KRT5, Maspin, MCM2, MCM3, MDM2, MMP9, MTA1, MYBL2, P14ARF, p27, P53, PI3KC2A, PR, PRAME, pS2, RAD51C,.3RB1, RIZ1, STK15, STMY3, SURV, TGFA, TOP2B, TP53BP2, TRAIL, TS, upa, VDR, VEGF, and ZNF217.

In particular embodiments, the array comprises polynucleotides hybridizing to at least 3, or at least 5, or at least 10, or at least 15, or at least 20, or all of the genes listed above.

In another specific embodiment, the array comprises polynucleotides hybridizing to the following genes: TP53BP2, GRB7, PR, CD68, Bcl2, KRT14, IRS1, CTSL, EstR1, Chk1, IGFBP2, BAG1, CEGP1, STK15, GSTM1, FHIT, RIZ1, AIB1, SURV, BBC3, IGF1R, p27, GATA3, ZNF217, EGFR, CD9, MYBL2, HIF1α, pS2, RIZ1, ErbB3, TOP2B, MDM2, RAD51C, KRT19, TS, Her2, KLK10, β-Catenin, γ-Catenin, MCM2, PI3KC2A, IGF1, TBP, CCNB1, FBXO5 and DR5.

The polynucleotides can be cDNAs, or oligonucleotides, and the solid surface on which they are displayed may, for example, be glass.

In another aspect, the invention concerns a method of predicting the likelihood of long-term survival of a patient diagnosed with invasive breast cancer, without the recurrence of breast cancer, comprising the steps of:

(1) determining the expression levels of the RNA transcripts or the expression products of genes or a gene set selected from the group consisting of

(a) TP53BP2, Bcl2, BAD, EPHX1, PDGFRβ, DIABLO, XIAP, YB1, CA9, and KRT8;

(b) GRB7, CD68, TOP2A, Bcl2, DIABLO, CD3, ID1, PPM1D, MCM6, and WISP1;

(c) PR, TP53BP2, PRAME, DIABLO, CTSL, IGFBP2, TIMP1, CA9, MMP9, and COX2;

(d) CD68, GRB7, TOP2A, Bcl2, DIABLO, CD3, ID1, PPM1D, MCM6, and WISP1;

(e) Bcl2, TP53BP2, BAD, EPHX1, PDGFRβ, DIABLO, XIAP, YB1, CA9, and KRT8;

(f) KRT14, KRT5, PRAME, TP53BP2, GUS1, AIB1, MCM3, CCNE1, MCM6, and ID1;

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(g) PRAME, TP53BP2, EstR1, DIABLO, CTSL, PPM1D, GRB7, DAPK1, BBC3, and VEGFB;

(h) CTSL2, GRB7, TOP2A, CCNB1, Bcl2, DIABLO, PRAME, EMS1, CA9, and EpCAM;

(i) EstR1, TP53BP2, PRAME, DIABLO, CTSL, PPM1D, GRB7, DAPK1, BBC3, and VEGFB;

(k) Chk1, PRAME, TP53BP2, GRB7, CA9, CTSL, CCNB1, TOP2A, tumor size, and IGFBP2;

(l) IGFBP2, GRB7, PRAME, DIABLO, CTSL, β-Catenin, PPM1D, Chk1, WISP1, and LOT1;

(m) HER2, TP53BP2, Bcl2, DIABLO, TIMP1, EPHX1, TOP2A, TRAIL, CA9, and AREG;

(n) BAG1, TP53BP2, PRAME, IL6, CCNB1, PAI1, AREG, tumor size, CA9, and Ki67;

(o) CEGPİ, TP53BP2, PRAME, DIABLO, Bcl2, COX2, CCNE1, STK15, and AKT2, and FGF18;

(p) STK15, TP53BP2, PRAME, IL6, CCNE1, AKT2, DIABLO, cMet, CCNE2, and COX2;

(q) KLK10, EstR1, TP53BP2, PRAME, DIABLO, CTSL, PPM1D, GRB7, DAPK1, and BBC3;

(r) AIB1, TP53BP2, Bcl2, DIABLO, TIMP1, CD3, p53, CA9, GRB7, and EPHX1

(s) BBC3, GRB7, CD68, PRAME, TOP2A, CCNB1, EPHX1, CTSL GSTM1, and APC;

(t) CD9, GRB7, CD68, TOP2A, Bcl2, CCNB1, CD3, DIABLO, ID1, and PPM1D;

(w) EGFR, KRT14, GRB7, TOP2A, CCNB1, CTSL, Bcl2, TP, KLK10, and CA9;

(x) HIF1α, PR, DIABLO, PRAME, Chk1, AKT2, GRB7, CCNE1, TOP2A, and CCNB1;

(y) MDM2, TP53BP2, DIABLO, Bcl2, AIB1, TIMP1, CD3, p53, CA9, and HER2;

(z) MYBL2, TP53BP2, PRAME, IL6, Bcl2, DIABLO, CCNE1, EPHX1, TIMP1, and CA9;

(aa) p27, TP53BP2, PRAME, DIABLO, Bcl2, COX2, CCNE1, STK15, AKT2, and ID1;

(ab) RAD51, GRB7, CD68, TOP2A, CIAP2, CCNB1, BAG1, IL6, FGFR1, and TP53BP2;

(ac) SURV, GRB7, TOP2A, PRAME, CTSL, GSTM1, CCNB1, VDR, CA9; and CCNE2;

(ad) TOP2B, TP53BP2, DIABLO, Bcl2, TIMP1, AIB1, CA9, p53, KRT8, and BAD;

(ae) ZNF217, GRB7, TP53BP2, PRAME, DIABLO, Bcl2, COX2, CCNE1, APC4, and β-Catenin,

in a breast cancer tissue sample obtained from the patient, normalized against the expression levels of all RNA transcripts or their expression products in said breast cancer tissue sample, or of a reference set of RNA transcripts or their products;

(2) subjecting the data obtained in step (1) to statistical analysis; and

(3) determining whether the likelihood of said long-term survival has increased or decreased.

In a further aspect, the invention concerns a method of predicting the likelihood of long-term survival of a patient diagnosed with estrogen receptor (ER)-positive invasive breast cancer, without the recurrence of breast cancer, comprising the steps of:

(1) determining the expression levels of the RNA transcripts or the expression products of genes of a gene set selected from the group consisting of CD68; CTSL; FBXO5; SURV; CCNB1; MCM2; Chk1; MYBL2; HIF1A; cMET; EGFR; TS; STK15, IGFR1; BCl2; HNF3A; TP53BP2; GATA3; BBC3; RAD51C; BAG1; IGFBP2; PR; CD9; RB1; EPHX1; CEGP1; TRAIL; DR5; p27; p53; MTA; RIZ1; ErbB3; TOP2B; EIF4E, wherein expression of the following genes in ER-positive cancer is indicative of a reduced likelihood of survival without cancer recurrence following surgery: CD68; CTSL; FBXO5; SURV; CCNB1; MCM2; Chk1; MYBL2; HIF1A; cMET; EGFR; TS; STK15, and wherein expression of the following genes is indicative of a better prognosis for survival without cancer recurrence following surgery: IGFR1; BCl2; HNF3A; TP53BP2; GATA3; BBC3; RAD51C; BAG1; IGFBP2; PR; CD9; RB1; EPHX1; CEGP1; TRAIL; DR5; p27; p53; MTA; RIZ1; ErbB3; TOP2B; EIF4E.

(2) subjecting the data obtained in step (1) to statistical analysis; and

(3) determining whether the likelihood of said long-term survival has increased or decreased.

In yet another aspect, the invention concerns a method of predicting the likelihood of long-term survival of a patient diagnosed with estrogen receptor (ER)-negative invasive breast cancer, without the recurrence of breast cancer, comprising determining the expression levels of the RNA transcripts or the expression products of genes of the gene set CCND1; UPA; HNF3A; CDH1; Her2; GRB7; AKT1; STMY3; α-Catenin; VDR; GRO1; KT14; KLK10; Maspin, TGFα, and FRP1, wherein expression of the following genes is indicative of a

reduced likelihood of survival without cancer recurrence: CCND1; UPA; HNF3A; CDH1; Her2; GRB7; AKT1; STMY3; α-Catenin; VDR; GRO1, and wherein expression of the following genes is indicative of a better prognosis for survival without cancer recurrence: KT14; KLK10; Maspin, TGFα, and FRP1.

In a different aspect, the invention concerns a method of preparing a personalized genomics profile for a patient, comprising the steps of:

(a) subjecting RNA extracted from a breast tissue obtained from the patient to gene expression analysis;

(b) determining the expression level of one or more genes selected from the breast cancer gene set listed in any one of Tables 1-5, wherein the expression level is normalized against a control gene or genes and optionally is compared to the amount found in a breast cancer reference tissue set; and

(c) creating a report summarizing the data obtained by the gene expression analysis.

The report may, for example, include prediction of the likelihood of long term survival of the patient and/or recommendation for a treatment modality of said patient.

In a further aspect, the invention concerns a method for amplification of a gene listed in Tables 5A and B by polymerase chain reaction (PCR), comprising performing said PCR by using an amplicon listed in Tables 5A and B and a primer-probe set listed in Tables 6A-F.

In a still further aspect, the invention concerns a PCR amplicon listed in Tables 5A and B.

In yet another aspect, the invention concerns a PCR primer-probe set listed in Tables 6A-F.

The invention further concerns a prognostic method comprising:

(a) subjecting a sample comprising breast cancer cells obtained from a patient to quantitative analysis of the expression level of the RNA transcript of at least one gene selected from the group consisting of GRB7, CD68, CTSL, Chk1, AIB1, CCNB1, MCM2, FBXO5, Her2, STK15, SURV, EGFR, MYBL2, HIF1α, and TS, or their product, and

(b) identifying the patient as likely to have a decreased likelihood of long-term survival without breast cancer recurrence if the normalized expression levels of the gene or genes, or their products, are elevated above a defined expression threshold.

In a different aspect, the invention concerns a prognostic method comprising:

(a) subjecting a sample comprising breast cancer cells obtained from a patient to quantitative analysis of the expression level of the RNA transcript of at least one gene selected from the group consisting of TP53BP2, PR, Bcl2, KRT14, EstR1, IGFBP2, BAG1, CEGP1, KLK10, β-Catenin, γ-Catenin, DR5, PI3KCA2, RAD51C, GSTM1, FHIT, RIZ1, BBC3, TBP, p27, IRS1, IGF1R, GATA3, ZNF217, CD9, pS2, ErbB3, TOP2B, MDM2, IGF1, and KRT19, and

(b) identifying the patient as likely to have an increased likelihood of long-term survival without breast cancer recurrence if the normalized expression levels of the gene or genes, or their products, are elevated above a defined expression threshold.

The invention further concerns a kit comprising one or more of (1) extraction buffer/reagents and protocol; (2) reverse transcription buffer/reagents and protocol; and (3) qPCR buffer/reagents and protocol suitable for performing any of the foregoing methods.

Description of the Tables

Table 1 is a list of genes, expression of which correlate with breast cancer survival. Results from a retrospective clinical trial. Binary statistical analysis.

Table 2 is a list of genes, expression of which correlates with breast cancer survival in estrogen receptor (ER) positive patients. Results from a retrospective clinical trial. Binary statistical analysis.

Table 3 is a list of genes, expression of which correlates with breast cancer survival in estrogen receptor (ER) negative patients. Results from a retrospective clinical trial. Binary statistical analysis.

Table 4 is a list of genes, expression of which correlates with breast cancer survival. Results from a retrospective clinical trial. Cox proportional hazards statistical analysis.

Tables 5A and B show a list of genes, expression of which correlate with breast cancer survival. Results from a retrospective clinical trial. The table includes accession numbers for the genes, and amplicon sequences used for PCR amplification.

Tables 6A-6F The table includes sequences for the forward and reverse primers (designated by "f" and "r", respectively) and probes (designated by "p") used for PCR amplification of the amplicons listed in Tables 5A-B.

Detailed Description of the Preferred Embodiment

A. Definitions

Unless defined otherwise, technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Singleton *et al.*, Dictionary of Microbiology and Molecular Biology 2nd ed., J. Wiley & Sons (New York, NY 1994), and March, Advanced Organic Chemistry Reactions, Mechanisms and Structure 4th ed., John Wiley & Sons (New York, NY 1992), provide one skilled in the art with a general guide to many of the terms used in the present application.

One skilled in the art will recognize many methods and materials similar or equivalent to those described herein, which could be used in the practice of the present invention. Indeed, the present invention is in no way limited to the methods and materials described. For purposes of the present invention, the following terms are defined below.

The term "microarray" refers to an ordered arrangement of hybridizable array elements, preferably polynucleotide probes, on a substrate.

The term "polynucleotide," when used in singular or plural, generally refers to any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. Thus, for instance, polynucleotides as defined herein include, without limitation, single- and double-stranded DNA, DNA including single- and double-stranded regions, single- and double-stranded RNA, and RNA including single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or include single- and double-stranded regions. In addition, the term "polynucleotide" as used herein refers to triple-stranded regions comprising RNA or DNA or both RNA and DNA. The strands in such regions may be from the same molecule or from different molecules. The regions may include all of one or more of the molecules, but more typically involve only a region of some of the molecules. One of the molecules of a triple-helical region often is an oligonucleotide. The term "polynucleotide" specifically includes cDNAs. The term includes DNAs (including cDNAs) and RNAs that contain one or more modified bases. Thus, DNAs or RNAs with backbones modified for stability or for other reasons are "polynucleotides" as that term is intended herein. Moreover, DNAs or RNAs comprising unusual bases, such as inosine, or modified bases, such as tritiated bases, are included within the term "polynucleotides" as defined herein. In general, the term "polynucleotide" embraces all chemically, enzymatically and/or metabolically modified forms of unmodified polynucleotides, as well as the chemical forms of DNA and RNA characteristic of viruses and cells, including simple and complex cells.

The term "oligonucleotide" refers to a relatively short polynucleotide, including, without limitation, single-stranded deoxyribonucleotides, single- or double-stranded ribonucleotides, RNA:DNA hybrids and double-stranded DNAs. Oligonucleotides, such as single-stranded DNA probe oligonucleotides, are often synthesized by chemical methods, for example using automated oligonucleotide synthesizers that are commercially available. However, oligonucleotides can be made by a variety of other methods, including *in vitro* recombinant DNA-mediated techniques and by expression of DNAs in cells and organisms.

The terms "differentially expressed gene," "differential gene expression" and their synonyms, which are used interchangeably, refer to a gene whose expression is activated to a higher or lower level in a subject suffering from a disease, specifically cancer, such as breast

cancer, relative to its expression in a normal or control subject. The terms also include genes whose expression is activated to a higher or lower level at different stages of the same disease. It is also understood that a differentially expressed gene may be either activated or inhibited at the nucleic acid level or protein level, or may be subject to alternative splicing to result in a different polypeptide product. Such differences may be evidenced by a change in mRNA levels, surface expression, secretion or other partitioning of a polypeptide, for example. Differential gene expression may include a comparison of expression between two or more genes or their gene products, or a comparison of the ratios of the expression between two or more genes or their gene products, or even a comparison of two differently processed products of the same gene, which differ between normal subjects and subjects suffering from a disease, specifically cancer, or between various stages of the same disease. Differential expression includes both quantitative, as well as qualitative, differences in the temporal or cellular expression pattern in a gene or its expression products among, for example, normal and diseased cells, or among cells which have undergone different disease events or disease stages. For the purpose of this invention, "differential gene expression" is considered to be present when there is at least an about two-fold, preferably at least about four-fold, more preferably at least about six-fold, most preferably at least about ten-fold difference between the expression of a given gene in normal and diseased subjects, or in various stages of disease development in a diseased subject.

The phrase "gene amplification" refers to a process by which multiple copies of a gene or gene fragment are formed in a particular cell or cell line. The duplicated region (a stretch of amplified DNA) is often referred to as "amplicon." Usually, the amount of the messenger RNA (mRNA) produced, *i.e.*, the level of gene expression, also increases in the proportion of the number of copies made of the particular gene expressed.

The term "diagnosis" is used herein to refer to the identification of a molecular or pathological state, disease or condition, such as the identification of a molecular subtype of head and neck cancer, colon cancer, or other type of cancer.

The term "prognosis" is used herein to refer to the prediction of the likelihood of cancer-attributable death or progression, including recurrence, metastatic spread, and drug resistance, of a neoplastic disease, such as breast cancer.

The term "prediction" is used herein to refer to the likelihood that a patient will respond either favorably or unfavorably to a drug or set of drugs, and also the extent of those

responses, or that a patient will survive, following surgical removal or the primary tumor and/or chemotherapy for a certain period of time without cancer recurrence. The predictive methods of the present invention can be used clinically to make treatment decisions by choosing the most appropriate treatment modalities for any particular patient. The predictive methods of the present invention are valuable tools in predicting if a patient is likely to respond favorably to a treatment regimen, such as surgical intervention, chemotherapy with a given drug or drug combination, and/or radiation therapy, or whether long-term survival of the patient, following sugery and/or termination of chemotherapy or other treatment modalities is likely.

The term "long-term" survival is used herein to refer to survival for at least 3 years, more preferably for at least 8 years, most preferably for at least 10 years following surgery or other treatment.

The term "tumor," as used herein, refers to all neoplastic cell growth and proliferation, whether malignant or benign, and all pre-cancerous and cancerous cells and tissues.

The terms "cancer" and "cancerous" refer to or describe the physiological condition in mammals that is typically characterized by unregulated cell growth. Examples of cancer include but are not limited to, breast cancer, colon cancer, lung cancer, prostate cancer, hepatocellular cancer, gastric cancer, pancreatic cancer, cervical cancer, ovarian cancer, liver cancer, bladder cancer, cancer of the urinary tract, thyroid cancer, renal cancer, carcinoma, melanoma, and brain cancer.

The "pathology" of cancer includes all phenomena that compromise the well-being of the patient. This includes, without limitation, abnormal or uncontrollable cell growth, metastasis, interference with the normal functioning of neighboring cells, release of cytokines or other secretory products at abnormal levels, suppression or aggravation of inflammatory or immunological response, neoplasia, premalignancy, malignancy, invasion of surrounding or distant tissues or organs, such as lymph nodes, etc.

"Stringency" of hybridization reactions is readily determinable by one of ordinary skill in the art, and generally is an empirical calculation dependent upon probe length, washing temperature, and salt concentration. In general, longer probes require higher temperatures for proper annealing, while shorter probes need lower temperatures. Hybridization generally depends on the ability of denatured DNA to reanneal when complementary strands are present in an environment below their melting temperature. The higher the degree of desired

homology between the probe and hybridizable sequence, the higher the relative temperature which can be used. As a result, it follows that higher relative temperatures would tend to make the reaction conditions more stringent, while lower temperatures less so. For additional details and explanation of stringency of hybridization reactions, see Ausubel et al., Current Protocols in Molecular Biology, Wiley Interscience Publishers, (1995).

"Stringent conditions" or "high stringency conditions", as defined herein, typically: (1) employ low ionic strength and high temperature for washing, for example 0.015 M sodium chloride/0.0015 M sodium citrate/0.1% sodium dodecyl sulfate at 50°C; (2) employ during hybridization a denaturing agent, such as formamide, for example, 50% (v/v) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50mM sodium phosphate buffer at pH 6.5 with 750 mM sodium chloride, 75 mM sodium citrate at 42°C; or (3) employ 50% formamide, 5 x SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 µg/ml), 0.1% SDS, and 10% dextran sulfate at 42°C, with washes at 42°C in 0.2 x SSC (sodium chloride/sodium citrate) and 50% formamide at 55°C, followed by a high-stringency wash consisting of 0.1 x SSC containing EDTA at 55°C.

"Moderately stringent conditions" may be identified as described by Sambrook et al., Molecular Cloning: A Laboratory Manual, New York: Cold Spring Harbor Press, 1989, and include the use of washing solution and hybridization conditions (e.g., temperature, ionic strength and %SDS) less stringent that those described above. An example of moderately stringent conditions is overnight incubation at 37°C in a solution comprising: 20% formamide, 5 x SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5 x Denhardt's solution, 10% dextran sulfate, and 20 mg/ml denatured sheared salmon sperm DNA, followed by washing the filters in 1 x SSC at about 37-50°C. The skilled artisan will recognize how to adjust the temperature, ionic strength, etc. as necessary to accommodate factors such as probe length and the like.

In the context of the present invention, reference to "at least one," "at least two," "at least five," etc. of the genes listed in any particular gene set means any one or any and all combinations of the genes listed.

The terms "expression threshold," and "defined expression threshold" are used interchangeably and refer to the level of a gene or gene product in question above which the gene or gene product serves as a predictive marker for patient survival without cancer

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recurrence. The threshold is defined experimentally from clinical studies such as those described in the Example below. The expression threshold can be selected either for maximum sensitivity, or for maximum selectivity, or for minimum error. The determination of the expression threshold for any situation is well within the knowledge of those skilled in the art.

B. Detailed Description

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of molecular biology (including recombinant techniques), microbiology, cell biology, and biochemistry, which are within the skill of the art. Such techniques are explained fully in the literature, such as, "Molecular Cloning: A Laboratory Manual", 2nd edition (Sambrook et al., 1989); "Oligonucleotide Synthesis" (M.J. Gait, ed., 1984); "Animal Cell Culture" (R.I. Freshney, ed., 1987); "Methods in Enzymology" (Academic Press, Inc.); "Handbook of Experimental Immunology", 4th edition (D.M. Weir & C.C. Blackwell, eds., Blackwell Science Inc., 1987); "Gene Transfer Vectors for Mammalian Cells" (J.M. Miller & M.P. Calos, eds., 1987); "Current Protocols in Molecular Biology" (F.M. Ausubel et al., eds., 1987); and "PCR: The Polymerase Chain Reaction", (Mullis et al., eds., 1994).

1. *Gene Expression Profiling*

In general, methods of gene expression profiling can be divided into two large groups: methods based on hybridization analysis of polynucleotides, and methods based on sequencing of polynucleotides. The most commonly used methods known in the art for the quantification of mRNA expression in a sample include northern blotting and *in situ* hybridization (Parker & Barnes, *Methods in Molecular Biology* 106:247-283 (1999)); RNAse protection assays (Hod, *Biotechniques* 13:852-854 (1992)); and reverse transcription polymerase chain reaction (RT-PCR) (Weis *et al., Trends in Genetics* 8:263-264 (1992)). Alternatively, antibodies may be employed that can recognize specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes. Representative methods for sequencing-based gene expression analysis include Serial Analysis of Gene Expression (SAGE), and gene expression analysis by massively parallel signature sequencing (MPSS).

2. *Reverse Transcriptase PCR (RT-PCR)*

Of the techniques listed above, the most sensitive and most flexible quantitative method is RT-PCR, which can be used to compare mRNA levels in different sample populations, in normal and tumor tissues, with or without drug treatment, to characterize patterns of gene expression, to discriminate between closely related mRNAs, and to analyze RNA structure.

The first step is the isolation of mRNA from a target sample. The starting material is typically total RNA isolated from human tumors or tumor cell lines, and corresponding normal tissues or cell lines, respectively. Thus RNA can be isolated from a variety of primary tumors, including breast, lung, colon, prostate, brain, liver, kidney, pancreas, spleen, thymus, testis, ovary, uterus, etc., tumor, or tumor cell lines, with pooled DNA from healthy donors. If the source of mRNA is a primary tumor, mRNA can be extracted, for example, from frozen or archived paraffin-embedded and fixed (e.g. formalin-fixed) tissue samples.

General methods for mRNA extraction are well known in the art and are disclosed in standard textbooks of molecular biology, including Ausubel *et al.*, Current Protocols of Molecular Biology, John Wiley and Sons (1997). Methods for RNA extraction from paraffin embedded tissues are disclosed, for example, in Rupp and Locker, *Lab Invest.* 56:A67 (1987), and De Andrés *et al., BioTechniques* 18:42044 (1995). In particular, RNA isolation can be performed using purification kit, buffer set and protease from commercial manufacturers, such as Qiagen, according to the manufacturer's instructions. For example, total RNA from cells in culture can be isolated using Qiagen RNeasy mini-columns. Other commercially available RNA isolation kits include MasterPure™ Complete DNA and RNA Purification Kit (EPICENTRE®, Madison, WI), and Paraffin Block RNA Isolation Kit (Ambion, Inc.). Total RNA from tissue samples can be isolated using RNA Stat-60 (Tel-Test). RNA prepared from tumor can be isolated, for example, by cesium chloride density gradient centrifugation.

As RNA cannot serve as a template for PCR, the first step in gene expression profiling by RT-PCR is the reverse transcription of the RNA template into cDNA, followed by its exponential amplification in a PCR reaction. The two most commonly used reverse transcriptases are avilo myeloblastosis virus reverse transcriptase (AMV-RT) and Moloney murine leukemia virus reverse transcriptase (MMLV-RT). The reverse transcription step is typically primed using specific primers, random hexamers, or oligo-dT primers, depending on the circumstances and the goal of expression profiling. For example, extracted RNA can be reverse-transcribed using a GeneAmp RNA PCR kit (Perkin Elmer, CA, USA), following the

manufacturer's instructions. The derived cDNA can then be used as a template in the subsequent PCR reaction.

Although the PCR step can use a variety of thermostable DNA-dependent DNA polymerases, it typically employs the Taq DNA polymerase, which has a 5'-3' nuclease activity but lacks a 3'-5' proofreading endonuclease activity. Thus, TaqMan® PCR typically utilizes the 5'-nuclease activity of Taq or Tth polymerase to hydrolyze a hybridization probe bound to its target amplicon, but any enzyme with equivalent 5' nuclease activity can be used. Two oligonucleotide primers are used to generate an amplicon typical of a PCR reaction. A third oligonucleotide, or probe, is designed to detect nucleotide sequence located between the two PCR primers. The probe is non-extendible by Taq DNA polymerase enzyme, and is labeled with a reporter fluorescent dye and a quencher fluorescent dye. Any laser-induced emission from the reporter dye is quenched by the quenching dye when the two dyes are located close together as they are on the probe. During the amplification reaction, the Taq DNA polymerase enzyme cleaves the probe in a template-dependent manner. The resultant probe fragments disassociate in solution, and signal from the released reporter dye is free from the quenching effect of the second fluorophore. One molecule of reporter dye is liberated for each new molecule synthesized, and detection of the unquenched reporter dye provides the basis for quantitative interpretation of the data.

TaqMan® RT-PCR can be performed using commercially available equipment, such as, for example, ABI PRISM 7700™ Sequence Detection System™ (Perkin-Elmer-Applied Biosystems, Foster City, CA, USA), or Lightcycler (Roche Molecular Biochemicals, Mannheim, Germany). In a preferred embodiment, the 5' nuclease procedure is run on a real-time quantitative PCR device such as the ABI PRISM 7700™ Sequence Detection System™. The system consists of a thermocycler, laser, charge-coupled device (CCD), camera and computer. The system amplifies samples in a 96-well format on a thermocycler. During amplification, laser-induced fluorescent signal is collected in real-time through fiber optics cables for all 96 wells, and detected at the CCD. The system includes software for running the instrument and for analyzing the data.

5'-Nuclease assay data are initially expressed as Ct, or the threshold cycle. As discussed above, fluorescence values are recorded during every cycle and represent the amount of product amplified to that point in the amplification reaction. The point when the fluorescent signal is first recorded as statistically significant is the threshold cycle (C_t).

To minimize errors and the effect of sample-to-sample variation, RT-PCR is usually performed using an internal standard. The ideal internal standard is expressed at a constant level among different tissues, and is unaffected by the experimental treatment. RNAs most frequently used to normalize patterns of gene expression are mRNAs for the housekeeping genes glyceraldehyde-3-phosphate-dehydrogenase (GAPDH) and β-actin.

A more recent variation of the RT-PCR technique is the real time quantitative PCR, which measures PCR product accumulation through a dual-labeled fluorigenic probe (i.e., TaqMan® probe). Real time PCR is compatible both with quantitative competitive PCR, where internal competitor for each target sequence is used for normalization, and with quantitative comparative PCR using a normalization gene contained within the sample, or a housekeeping gene for RT-PCR. For further details see, e.g. Held *et al., Genome Research* 6:986-994 (1996).

The steps of a representative protocol for profiling gene expression using fixed, paraffin-embedded tissues as the RNA source, including mRNA isolation, purification, primer extension and amplification are given in various published journal articles {for example: T.E. Godfrey et al,. J. Molec. Diagnostics 2: 84-91 [2000]; K. Specht et al., Am. J. Pathol. 158: 419-29 [2001]}. Briefly, a representative process starts with cutting about 10 μm thick sections of paraffin-embedded tumor tissue samples. The RNA is then extracted, and protein and DNA are removed. After analysis of the RNA concentration, RNA repair and/or amplification steps may be included, if necessary, and RNA is reverse transcribed using gene specific promoters followed by RT-PCR.

According to one aspect of the present invention, PCR primers and probes are designed based upon intron sequences present in the gene to be amplified. In this embodiment, the first step in the primer/probe design is the delineation of intron sequences within the genes. This can be done by publicly available software, such as the DNA BLAT software developed by Kent, W.J., *Genome Res.* 12(4):656-64 (2002), or by the BLAST software including its variations. Subsequent steps follow well established methods of PCR primer and probe design.

In order to avoid non-specific signals, it is important to mask repetitive sequences within the introns when designing the primers and probes. This can be easily accomplished by using the Repeat Masker program available on-line through the Baylor College of Medicine, which screens DNA sequences against a library of repetitive elements and returns a

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query sequence in which the repetitive elements are masked. The masked intron sequences can then be used to design primer and probe sequences using any commercially or otherwise publicly available primer/probe design packages, such as Primer Express (Applied Biosystems); MGB assay-by–design (Applied Biosystems); Primer3 (Steve Rozen and Helen J. Skaletsky (2000) Primer3 on the WWW for general users and for biologist programmers. In: Krawetz S, Misener S (eds) *Bioinformatics Methods and Protocols: Methods in Molecular Biology*. Humana Press, Totowa, NJ, pp 365-386)

The most important factors considered in PCR primer design include primer length, melting temperature (Tm), and G/C content, specificity, complementary primer sequences, and 3'-end sequence. In general, optimal PCR primers are generally 17-30 bases in length, and contain about 20-80%, such as, for example, about 50-60% G+C bases. Tm's between 50 and 80 °C, e.g. about 50 to 70 °C are typically preferred.

For further guidelines for PCR primer and probe design see, e.g. Dieffenbach, C.W. *et al.*, "General Concepts for PCR Primer Design" in: *PCR Primer, A Laboratory Manual*, Cold Spring Harbor Laboratory Press, New York, 1995, pp. 133-155; Innis and Gelfand, "Optimization of PCRs" in: *PCR Protocols, A Guide to Methods and Applications*, CRC Press, London, 1994, pp. 5-11; and Plasterer, T.N. Primerselect: Primer and probe design. *Methods Mol. Biol.* 70:520-527 (1997).

3. *Microarrays*

Differential gene expression can also be identified, or confirmed using the microarray technique. Thus, the expression profile of breast cancer-associated genes can be measured in either fresh or paraffin-embedded tumor tissue, using microarray technology. In this method, polynucleotide sequences of interest (including cDNAs and oligonucleotides) are plated, or arrayed, on a microchip substrate. The arrayed sequences are then hybridized with specific DNA probes from cells or tissues of interest. Just as in the RT-PCR method, the source of mRNA typically is total RNA isolated from human tumors or tumor cell lines, and corresponding normal tissues or cell lines. Thus RNA can be isolated from a variety of primary tumors or tumor cell lines. If the source of mRNA is a primary tumor, mRNA can be extracted, for example, from frozen or archived paraffin-embedded and fixed (e.g. formalin-fixed) tissue samples, which are routinely prepared and preserved in everyday clinical practice.

In a specific embodiment of the microarray technique, PCR amplified inserts of cDNA clones are applied to a substrate in a dense array. Preferably at least 10,000 nucleotide sequences are applied to the substrate. The microarrayed genes, immobilized on the microchip at 10,000 elements each, are suitable for hybridization under stringent conditions. Fluorescently labeled cDNA probes may be generated through incorporation of fluorescent nucleotides by reverse transcription of RNA extracted from tissues of interest. Labeled cDNA probes applied to the chip hybridize with specificity to each spot of DNA on the array. After stringent washing to remove non-specifically bound probes, the chip is scanned by confocal laser microscopy or by another detection method, such as a CCD camera. Quantitation of hybridization of each arrayed element allows for assessment of corresponding mRNA abundance. With dual color fluorescence, separately labeled cDNA probes generated from two sources of RNA are hybridized pairwise to the array. The relative abundance of the transcripts from the two sources corresponding to each specified gene is thus determined simultaneously. The miniaturized scale of the hybridization affords a convenient and rapid evaluation of the expression pattern for large numbers of genes. Such methods have been shown to have the sensitivity required to detect rare transcripts, which are expressed at a few copies per cell, and to reproducibly detect at least approximately two-fold differences in the expression levels (Schena *et al., Proc. Natl. Acad. Sci. USA* 93(2):106-149 (1996)). Microarray analysis can be performed by commercially available equipment, following manufacturer's protocols, such as by using the Affymetrix GenChip technology, or Incyte's microarray technology.

The development of microarray methods for large-scale analysis of gene expression makes it possible to search systematically for molecular markers of cancer classification and outcome prediction in a variety of tumor types.

4. *Serial Analysis of Gene Expression (SAGE)*

Serial analysis of gene expression (SAGE) is a method that allows the simultaneous and quantitative analysis of a large number of gene transcripts, without the need of providing an individual hybridization probe for each transcript. First, a short sequence tag (about 10-14 bp) is generated that contains sufficient information to uniquely identify a transcript, provided that the tag is obtained from a unique position within each transcript. Then, many transcripts are linked together to form long serial molecules, that can be sequenced, revealing the identity of the multiple tags simultaneously. The expression pattern of any population of transcripts

can be quantitatively evaluated by determining the abundance of individual tags, and identifying the gene corresponding to each tag. For more details see, e.g. Velculescu *et al.*, *Science* 270:484-487 (1995); and Velculescu *et al.*, *Cell* 88:243-51 (1997).

5. *MassARRAY Technology*

The MassARRAY (Sequenom, San Diego, California) technology is an automated, high-throughput method of gene expression analysis using mass spectrometry (MS) for detection. According to this method, following the isolation of RNA, reverse transcription and PCR amplification, the cDNAs are subjected to primer extension. The cDNA-derived primer extension products are purified, and dipensed on a chip array that is pre-loaded with the components needed for MALTI-TOF MS sample preparation. The various cDNAs present in the reaction are quantitated by analyzing the peak areas in the mass spectrum obtained.

6. *Gene Expression Analysis by Massively Parallel Signature Sequencing (MPSS)*

This method, described by Brenner *et al.*, *Nature Biotechnology* 18:630-634 (2000), is a sequencing approach that combines non-gel-based signature sequencing with *in vitro* cloning of millions of templates on separate 5 μm diameter microbeads. First, a microbead library of DNA templates is constructed by *in vitro* cloning. This is followed by the assembly of a planar array of the template-containing microbeads in a flow cell at a high density (typically greater than 3 x 10^6 microbeads/cm^2). The free ends of the cloned templates on each microbead are analyzed simultaneously, using a fluorescence-based signature sequencing method that does not require DNA fragment separation. This method has been shown to simultaneously and accurately provide, in a single operation, hundreds of thousands of gene signature sequences from a yeast cDNA library.

7. *Immunohistochemistry*

Immunohistochemistry methods are also suitable for detecting the expression levels of the prognostic markers of the present invention. Thus, antibodies or antisera, preferably polyclonal antisera, and most preferably monoclonal antibodies specific for each marker are used to detect expression. The antibodies can be detected by direct labeling of the antibodies themselves, for example, with radioactive labels, fluorescent labels, hapten labels such as, biotin, or an enzyme such as horse radish peroxidase or alkaline phosphatase. Alternatively, unlabeled primary antibody is used in conjunction with a labeled secondary antibody, comprising antisera, polyclonal antisera or a monoclonal antibody specific for the primary

antibody. Immunohistochemistry protocols and kits are well known in the art and are commercially available.

8. *Proteomics*

The term "proteome" is defined as the totality of the proteins present in a sample (e.g. tissue, organism, or cell culture) at a certain point of time. Proteomics includes, among other things, study of the global changes of protein expression in a sample (also referred to as "expression proteomics"). Proteomics typically includes the following steps: (1) separation of individual proteins in a sample by 2-D gel electrophoresis (2-D PAGE); (2) identification of the individual proteins recovered from the gel, e.g. my mass spectrometry or N-terminal sequencing, and (3) analysis of the data using bioinformatics. Proteomics methods are valuable supplements to other methods of gene expression profiling, and can be used, alone or in combination with other methods, to detect the products of the prognostic markers of the present invention.

9. *General Description of the mRNA Isolation, Purification and Amplification*

The steps of a representative protocol for profiling gene expression using fixed, paraffin-embedded tissues as the RNA source, including mRNA isolation, purification, primer extension and amplification are given in various published journal articles {for example: T.E. Godfrey et al. J. Molec. Diagnostics 2: 84-91 [2000]; K. specht et al., Am. J. Pathol. 158: 419-29 [2001]}. Briefly, a representative process starts with cutting about 10 μm thick sections of paraffin-embedded tumor tissue samples. The RNA is then extracted, and protein and DNA are removed. After analysis of the RNA concentration, RNA repair and/or amplification steps may be included, if necessary, and RNA is reverse transcribed using gene specific promoters followed by RT-PCR. Finally, the data are analyzed to identify the best treatment option(s) available to the patient on the basis of the characteristic gene expression pattern identified in the tumor sample examined.

10. *Breast Cancer Gene Set, Assayed Gene Subsequences, and Clinical Application of Gene Expression Data*

An important aspect of the present invention is to use the measured expression of certain genes by breast cancer tissue to provide prognostic information. For this purpose it is necessary to correct for (normalize away) both differences in the amount of RNA assayed and variability in the quality of the RNA used. Therefore, the assay typically measures and incorporates the expression of certain normalizing genes, including well known housekeeping

genes, such as GAPDH and Cyp1. Alternatively, normalization can be based on the mean or median signal (Ct) of all of the assayed genes or a large subset thereof (global normalization approach). On a gene-by-gene basis, measured normalized amount of a patient tumor mRNA is compared to the amount found in a breast cancer tissue reference set. The number (N) of breast cancer tissues in this reference set should be sufficiently high to ensure that different reference sets (as a whole) behave essentially the same way. If this condition is met, the identity of the individual breast cancer tissues present in a particular set will have no significant impact on the relative amounts of the genes assayed. Usually, the breast cancer tissue reference set consists of at least about 30, preferably at least about 40 different FPE breast cancer tissue specimens. Unless noted otherwise, normalized expression levels for each mRNA/tested tumor/patient will be expressed as a percentage of the expression level measured in the reference set. More specifically, the reference set of a sufficiently high number (e.g. 40) of tumors yields a distribution of normalized levels of each mRNA species. The level measured in a particular tumor sample to be analyzed falls at some percentile within this range, which can be determined by methods well known in the art. Below, unless noted otherwise, reference to expression levels of a gene assume normalized expression relative to the reference set although this is not always explicitly stated.

Further details of the invention will be described in the following non-limiting Example

Example

A Phase II Study of Genc Expression in 79 Malignant Breast Tumors

A gene expression study was designed and conducted with the primary goal to molecularly characterize gene expression in paraffin-embedded, fixed tissue samples of invasive breast ductal carcinoma, and to explore the correlation between such molecular profiles and disease-free survival.

Study design

Molecular assays were performed on paraffin-embedded, formalin-fixed primary breast tumor tissues obtained from 79 individual patients diagnosed with invasive breast cancer. All patients in the study had 10 or more positive nodes. Mean age was 57 years, and mean clinical tumor size was 4.4 cm. Patients were included in the study only if

histopathologic assessment, performed as described in the Materials and Methods section, indicated adequate amounts of tumor tissue and homogeneous pathology.

Materials and Methods

Each representative tumor block was characterized by standard histopathology for diagnosis, semi-quantitative assessment of amount of tumor, and tumor grade. A total of 6 sections (10 microns in thickness each) were prepared and placed in two Costar Brand Microcentrifuge Tubes (Polypropylene, 1.7 mL tubes, clear; 3 sections in each tube). If the tumor constituted less than 30% of the total specimen area, the sample may have been crudely dissected by the pathologist, using gross microdissection, putting the tumor tissue directly into the Costar tube.

If more than one tumor block was obtained as part of the surgical procedure, the block most representative of the pathology was used for analysis.

Gene Expression Analysis

mRNA was extracted and purified from fixed, paraffin-embedded tissue samples, and prepared for gene expression analysis as described in section 9 above.

Molecular assays of quantitative gene expression were performed by RT-PCR, using the ABI PRISM 7900™ Sequence Detection System™ (Perkin-Elmer-Applied Biosystems, Foster City, CA, USA). ABI PRISM 7900™ consists of a thermocycler, laser, charge-coupled device (CCD), camera and computer. The system amplifies samples in a 384-well format on a thermocycler. During amplification, laser-induced fluorescent signal is collected in real-time through fiber optics cables for all 384 wells, and detected at the CCD. The system includes software for running the instrument and for analyzing the data.

Analysis and Results

Tumor tissue was analyzed for 185 cancer-related genes and 7 reference genes. The threshold cycle (CT) values for each patient were normalized based on the median of the 7 reference genes for that particular patient. Clinical outcome data were available for all patients from a review of registry data and selected patient charts.

Outcomes were classified as:

0 died due to breast cancer or to unknown cause or alive with breast cancer recurrence;

1 alive without breast cancer recurrence or died due to a cause other than breast cancer

Analysis was performed by:

1. Analysis of the relationship between normalized gene expression and the binary outcomes of 0 or 1.

2. Analysis of the relationship between normalized gene expression and the time to outcome (0 or 1 as defined above) where patients who were alive without breast cancer recurrence or who died due to a cause other than breast cancer were censored. This approach was used to evaluate the prognostic impact of individual genes and also sets of multiple genes.

Analysis of patients with invasive breast carcinoma by binary approach

In the first (binary) approach, analysis was performed on all 79 patients with invasive breast carcinoma. A t test was performed on the groups of patients classified as either no recurrence and no breast cancer related death at three years, versus recurrence, or breast cancer-related death at three years, and the p-values for the differences between the groups for each gene were calculated.

Table 1 lists the 47 genes for which the p-value for the differences between the groups was <0.10. The first column of mean expression values pertains to patients who neither had a metastatic recurrence of nor died from breast cancer. The second column of mean expression values pertains to patients who either had a metastatic recurrence of or died from breast cancer.

Table 1

	Mean	Mean	t-value	df	p	Valid N	Valid N
Bcl2	-0.15748	-1.22816	4.00034	75	0.000147	35	42
PR	-2.67225	-5.49747	3.61540	75	0.000541	35	42
IGF1R	-0.59390	-1.71506	3.49158	75	0.000808	35	42
BAG1	0.18844	-0.68509	3.42973	75	0.000985	35	42
CD68	-0.52275	0.10983	-3.41186	75	0.001043	35	42
EstR1	-0.35581	-3.00699	3.32190	75	0.001384	35	42
CTSL	-0.64894	-0.09204	-3.26781	75	0.001637	35	42
IGFBP2	-0.81181	-1.78398	3.24158	75	0.001774	35	42
GATA3	1.80525	0.57428	3.15608	75	0.002303	35	42
TP53BP2	-4.71118	-6.09289	3.02888	75	0.003365	35	42
EstR1	3.67801	1.64693	3.01073	75	0.003550	35	42
CEGP1	-2.02566	-4.25537	2.85620	75	0.005544	35	42
SURV	-3.67493	-2.96982	-2.70544	75	0.008439	35	42
p27	0.80789	0.28807	2.55401	75	0.012678	35	42
Chk1	-3.37981	-2.80389	-2.46979	75	0.015793	35	42
BBC3	-4.71789	-5.62957	2.46019	75	0.016189	35	42

ZNF217	1.10038	0.62730	2.42282	75	0.017814	35	42
EGFR	-2.88172	-2.20556	-2.34774	75	0.021527	35	42
CD9	1.29955	0.91025	2.31439	75	0.023386	35	42
MYBL2	-3.77489	-3.02193	-2.29042	75	0.024809	35	42
HIF1A	-0.44248	0.03740	-2.25950	75	0.026757	35	42
GRB7	-1.96063	-1.05007	-2.25801	75	0.026854	35	42
pS2	-1.00691	-3.13749	2.24070	75	0.028006	35	42
RIZ1	-7.62149	-8.38750	2.20226	75	0.030720	35	42
ErbB3	-6.89508	-7.44326	2.16127	75	0.033866	35	42
TOP2B	0.45122	0.12665	2.14616	75	0.035095	35	42
MDM2	1.09049	0.69001	2.10967	75	0.038223	35	42
PRAME	-6.40074	-7.70424	2.08126	75	0.040823	35	42
GUS	-1.51683	-1.89280	2.05200	75	0.043661	35	42
RAD51C	-5.85618	-6.71334	2.04575	75	0.044288	35	42
AIB1	-3.08217	-2.28784	-2.00600	75	0.048462	35	42
STK15	-3.11307	-2.59454	-2.00321	75	0.048768	35	42
GAPDH	-0.35829	-0.02292	-1.94326	75	0.055737	35	42
FHIT	-3.00431	-3.67175	1.86927	75	0.065489	35	42
KRT19	2.52397	2.01694	1.85741	75	0.067179	35	42
TS	-2.83607	-2.29048	-1.83712	75	0.070153	35	42
GSTM1	-3.69140	-4.38623	1.83397	75	0.070625	35	42
G-Catenin	0.31875	-0.15524	1.80823	75	0.074580	35	42
AKT2	0.78858	0.46703	1.79276	75	0.077043	35	42
CCNB1	-4.26197	-3.51628	-1.78803	75	0.077810	35	42
PI3KC2A	-2.27401	-2.70265	1.76748	75	0.081215	35	42
FBXO5	-4.72107	-4.24411	-1.75935	75	0.082596	35	42
DR5	-5.80850	-6.55501	1.74345	75	0.085353	35	42
CIAP1	-2.81825	-3.09921	1.72480	75	0.088683	35	42
MCM2	-2.87541	-2.50683	-1.72061	75	0.089445	35	42
CCND1	1.30995	0.80905	1.68794	75	0.095578	35	42
EIF4E	-5.37657	-6.47156	1.68169	75	0.096788	35	42

In the foregoing Table 1, negative t-values indicate higher expression, associated with worse outcomes, and, inversely, higher (positive) t-values indicate higher expression associated with better outcomes. Thus, for example, elevated expression of the CD68 gene (t-value = -3.41, CT mean alive< CT mean deceased) indicates a reduced likelihood of disease free survival. Similarly, elevated expression of the BCl2 gene (t-value = 4.00; CT mean alive> CT mean deceased) indicates an increased likelihood of disease free survival.

Based on the data set forth in Table 1, the expression of any of the following genes in breast cancer above a defined expression threshold indicates a reduced likelihood of survival without cancer recurrence following surgery: Grb7, CD68, CTSL, Chk1, Her2, STK15, AIB1, SURV, EGFR, MYBL2, HIF1α.

Based on the data set forth in Table 1, the expression of any of the following genes in breast cancer above a defined expression threshold indicates a better prognosis for survival

without cancer recurrence following surgery: TP53BP2, PR, Bcl2, KRT14, EstR1, IGFBP2, BAG1, CEGP1, KLK10, β Catenin, GSTM1, FHIT, Riz1, IGF1, BBC3, IGFR1, TBP, p27, IRS1, IGF1R, GATA3, CEGP1, ZNF217, CD9, pS2, ErbB3, TOP2B, MDM2, RAD51, and KRT19.

Analysis of ER positive patients by binary approach

57 patients with normalized CT for estrogen receptor (ER) >0 (i.e., ER positive patients) were subjected to separate analysis. A t test was performed on the two groups of patients classified as either no recurrence and no breast cancer related death at three years, or recurrence or breast cancer-related death at three years, and the p-values for the differences between the groups for each gene were calculated. Table 2, below, lists the genes where the p-value for the differences between the groups was <0.105. The first column of mean expression values pertains to patients who neither had a metastatic recurrence nor died from breast cancer. The second column of mean expression values pertains to patients who either had a metastatic recurrence of or died from breast cancer.

Table 2

	Mean	Mean	t-value	df	p	Valid N	Valid N
IGF1R	-0.13975	-1.00435	3.65063	55	0.000584	30	27
Bcl2	0.15345	-0.70480	3.55488	55	0.000786	30	27
CD68	-0.54779	0.19427	-3.41818	55	0.001193	30	27
HNF3A	0.39617	-0.63802	3.20750	55	0.002233	30	27
CTSL	-0.66726	0.00354	-3.20692	55	0.002237	30	27
TP53BP2	-4.81858	-6.44425	3.13698	55	0.002741	30	27
GATA3	2.33386	1.40803	3.02958	55	0.003727	30	27
BBC3	-4.54979	-5.72333	2.91943	55	0.005074	30	27
RAD51C	-5.63363	-6.94841	2.85475	55	0.006063	30	27
BAG1	0.31087	-0.50669	2.61524	55	0.011485	30	27
IGFBP2	-0.49300	-1.30983	2.59121	55	0.012222	30	27
FBXO5	-4.86333	-4.05564	-2.56325	55	0.013135	30	27
EstR1	0.68368	-0.66555	2.56090	55	0.013214	30	27
PR	-1.89094	-3.86602	2.52803	55	0.014372	30	27
SURV	-3.87857	-3.10970	-2.49622	55	0.015579	30	27
CD9	1.41691	0.91725	2.43043	55	0.018370	30	27
RB1	-2.51662	-2.97419	2.41221	55	0.019219	30	27
EPHX1	-3.91703	-5.85097	2.29491	55	0.025578	30	27
CEGP1	-1.18600	-2.95139	2.26608	55	0.027403	30	27
CCNB1	-4.44522	-3.35763	-2.25148	55	0.028370	30	27
TRAIL	0.34893	-0.56574	2.20372	55	0.031749	30	27
EstR1	4.60346	3.60340	2.20223	55	0.031860	30	27
DR5	-5.71827	-6.79088	2.14548	55	0.036345	30	27
MCM2	-2.96800	-2.48458	-2.10518	55	0.039857	30	27
Chk1	-3.46968	-2.85708	-2.08597	55	0.041633	30	27
p27	0.94714	0.49656	2.04313	55	0.045843	30	27
MYBL2	-3.97810	-3.14837	-2.02921	55	0.047288	30	27
GUS	-1.42486	-1.82900	1.99758	55	0.050718	30	27

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P53	-1.08810	-1.47193	1.92087	55	0.059938	30	27
HIF1A	-0.40925	0.11688	-1.91278	55	0.060989	30	27
cMet	-6.36835	-5.58479	-1.88318	55	0.064969	30	27
EGFR	-2.95785	-2.28105	-1.86840	55	0.067036	30	27
MTA1	-7.55365	-8.13656	1.81479	55	0.075011	30	27
RIZ1	-7.52785	-8.25903	1.79518	55	0.078119	30	27
ErbB3	-6.62488	-7.10826	1.79255	55	0.078545	30	27
TOP2B	0.54974	0.27531	1.74888	55	0.085891	30	27
EIF4E	-5.06603	-6.31426	1.68030	55	0.098571	30	27
TS	-2.95042	-2.36167	-1.67324	55	0.099959	30	27
STK15	-3.25010	-2.72118	-1.64822	55	0.105010	30	27

For each gene, a classification algorithm was utilized to identify the best threshold value (CT) for using each gene alone in predicting clinical outcome.

Based on the data set forth in Table 2, expression of the following genes in ER-positive cancer above a defined expression level is indicative of a reduced likelihood of survival without cancer recurrence following surgery: CD68; CTSL; FBXO5; SURV; CCNB1; MCM2; Chk1; MYBL2; HIF1A; cMET; EGFR; TS; STK15. Many of these genes (CD68, CTSL, SURV, CCNB1, MCM2, Chk1, MYBL2, EGFR, and STK15) were also identified as indicators of poor prognosis in the previous analysis, not limited to ER-positive breast cancer. Based on the data set forth in Table 2, expression of the following genes in ER-positive cancer above a defined expression level is indicative of a better prognosis for survival without cancer recurrence following surgery: IGFR1; BCl2; HNF3A; TP53BP2; GATA3; BBC3; RAD51C; BAG1; IGFBP2; PR; CD9; RB1; EPHX1; CEGP1; TRAIL; DR5; p27; p53; MTA; RIZ1; ErbB3; TOP2B; EIF4E. Of the latter genes, IGFR1; BCl2; TP53BP2; GATA3; BBC3; RAD51C; BAG1; IGFBP2; PR; CD9; CEGP1; DR5; p27; RIZ1; ErbB3; TOP2B; EIF4E have also been identified as indicators of good prognosis in the previous analysis, not limited to ER-positive breast cancer.

Analysis of ER negative patients by binary approach

Twenty patients with normalized CT for estrogen receptor (ER) <1.6 (i.e., ER negative patients) were subjected to separate analysis. A t test was performed on the two groups of patients classified as either no recurrence and no breast cancer related death at three years, or recurrence or breast cancer-related death at three years, and the p-values for the differences between the groups for each gene were calculated. Table 3 lists the genes where the p-value for the differences between the groups was <0.118. The first column of mean expression values pertains to patients who neither had a metastatic recurrence nor died from breast

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cancer. The second column of mean expression values pertains to patients who either had a metastatic recurrence of or died from breast cancer.

Table 3

	Mean	Mean	t-value	df	p	Valid N	Valid N
KRT14	-1.95323	-6.69231	4.03303	18	0.000780	5	15
KLK10	-2.68043	-7.11288	3.10321	18	0.006136	5	15
CCND1	-1.02285	0.03732	-2.77992	18	0.012357	5	15
Upa	-0.91272	-0.04773	-2.49460	18	0.022560	5	15
HNF3A	-6.04780	-2.36469	-2.43148	18	0.025707	5	15
Maspin	-3.56145	-6.18678	2.40169	18	0.027332	5	15
CDH1	-3.54450	-2.34984	-2.38755	18	0.028136	5	15
HER2	-1.48973	1.53108	-2.35826	18	0.029873	5	15
GRB7	-2.55289	0.00036	-2.32890	18	0.031714	5	15
AKT1	-0.36849	0.46222	-2.29737	18	0.033807	5	15
TGFA	-4.03137	-5.67225	2.28546	18	0.034632	5	15
FRP1	1.45776	-1.39459	2.27884	18	0.035097	5	15
STMY3	-1.59610	-0.26305	-2.23191	18	0.038570	5	15
Contig 27882	-4.27585	-7.34338	2.18700	18	0.042187	5	15
A-Catenin	-1.19790	-0.39085	-2.15624	18	0.044840	5	15
VDR	-4.37823	-2.37167	-2.15620	18	0.044844	5	15
GRO1	-3.65034	-5.97002	2.12286	18	0.047893	5	15
MCM3	-3.86041	-5.55078	2.10030	18	0.050061	5	15
B-actin	4.69672	5.19190	-2.04951	18	0.055273	5	15
HIF1A	-0.64183	-0.10566	-2.02301	18	0.058183	5	15
MMP9	-8.90613	-7.35163	-1.88747	18	0.075329	5	15
VEGF	0.37904	1.10778	-1.87451	18	0.077183	5	15
PRAME	-4.95855	-7.41973	1.86668	18	0.078322	5	15
AIB1	-3.12245	-1.92934	-1.86324	18	0.078829	5	15
KRT5	-1.32418	-3.62027	1.85919	18	0.079428	5	15
KRT18	1.08383	2.25369	-1.83831	18	0.082577	5	15
KRT17	-0.69073	-3.56536	1.78449	18	0.091209	5	15
P14ARF	-1.87104	-3.36534	1.63923	18	0.118525	5	15

Based on the data set forth in Table 3, expression of the following genes in ER-negative cancer above a defined expression level is indicative of a reduced likelihood of survival without cancer recurrence ($p<0.05$): CCND1; UPA; HNF3A; CDH1; Her2; GRB7; AKT1; STMY3; α-Catenin; VDR; GRO1. Only 2 of these genes (Her2 and Grb7) were also identified as indicators of poor prognosis in the previous analysis, not limited to ER-negative breast cancer. Based on the data set forth in Table 3, expression of the following genes in ER-negative cancer above a defined expression level is indicative of a better prognosis for survival without cancer recurrence (KT14; KLK10; Maspin, TGFα, and FRP1. Of the latter genes, only KLK10 has been identified as an indicator of good prognosis in the previous analysis, not limited to ER-negative breast cancer.

Analysis of multiple genes and indicators of outcome

Two approaches were taken in order to determine whether using multiple genes would provide better discrimination between outcomes.

First, a discrimination analysis was performed using a forward stepwise approach. Models were generated that classified outcome with greater discrimination than was obtained with any single gene alone.

According to a second approach (time-to-event approach), for each gene a Cox Proportional Hazards model (see, e.g. Cox, D. R., and Oakes, D. (1984), *Analysis of Survival Data*, Chapman and Hall, London, New York) was defined with time to recurrence or death as the dependent variable, and the expression level of the gene as the independent variable. The genes that have a p-value < 0.10 in the Cox model were identified. For each gene, the Cox model provides the relative risk (RR) of recurrence or death for a unit change in the expression of the gene. One can choose to partition the patients into subgroups at any threshold value of the measured expression (on the CT scale), where all patients with expression values above the threshold have higher risk, and all patients with expression values below the threshold have lower risk, or vice versa, depending on whether the gene is an indicator of bad (RR>1.01) or good (RR<1.01) prognosis. Thus, any threshold value will define subgroups of patients with respectively increased or decreased risk. The results are summarized in Table 4. The third column, with the heading: exp(coef), shows RR values.

Table 4

Gene	coef	exp(coef)	se(coef)	z	p
TP53BP2	-0.21892	0.803386	0.068279	-3.20625	0.00134
GRB7	0.235697	1.265791	0.073541	3.204992	0.00135
PR	-0.10258	0.90251	0.035864	-2.86018	0.00423
CD68	0.465623	1.593006	0.167785	2.775115	0.00552
Bcl2	-0.26769	0.765146	0.100785	-2.65603	0.00791
KRT14	-0.11892	0.887877	0.046938	-2.53359	0.0113
PRAME	-0.13707	0.871912	0.054904	-2.49649	0.0125
CTSL	0.431499	1.539564	0.185237	2.329444	0.0198
EstR1	-0.07686	0.926018	0.034848	-2.20561	0.0274
Chk1	0.284466	1.329053	0.130823	2.174441	0.0297
IGFBP2	-0.2152	0.806376	0.099324	-2.16669	0.0303
HER2	0.155303	1.168011	0.072633	2.13818	0.0325
BAG1	-0.22695	0.796959	0.106377	-2.13346	0.0329
CEGP1	-0.07879	0.924236	0.036959	-2.13177	0.033
STK15	0.27947	1.322428	0.132762	2.105039	0.0353
KLK10	-0.11028	0.895588	0.05245	-2.10248	0.0355
B.Catenin	-0.16536	0.847586	0.084796	-1.95013	0.0512
EstR1	-0.0803	0.922842	0.042212	-1.90226	0.0571
GSTM1	-0.13209	0.876266	0.072211	-1.82915	0.0674
TOP2A	-0.11148	0.894512	0.061855	-1.80222	0.0715
AIB1	0.152968	1.165288	0.086332	1.771861	0.0764
FHIT	-0.15572	0.855802	0.088205	-1.7654	0.0775
RIZ1	-0.17467	0.839736	0.099464	-1.75609	0.0791
SURV	0.185784	1.204162	0.106625	1.742399	0.0814
IGF1	-0.10499	0.900338	0.060482	-1.73581	0.0826
BBC3	-0.1344	0.874243	0.077613	-1.73163	0.0833
IGF1R	-0.13484	0.873858	0.077889	-1.73115	0.0834
DIABLO	0.284336	1.32888	0.166556	1.707148	0.0878
TBP	-0.34404	0.7089	0.20564	-1.67303	0.0943
p27	-0.26002	0.771033	0.1564	-1.66256	0.0964
IRS1	-0.07585	0.926957	0.046096	-1.64542	0.0999

The binary and time-to-event analyses, with few exceptions, identified the same genes as prognostic markers. For example, comparison of Tables 1 and 4 shows that 10 genes were represented in the top 15 genes in both lists. Furthermore, when both analyses identified the same gene at [$p<0.10$], which happened for 21 genes, they were always concordant with respect to the direction (positive or negative sign) of the correlation with survival/recurrence. Overall, these results strengthen the conclusion that the identified markers have significant prognostic value.

For Cox models comprising more than two genes (multivariate models), stepwise entry of each individual gene into the model is performed, where the first gene entered is pre-selected from among those genes having significant univariate p-values, and the gene selected

for entry into the model at each subsequent step is the gene that best improves the fit of the model to the data. This analysis can be performed with any total number of genes. In the analysis the results of which are shown below, stepwise entry was performed for up to 10 genes.

Multivariate analysis is performed using the following equation:

RR=exp[coef(geneA) x Ct(geneA) + coef(geneB) x Ct(geneB) + coef(geneC) x Ct(geneC) + ...].

In this equation, coefficients for genes that are predictors of beneficial outcome are positive numbers and coefficients for genes that are predictors of unfavorable outcome are negative numbers. The "Ct" values in the equation are ΔCts, i.e. reflect the difference between the average normalized Ct value for a population and the normalized Ct measured for the patient in question. The convention used in the present analysis has been that ΔCts below and above the population average have positive signs and negative signs, respectively (reflecting greater or lesser mRNA abundance). The relative risk (RR) calculated by solving this equation will indicate if the patient has an enhanced or reduced chance of long-term survival without cancer recurrence.

Multivariate gene analysis of 79 patients with invasive breast carcinoma

A multivariate stepwise analysis, using the Cox Proportional Hazards Model, was performed on the gene expression data obtained for all 79 patients with invasive breast carcinoma. The following ten-gene sets have been identified by this analysis as having particularly strong predictive value of patient survival :

(a) TP53BP2, Bcl2, BAD, EPHX1, PDGFRβ, DIABLO, XIAP, YB1, CA9, and KRT8.

(b) GRB7, CD68, TOP2A, Bcl2, DIABLO, CD3, ID1, PPM1D, MCM6, and WISP1.

(c) PR, TP53BP2, PRAME, DIABLO, CTSL, IGFBP2, TIMP1, CA9, MMP9, and COX2.

(d) CD68, GRB7, TOP2A, Bcl2, DIABLO, CD3, ID1, PPM1D, MCM6, and WISP1.

(e) Bcl2, TP53BP2, BAD, EPHX1, PDGFRβ, DIABLO, XIAP, YB1, CA9, and KRT8.

(f) KRT14, KRT5, PRAME, TP53BP2, GUS1, AIB1, MCM3, CCNE1, MCM6, and ID1.

(g) PRAME, TP53BP2, EstR1, DIABLO, CTSL, PPM1D, GRB7, DAPK1, BBC3, and VEGFB.

(h) CTSL2, GRB7, TOP2A, CCNB1, Bcl2, DIABLO, PRAME, EMS1, CA9, and EpCAM.

(i) EstR1, TP53BP2, PRAME, DIABLO, CTSL, PPM1D, GRB7, DAPK1, BBC3, and VEGFB.

(k) Chk1, PRAME, p53BP2, GRB7, CA9, CTSL, CCNB1, TOP2A, tumor size, and IGFBP2.

(l) IGFBP2, GRB7, PRAME, DIABLO, CTSL, β-Catenin, PPM1D, Chk1, WISP1, and LOT1.

(m) HER2, TP53BP2, Bcl2, DIABLO, TIMP1, EPHX1, TOP2A, TRAIL, CA9, and AREG.

(n) BAG1, TP53BP2, PRAME, IL6, CCNB1, PAI1, AREG, tumor size, CA9, and Ki67.

(o) CEGP1, TP53BP2, PRAME, DIABLO, Bcl2, COX2, CCNE1, STK15, and AKT2, and FGF18.

(p) STK15, TP53BP2, PRAME, IL6, CCNE1, AKT2, DIABLO, cMet, CCNE2, and COX2.

(q) KLK10, EstR1, TP53BP2, PRAME, DIABLO, CTSL, PPM1D, GRB7, DAPK1, and BBC3.

(r) AIB1, TP53BP2, Bcl2, DIABLO, TIMP1, CD3, p53, CA9, GRB7, and EPHX1

(s) BBC3, GRB7, CD68, PRAME, TOP2A, CCNB1, EPHX1, CTSL GSTM1, and APC.

(t) CD9, GRB7, CD68, TOP2A, Bcl2, CCNB1, CD3, DIABLO, ID1, and PPM1D.

(w) EGFR, KRT14, GRB7, TOP2A, CCNB1, CTSL, Bcl2, TP, KLK10, and CA9.

(x) HIF1α, PR, DIABLO, PRAME, Chk1, AKT2, GRB7, CCNE1, TOP2A, and CCNB1.

(y) MDM2, TP53BP2, DIABLO, Bcl2, AIB1, TIMP1, CD3, p53, CA9, and HER2.

(z) MYBL2, TP53BP2, PRAME, IL6, Bcl2, DIABLO, CCNE1, EPHX1, TIMP1, and CA9.

(aa) p27, TP53BP2, PRAME, DIABLO, Bcl2, COX2, CCNE1, STK15, AKT2, and ID1.

(ab) RAD51, GRB7, CD68, TOP2A, CIAP2, CCNB1, BAG1, IL6, FGFR1, and TP53BP2.

(ac) SURV, GRB7, TOP2A, PRAME, CTSL, GSTM1, CCNB1, VDR, CA9, and CCNE2.

(ad) TOP2B, TP53BP2, DIABLO, Bcl2, TIMP1, AIB1, CA9, p53, KRT8, and BAD.

(ae) ZNF217, GRB7, p53BP2, PRAME, DIABLO, Bcl2, COX2, CCNE1, APC4, and β-Catenin.

While the present invention has been described with reference to what are considered to be the specific embodiments, it is to be understood that the invention is not limited to such embodiments. To the contrary, the invention is intended to cover various modifications and equivalents included within the scope of the appended claims. For example, while the disclosure focuses on the identification of various breast cancer associated genes and gene sets, and on the personalized prognosis of breast cancer, similar genes, gene sets and methods concerning other types of cancer are specifically within the scope herein.

Table 5A

Gene	Accession	Seq
AIB1	NM_006534	GCGGCGAGTTTCCGATTTAAAGCTGAGCTGCGAGGAAAATGGCGGCGGGAGGATCAAAATACTTGCTGGATGGTGGACTCA
AKT1	NM_005163	CGCTTCTATGGCGCTGAGATTGTGTCAGCCCTGGACTACCTGCACTCGGAGAAGAACGTGGTGTACCGGGA
AKT2	NM_001626	TCCTGCCACCCTTCAAACCTCAGGTCACGTCCGAGGTCGACACAAGGTACTTCGATGATGAATTTACCGCC
APC	NM_000038	GGACAGCAGGAATGTGTTTCTCCATACAGGTCACGGGGAGCCAATGGTTCAGAAACAAATCGAGTGGGT
AREG	NM_001657	TGTGAGTGAAATGCCTTCTAGTAGTGAACCGTCCTCGGGAGCCGACTATGACTACTCAGAAGAGTATGATAACGAACCACAA
B-actin	NM_001101	CAGCAGATGTGGATCAGCAAGCAGGAGTATGACGAGTCCGGCCCCTCCATCGTCCACCGCAAATGC
B-Catenin	NM_001904	GGCTCTTGTGCGTACTGTCCTTCGGGCTGGTGACAGGGAAGACATCACTGAGCCTGCCATCTGTGCTCTTCGTCATCTGA
BAD	NM_032989	GGGTCAGGTGCCTCGAGATCGGGCTTGGGCCCAGAGCATGTTCCAGATCCCAGAGTTTGAGCCGAGTGAGCAG
BAG1	NM_004323	CGTTGTCAGCACTTGGAATACAAGATGGTTGCCGGGTCATGTTAATTGGGAAAAAGAACAGTCCACAGGAAGAGGTTGAAC
BBC3	NM_014417	CCTGGAGGGTCCTGTACAATCTCATCATGGGACTCCTGCCCTTACCCAGGGGCCACAGAGCCCCCGAGATGGAGCCCAATTAG
Bcl2	NM_000633	CAGATGGACCTAGTACCCACTGAGATTTCCACGCCGAAGGACAGCGATGGGAAAAATGCCCTTAAATCATAGG
CA9	NM_001216	ATCCTAGCCCTGGTTTTTGGCCTCCTTTTTGCTGTCACCAGCGTCGCGTTCCTTGTGCAGATGAGAAGGCAG
CCNB1	NM_031966	TTCAGGTTGTTGCAGGAGACCATGTACATGACTGTCTCCATTATTGATCGGTTCATGCAGAATAATTGTGTGCCCAAGAAGATG
CCND1	NM_001758	GCATGTTCGTGGCCTCTAAGATGAAGGAGACCATCCCCCTGACGGCCGAGAAGCTGTGCATCTACACCG
CCNE1	NM_001238	AAAGAAGATGATGACCGGGTTTACCCAAACTCAACGTGCAAGCCTCGGATTATTGCACCATCCAGAGGCTC
CCNE2	NM_057749	ATGCTGTGGCTCCTTCCTAACTGGGGCTTTCTTGACATGTAGGTTGCTTGGTAATAACCTTTTTGTATATCACAATTTGGGT
CD3z	NM_000734	AGATGAAGTGGAAGGCGCTTTTCACCGCGGCCATCCTGCAGGCACAGTTGCCGATTACAGAGGCA
CD68	NM_001251	TGGTTCCCAGCCCTGTGTCCACCTCCAAGCCCAGATTCAGATTCGAGTCATGTACACAACCCAGGGTGGAGGAG
CD9	NM_001769	GGGCGTGGAACAGTTTATCTCAGACATCTGCCCCAAGAAGGACGTACTCGAAACCTTCACCGTG
CDH1	NM_004360	TGAGTGTCCCCCGGTATCTTCCCCGCCCTGCCAATCCCGATGAAATTGGAAATTTTATTGATGAAAATCTGAAAGCGGCTG
CEGP1	NM_020974	TGACAATCAGCACACCTGCATTCACCGCTCGGAAGAGGGCCTGAGCTGCATGAATAAGGATCACGGCTGTAGTCACA
Chk1	NM_001274	GATAAATTGGTACAAGGGATCAGCTTTTCCCAGCCCACATGTCCTGATCATATGCTTTTGAATAGTCAGTTACTTGGCACCC
cIAP1	NM_001166	TGCCTGTGGTGGGAAGCTCAGTAACTGGGAACCAAAGGATGATGCTATGTCAGAACACCGGAGGCATTTTCC
cIAP2	NM_001165	GGATATTTCCGTGGCTCTTATTCAAACTCTCCATCAAATCCTGTAAACTCCAGAGCAAATCAAGATTTTTCTGCCTTGATGAGAAG
cMet	NM_000245	GACATTTCCAGTCCTGCAGTCAATGCCTCTCTGCCCCACCCTTTGTTCAGTGTGGCTGGTGCCACGACAAATGTGTGCGATCGGAG
Contig 278	AK000818	GGCATCCTGGCCCAAAGTTTCCCAAATCCAGGCGGCTAGAGGCCCACTGCTTCCCAACTACCAGCTGAGGGGGTC
COX2	NM_000963	TCTGCAGAGTTGGAAGCACTCTATGGTGACATCGATGCTGTGGAGCTGTATCCTGCCGTTCTGGTAGAAAAGCCTCGGC
CTSL	NM_001912	GGGAGGCTTATCTCACTGAGTGAGCAGAATCTGGTAGACTGCTCTGGGCCTCAAGGCAATGAAGGCTGCAATGG
GTSL2	NM_001333	TGTCTCACTGAGCGAGCAGAATCTGGTGGACTGTTCGCGTCCTCAAGGCAATCAGGGCTGCAATGGT
DAPK1	NM_004938	CGCTGACATCATGAATGTTCCTCGACCGGCTGGAGGCGAGTTTGGATATGACAAAGACACATCGTTGCTGAAAGAGA
DIABLO	NM_019887	CACAATGGCGGCTCTGAAGAGTTGGCTGTCGCGCAGCGTAACTTCATTCTTCAGGTACAGACAGTGTTTGTGT
DR5	NM_003842	CTCTGAGACAGTGCTTCGATGACTTTGCAGACTTGGTGCCCTTTGACTCCTGGGAGCCGCTCATGAGGAAGTTGGGCCTCATGG
EGFR	NM_005228	TGTCGATGGACTTCCAGAACCACCTGGGCAGCTGCCAAAAGTGTGATCCAAGCTGTCCCAAT
EIF4E	NM_001968	GATCTAAGATGGCGACTGTCGAACCGGAAACCACCCCTACTCCTAATCCCCCGACTACAGAAGAGGAGAAAACGGAATCTAA
EMS1	NM_005231	GGCAGTGTCACTGAGTCCTTGAAATCCTCCCCTGCCCCGCGGGTCTCTGGATTGGGACGCACAGTGCA
EpCAM	NM_002354	GGGCCCTCCAGAACAATGATGGGCTTTATGATCCTGACTGCGATGAGAGCGGGCTCTTTAAGGCCAAGCAGTGCA
EPHX1	NM_000120	ACCGTAGGCTCTGCTCTGAATGACTCTCCTGTGGGTCTGGCTGCCTATATTCTAGAGAAGTTTTCCACCTGGACCA
ErbB3	NM_001982	CGGTTATGTCATGCCAGATACACACCTCAAAGGTACTCCCTCCTCCCGGGAAGGCACCCTTTCTTCAGTGGGTCTCAGTTC
EstR1	NM_000125	CGTGGTGCCCCCTCTATGACCTGCTGCTGGAGATGCTGGACGCCCACCGCCTACATGCGCCCACTAGCC
FBXO5	NM_012177	GGCTATTCCTCATTTTCTCTACAAAGTGGCCTCAGTGAACATGAAGAAGGTAGCCTCCTGGAGGAGAATTTCGGTGACAGTCTACAATCC
FGF18	NM_003862	CGGTAGTCAAGTCCGGATCAAGGGCAAGGAGACGGAATTCTACCTGTGCATGAACCGCAAAGGCAAGC
FGFR1	NM_023109	CACGGGACATTCACCACATCGACTACTATAAAAAGACAACCAACGGCCGACTGCCTGTGAAGTGGATGGCACCC
FHIT	NM_002012	CCAGTGGAGCGCTTCCATGACCTGCGTCCTGATGAAGTGGCCGATTTGTTTCAGACGACCCAGAGAG
FRP1	NM_003012	TTGGTACCTGTGGGTTAGCATCAAGTTCTCCCCAGGGTAGAATTCAATCAGAGCTCCAGTTTGCATTTGGATGTG
G-Caterin	NM_002230	TCAGCAGCAAGGGCATCATGGAGGAGGATGAGGCCTGCGGGCGCCAGTACACGCTCAAGAAAACCACC
GAPDH	NM_002046	ATTCCACCCATGGCAAATTCCATGGCACCGTCAAGGCTGAGAACGGGAAGCTTGTCATCAATGGAAATCCCATC
GATA3	NM_002051	CAAAGGAGCTCACTGTGGTGTCTGTGTTCCAACCACTGAATCTGGACCCCATCTGTGAATAAGCCATTCTGACTC
GRB7	NM_005310	CCATCTGCATCCATCTTGTTTGGGCTCCCCACCCTTGAGAAGTGCCTCAGATAATACCCTGGTGGCC
GRO1	NM_001511	CGAAAAGATGCTGAACAGTGACAAATCCAACTGACCAGAAGGGAGGAGGAAGCTCACTGGTGGCTGTTCCTGA
GSTM1	NM_000561	AAGCTATGAGGAAAAGAAGTACACGATGGGGGACGCTCCTGATTATGACAGAAGCCAGTGGCTGAATGAAAAATTCAAGCTGGGCC
GUS	NM_000181	CCCACTCAGTAGCCAAGTCACAATGTTTGGAAAACAGCCCGTTTACTTGAGCAAGACTGATACCACCTGCGTG
HER2	NM_004448	CGGTGTGAGAAGTGCAGCAAGCCCTGTGCCCGAGTGTGCTATGGTCTGGGCATGGAGCACTTGCGAGAGG
HIF1A	NM_001530	TGAACATAAAGTCTGCAACATGGAAGGTATTGCACTGCACAGGCCACATTCACGTATATGATACCAACAGTAACCAACCTCA
HNF3A	NM_004496	TCCAGGATGTTAGGAACTGTGAAGATGGAAGGGCATGAAACCAGCGACTGGAACAGCTACTACGCAGACACGC
ID1	NM_002165	AGAACCGCAAGGTGAGCAAGGTGGAGATTCTCCAGCACGTCATCGACTACATCAGGGACCTTCAGTTGGA
IGF1	NM_000618	TCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTATTGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCG
IGF1R	NM_000875	GCATGGTAGCCGAAGATTTCACAGTCAAAATCGGAGATTTTGGTATGACGCGAGATATCTATGAGACAGACTATTACCGGAAA
IGFBP2	NM_000597	GTGGACAGCACCATGAACATGTTGGGCGGGGGAGGCAGTGCTGGCCGGAAGCCCCTCAAGTCGGGTATGAAGG
IL8	NM_000600	CCTGAACCTTCCAAAGATGGCTGAAAAAGATGGATGCTTCCAATCTGGATTCAATGAGGAGACTTGCCTGGT
IRS1	NM_005544	CCACAGCTCACCTTCTGTCAGGTGTCCATCCCAGCTCCAGCCAGCTCCCAGAGAGGAAGAGACTGGCACTGAGG
KI-67	NM_002417	CGGACTTTGGGTGCGACTTGACGAGCGGTGGTTCGACAAGTGGCCTTGCGGGCCGGATCGTCCCAGTGGAAGAGTTGTAA
KLK10	NM_002776	GCCCAGAGGCTCCATCGTCCATCCTCTTCCTCCCCAGTCGGCTGAACTCTCCCCTTGTCTGCACTGTTCAAACCTCTG
KRT14	NM_000526	GGCCTGCTGAGATCAAAGACTACAGTCCCTACTTCAAGACCATTGAGGACCTGAGGAACAAGATTCTCACAGCCACAGTGGAC
KRT17	NM_000422	CGAGGATTGGTTCTTCAGCAAGACAGAGGAACTGAACCGCGAGGTGGCCACCAACAGTGAGCTGGTGCAGAGT
KRT18	NM_000224	AGAGATCGAGGCTCTCAAGGAGGAGCTGCTCTTCATGAAGAAGAACCACGAAGAGGAAGTAAAAGGCC
KRT19	NM_002276	TGAGCGGCAGAATCAGGAGTACCAGCGGCTCATGGACATCAAGTCGCGGCTGGAGCAGGAGATTGCCACCTACCGCA
KRT5	NM_000424	TCAGTGGAGAAGGAGTTGGACCAGTCAACATCTCTGTTGTCACAAGCAGTGTTTCCTCTGGATATGGCA
KRT8	NM_002273	GGATGAAGCTTACATGAACAAGGTAGAGCTGGAGTCTCGCCTGGAAGGGCTGACCGACGAGATCAACTTCCTCAGGCAGCTATATG
LOT1 varia	NM_002656	GGAAAGACCACCTGAAAAACCACCTCCAGACCCACGACCCCAACAAAATGGCCTTTGGGTGTGAGGAGTGTGGGAAGAAGTAC
Maspin	NM_002639	CAGATGGCCACTTTGAGAACATTTTAGCTGACAACAGTGTGAACGACCAGACCAAAATCCTTGTGGTTAATGCTGCC
MCM2	NM_004526	GACTTTTGCCCGCTACCTTTCATTCCGGCGTGACAACAATGAGCTGTTGCTCTTCATACTGAAGCAGTTAGTGGC
MCM3	NM_002388	GGAGAACAATCCCCTTGAGACAGAATATGGCCTTTCTGTCTACAAGGATCACCAGACCATCACCATCCAGGAGAT
MCM6	NM_005915	TGATGGTCCTATGTGTCACATTCATCACAGGTTTCATACCAACACAGGCTTCAGCACTTCCTTTGGTGTGTTTCCTGTCCCA
MDM2	NM_002392	CTACAGGGACGCCATCGAATCCGGATCTTGATGCTGGTGTAAGTGAACATTCAGGTGATTGGTTGGAT
MMP9	NM_004994	GAGAACCAATCTCACCGACAGGCAGCTGGCAGAGGAATACCTGTACCGCTATGGTTACACTCGGGTG
MTA1	NM_004689	CCGCCCTCACCTGAAGAGAAACGCGCTCCTTGGCGGACACTGGGGGAGGAGAGGAAGAAGCGCGGCTAACTTATTCC
MYBL2	NM_002466	GCCGAGATCGCCAAGATGTTGCCAGGGAGGACAGACAATGCTGTGAAGAATCACTGGAACTCTACCATCAAAAG
P14ARF	578535	CCCTCGTGCTGATGCTACTGAGGAGCCAGCGTCTAGGGCAGCAGCCGCTTCCTAGAAGACCAGGTCATGATG
p27	NM_004064	CGGTGGACCACGAAGAGTTAACCCGGGACTTGGAGAAGCACTGCAGAGACATGGAAGAGGCGAGCC
P53	NM_000546	CTTTGAACCCTTGCTTGCAATAGGTGTGCGTCAGAAGCACCCAGGACTTCCATTTGCTTTGTCCCGGG
PAI1	NM_000602	CCGCAACGTGGTTTTCTCACCCTATGGGGTGGCCTCGGTGTTGGCCATGCTCCAGCTGACAACAGGAGGAGAAACCCAGCA
PDGFRb	NM_002609	CCAGCTCTCCTTCCAGCTACAGATCAATGTCCCTGTCCGAGTGCTGGAGCTAAGTGAGAGCCACCC
PI3KC2A	NM_002645	ATACCAATCACCGCACAAACCCAGGCTATTTGTTAAGTCCAGTCACAGCGCAAAGAAACATATGCGGAGAAAATGCTAGTGTG
PPM1D	NM_003620	GCCATCCGCAAAGGCTTTCTCGCTTGTCACCTTGCCATGTGGAAGAAACTGGCGGAATGGCC
PR	NM_000926	GCATCAGGCTGTCATTATGGTGTCCTTACCTGTGGGAGCTGTAAGGTCTTCTTTAAGAGGGCAATGGAAGGGCAGCACAACTACT
PRAME	NM_006115	TCTCCATATCTGCCTTGCAGAGTCTCCTGCAGCACCTCATCGGGCTGAGCAATCTGACCCACGTGC
pS2	NM_003225	GCCCTCCCAGTGTGCAAATAAGGGCTGCTGTTTCGACGACACCGTTCGTGGGGTCCCCTGGTGCTTCTATCCTAATACCATCGACG
RAD51C	NM_058216	GAACTTCTTGAGCAGGAGCATACCCAGGGCTTCATAATCACCTTCTGTTCAGCACTAGATGATATTCTTGGGGGTGGA
RB1	NM_000321	CGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCC
RIZ1	NM_012231	CCAGACGAGCGATTAGAAGCGGCAGCTTGTGAGGTGAATGATTTGGGGGAAGAGGAGGAGGAGGAAGAGGAGGA
STK15	NM_003600	CATCTTCCAGGAGGACCACTCTCTGTGGCACCCTGGACTACCTGCCCCCTGAAATGATTGAAGGTCGGA
STMY3	NM_005940	CCTGGAGGCTGCAACATAGCTCAATCCTGTCCCAGGCCGGATCCTCCTGAAGCCCTTTTCGCAGCACTGCTATCCTCCAAAGCCATTGTA

Table 5B

SURV	NM_001168	TGTTTTGATTCCCGGGCTTACCAGGTGAGAAGTGAGGGAGGAAGAAGGCAGTGTCCCTTTTGCTAGAGCTGACAGCTTTG
TBP	NM_003194	GCCCGAAACGCCGAATATAATCCCAAGCGGTTTGCTGCGGTAATCATGAGGATAAGAGAGCCACG
TGFA	NM_003236	GGTGTGCCACAGACCTTCCTACTTGGCCTGTAATCACGTGTGCAGCCTTTTGTGGGCCTTCAAAACTCTGTCAAGAACTCCGT
TIMP1	NM_003254	TCCCTGCGGTCCCAGATAGCCTGAATCCTGCCCGGAGTGGAACTGAAGCCTGCACAGTGTCCACCCTGTTCCCAC
TOP2A	NM_001067	AATCCAAGGGGGAGAGTGATGACTTCCATATGGACTTTGACTCAGCTGTGGCTCCTCGGGCAAAATCTGTAC
TOP2B	NM_001068	TGTGGACATCTTCCCCTCAGACTTCCCTACTGAGCCACCTTCTCTGCCACGAACCGGTCGGGCTAG
TP	NM_001953	CTATATGCAGCCAGAGATGTGACAGCCACCGTGGACAGCCTGCCACTCATCACAGCCTCCATTCTCAGTAAGAAACTCGTGG
TP53BP2	NM_005426	GGGCCAAATATTCAGAAGCTTTTATATCAGAGGACCACCATAGCGGCCATGGAGACCATCTCTGTCCCATCATACCCATCC
TRAIL	NM_003810	CTTCACAGTGCTCCTGCAGTCTCTCTGTGTGGCTGTAACTTACGTGTACTTTACCAACGAGCTGAAGCAGATG
TS	NM_001071	GCCTCGGTGTGCCTTTCAACATCGCCAGCTACGCCCTGCTCACGTACATGATTGCGCACATCACG
upa	NM_002658	GTGGATGTGCCCTGAAGGACAAGCCAGGCGTCTACACGAGAGTCTCACACTTCTTACCCTGGATCCGCAG
VDR	NM_000376	GCCCTGGATTTCAGAAAGAGCCAAGTCTGGATCTGGGACCGTTTCGTTCGTTCGCTGGCTTGTAACT
VEGF	NM_003376	CTGCTGTCTTGGGTGCATTGGAGCCTTGCCTTGCTGCTCTACCTCCACCATGCCAAGTGGTCCCAGGCTGC
VEGFB	NM_003377	TGACGATGGCCTGGAGTGTGTGCCCACTGGGCAGCACCAAGTCCGGATGCAGATCCTCATGATCCGGTACC
WISP1	NM_003882	AGAGGCATCCATGAACTTCACACTTGCGGGCTGCATCAGCACACGCTCCTATCAACCCAAGTACTGTGGAGTTTG
XIAP	NM_001167	GCAGTTGGAAGACACAGGAAAGTATCCCCAAATTGCAGATTTATCAACGGCTTTTATCTTGAAAATAGTGCCACGCA
YB-1	NM_004559	AGACTGTGGAGTTTGATGTTGTTGAAGGAGAAAAGGGTGCGGAGGCAGCAAATGTTACAGGTCCTGGTGGTGTTCC
ZNF217	NM_006526	ACCCAGTAGCAAGGAGAAGCCCACTCACTGCTCCGAGTGCGGCAAAGCTTTCAGAACCTACCACCAGCTG

Table 6A

Gene	Accession	Probe Name	Seq	Len
AIB1	NM_006534	S1994/AIB1.f3	GCGGCGAGTTTCCGATTTA	19
AIB1	NM_006534	S1995/AIB1.r3	TGAGTCCACCATCCAGCAAGT	21
AIB1	NM_006534	S5055/AIB1.p3	ATGGCGGCGGGAGGATCAAAA	21
AKT1	NM_005163	S0010/AKT1.f3	CGCTTCTATGGCGCTGAGAT	20
AKT1	NM_005163	S0012/AKT1.r3	TCCCGGTACACCACGTTCTT	20
AKT1	NM_005163	S4776/AKT1.p3	CAGCCCTGGACTACCTGCACTCGG	24
AKT2	NM_001626	S0828/AKT2.f3	TCCTGCCACCCTTCAAACC	19
AKT2	NM_001626	S0829/AKT2.r3	GGCGGTAAATTCATCATCGAA	21
AKT2	NM_001626	S4727/AKT2.p3	CAGGTCACGTCCGAGGTCGACACA	24
APC	NM_000038	S0022/APC.f4	GGACAGCAGGAATGTGTTTC	20
APC	NM_000038	S0024/APC.r4	ACCCACTCGATTTGTTTCTG	20
APC	NM_000038	S4888/APC.p4	CATTGGCTCCCCGTGACCTGTA	22
AREG	NM_001657	S0025/AREG.f2	TGTGAGTGAAATGCCTTCTAGTAGTGA	27
AREG	NM_001657	S0027/AREG.r2	TTGTGGTTCGTTATCATACTCTTCTGA	27
AREG	NM_001657	S4889/AREG.p2	CCGTCCTCGGGAGCCGACTATGA	23
B-actin	NM_001101	S0034/B-actl.f2	CAGCAGATGTGGATCAGCAAG	21
B-actin	NM_001101	S0036/B-acti.r2	GCATTTGCGGTGGACGAT	18
B-actin	NM_001101	S4730/B-acti.p2	AGGAGTATGACGAGTCCGGCCCC	23
B-Catenin	NM_001904	S2150/B-Cate.f3	GGCTCTTGTGCGTACTGTCCTT	22
B-Catenin	NM_001904	S2151/B-Cate.r3	TCAGATGACGAAGAGCACAGATG	23
B-Catenin	NM_001904	S5046/B-Cate.p3	AGGCTCAGTGATGTCTTCCCTGTCACCAG	29
BAD	NM_032989	S2011/BAD.f1	GGGTCAGGTGCCTCGAGAT	19
BAD	NM_032989	S2012/BAD.r1	CTGCTCACTCGGCTCAAACTC	21
BAD	NM_032989	S5058/BAD.p1	TGGGCCCAGAGCATGTTCCAGATC	24
BAG1	NM_004323	S1386/BAG1.f2	CGTTGTCAGCACTTGGAATACAA	23
BAG1	NM_004323	S1387/BAG1.r2	GTTCAACCTCTTCCTGTGGACTGT	24
BAG1	NM_004323	S4731/BAG1.p2	CCCAATTAACATGACCCGGCAACCAT	26
BBC3	NM_014417	S1584/BBC3.f2	CCTGGAGGGTCCTGTACAAT	20
BBC3	NM_014417	S1585/BBC3.r2	CTAATTGGGCTCCATCTCG	19
BBC3	NM_014417	S4890/BBC3.p2	CATCATGGGACTCCTGCCCTTACC	24
Bcl2	NM_000633	S0043/Bcl2.f2	CAGATGGACCTAGTACCCACTGAGA	25
Bcl2	NM_000633	S0045/Bcl2.r2	CCTATGATTTAAGGGCATTTTTCC	24
Bcl2	NM_000633	S4732/Bcl2.p2	TTCCACGCCGAAGGACAGCGAT	22
CA9	NM_001216	S1398/CA9.f3	ATCCTAGCCCTGGTTTTTGG	20
CA9	NM_001216	S1399/CA9.r3	CTGCCTTCTCATCTGCACAA	20
CA9	NM_001216	S4938/CA9.p3	TTTGCTGTCACCAGCGTCGC	20
CCNB1	NM_031966	S1720/CCNB1.f2	TTCAGGTTGTTGCAGGAGAC	20
CCNB1	NM_031966	S1721/CCNB1.r2	CATCTTCTTGGGCACACAAT	20
CCNB1	NM_031966	S4733/CCNB1.p2	TGTCTCCATTATTGATCGGTTCATGCA	27
CCND1	NM_001758	S0058/CCND1.f3	GCATGTTCGTGGCCTCTAAGA	21
CCND1	NM_001758	S0060/CCND1.r3	CGGTGTAGATGCACAGCTTCTC	22
CCND1	NM_001758	S4986/CCND1.p3	AAGGAGACCATCCCCCTGACGGC	23
CCNE1	NM_001238	S1446/CCNE1.f1	AAAGAAGATGATGACCGGGTTTAC	24
CCNE1	NM_001238	S1447/CCNE1.r1	GAGCCTCTGGATGGTGCAAT	20
CCNE1	NM_001238	S4944/CCNE1.p1	CAAACTCAACGTGCAAGCCTCGGA	24
CCNE2	NM_057749	S1458/CCNE2.f2	ATGCTGTGGCTCCTTCCTAACT	22
CCNE2	NM_057749	S1459/CCNE2.r2	ACCCAAATTGTGATATACAAAAAGGTT	27
CCNE2	NM_057749	S4945/CCNE2.p2	TACCAAGCAACCTACATGTCAAGAAAGCCC	30
CD3z	NM_000734	S0064/CD3z.f1	AGATGAAGTGGAAGGCGCTT	20
CD3z	NM_000734	S0066/CD3z.r1	TGCCTCTGTAATCGGCAACTG	21
CD3z	NM_000734	S4988/CD3z.p1	CACCGCGGCCATCCTGCA	18
CD68	NM_001251	S0067/CD68.f2	TGGTTCCCAGCCCTGTGT	18
CD68	NM_001251	S0069/CD68.r2	CTCCTCCACCCTGGGTTGT	19
CD68	NM_001251	S4734/CD68.p2	CTCCAAGCCCAGATTCAGATTCGAGTCA	28
CD9	NM_001769	S0686/CD9.f1	GGGCGTGGAACAGTTTATCT	20
CD9	NM_001769	S0687/CD9.r1	CACGGTGAAGGTTTCGAGT	19
CD9	NM_001769	S4792/CD9.p1	AGACATCTGCCCCAAGAAGGACGT	24
CDH1	NM_004360	S0073/CDH1.f3	TGAGTGTCCCCCGGTATCTTC	21
CDH1	NM_004360	S0075/CDH1.r3	CAGCCGCTTTCAGATTTTCAT	21
CDH1	NM_004360	S4990/CDH1.p3	TGCCAATCCCGATGAAATTGGAAATTT	27
CEGP1	NM_020974	S1494/CEGP1.f2	TGACAATCAGCACACCTGCAT	21

Table 6B

CEGP1	NM_020974	S1495/CEGP1.r2	TGTGACTACAGCCGTGATCCTTA	23
CEGP1	NM_020974	S4735/CEGP1.p2	CAGGCCCTCTTCCGAGCGGT	20
Chk1	NM_001274	S1422/Chk1.f2	GATAAATTGGTACAAGGGATCAGCTT	26
Chk1	NM_001274	S1423/Chk1.r2	GGGTGCCAAGTAACTGACTATTCA	24
Chk1	NM_001274	S4941/Chk1.p2	CCAGCCCACATGTCCTGATCATATGC	26
ClAP1	NM_001166	S0764/ClAP1.f2	TGCCTGTGGTGGGAAGCT	18
ClAP1	NM_001166	S0765/ClAP1.r2	GGAAAATGCCTCCGGTGTT	19
ClAP1	NM_001166	S4802/ClAP1.p2	TGACATAGCATCATCCTTTGGTTCCCAGTT	30
clAP2	NM_001165	S0076/clAP2.f2	GGATATTTCCGTGGCTCTTATTCA	24
clAP2	NM_001165	S0078/clAP2.r2	CTTCTCATCAAGGCAGAAAAATCTT	25
clAP2	NM_001165	S4991/clAP2.p2	TCTCCATCAAATCCTGTAAACTCCAGAGCA	30
cMet	NM_000245	S0082/cMet.f2	GACATTTCCAGTCCTGCAGTCA	22
cMet	NM_000245	S0084/cMet.r2	CTCCGATCGCACACATTTGT	20
cMet	NM_000245	S4993/cMet.p2	TGCCTCTCTGCCCCACCCTTTGT	23
Contig 27882	AK000618	S2633/Contig.f3	GGCATCCTGGCCCAAAGT	18
Contig 27882	AK000618	S2634/Contig.r3	GACCCCCTCAGCTGGTAGTTG	21
Contig 27882	AK000618	S4977/Contig.p3	CCCAAATCCAGGCGGCTAGAGGC	23
COX2	NM_000963	S0088/COX2.f1	TCTGCAGAGTTGGAAGCACTCTA	23
COX2	NM_000963	S0090/COX2.r1	GCCGAGGCTTTTCTACCAGAA	21
COX2	NM_000963	S4995/COX2.p1	CAGGATACAGCTCCACAGCATCGATGTC	28
CTSL	NM_001912	S1303/CTSL.f2	GGGAGGCTTATCTCACTGAGTGA	23
CTSL	NM_001912	S1304/CTSL.r2	CCATTGCAGCCTTCATTGC	19
CTSL	NM_001912	S4899/CTSL.p2	TTGAGGCCCAGAGCAGTCTACCAGATTCT	29
CTSL2	NM_001333	S4354/CTSL2.f1	TGTCTCACTGAGCGAGCAGAA	21
CTSL2	NM_001333	S4355/CTSL2.r1	ACCATTGCAGCCCTGATTG	19
CTSL2	NM_001333	S4356/CTSL2.p1	CTTGAGGACGCGAACAGTCCACCA	24
DAPK1	NM_004938	S1768/DAPK1.f3	CGCTGACATCATGAATGTTCCT	22
DAPK1	NM_004938	S1769/DAPK1.r3	TCTCTTTCAGCAACGATGTGTCTT	24
DAPK1	NM_004938	S4927/DAPK1.p3	TCATATCCAAACTCGCCTCCAGCCG	25
DIABLO	NM_019887	S0808/DIABLO.f1	CACAATGGCGGCTCTGAAG	19
DIABLO	NM_019887	S0809/DIABLO.r1	ACACAAACACTGTCTGTACCTGAAGA	26
DIABLO	NM_019887	S4813/DIABLO.p1	AAGTTACGCTGCGCGACAGCCAA	23
DR5	NM_003842	S2551/DR5.f2	CTCTGAGACAGTGCTTCGATGACT	24
DR5	NM_003842	S2552/DR5.r2	CCATGAGGCCCAACTTCCT	19
DR5	NM_003842	S4979/DR5.p2	CAGACTTGGTGCCCTTTGACTCC	23
EGFR	NM_005228	S0103/EGFR.f2	TGTCGATGGACTTCCAGAAC	20
EGFR	NM_005228	S0105/EGFR.r2	ATTGGGACAGCTTGGATCA	19
EGFR	NM_005228	S4999/EGFR.p2	CACCTGGGCAGCTGCCAA	18
EIF4E	NM_001968	S0106/EIF4E.f1	GATCTAAGATGGCGACTGTCGAA	23
EIF4E	NM_001968	S0108/EIF4E.r1	TTAGATTCCGTTTTCTCCTCTTCTG	25
EIF4E	NM_001968	S5000/EIF4E.p1	ACCACCCCTACTCCTAATCCCCCGACT	27
EMS1	NM_005231	S2663/EMS1.f1	GGCAGTGTCACTGAGTCCTTGA	22
EMS1	NM_005231	S2664/EMS1.r1	TGCACTGTGCGTCCCAAT	18
EMS1	NM_005231	S4956/EMS1.p1	ATCCTCCCCTGCCCCGCG	18
EpCAM	NM_002354	S1807/EpCAM.f1	GGGCCCTCCAGAACAATGAT	20
EpCAM	NM_002354	S1808/EpCAM.r1	TGCACTGCTTGGCCTTAAAGA	21
EpCAM	NM_002354	S4984/EpCAM.p1	CCGCTCTCATCGCAGTCAGGATCAT	25
EPHX1	NM_000120	S1865/EPHX1.f2	ACCGTAGGCTCTGCTCTGAA	20
EPHX1	NM_000120	S1866/EPHX1.r2	TGGTCCAGGTGGAAAACTTC	20
EPHX1	NM_000120	S4754/EPHX1.p2	AGGCAGCCAGACCCACAGGA	20
ErbB3	NM_001982	S0112/ErbB3.f1	CGGTTATGTCATGCCAGATACAC	23
ErbB3	NM_001982	S0114/ErbB3.r1	GAACTGAGACCCACTGAAGAAAGG	24
ErbB3	NM_001982	S5002/ErbB3.p1	CCTCAAAGGTACTCCCTCCTCCCGG	25
EstR1	NM_000125	S0115/EstR1.f1	CGTGGTGCCCCTCTATGAC	19
EstR1	NM_000125	S0117/EstR1.r1	GGCTAGTGGGCGCATGTAG	19
EstR1	NM_000125	S4737/EstR1.p1	CTGGAGATGCTGGACGCCC	19
FBXO5	NM_012177	S2017/FBXO5.r1	GGATTGTAGACTGTCACCGAAATTC	25
FBXO5	NM_012177	S2018/FBXO5.f1	GGCTATTCCTCATTTTCTCTACAAAGTG	28
FBXO5	NM_012177	S5061/FBXO5.p1	CCTCCAGGAGGCTACCTTCTTCATGTTCAC	30
FGF18	NM_003862	S1665/FGF18.f2	CGGTAGTCAAGTCCGGATCAA	21
FGF18	NM_003862	S1666/FGF18.r2	GCTTGCCTTTGCGGTTCA	18
FGF18	NM_003862	S4914/FGF18.p2	CAAGGAGACGGAATTCTACCTGTGC	25

Table 6C

FGFR1	NM_023109	S0818/FGFR1.f3	CACGGGACATTCACCACATC	20
FGFR1	NM_023109	S0819/FGFR1.r3	GGGTGCCATCCACTTCACA	19
FGFR1	NM_023109	S4816/FGFR1.p3	ATAAAAAGACAACCAACGGCCGACTGC	27
FHIT	NM_002012	S2443/FHIT.f1	CCAGTGGAGCGCTTCCAT	18
FHIT	NM_002012	S2444/FHIT.r1	CTCTCTGGGTCGTCTGAAACAA	22
FHIT	NM_002012	S2445/FHIT.p1	TCGGCCACTTCATCAGGACGCAG	23
FHIT	NM_002012	S4921/FHIT.p1	TCGGCCACTTCATCAGGACGCAG	23
FRP1	NM_003012	S1804/FRP1.f3	TTGGTACCTGTGGGTTAGCA	20
FRP1	NM_003012	S1805/FRP1.r3	CACATCCAAATGCAAACTGG	20
FRP1	NM_003012	S4983/FRP1.p3	TCCCCAGGGTAGAATTCAATCAGAGC	26
G-Catenin	NM_002230	S2153/G-Cate.f1	TCAGCAGCAAGGGCATCAT	19
G-Catenin	NM_002230	S2154/G-Cate.r1	GGTGGTTTTCTTGAGCGTGTACT	23
G-Catenin	NM_002230	S5044/G-Cate.p1	CGCCCGCAGGCCTCATCCT	19
GAPDH	NM_002046	S0374/GAPDH.f1	ATTCCACCCATGGCAAATTC	20
GAPDH	NM_002046	S0375/GAPDH.r1	GATGGGATTTCCATTGATGACA	22
GAPDH	NM_002046	S4738/GAPDH.p1	CCGTTCTCAGCCTTGACGGTGC	22
GATA3	NM_002051	S0127/GATA3.f3	CAAAGGAGCTCACTGTGGTGTCT	23
GATA3	NM_002051	S0129/GATA3.r3	GAGTCAGAATGGCTTATTCACAGATG	26
GATA3	NM_002051	S5005/GATA3.p3	TGTTCCAACCACTGAATCTGGACC	24
GRB7	NM_005310	S0130/GRB7.f2	CCATCTGCATCCATCTTGTT	20
GRB7	NM_005310	S0132/GRB7.r2	GGCCACCAGGGTATTATCTG	20
GRB7	NM_005310	S4726/GRB7.p2	CTCCCCACCCTTGAGAAGTGCCT	23
GRO1	NM_001511	S0133/GRO1.f2	CGAAAAGATGCTGAACAGTGACA	23
GRO1	NM_001511	S0135/GRO1.r2	TCAGGAACAGCCACCAGTGA	20
GRO1	NM_001511	S5006/GRO1.p2	CTTCCTCCTCCCTTCTGGTCAGTTGGAT	28
GSTM1	NM_000561	S2026/GSTM1.r1	GGCCCAGCTTGAATTTTTCA	20
GSTM1	NM_000561	S2027/GSTM1.f1	AAGCTATGAGGAAAAGAAGTACACGAT	27
GSTM1	NM_000561	S4739/GSTM1.p1	TCAGCCACTGGCTTCTGTCATAATCAGGAG	30
GUS	NM_000181	S0139/GUS.f1	CCCACTCAGTAGCCAAGTCA	20
GUS	NM_000181	S0141/GUS.r1	CACGCAGGTGGTATCAGTCT	20
GUS	NM_000181	S4740/GUS.p1	TCAAGTAAACGGGCTGTTTTCCAAACA	27
HER2	NM_004448	S0142/HER2.f3	CGGTGTGAGAAGTGCAGCAA	20
HER2	NM_004448	S0144/HER2.r3	CCTCTCGCAAGTGCTCCAT	19
HER2	NM_004448	S4729/HER2.p3	CCAGACCATAGCACACTCGGGCAC	24
HIF1A	NM_001530	S1207/HIF1A.f3	TGAACATAAAGTCTGCAACATGGA	24
HIF1A	NM_001530	S1208/HIF1A.r3	TGAGGTTGGTTACTGTTGGTATCATATA	28
HIF1A	NM_001530	S4753/HIF1A.p3	TTGCACTGCACAGGCCACATTCAC	24
HNF3A	NM_004496	S0148/HNF3A.f1	TCCAGGATGTTAGGAACTGTGAAG	24
HNF3A	NM_004496	S0150/HNF3A.r1	GCGTGTCTGCGTAGTAGCTGTT	22
HNF3A	NM_004496	S5008/HNF3A.p1	AGTCGCTGGTTTCATGCCCTTCCA	24
ID1	NM_002165	S0820/ID1.f1	AGAACCGCAAGGTGAGCAA	19
ID1	NM_002165	S0821/ID1.r1	TCCAACTGAAGGTCCCTGATG	21
ID1	NM_002165	S4832/ID1.p1	TGGAGATTCTCCAGCACGTCATCGAC	26
IGF1	NM_000618	S0154/IGF1.f2	TCCGGAGCTGTGATCTAAGGA	21
IGF1	NM_000618	S0156/IGF1.r2	CGGACAGAGCGAGCTGACTT	20
IGF1	NM_000618	S5010/IGF1.p2	TGTATTGCGCACCCCTCAAGCCTG	24
IGF1R	NM_000875	S1249/IGF1R.f3	GCATGGTAGCCGAAGATTTCA	21
IGF1R	NM_000875	S1250/IGF1R.r3	TTTCCGGTAATAGTCTGTCTCATAGATATC	30
IGF1R	NM_000875	S4895/IGF1R.p3	CGCGTCATACCAAAATCTCCGATTTTGA	28
IGFBP2	NM_000597	S1128/IGFBP2.f1	GTGGACAGCACCATGAACA	19
IGFBP2	NM_000597	S1129/IGFBP2.r1	CCTTCATACCCGACTTGAGG	20
IGFBP2	NM_000597	S4837/IGFBP2.p1	CTTCCGGCCAGCACTGCCTC	20
IL6	NM_000600	S0760/IL6.f3	CCTGAACCTTCCAAAGATGG	20
IL6	NM_000600	S0761/IL6.r3	ACCAGGCAAGTCTCCTCATT	20
IL6	NM_000600	S4800/IL6.p3	CCAGATTGGAAGCATCCATCTTTTTCA	27
IRS1	NM_005544	S1943/IRS1.f3	CCACAGCTCACCTTCTGTCA	20
IRS1	NM_005544	S1944/IRS1.r3	CCTCAGTGCCAGTCTCTTCC	20
IRS1	NM_005544	S5050/IRS1.p3	TCCATCCCAGCTCCAGCCAG	20
KI-67	NM_002417	S0436/Ki-67.f2	CGGACTTTGGGTGCGACTT	19
KI-67	NM_002417	S0437/Ki-67.r2	TTACAACTCTTCCACTGGGACGAT	24
KI-67	NM_002417	S4741/Ki-67.p2	CCACTTGTCGAACCACCGCTCGT	23
KLK10	NM_002776	S2624/KLK10.f3	GCCCAGAGGCTCCATCGT	18

Table 6D

KLK10	NM_002776	S2625/KLK10.r3	'CAGAGGTTTGAACAGTGCAGACA	23
KLK10	NM_002776	S4978/KLK10.p3	CCTCTTCCTCCCCAGTCGGCTGA	23
KRT14	NM_000526	S1853/KRT14.f1	GGCCTGCTGAGATCAAAGAC	20
KRT14	NM_000526	S1854/KRT14.r1	GTCCACTGTGGCTGTGAGAA	20
KRT14	NM_000526	S5037/KRT14.p1	TGTTCCTCAGGTCCTCAATGGTCTTG	26
KRT17	NM_000422	S0172/KRT17.f2	CGAGGATTGGTTCTTCAGCAA	21
KRT17	NM_000422	S0174/KRT17.r2	ACTCTGCACCAGCTCACTGTTG	22
KRT17	NM_000422	S5013/KRT17.p2	CACCTCGCGGTTCAGTTCCTCTGT	24
KRT18	NM_000224	S1710/KRT18.f2	AGAGATCGAGGCTCTCAAGG	20
KRT18	NM_000224	S1711/KRT18.r2	GGCCTTTTACTTCCTCTTCG	20
KRT18	NM_000224	S4762/KRT18.p2	TGGTTCTTCTTCATGAAGAGCAGCTCC	27
KRT19	NM_002276	S1515/KRT19.f3	TGAGCGGCAGAATCAGGAGTA	21
KRT19	NM_002276	S1516/KRT19.r3	TGCGGTAGGTGGCAATCTC	19
KRT19	NM_002276	S4866/KRT19.p3	CTCATGGACATCAAGTCGCGGCTG	24
KRT5	NM_000424	S0175/KRT5.f3	TCAGTGGAGAAGGAGTTGGA	20
KRT5	NM_000424	S0177/KRT5.r3	TGCCATATCCAGAGGAAACA	20
KRT5	NM_000424	S5015/KRT5.p3	CCAGTCAACATCTCTGTTGTCACAAGCA	28
KRT8	NM_002273	S2588/KRT8.f3	GGATGAAGCTTACATGAACAAGGTAGA	27
KRT8	NM_002273	S2589/KRT8.r3	CATATAGCTGCCTGAGGAAGTTGAT	25
KRT8	NM_002273	S4952/KRT8.p3	CGTCGGTCAGCCCTTCCAGGC	21
LOT1 variant 1	NM_002656	S0692/LOT1 v.f2	GGAAAGACCACCTGAAAAACCA	22
LOT1 variant 1	NM_002656	S0693/LOT1 v.r2	GTACTTCTTCCCACACTCCTCACA	24
LOT1 variant 1	NM_002656	S4793/LOT1 v.p2	ACCCACGACCCCAACAAAATGGC	23
Maspin	NM_002639	S0836/Maspin.f2	CAGATGGCCACTTTGAGAACATT	23
Maspin	NM_002639	S0837/Maspin.r2	GGCAGCATTAACCACAAGGATT	22
Maspin	NM_002639	S4835/Maspin.p2	AGCTGACAACAGTGTGAACGACCAGACC	28
MCM2	NM_004526	S1602/MCM2.f2	GACTTTTGCCCGCTACCTTTC	21
MCM2	NM_004526	S1603/MCM2.r2	GCCACTAACTGCTTCAGTATGAAGAG	26
MCM2	NM_004526	S4900/MCM2.p2	ACAGCTCATTGTTGTCACGCCGGA	24
MCM3	NM_002388	S1524/MCM3.f3	GGAGAACAATCCCCTTGAGA	20
MCM3	NM_002388	S1525/MCM3.r3	ATCTCCTGGATGGTGATGGT	20
MCM3	NM_002388	S4870/MCM3.p3	TGGCCTTTCTGTCTACAAGGATCACCA	27
MCM6	NM_005915	S1704/MCM6.f3	TGATGGTCCTATGTGTCACATTCA	24
MCM6	NM_005915	S1705/MCM6.r3	TGGGACAGGAAACACACCAA	20
MCM6	NM_005915	S4919/MCM6.p3	CAGGTTTCATACCAACACAGGCTTCAGCAC	30
MDM2	NM_002392	S0830/MDM2.f1	CTACAGGGACGCCATCGAA	19
MDM2	NM_002392	S0831/MDM2.r1	ATCCAACCAATCACCTGAATGTT	23
MDM2	NM_002392	S4834/MDM2.p1	CTTACACCAGCATCAAGATCCGG	23
MMP9	NM_004994	S0656/MMP9.f1	GAGAACCAATCTCACCGACA	20
MMP9	NM_004994	S0657/MMP9.r1	CACCCGAGTGTAACCATAGC	20
MMP9	NM_004994	S4760/MMP9.p1	ACAGGTATTCCTCTGCCAGCTGCC	24
MTA1	NM_004689	S2369/MTA1.f1	CCGCCCTCACCTGAAGAGA	19
MTA1	NM_004689	S2370/MTA1.r1	GGAATAAGTTAGCCGCGCTTCT	22
MTA1	NM_004689	S4855/MTA1.p1	CCCAGTGTCCGCCAAGGAGCG	21
MYBL2	NM_002466	S3270/MYBL2.f1	GCCGAGATCGCCAAGATG	18
MYBL2	NM_002466	S3271/MYBL2.r1	CTTTTGATGGTAGAGTTCCAGTGATTC	27
MYBL2	NM_002466	S4742/MYBL2.p1	CAGCATTGTCTGTCCTCCCTGGCA	24
P14ARF	S78535	S2842/P14ARF.f1	CCCTCGTGCTGATGCTACT	19
P14ARF	S78535	S2843/P14ARF.r1	CATCATGACCTGGTCTTCTAGG	22
P14ARF	S78535	S4971/P14ARF.p1	CTGCCCTAGACGCTGGCTCCTC	22
p27	NM_004064	S0205/p27.f3	CGGTGGACCACGAAGAGTTAA	21
p27	NM_004064	S0207/p27.r3	GGCTCGCCTCTTCCATGTC	19
p27	NM_004064	S4750/p27.p3	CCGGGACTTGGAGAAGCACTGCA	23
P53	NM_000546	S0208/P53.f2	CTTTGAACCCTTGCTTGCAA	20
P53	NM_000546	S0210/P53.r2	CCCGGGACAAAGCAAATG	18
P53	NM_000546	S5065/P53.p2	AAGTCCTGGGTGCTTCTGACGCACA	25
PAI1	NM_000602	S0211/PAI1.f3	CCGCAACGTGGTTTTCTCA	19
PAI1	NM_000602	S0213/PAI1.r3	TGCTGGGTTTCTCCTCCTGTT	21
PAI1	NM_000602	S5066/PAI1.p3	CTCGGTGTTGGCCATGCTCCAG	22
PDGFRb	NM_002609	S1346/PDGFRb.f3	CCAGCTCTCCTTCCAGCTAC	20
PDGFRb	NM_002609	S1347/PDGFRb.r3	GGGTGGCTCTCACTTAGCTC	20
PDGFRb	NM_002609	S4931/PDGFRb.p3	ATCAATGTCCCTGTCCGAGTGCTG	24

Table 6E

PI3KC2A	NM_002645	S2020/PI3KC2.r1	CACACTAGCATTTTCTCCGCATA	23
PI3KC2A	NM_002645	S2021/PI3KC2.f1	ATACCAATCACCGCACAAACC	21
PI3KC2A	NM_002645	S5062/PI3KC2.p1	TGCGCTGTGACTGGACTTAACAAATAGCCT	30
PPM1D	NM_003620	S3159/PPM1D.f1	GCCATCCGCAAAGGCTTT	18
PPM1D	NM_003620	S3160/PPM1D.r1	GGCCATTCCGCCAGTTTC	18
PPM1D	NM_003620	S4856/PPM1D.p1	TCGCTTGTCACCTTGCCATGTGG	23
PR	NM_000926	S1336/PR.f6	GCATCAGGCTGTCATTATGG	20
PR	NM_000926	S1337/PR.r6	AGTAGTTGTGCTGCCCTTCC	20
PR	NM_000926	S4743/PR.p6	TGTCCTTACCTGTGGGAGCTGTAAGGTC	28
PRAME	NM_006115	S1985/PRAME.f3	TCTCCATATCTGCCTTGCAGAGT	23
PRAME	NM_006115	S1986/PRAME.r3	GCACGTGGGTCAGATTGCT	19
PRAME	NM_006115	S4756/PRAME.p3	TCCTGCAGCACCTCATCGGGCT	22
pS2	NM_003225	S0241/pS2.f2	GCCCTCCCAGTGTGCAAAT	19
pS2	NM_003225	S0243/pS2.r2	CGTCGATGGTATTAGGATAGAAGCA	25
pS2	NM_003225	S5026/pS2.p2	TGCTGTTTCGACGACACCGTTCG	23
RAD51C	NM_058216	S2606/RAD51C.f3	GAACTTCTTGAGCAGGAGCATACC	24
RAD51C	NM_058216	S2607/RAD51C.r3	TCCACCCCCAAGAATATCATCTAGT	25
RAD51C	NM_058216	S4764/RAD51C.p3	AGGGCTTCATAATCACCTTCTGTTC	25
RB1	NM_000321	S2700/RB1.f1	CGAAGCCCTTACAAGTTTCC	20
RB1	NM_000321	S2701/RB1.r1	GGACTCTTCAGGGGTGAAAT	20
RB1	NM_000321	S4765/RB1.p1	CCCTTACGGATTCCTGGAGGGAAC	24
RIZ1	NM_012231	S1320/RIZ1.f2	CCAGACGAGCGATTAGAAGC	20
RIZ1	NM_012231	S1321/RIZ1.r2	TCCTCCTCTTCCTCCTCCTC	20
RIZ1	NM_012231	S4761/RIZ1.p2	TGTGAGGTGAATGATTTGGGGGA	23
STK15	NM_003600	S0794/STK15.f2	CATCTTCCAGGAGGACCACT	20
STK15	NM_003600	S0795/STK15.r2	TCCGACCTTCAATCATTTCA	20
STK15	NM_003600	S4745/STK15.p2	CTCTGTGGCACCCTGGACTACCTG	24
STMY3	NM_005940	S2067/STMY3.f3	CCTGGAGGCTGCAACATACC	20
STMY3	NM_005940	S2068/STMY3.r3	TACAATGGCTTTGGAGGATAGCA	23
STMY3	NM_005940	S4746/STMY3.p3	ATCCTCCTGAAGCCCTTTTCGCAGC	25
SURV	NM_001168	S0259/SURV.f2	TGTTTTGATTCCCGGGCTTA	20
SURV	NM_001168	S0261/SURV.r2	CAAAGCTGTCAGCTCTAGCAAAAG	24
SURV	NM_001168	S4747/SURV.p2	TGCCTTCTTCCTCCCTCACTTCTCACCT	28
TBP	NM_003194	S0262/TBP.f1	GCCCGAAACGCCGAATATA	19
TBP	NM_003194	S0264/TBP.r1	CGTGGCTCTCTTATCCTCATGAT	23
TBP	NM_003194	S4751/TBP.p1	TACCGCAGCAAACCGCTTGGG	21
TGFA	NM_003236	S0489/TGFA.f2	GGTGTGCCACAGACCTTCCT	20
TGFA	NM_003236	S0490/TGFA.r2	ACGGAGTTCTTGACAGAGTTTTGA	24
TGFA	NM_003236	S4768/TGFA.p2	TTGGCCTGTAATCACCTGTGCAGCCTT	27
TIMP1	NM_003254	S1695/TIMP1.f3	TCCCTGCGGTCCCAGATAG	19
TIMP1	NM_003254	S1696/TIMP1.r3	GTGGGAACAGGGTGGACACT	20
TIMP1	NM_003254	S4918/TIMP1.p3	ATCCTGCCCGGAGTGGAACTGAAGC	25
TOP2A	NM_001067	S0271/TOP2A.f4	AATCCAAGGGGGAGAGTGAT	20
TOP2A	NM_001067	S0273/TOP2A.r4	GTACAGATTTTGCCCGAGGA	20
TOP2A	NM_001067	S4777/TOP2A.p4	CATATGGACTTTGACTCAGCTGTGGC	26
TOP2B	NM_001068	S0274/TOP2B.f2	TGTGGACATCTTCCCCTCAGA	21
TOP2B	NM_001068	S0276/TOP2B.r2	CTAGCCCGACCGGTTCGT	18
TOP2B	NM_001068	S4778/TOP2B.p2	TTCCCTACTGAGCCACCTTCTCTG	24
TP	NM_001953	S0277/TP.f3	CTATATGCAGCCAGAGATGTGACA	24
TP	NM_001953	S0279/TP.r3	CCACGAGTTTCTTACTGAGAATGG	24
TP	NM_001953	S4779/TP.p3	ACAGCCTGCCACTCATCACAGCC	23
TP53BP2	NM_005426	S1931/TP53BP.f2	GGGCCAAATATTCAGAAGC	19
TP53BP2	NM_005426	S1932/TP53BP.r2	GGATGGGTATGATGGGACAG	20
TP53BP2	NM_005426	S5049/TP53BP.p2	CCACCATAGCGGCCATGGAG	20
TRAIL	NM_003810	S2539/TRAIL.f1	CTTCACAGTGCTCCTGCAGTCT	22
TRAIL	NM_003810	S2540/TRAIL.r1	CATCTGCTTCAGCTCGTTGGT	21
TRAIL	NM_003810	S4980/TRAIL.p1	AAGTACACGTAAGTTACAGCCACACA	26
TS	NM_001071	S0280/TS.f1	GCCTCGGTGTGCCTTTCA	18
TS	NM_001071	S0282/TS.r1	CGTGATGTGCGCAATCATG	19
TS	NM_001071	S4780/TS.p1	CATCGCCAGCTACGCCCTGCTC	22
upa	NM_002658	S0283/upa.f3	GTGGATGTGCCCTGAAGGA	19
upa	NM_002658	S0285/upa.r3	CTGCGGATCCAGGGTAAGAA	20

Table 6F

upa	NM_002658	S4769/upa.p3	AAGCCAGGCGTCTACACGAGAGTCTCAC	28
VDR	NM_000376	S2745/VDR.f2	GCCCTGGATTTCAGAAAGAG	20
VDR	NM_000376	S2746/VDR.r2	AGTTACAAGCCAGGGAAGGA	20
VDR	NM_000376	S4962/VDR.p2	CAAGTCTGGATCTGGGACCCTTTCC	25
VEGF	NM_003376	S0286/VEGF.f1	CTGCTGTCTTGGGTGCATTG	20
VEGF	NM_003376	S0288/VEGF.r1	GCAGCCTGGGACCACTTG	18
VEGF	NM_003376	S4782/VEGF.p1	TTGCCTTGCTGCTCTACCTCCACCA	25
VEGFB	NM_003377	S2724/VEGFB.f1	TGACGATGGCCTGGAGTGT	19
VEGFB	NM_003377	S2725/VEGFB.r1	GGTACCGGATCATGAGGATCTG	22
VEGFB	NM_003377	S4960/VEGFB.p1	CTGGGCAGCACCAAGTCCGGA	21
WISP1	NM_003882	S1671/WISP1.f1	AGAGGCATCCATGAACTTCACA	22
WISP1	NM_003882	S1672/WISP1.r1	CAAACTCCACAGTACTTGGGTTGA	24
WISP1	NM_003882	S4915/WISP1.p1	CGGGCTGCATCAGCACACGC	20
XIAP	NM_001167	S0289/XIAP.f1	GCAGTTGGAAGACACAGGAAAGT	23
XIAP	NM_001167	S0291/XIAP.r1	TGCGTGGCACTATTTTCAAGA	21
XIAP	NM_001167	S4752/XIAP.p1	TCCCCAAATTGCAGATTTATCAACGGC	27
YB-1	NM_004559	S1194/YB-1.f2	AGACTGTGGAGTTTGATGTTGTTGA	25
YB-1	NM_004559	S1195/YB-1.r2	GGAACACCACCAGGACCTGTAA	22
YB-1	NM_004559	S4843/YB-1.p2	TTGCTGCCTCCGCACCCTTTTCT	23
ZNF217	NM_006526	S2739/ZNF217.f3	ACCCAGTAGCAAGGAGAAGC	20
ZNF217	NM_006526	S2740/ZNF217.r3	CAGCTGGTGGTAGGTTCTGA	20
ZNF217	NM_006526	S4961/ZNF217.p3	CACTCACTGCTCCGAGTGCGG	21

WHAT IS CLAIMED IS:

1. A method of predicting the likelihood of long-term survival of a breast cancer patient without the recurrence of breast cancer, comprising determining the expression level of one or more prognostic RNA transcripts or their expression products in a breast cancer tissue sample obtained from said patient, normalized against the expression level of all RNA transcripts or their products in said breast cancer tissue sample, or of a reference set of RNA transcripts or their expression products, wherein the prognostic RNA transcript is the transcript of one or more genes selected from the group consisting of: TP53BP2, GRB7, PR, CD68, Bc12, KRT14, IRS1, CTSL, EstR1, Chkl, IGFBP2, BAG1, CEGP1, STK15, GSTM1, FHIT, RIZ1, AIB1, SURV, BBC3, IGF1R, p27, GATA3, ZNF217, EGFR, CD9, MYBL2, HIFlα, pS2, ErbB3, TOP2B, MDM2, RAD51C, KRT19, TS, Her2, KLK10, β-Catenin, γ-Catenin, MCM2, PI3KC2A, IGF1, TBP, CCNB1, FBXO5, and DR5,

wherein expression of one or more of GRB7, CD68, CTSL, Chkl, AIB1, CCNB1, MCM2, FBXO5, Her2, STK15, SURV, EGFR, MYBL2, HIF1α, and TS indicates a decreased likelihood of long-term survival without breast cancer recurrence, and the expression of one or more of TP53BP2, PR, Bc12, KRT14, EstR1, IGFBP2, BAG1, CEGP1, KLK10, β-Catenin, γ-Catenin, DRS, PI3KCA2, RAD51C, GSTM1, FHIT, RIZ1, BBC3, TBP, p27, IRS1, IGF1R, GATA3, ZNF217, CD9, pS2, ErbB3, TOP2B, MDM2, IGF1, and KRT19 indicates an increased likelihood of long-term survival without breast cancer recurrence.

2. The method of claim 1 comprising determining the expression level of at least two of said prognostic RNA transcripts or their expression products.

3. The method of claim 1 comprising determining the expression level of at least 5 of said prognostic RNA transcripts or their expression products.

4. The method of claim 1 comprising determining the expression level of at least 10 of said prognostic RNA transcripts or their expression products.

5. The method of claim 1 comprising determining the expression level of at least 15 of said prognostic transcripts of their expression products.

6. The method of claim 1 wherein the breast cancer is invasive breast carcinoma.

7. The method of claim 1 wherein the expression level of one or more prognostic RNA transcripts is determined.

8. The method of claim 1 wherein said RNA is isolated from a fixed, wax-embedded breast cancer tissue specimen of said patient.

9. The method of claim 1 wherein said RNA is isolated from core biopsy tissue or fine needle aspirate cells.

10. An array comprising polynucleotides hybridizing to two or more of the following genes: α-Catenin, AIB1, AKT1, AKT2, β-actin, BAG1, BBC3, Bcl2, CCNB1, CCND1, CD68, CD9, CDH1, CEGP1, Chkl, CIAP1, cMet.2, Contig 27882, CTSL, DR5, EGFR, EIF4E, EPHX1, ErbB3, EstR1, FBXO5, FHIT1 FRP1, GAPDH, GATA3, G-Catenin, GRB7, GRO1, GSTM1, GUS, HER2, HIF1A, HNF3A, IGF1R, IGFBP2, KLK10, KRT14, KRT17, KRT18, KRT19, KRT5, Maspin, MCM2, MCM3, MDM2, MMP9, MTA1, MYBL2, P14ARF, p27, P53, PI3KC2A, PR, PRAME, pS2, RAD51C,.3RB1, RIZ1, STK15, STMY3, SURV, TGFA, TOP2B, TP53BP2, TRAIL, TS, upa, VDR, VEGF, and ZNF217.

11. The array of claim 10 comprising polynucleotides hybridizing to at least 3 of said genes.

12. The array of claim 10 comprising polynucleotides hybridizing to at least 5 of said genes.

13. The array of claim 10 comprising polynucleotides hybridizing to at least 10 of said genes.

14. The array of claim 10 comprising polynucleotides hybridizing to the following genes: TP53BP2, GRB7, PR, CD68, Bc12, KRT14, IRS1, CTSL, EstR1, Chkl, IGFBP2, BAG1, CEGP1, STK15, GSTM1, FHIT, RIZ1, AIB1, SURV, BBC3, IGF1R, p27, GATA3, ZNF217, EGFR, CD9, MYBL2, HIF1α, pS2, RIZ1, ErbB3, TOP2B, MDM2, RAD51C, KRT19, TS, Her2, KLK10, β-Catenin, γ-Catenin, MCM2, PI3KC2A, IGF1, TBP, CCNB1, FBXO5 and DR5.

15. The array of claim 10 or claim 14 wherein said polynucleotides are cDNAs.

16. The array of claim 15 wherein said cDNAs are about 500 to 5000 bases long.

17. The array of claim 10 or claim 14 wherein said polynucleotides are oligonucleotides.

18. The array of claim 17 wherein said oligonucleotides are about 20 to 80 bases long.

19. The array of claim 10 or claim 14 wherein the solid surface is glass.

20. The array of claim 19 which comprises about 330,000 oligonucleotides.

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

(1) determining the expression levels of the RNA transcripts or the expression products of genes or a gene set selected from the group consisting of

(a) TP53BP2, Bc12, BAD, EPHX1, PDGFRβ, DIABLO, XIAP, YB1, CA9, and KRT8;

(b) GRB7, CD68, TOP2A, Bc12, DIABLO, CD3, ID1, PPM1D, MCM6, and WISP1;

(c) PR, TP53BP2, PRAME, DIABLO, CTSL, IGFBP2, TIMP1, CA9, MMP9, and COX2;

(d) CD68, GRB7, TOP2A, Bc12, DIABLO, CD3, ID1, PPM1D, MCM6, and WISP1;

(e) Bc12, TP53BP2, BAD, EPHX1, PDGFRβ, DIABLO, XIAP, YB1, CA9, and KRT8;

(f) KRT14, KRT5, PRAME, TP53BP2, GUS1, AIB1, MCM3, CCNE1, MCM6, and ID1;

(g) PRAME, TP53BP2, EstR1, DIABLO, CTSL, PPM1D, GRB7, DAPK1, BBC3, and VEGFB;

(h) CTSL2, GRB7, TOP2A, CCNB1, Bc12, DIABLO, PRAME, EMS1, CA9, and EpCAM;

(i) EstR1, TP53BP2, PRAME, DIABLO, CTSL, PPM1D, GRB7, DAPK1, BBC3, and VEGFB;

(k) Chkl, PRAME, TP53BP2, GRB7, CA9, CTSL, CCNB1, TOP2A, tumor size, and IGFBP2;

(1) IGFBP2, GRB7, PRAME, DIABLO, CTSL, β-Catenin, PPM1D, Chkl, WISP1, and LOT1;

(m) HER2, TP53BP2, Bc12, DIABLO, TIMP1, EPHX1, TOP2A, TRAIL, CA9, and AREG;

(n) BAG1, TP53BP2, PRAME, IL6, CCNB1, PAI1 AREG, tumor size, CA9, and Ki67;

(o) CEGP1, TP53BP2, PRAME, DIABLO, Bc12, COX2, CCNE1, STK15, and AKT2, and FGF18;

(p) STK15, TP53BP2, PRAME, IL6, CCNE1, AKT2, DIABLO, cMet, CCNE2, and COX2;

(q) KLK10, EstR1, TP53BP2, PRAME, DIABLO, CTSL, PPM1D, GRB7, DAPK1, and BBC3;

(r) AIB1, TP53BP2, Bc12, DIABLO, TIMP1, CD3, p53, CA9, GRB7, and EPHX1

(s) BBC3, GRB7, CD68, PRAME, TOP2A, CCNB1, EPHX1, CTSL GSTM1, and APC;

(t) CD9, GRB7, CD68, TOP2A, Bc12, CCNB1, CD3, DIABLO, ID1, and PPM1D;

(w) EGFR, KRT14, GRB7, TOP2A, CCNB1, CTSL, Bc12, TP, KLK10, and CA9;

(x) HIF1α, PR, DIABLO, PRAME, Chkl, AKT2, GRB7, CCNE1, TOP2A, and CCNB1;

(y) MDM2, TP53BP2, DIABLO, Bc12, AIB1, TIMP1, CD3, p53, CA9, and HER2;

(z) MYBL2, TP53BP2, PRAME, IL6, Bc12, DIABLO, CCNE1, EPHX1, TIMP1, and CA9;

(aa) p27, TP53BP2, PRAME, DIABLO, Bc12, COX2, CCNE1, STK15, AKT2, and ID1;

(ab) RAD51, GRB7, CD68, TOP2A, CIAP2, CCNB1, BAG1, IL6, FGFR1, and TP53BP2;

(ac) SURV, GRB7, TOP2A, PRAME, CTSL, GSTM1, CCNB1, VDR, CA9; and CCNE2;

(ad) TOP2B, TP53BP2, DIABLO, Bc12, TIMP1, AIB1, CA9, p53, KRT8, and BAD;

(ae) ZNF217, GRB7, TP53BP2, PRAME, DIABLO, Bc12, COX2, CCNE1, APC4, and β-Catenin,

in a breast cancer tissue sample obtained from said patient, normalized against the expression levels of all RNA transcripts or their expression products in said breast cancer tissue sample, or of a reference set of RNA transcripts or their products;

(2) subjecting the data obtained in step (1) to statistical analysis; and

(3) determining whether the likelihood of said long-term survival has increased or decreased.

22. A method of predicting the likelihood of long-term survival of a patient diagnosed with estrogen receptor (ER)-positive invasive breast cancer, without the recurrence of breast cancer, comprising the steps of:

(1) determining the expression levels of the RNA transcripts or the expression products of genes of a gene set selected from the group consisting of CD68; CTSL; FBXO5; SURV; CCNB1; MCM2; Chkl; MYBL2; HIF1A; cMET; EGFR; TS; STK15, IGFR1; BC12; HNF3A; TP53BP2; GATA3; BBC3; RAD51C; BAG1; IGFBP2; PR; CD9; RB1; EPHX1; CEGP1; TRAIL; DR5; p27; p53; MTA; RIZ1; ErbB3; T OP2B ; EIF4E, wherein expression of the following genes in ER-positive cancer is indicative of a reduced likelihood of survival without cancer recurrence following surgery: CD68; CTSL; FBXO5; SURV; CCNB1; MCM2; Chkl; MYBL2; HIF1A; cMET; EGFR; TS; STK15, and wherein expression of the following genes is indicative of a better prognosis for survival without cancer recurrence following surgery: IGFR1; BC12; HNF3A; TP53BP2; GATA3; BBC3; RAD51C; BAG1; IGFBP2; PR; CD9; RB1; EPHX1; CEGP1; TRAIL; DR5; p27; p53; MTA; RIZ1; ErbB3; TOP2B;

(2) subjecting the data obtained in step (1) to statistical analysis; and

(3) determining whether the likelihood of said long-term survival has increased or decreased.

23. The method of claim 21 or 22 wherein said statistical analysis is performed by using the Cox Proportional Hazards model.

24. A method of predicting the likelihood of long-term survival of a patient diagnosed with estrogen receptor (ER)-negative invasive breast cancer, without the recurrence of breast cancer, comprising determining the expression levels of the RNA transcripts or the expression products of genes of the gene set CCND1; UPA; HNF3A; CDH1; Her2; GRB7; AKT1; STMY3; α-Catenin; VDR; GRO1; KT14; KLK10; Maspin, TGFα, and FRP1, wherein expression of the following genes is indicative of a reduced likelihood of survival without cancer recurrence: CCND1; UPA; HNF3A; CDH1; Her2; GRB7; AKT1; STMY3; α-Catenin; VDR; GRO1, and wherein expression of the following genes is indicative of a better prognosis for survival without cancer recurrence: KT14; KLK10; Maspin, TGFα, and FRP1.

25. A method of preparing a personalized genomics profile for a patient, comprising the steps of:

(a) subjecting RNA extracted from a breast tissue obtained from the patient to gene expression analysis;

(b) determining the expression level of one or more genes selected from the breast cancer gene set listed in any one of Tables 1-5, wherein the expression level is normalized against a control gene or genes and optionally is compared to the amount found in a breast cancer reference tissue set; and

(c) creating a report summarizing the data obtained by said gene expression analysis.

26. The method of claim 25, wherein said breast tissue comprises breast cancer cells.

27. The method of claim 26 wherein said breast tissue is obtained from a fixed, paraffin-embedded biopsy sample.

28. The method of claim 27 wherein said RNA is fragmented.

29. The method of claim 25 wherein said report includes prediction of the likelihood of long term survival of the patient.

30. The method of claim 25 wherein said report includes recommendation for a treatment modality of said patient.

31. A method for amplification of a gene listed in Tables 5A and B by polymerase chain reaction (PCR), comprising performing said PCR by using an amplicon listed in Tables 5A and B and a primer-probe set listed in Tables 6A-F.

32. A PCR amplicon listed in Tables 5A and B.

33. A PCR primer-probe set listed in Tables 6A-F.

34. A prognostic method comprising:

(a) subjecting a sample comprising breast cancer cells obtained from a patient to quantitative analysis of the expression level of the RNA transcript of at least one gene selected from the group consisting of GRB7, CD68, CTSL, Chkl, AIB1, CCNB1, MCM2, FBXO5, Her2, STK15, SURV, EGFR, MYBL2, HIFlα, and TS, or their product, and

(b) identifying the patient as likely to have a decreased likelihood of long-term survival without breast cancer recurrence if the normalized expression levels of said gene or genes, or their products, are elevated above a defined expression threshold.

35. A prognostic method comprising:

(a) subjecting a sample comprising breast cancer cells obtained from a patient to quantitative analysis of the expression level of the RNA transcript of at least one gene selected from the group consisting of TP53BP2, PR, Bc12, KRT14, EstR1, IGFBP2, BAG1, CEGP1, KLK10, β-Catenin, γ-Catenin, DR5, PI3KCA2, RAD51C, GSTM1, FHIT, RIZ1, BBC3, TBP, p27, IRS1, IGF1R, GATA3, ZNF217, CD9, pS2, ErbB3, TOP2B, MDM2, IGF1, and KRT19, and

(b) identifying the patient as likely to have an increased likelihood of long-term survival without breast cancer recurrence if the normalized expression levels of said gene or genes, or their products, are elevated above a defined expression threshold.

36. The method of claim 1 wherein the levels of the RNA transcripts of said genes are normalized relative to the mean level of the RNA transcript or the product of two or more housekeeping genes.

37. The method of claim 34 or 35 wherein the housekeeping genes are selected from the group consisting of glyceraldehyde-3-phosphate dehydrogenase (GAPDH), Cyp, albumin, actins, tubulins, cyclophilin hypoxantine phosphoribosyltransferase (HRPT), L32, 28S, and 18S.

38. The method of claim 34 or 35 wherein the sample is subjected to global gene expression analysis of all genes present above the limit of detection.

39. The method of claim 37 wherein the levels of the RNA transcripts of said genes are normalized relative to the mean signal of the RNA transcripts or the products of all assayed genes or a subset thereof.

40. The method of claim 38 wherein the level of RNA transcripts is determined by quantitative RT-PCR (qRT-PCR), and the signal is a Ct value.

41. The method of claim 39 wherein the assayed genes include at least 50 cancer related genes.

42. The method of claim 39 wherein the assayed genes includes at least 100 cancer related genes.

43. The method of claim 34 or 35 wherein said patient is human.

44. The method of claim 42 wherein said sample is a fixed, paraffin-embedded tissue (FPET) sample, or fresh or frozen tissue sample.

45. The method of claim 42 wherein said sample is a tissue sample from fine needle, core, or other types of biopsy.

46. The method of claim 42 wherein said quantitative analysis is performed by 30 qRT-PCR.

47. The method of claim 42 wherein said quantitative analysis is performed by quantifying the products of said genes.

48. The method of claim 45 wherein said products are quantified by immunohistochemistry or by proteomics technology.

49. The method of claim 34 further comprising the step of preparing a report indicating that the patient has a decreased likelihood of long-term survival without breast cancer recurrence.

50. The method of claim 35 further comprising the step of preparing a report indicating that the patient has an increased likelihood of long-term survival without breast cancer recurrence.

51. A kit comprising one or more of (1) extraction buffer/reagents and protocol; (2) reverse transcription buffer/reagents and protocol; and (3) qPCR buffer/reagents and protocol suitable for performing the method of any one of claims 1, 34 and 35.