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(54) Title: BREAST CANCER PROGNOSIS SIGNATURES

(57) Abstract: The invention provides for molecular classification of disease and, particularly, molecular markers for breast cancer prognosis and methods and systems of use thereof.



BREAST CANCER PROGNOSIS SIGNATURES

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the priority benefit of U.S. Provisional Application Serial Nos. 61/678,838 (filed on August 2, 2012), 61/673,538 (filed on July 19, 2012), 61/587,455 (filed on January 17, 2012), each of which is hereby incorporated by reference in its entirety.

FIELD OF THE INVENTION

[0002] The invention generally relates to a molecular classification of disease and particularly to molecular markers for breast cancer prognosis and methods of use thereof.

BACKGROUND OF THE INVENTION

[0003] Cancer is a major public health problem, accounting for roughly 25% of all deaths in the United States. *American Cancer Society, FACTS AND FIGURES 2010*. Though many treatments have been devised for various cancers, these treatments often vary in severity of side effects. It is useful for clinicians to know how aggressive a patient's cancer is in order to determine how aggressively to treat the cancer.

SUMMARY OF THE INVENTION

[0004] Inventors previously discovered that the expression of those genes whose expression closely tracks the cell cycle ("cell-cycle genes," "CCGs," or "CCP genes" as further defined below) is particularly useful in determining the prognosis in a patient having breast cancer. *See* WO/2010/080933 (also corresponding U.S. Application No. 13/177,887) and WO/2012/006447 (also related U.S. Application No. 13/178,380), each of which is incorporated herein by reference. The inventors have discovered new CCG panels that are similarly prognostic in cancer (e.g., Panels H, I, J, L, M, N & O in Tables 10, 11 & 25 below; "sub-panels" of Panel O in Tables 30 to 34 below). It has now been surprisingly discovered that the expression of certain additional genes, e.g.,

the *ABCC5* and *PGR* genes, each alone or together, is also prognostic, and adds significant prediction power to CCG expression in the prognosis of breast cancer.

[0005] Accordingly, in a first aspect, the present invention provides a method for determining gene expression in a tumor sample from a patient identified as having breast cancer. Generally, the method includes at least the following steps: (1) obtaining one or more tumor samples from a patient identified as having breast cancer; (2) determining the expression of a panel of genes in said tumor sample(s) including at least 4 cell-cycle genes, *ABCC5*, and *PGR*; and (3) providing a test value by (a) weighting the determined expression of each of a plurality of test genes selected from said panel of genes with a predefined coefficient, and (b) combining the weighted expression to provide said test value, wherein at least 50%, at least 75% or at least 90% of said plurality of test genes are cell-cycle genes (or wherein cell-cycle genes represent at least 50%, at least 75% or at least 85% of the combined weight used to provide the test value). In some embodiments, one or both of *ABCC5* and/or *PGR* is a test gene used to provide the test value. In some embodiments, neither *ABCC5* nor *PGR* is a test gene used to provide the test value.

[0006] In another aspect, the present invention provides a method for determining the prognosis in a patient having breast cancer or the likelihood of breast cancer recurrence, which comprises: determining in a tumor sample from the patient the expression of the *ABCC5* gene, and using the expression of the *ABCC5* gene in determining the prognosis of the breast cancer in the patient, or predicting the breast cancer outcome, the likelihood of breast cancer recurrence or probability of post-surgery distant metastasis-free survival. Optionally, but not necessarily, the method further comprises a step of determining in the same or a different tumor sample from the patient the expression of the *PGR* gene. In some embodiments, the patient is *ER*⁺ and node negative. In some embodiments, the patient is *ER*⁺ and node negative, has undergone surgery to remove some or all of the tumor in her breast, and is placed on hormone therapy.

[0007] In another aspect, the present invention provides a method for determining the prognosis in a patient having breast cancer or the likelihood of breast cancer recurrence, which comprises: determining in a tumor sample from the patient the expression of the *PGR* gene, and using the expression of the *PGR* gene in determining the prognosis of the breast cancer in the patient, or predicting the breast cancer outcome, the likelihood of breast cancer recurrence or probability of post-surgery distant metastasis-free survival. In some embodiments, the patient is

ER⁺ and node negative. In some embodiments, the patient is *ER*⁺ and node negative, has undergone surgery to remove some or all of the tumor in her breast, and is placed on hormone therapy. In some embodiments, the method further comprises determining whether the patient has undergone hormonal therapy. In these embodiments, if the patient has undergone hormonal therapy, then the method further comprises correlating increased *PGR* expression to better prognosis. Conversely, if the patient has not undergone hormonal therapy, then the method further comprises correlating increased *PGR* expression to worse prognosis. In some embodiments, the method comprises correlating increased *PGR* expression to an increased likelihood of response to hormonal therapy.

[0008] In yet another aspect, the present invention provides a method for determining in a patient the prognosis of breast cancer or the likelihood of breast cancer recurrence, which comprises: determining in a sample from the patient the expression of a plurality of test genes comprising at least 6, 8, 10 or 15 or more cell-cycle genes, determining in the same or different sample from the patient the expression of the *ABCC5* gene and/or the *PGR* gene, and using the expression of said plurality of test genes and the expression of the *ABCC5* gene and/or the *PGR* gene in determining the prognosis of the breast cancer in the patient, or predicting the breast cancer outcome, the likelihood of breast cancer recurrence or probability of post-surgery distant metastasis-free survival. In some embodiments, the patient is *ER*⁺ and node negative. In some embodiments, the patient is *ER*⁺ and node negative, has undergone surgery to remove some or all of the tumor in her breast, and is placed on hormone therapy.

[0009] Clinical parameters may be combined with the information gained from CCG, *ABCC5*, and/or *PGR* analysis. Thus, in yet another aspect, the present invention provides a method for determining in a patient the prognosis of breast cancer or the likelihood of breast cancer recurrence, which comprises: determining in a sample from the patient the expression of a plurality of test genes comprising at least 6, 8, 10 or 15 or more cell-cycle genes, determining in the same or different sample from the patient the expression of the *ABCC5* gene and/or the *PGR* gene, determining at least one clinical parameter for the patient (*e.g.*, age, tumor size, node status, tumor stage), and using the expression of said plurality of test genes and the expression of the *ABCC5* gene and/or the *PGR* gene, and the clinical parameter(s), in determining the prognosis of the breast cancer in the patient, or predicting the breast cancer outcome, the likelihood of breast cancer recurrence or

probability of post-surgery distant metastasis-free survival. In some embodiments, the CCG, *ABCC5*, and/or *PGR* information and the clinical parameter information are combined to yield a quantitative (e.g., numerical) evaluation of the prognosis of the breast cancer in the patient, or the breast cancer outcome, the likelihood of breast cancer recurrence or probability of post-surgery distant metastasis-free survival.

[0010] In one aspect, the present invention provides a method for treating breast cancer, which comprises: determining in a tumor sample from a patient the expression of the *ABCC5* and/or *PGR* gene, and recommending, prescribing or administering a particular treatment regimen (e.g., a treatment regimen comprising chemotherapy, such as adjuvant or neoadjuvant chemotherapy) based at least in part on the determined *ABCC5* and/or *PGR* expression. In some embodiments, a treatment regimen comprising chemotherapy is recommended, prescribed or administered based at least in part on the determination that the tumor sample has an increased level of *ABCC5* expression. In some embodiments, a treatment regimen comprising hormonal therapy is recommended, prescribed or administered based at least in part on the determination that the tumor sample has an increased level of *PGR* expression. In some embodiments, if an increased level of *ABCC5* and/or a decreased *PGR* expression is determined then the method further comprises administering to the patient a regimen comprising chemotherapy (and/or radiation) and not comprising hormonal therapy.

[0011] In another aspect, the present invention provides a method for treating breast cancer in a patient, which comprises: determining in a sample from the patient the expression of a plurality of test genes comprising at least 6, 8, 10 or 15 or more cell-cycle genes, determining in the same or different sample from the patient the expression of the *ABCC5* gene and/or the *PGR* gene, and recommending, prescribing or administering a particular treatment regimen (e.g., a treatment regimen comprising chemotherapy) based in part on the determined expression of the plurality of test genes, as well as the determined *ABCC5* and/or *PGR* expression. In some embodiments, a treatment regimen comprising a non-hormonal therapy agent (e.g., chemotherapy) or radiotherapy is recommended, prescribed or administered based at least in part on any of (1) an increased level of the plurality of test genes, (2) an increased level of *ABCC5* expression, and/or (3) decreased level of *PGR* expression. In some embodiments, a treatment regimen comprising a non-hormonal therapy agent (e.g., chemotherapy) or radiotherapy is recommended, prescribed or administered based at

least in part on any two of (1) an increased level of the plurality of test genes, (2) an increased level of *ABCC5* expression, and/or (3) decreased level of *PGR* expression. In some embodiments, a treatment regimen comprising a non-hormonal therapy agent (e.g., chemotherapy) or radiotherapy is recommended, prescribed or administered based at least in part on (1) an increased level of the plurality of test genes, (2) an increased level of *ABCC5* expression, and (3) decreased level of *PGR* expression. In some embodiments, a treatment regimen comprising a non-hormonal therapy agent (e.g., chemotherapy) or radiotherapy, and not comprising hormonal therapy, is recommended, prescribed or administered based at least in part on any of (1) an increased level of the plurality of test genes, (2) an increased level of *ABCC5* expression, and/or (3) decreased level of *PGR* expression. In some embodiments, a treatment regimen comprising hormonal therapy is recommended, prescribed or administered based at least in part on increased level of *PGR* expression.

[0012] In some embodiments of the methods described above, the patient is *ER*⁺ and node negative. In some embodiments, the patient is *ER*⁺ and node negative, has undergone surgery to remove the tumor in her breast, and is placed on hormone therapy. In some embodiments of the methods described above, the patient is *ER*⁺ and node positive.

[0013] In some embodiments, the plurality of test genes includes at least 8 cell-cycle genes, or at least 10, 15, 20, 25 or 30 cell-cycle genes. In some embodiments, at least 10%, 15%, 20%, 25%, 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95%, or 99% of the plurality of test genes are cell-cycle genes. In some embodiments, all of the test genes are cell-cycle genes.

[0014] In some embodiments, the step of determining the expression of the plurality of test genes in the tumor sample comprises measuring the amount of mRNA in the tumor sample transcribed from each of from 6 to about 200 cell-cycle genes; and measuring the amount of mRNA of one or more housekeeping genes in the tumor sample.

[0015] In some embodiments, the step of determining the expression of the plurality of test genes in the tumor sample comprises (1) determining in a tumor sample from a patient having breast cancer the expression of a panel of genes in said tumor sample including at least 4 or at least 8 cell-cycle genes; and (2) providing a “CCG score” by (a) weighting the determined expression of each of a plurality of test genes selected from the panel of genes with a predefined coefficient, and (b) combining the weighted expression to provide the CCG score, wherein at least 50%, at least 75%

or at least 85% of the plurality of test genes are cell-cycle genes (or wherein cell-cycle genes represent at least 50%, at least 75% or at least 85% of the combined weight used to provide the CCG score).

[0016] In some embodiments, the prognosis method comprises (1) determining in a tumor sample from a patient having breast cancer the expression of a panel of genes including at least 4, 8, 10 or 15 cell-cycle genes; (2) providing a “CCG score” by (a) weighting the determined expression of each of a plurality of test genes selected from the panel of genes with a predefined coefficient, and (b) combining the weighted expression to provide the CCG score, wherein at least 50%, at least 75% or at least 85% of the plurality of test genes are cell-cycle genes; (3) determining in a tumor sample from a patient having breast cancer the expression of the *ABCC5* gene; and (4) providing a test value by weighting the determined CCG score and the determined expression of the *ABCC5* gene with their respective predefined coefficients and combining the weighted expression.

[0017] In some embodiments, the prognosis method comprises (1) determining in a tumor sample from a patient having breast cancer the expression of a panel of genes including at least 4 or at least 8 or 10 or 15 cell-cycle genes; (2) providing a “CCG score” by (a) weighting the determined expression of each of a plurality of test genes selected from the panel of genes with a predefined coefficient, and (b) combining the weighted expression to provide the CCG score, wherein at least 50%, at least 75% or at least 85% of the plurality of test genes are cell-cycle genes; (3) determining in a tumor sample from a patient having breast cancer the expression of the *PGR* gene; and (4) providing a test value by weighting the determined CCG score and the determined expression of the *PGR* gene with their respective predefined coefficients and combining the weighted expression.

[0018] In one aspect of the present invention, a method is provided for determining gene expression in a tumor sample from a patient identified as having breast cancer, prostate cancer, lung cancer, bladder cancer, or brain cancer. Generally, the method includes at least the following steps: (1) obtaining a tumor sample from a patient identified as having breast cancer, prostate cancer, lung cancer, bladder cancer, or brain cancer; (2) determining the expression of a panel of genes in said tumor sample including at least 2, 3, 4, 5 or 6 cell-cycle genes chosen from the group of genes in any of Panels H, I, J, L, M, N & O (including “sub-panels” of Panel O in Tables 30 to 34); and (3) providing a test value by (a) weighting the determined expression of each of a plurality of test genes

selected from said panel of genes with a predefined coefficient, and (b) combining the weighted expression to provide said test value, wherein at least 50%, at least 75% or at least 90% of said plurality of test genes are cell-cycle genes.

[0019] In some embodiments, the plurality of test genes includes at least 8 cell-cycle genes, or at least 10, 15, 20, or 25 cell-cycle genes from any of Panels H, I, J, L, M, N & O (at least 2, 3, 4, 5, or 6 of which are in a sub-panel of Panel O in Tables 30 to 34). In some embodiments, all of the test genes are cell-cycle genes. In some embodiments, the plurality of test genes includes at least 8, 10, 15, 20, or 25 genes from any of Panels H, I, J, L, M, N & O (at least 2, 3, 4, 5, or 6 of which are in a sub-panel of Panel O in Tables 30 to 34).

[0020] In another aspect of the present invention, a method is provided for determining the prognosis of breast cancer, prostate cancer, lung cancer, bladder cancer or brain cancer, which comprises determining in a tumor sample from a patient diagnosed of breast cancer, prostate cancer, lung cancer, bladder cancer or brain cancer, the expression of at least 6, 8 or 10 cell-cycle genes in any of Panels H, I, J, L, M, N & O (at least 2, 3, 4, 5, or 6 of which are in a sub-panel of Panel O in Tables 30 to 34), wherein overexpression of said at least 6, 8 or 10 cell-cycle genes indicates a poor prognosis or an increased likelihood of recurrence of cancer in the patient.

[0021] In one embodiment, the prognosis method comprises (1) determining in a tumor sample from a patient diagnosed of breast cancer, prostate cancer, lung cancer, bladder cancer or brain cancer, the expression of a panel of genes in said tumor sample including at least 4 or at least 8 cell-cycle genes in any of Panels H, I, J, L, M, N & O (at least 2, 3, 4, 5, or 6 of which are in a sub-panel of Panel O in Tables 30 to 34); and (2) providing a test value by (a) weighting the determined expression of each of a plurality of test genes selected from the panel of genes with a predefined coefficient, and (b) combining the weighted expression to provide the test value, wherein at least 50%, at least 75% or at least 85% of the plurality of test genes are cell-cycle genes in any of Panels H, I, J, L, M, N & O (including at least 2, 3, 4, 5, or 6 genes in a sub-panel of Panel O in Tables 30 to 34), and wherein an increased level of overall expression of the plurality of test genes indicates a poor prognosis, whereas if there is no increase in the overall expression of the test genes, it would indicate a good prognosis or a low likelihood of recurrence of cancer in the patient.

[0022] In preferred embodiments, the prognosis method further includes a step of comparing the test value provided in step (2) above to one or more reference values, and correlating

the test value to a risk of cancer progression or risk of cancer recurrence. Optionally an increased likelihood of poor prognosis is indicated if the test value is greater than the reference value.

[0023] In yet another aspect, the present invention also provides a method of treating cancer in a patient identified as having breast cancer, prostate cancer, lung cancer, bladder cancer or brain cancer, comprising: (1) determining in a tumor sample from a patient diagnosed of breast cancer, prostate cancer, lung cancer, bladder cancer or brain cancer, the expression of a panel of genes in the tumor sample including at least 4 or at least 8 cell-cycle genes in any of Panels H, I, J, L, M, N & O (at least 2, 3, 4, 5, or 6 of which are in a sub-panel of Panel O in Tables 30 to 34); (2) providing a test value by (a) weighting the determined expression of each of a plurality of test genes selected from said panel of genes with a predefined coefficient, and (b) combining the weighted expression to provide said test value, wherein at least 50% or 75% or 85% of the plurality of test genes are cell-cycle genes, wherein an increased level of expression of the plurality of test genes indicates a poor prognosis, and an un-increased level of expression of the plurality of test genes indicates a good prognosis; and recommending, prescribing or administering a treatment regimen or watchful waiting based on the prognosis provided in step (2).

[0024] The present invention further provides a diagnostic kit for determining the prognosis of breast cancer in a patient, comprising, in a compartmentalized container, a plurality of oligonucleotides hybridizing to at least 8 test genes, wherein less than 10%, 30% or less than 40% of all of the at least 8 test genes are non-cell-cycle genes; one or more oligonucleotides hybridizing to the *ABCC5* gene. Optionally but not necessarily, the kit further includes one or more oligonucleotides hybridizing to the *PGR* gene. The kit may further include one or more oligonucleotides hybridizing to at least one housekeeping gene. The oligonucleotides can be hybridizing probes for hybridization with the genes under stringent conditions or primers suitable for PCR amplification of the genes. In one embodiment, the kit consists essentially of, in a compartmentalized container, a first plurality of PCR reaction mixtures for PCR amplification of from 5 or 10 to about 300 test genes, wherein at least 30% or 50%, at least 60% or at least 80% of such test genes are cell-cycle genes, and wherein each reaction mixture comprises a PCR primer pair for PCR amplifying one of the test genes; and a second plurality of PCR reaction mixtures for PCR amplification of the *ABCC5* and/or *PGR* gene. In some embodiments the kit comprises one or more computer software programs for calculating a test value representing the expression of the test genes

(either the overall expression of all test genes or of some subset) and the expression of the *ABCC5* and/or *PGR* gene, and for comparing this test value to some reference value. In some embodiments such computer software is programmed to weight the test genes such that cell-cycle genes are weighted to contribute at least 50%, at least 75% or at least 85% of the test value. In some embodiments such computer software is programmed to communicate (*e.g.*, display) that the patient has an increased likelihood of response to a treatment regimen comprising chemotherapy if the test value is greater than the reference value (*e.g.*, by more than some predetermined amount).

[0025] The present invention also provides the use of (1) a plurality of oligonucleotides hybridizing to at least 4 or at least 8 cell-cycle genes; and (2) one or more oligonucleotides hybridizing to the *ABCC5* and/or *PGR* gene, for the manufacture of a diagnostic product for determining the expression of the test genes in a tumor sample from a patient having breast cancer, for the prognosis of breast cancer in the patient, wherein an increased level of the overall expression of the test genes indicates an increased likelihood, whereas no increase in the overall expression of the test genes indicates no increased likelihood. In some embodiments, the oligonucleotides are PCR primers suitable for PCR amplification of the test genes. In other embodiments, the oligonucleotides are probes hybridizing to the test genes under stringent conditions. In some embodiments, the plurality of oligonucleotides are probes for hybridization under stringent conditions to, or are suitable for PCR amplification of, from 4 to about 300 test genes, at least 50%, 70% or 80% or 90% of the test genes being cell-cycle genes. In some other embodiments, the plurality of oligonucleotides are hybridization probes for, or are suitable for PCR amplification of, from 20 to about 300 test genes, at least 30%, 40%, 50%, 70% or 80% or 90% of the test genes being cell-cycle genes.

[0026] The present invention further provides a system for determining breast cancer prognosis in a patient, comprising: (1) a sample analyzer for determining the expression levels of a panel of genes in a tumor sample including at least 4 cell-cycle genes, and the expression levels of the *ABCC5* and/or *PGR* genes, wherein the sample analyzer contains the tumor sample, mRNA molecules expressed from the panel of genes and extracted from the sample, or cDNA molecules from said mRNA molecules; (2) a first computer program for (a) receiving gene expression data on at least 4 test genes selected from the panel of genes, and the *ABCC5* and/or *PGR* genes, (b) weighting the determined expression of each of the test genes with a predefined coefficient, and (c)

combining the weighted expression to provide a test value, wherein at least 50%, at least at least 75% of at least 4 test genes are cell-cycle genes; and (3) a second computer program for comparing the test value to one or more reference values each associated with a predetermined likelihood of breast cancer recurrence or post-surgery distant metastasis-free survival. In some embodiments, the system further comprises a display module displaying the comparison between the test value and the one or more reference values, or displaying a result of the comparing step.

[0027] Unless otherwise defined, all 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 pertains. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. In case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

[0028] Other features and advantages of the invention will be apparent from the following Detailed Description, and from the Claims.

BRIEF DESCRIPTION OF THE DRAWINGS

[0029] Figure 1 illustrates the relationship between *PGR* qPCR expression and PR IHC expression in the breast tumor samples assayed.

[0030] Figure 2 is a Kaplan Meier plot of distant metastasis-free survival for CCP score quartiles in the breast tumor samples assayed.

[0031] Figure 3 is an illustration of an example of a system useful in certain aspects and embodiments of the invention.

[0032] Figure 4 is a flowchart illustrating an example of a computer-implemented method of the invention.

[0033] Figure 5 is a Kaplan Meier plot of distant metastasis-free survival for PR IHC in the breast tumor samples assayed.

[0034] Figure 6 is a Kaplan Meier plot of distant metastasis-free survival for *ABCC5* expression quartiles in the breast tumor samples assayed.

[0035] Figure 7 is a plot showing the relationship between CCP score and response to neoadjuvant therapy.

DETAILED DESCRIPTION OF THE INVENTION

[0036] The present invention is based in part on the discovery that the expression levels of the *ABCC5* and *PGR* genes in breast tumor sample from a breast cancer patient correlate with the prognosis of the breast cancer, and that they add significant prediction power when combined with cell-cycle genes (“CCGs”).

[0037] “Cell-cycle gene” and “CCG” herein refer to a gene whose expression level closely tracks the progression of the cell through the cell-cycle. *See, e.g.*, Whitfield *et al.*, MOL. BIOL. CELL (2002) 13:1977-2000. The term “cell-cycle progression” or “CCP” will also be used in this application and will generally be interchangeable with CCG (*i.e.*, a CCP gene is a CCG; a CCP score is a CCG score). More specifically, CCGs show periodic increases and decreases in expression that coincide with certain phases of the cell cycle—*e.g.*, *STK15* and *PLK* show peak expression at G2/M. *Id.* Often CCGs have clear, recognized cell-cycle related function —*e.g.*, in DNA synthesis or repair, in chromosome condensation, in cell-division, etc. However, some CCGs have expression levels that track the cell-cycle without having an obvious, direct role in the cell-cycle—*e.g.*, *UBE2S* encodes a ubiquitin-conjugating enzyme, yet its expression closely tracks the cell-cycle. Thus a CCG according to the present invention need not have a recognized role in the cell-cycle. Exemplary CCGs are listed in Tables 1, 2, 3, 5, 6, 7, 8 & 9. A fuller discussion of CCGs, including an extensive (though not exhaustive) list of CCGs, can be found in International Application No. PCT /US2010/020397 (pub. no. WO/2010/080933) (*see, e.g.*, Table 1 in WO/2010/080933). International Application No. PCT/US2010/020397 (pub. no. WO/2010/080933 (see also corresponding U.S. Application No. 13/177,887)) and International Application No. PCT/US2011/043228 (pub no. WO/2012/006447 (see also related U.S. Application No. 13/178,380)) and their contents are hereby incorporated by reference in their entirety.

[0038] Whether a particular gene is a CCG may be determined by any technique known in the art, including those taught in Whitfield *et al.*, MOL. BIOL. CELL (2002) 13:1977-2000; Whitfield *et al.*, MOL. CELL. BIOL. (2000) 20:4188-4198; WO/2010/080933 (¶ [0039]). All of the CCGs in Table 1 below form a panel of CCGs (“Panel A”) useful in the invention. As will be shown

detail throughout this document, individual CCGs (e.g., CCGs in Table 1) and subsets of these genes can also be used in the invention.

Table 1

Gene Symbol	Entrez GeneID	ABI Assay ID	RefSeq Accession Nos.
<i>APOBEC3B*</i>	9582	Hs00358981_m1	NM_004900.3
<i>ASF1B*</i>	55723	Hs00216780_m1	NM_018154.2
<i>ASPM*</i>	259266	Hs00411505_m1	NM_018136.4
<i>ATAD2*</i>	29028	Hs00204205_m1	NM_014109.3
<i>BIRC5*</i>	332	Hs00153353_m1; Hs03043576_m1	NM_001012271.1; NM_001012270.1; NM_001168.2
<i>BLM*</i>	641	Hs00172060_m1	NM_000057.2
<i>BUB1</i>	699	Hs00177821_m1	NM_004336.3
<i>BUB1B*</i>	701	Hs01084828_m1	NM_001211.5
<i>C12orf48*</i>	55010	Hs00215575_m1	NM_017915.2
<i>C18orf24*</i>	220134	Hs00536843_m1	NM_145060.3; NM_001039535.2
<i>C1orf135*</i>	79000	Hs00225211_m1	NM_024037.1
<i>C21orf45*</i>	54069	Hs00219050_m1	NM_018944.2
<i>CCDC99*</i>	54908	Hs00215019_m1	NM_017785.4
<i>CCNA2*</i>	890	Hs00153138_m1	NM_001237.3
<i>CCNB1*</i>	891	Hs00259126_m1	NM_031966.2
<i>CCNB2*</i>	9133	Hs00270424_m1	NM_004701.2
<i>CCNE1*</i>	898	Hs01026536_m1	NM_001238.1; NM_057182.1
<i>CDC2*</i>	983	Hs00364293_m1	NM_033379.3; NM_001130829.1; NM_001786.3
<i>CDC20*</i>	991	Hs03004916_g1	NM_001255.2
<i>CDC45L*</i>	8318	Hs00185895_m1	NM_003504.3
<i>CDC6*</i>	990	Hs00154374_m1	NM_001254.3
<i>CDC43*</i>	83461	Hs00229905_m1	NM_031299.4
<i>CDC48*</i>	55143	Hs00983655_m1	NM_018101.2
<i>CDKN3*</i>	1033	Hs00193192_m1	NM_001130851.1; NM_005192.3

<i>CDTI*</i>	81620	Hs00368864_m1	NM_030928.3
<i>CENPA</i>	1058	Hs00156455_m1	NM_001042426.1; NM_001809.3
<i>CENPE*</i>	1062	Hs00156507_m1	NM_001813.2
<i>CENPF*</i>	1063	Hs00193201_m1	NM_016343.3
<i>CENPI*</i>	2491	Hs00198791_m1	NM_006733.2
<i>CENPM*</i>	79019	Hs00608780_m1	NM_024053.3
<i>CENPN*</i>	55839	Hs00218401_m1	NM_018455.4; NM_001100624.1; NM_001100625.1
<i>CEP55*</i>	55165	Hs00216688_m1	NM_018131.4; NM_001127182.1
<i>CHEK1*</i>	1111	Hs00967506_m1	NM_001114121.1; NM_001114122.1; NM_001274.4
<i>CKAP2*</i>	26586	Hs00217068_m1	NM_018204.3; NM_001098525.1
<i>CKS1B*</i>	1163	Hs01029137_g1	NM_001826.2
<i>CKS2*</i>	1164	Hs01048812_g1	NM_001827.1
<i>CTPS*</i>	1503	Hs01041851_m1	NM_001905.2
<i>CTSL2*</i>	1515	Hs00952036_m1	NM_001333.2
<i>DBF4*</i>	10926	Hs00272696_m1	NM_006716.3
<i>DDX39*</i>	10212	Hs00271794_m1	NM_005804.2
<i>DLGAP5/ DLG7*</i>	9787	Hs00207323_m1	NM_014750.3
<i>DONSON*</i>	29980	Hs00375083_m1	NM_017613.2
<i>DSN1*</i>	79980	Hs00227760_m1	NM_024918.2
<i>DTL*</i>	51514	Hs00978565_m1	NM_016448.2
<i>E2F8*</i>	79733	Hs00226635_m1	NM_024680.2
<i>ECT2*</i>	1894	Hs00216455_m1	NM_018098.4
<i>ESPL1*</i>	9700	Hs00202246_m1	NM_012291.4
<i>EXO1*</i>	9156	Hs00243513_m1	NM_130398.2; NM_003686.3; NM_006027.3

<i>EZH2*</i>	2146	Hs00544830_m1	NM_152998.1; NM_004456.3
<i>FANCI*</i>	55215	Hs00289551_m1	NM_018193.2; NM_001113378.1
<i>FBXO5*</i>	26271	Hs03070834_m1	NM_001142522.1; NM_012177.3
<i>FOXMI*</i>	2305	Hs01073586_m1	NM_202003.1; NM_202002.1; NM_021953.2
<i>GINSI*</i>	9837	Hs00221421_m1	NM_021067.3
<i>GMPS*</i>	8833	Hs00269500_m1	NM_003875.2
<i>GPSM2*</i>	29899	Hs00203271_m1	NM_013296.4
<i>GTSE1*</i>	51512	Hs00212681_m1	NM_016426.5
<i>H2AFX*</i>	3014	Hs00266783_s1	NM_002105.2
<i>HMMR*</i>	3161	Hs00234864_m1	NM_001142556.1; NM_001142557.1; NM_012484.2; NM_012485.2
<i>HNI*</i>	51155	Hs00602957_m1	NM_001002033.1; NM_001002032.1; NM_016185.2
<i>KIAA0101*</i>	9768	Hs00207134_m1	NM_014736.4
<i>KIF11*</i>	3832	Hs00189698_m1	NM_004523.3
<i>KIF15*</i>	56992	Hs00173349_m1	NM_020242.2
<i>KIF18A*</i>	81930	Hs01015428_m1	NM_031217.3
<i>KIF20A*</i>	10112	Hs00993573_m1	NM_005733.2
<i>KIF20B/ MPHOSPH1*</i>	9585	Hs01027505_m1	NM_016195.2
<i>KIF23*</i>	9493	Hs00370852_m1	NM_138555.1; NM_004856.4
<i>KIF2C*</i>	11004	Hs00199232_m1	NM_006845.3
<i>KIF4A*</i>	24137	Hs01020169_m1	NM_012310.3
<i>KIFC1*</i>	3833	Hs00954801_m1	NM_002263.3
<i>KPNA2</i>	3838	Hs00818252_g1	NM_002266.2

<i>LMNB2*</i>	84823	Hs00383326_m1	NM_032737.2
<i>MAD2L1</i>	4085	Hs01554513_g1	NM_002358.3
<i>MCAM*</i>	4162	Hs00174838_m1	NM_006500.2
<i>MCM10*</i>	55388	Hs00960349_m1	NM_018518.3; NM_182751.1
<i>MCM2*</i>	4171	Hs00170472_m1	NM_004526.2
<i>MCM4*</i>	4173	Hs00381539_m1	NM_005914.2; NM_182746.1
<i>MCM6*</i>	4175	Hs00195504_m1	NM_005915.4
<i>MCM7*</i>	4176	Hs01097212_m1	NM_005916.3; NM_182776.1
<i>MELK</i>	9833	Hs00207681_m1	NM_014791.2
<i>MKI67*</i>	4288	Hs00606991_m1	NM_002417.3
<i>MYBL2*</i>	4605	Hs00231158_m1	NM_002466.2
<i>NCAPD2*</i>	9918	Hs00274505_m1	NM_014865.3
<i>NCAPG*</i>	64151	Hs00254617_m1	NM_022346.3
<i>NCAPG2*</i>	54892	Hs00375141_m1	NM_017760.5
<i>NCAPH*</i>	23397	Hs01010752_m1	NM_015341.3
<i>NDC80*</i>	10403	Hs00196101_m1	NM_006101.2
<i>NEK2*</i>	4751	Hs00601227_mH	NM_002497.2
<i>NUSAP1*</i>	51203	Hs01006195_m1	NM_018454.6; NM_001129897.1; NM_016359.3
<i>OIP5*</i>	11339	Hs00299079_m1	NM_007280.1
<i>ORC6L*</i>	23594	Hs00204876_m1	NM_014321.2
<i>PAICS*</i>	10606	Hs00272390_m1	NM_001079524.1; NM_001079525.1; NM_006452.3
<i>PBK*</i>	55872	Hs00218544_m1	NM_018492.2
<i>PCNA*</i>	5111	Hs00427214_g1	NM_182649.1; NM_002592.2
<i>PDSSI*</i>	23590	Hs00372008_m1	NM_014317.3
<i>PLK1*</i>	5347	Hs00153444_m1	NM_005030.3

<i>PLK4*</i>	10733	Hs00179514_m1	NM_014264.3
<i>POLE2*</i>	5427	Hs00160277_m1	NM_002692.2
<i>PRCI*</i>	9055	Hs00187740_m1	NM_199413.1; NM_199414.1; NM_003981.2
<i>PSMA7*</i>	5688	Hs00895424_m1	NM_002792.2
<i>PSRC1*</i>	84722	Hs00364137_m1	NM_032636.6; NM_001005290.2; NM_001032290.1; NM_001032291.1
<i>PTTGI*</i>	9232	Hs00851754_u1	NM_004219.2
<i>RACGAP1*</i>	29127	Hs00374747_m1	NM_013277.3
<i>RAD51*</i>	5888	Hs00153418_m1	NM_133487.2; NM_002875.3
<i>RAD51API*</i>	10635	Hs01548891_m1	NM_001130862.1; NM_006479.4
<i>RAD54B*</i>	25788	Hs00610716_m1	NM_012415.2
<i>RAD54L*</i>	8438	Hs00269177_m1	NM_001142548.1; NM_003579.3
<i>RFC2*</i>	5982	Hs00945948_m1	NM_181471.1; NM_002914.3
<i>RFC4*</i>	5984	Hs00427469_m1	NM_181573.2; NM_002916.3
<i>RFC5*</i>	5985	Hs00738859_m1	NM_181578.2; NM_001130112.1; NM_001130113.1; NM_007370.4
<i>RNASEH2A*</i>	10535	Hs00197370_m1	NM_006397.2
<i>RRM2*</i>	6241	Hs00357247_g1	NM_001034.2
<i>SHCBP1*</i>	79801	Hs00226915_m1	NM_024745.4
<i>SMC2*</i>	10592	Hs00197593_m1	NM_001042550.1; NM_001042551.1; NM_006444.2

<i>SPAG5*</i>	10615	Hs00197708_m1	NM_006461.3
<i>SPC25*</i>	57405	Hs00221100_m1	NM_020675.3
<i>STIL*</i>	6491	Hs00161700_m1	NM_001048166.1; NM_003035.2
<i>STMN1*</i>	3925	Hs00606370_m1; Hs01033129_m1	NM_005563.3; NM_203399.1
<i>TACC3*</i>	10460	Hs00170751_m1	NM_006342.1
<i>TIMELESS*</i>	8914	Hs01086966_m1	NM_003920.2
<i>TK1*</i>	7083	Hs01062125_m1	NM_003258.4
<i>TOP2A*</i>	7153	Hs00172214_m1	NM_001067.2
<i>TPX2*</i>	22974	Hs00201616_m1	NM_012112.4
<i>TRIP13*</i>	9319	Hs01020073_m1	NM_004237.2
<i>TTK*</i>	7272	Hs00177412_m1	NM_003318.3
<i>TUBA1C*</i>	84790	Hs00733770_m1	NM_032704.3
<i>TYMS*</i>	7298	Hs00426591_m1	NM_001071.2
<i>UBE2C</i>	11065	Hs00964100_g1	NM_181799.1; NM_181800.1; NM_181801.1; NM_181802.1; NM_181803.1; NM_007019.2
<i>UBE2S</i>	27338	Hs00819350_m1	NM_014501.2
<i>VRK1*</i>	7443	Hs00177470_m1	NM_003384.2
<i>ZWILCH*</i>	55055	Hs01555249_m1	NM_017975.3; NR_003105.1
<i>ZWINT*</i>	11130	Hs00199952_m1	NM_032997.2; NM_001005413.1; NM_007057.3

* 124-gene subset of CCGs useful in the invention ("Panel B"). ABI Assay ID means the catalogue ID number for the gene expression assay commercially available from Applied Biosystems Inc. (Foster City, CA) for the particular gene.

[0039] The *ABCC5* gene (Entrez GeneID no. 10057) is also known as “ATP-binding cassette, sub-family C (CFTR/MRP), member 5.” Its expression can be determined by, e.g., using ABI Assay ID Hs00981085_m1. The *PGR* gene (Entrez GeneID no. 5241) is also known as “progesterone receptor gene” and its expression can be determined by, e.g., using ABI Assay ID Hs00172183_m1.

[0040] Accordingly, in one aspect, the present invention provides a method for determining the prognosis in a patient having breast cancer or the likelihood of breast cancer recurrence. Generally, the method comprises: determining in a sample from the patient the expression of the *ABCC5* gene, and using the expression of the *ABCC5* gene in determining the prognosis of the breast cancer in the patient, or predicting the breast cancer outcome, the likelihood of breast cancer recurrence or probability of post-surgery distant metastasis-free survival. In some embodiments, the method comprises correlating an increased expression level of the *ABCC5* gene to a poor prognosis, increased likelihood of cancer recurrence, and decreased probability of post-surgery distant metastasis-free survival. In one embodiment, the method further comprises determining in the same or different sample from the patient the expression of the *PGR* gene, and using the expression of the *PGR* gene in combination with that of the *ABCC5* gene in determining the prognosis of the breast cancer in the patient, or predicting the breast cancer outcome, the likelihood of breast cancer recurrence or probability of post-surgery distant metastasis-free survival.

[0041] In another aspect, the present invention provides a method for determining the prognosis in a patient having breast cancer or the likelihood of breast cancer recurrence, which comprises: determining in a tumor sample from the patient the expression of the *PGR* gene, and using the expression of the *PGR* gene in determining the prognosis of the breast cancer in the patient, or predicting the breast cancer outcome, the likelihood of breast cancer recurrence or probability of post-surgery distant metastasis-free survival. In some embodiments, the method comprises correlating an increased expression level of the *PGR* gene, in patients who have received hormonal therapy, to a better prognosis, decreased likelihood of cancer recurrence, and increased probability of post-surgery distant metastasis-free survival. Conversely, the method comprises correlating an increased expression level of the *PGR* gene, in patients who have not received hormonal therapy, to a worse prognosis, increased likelihood of cancer recurrence, and decreased probability of post-surgery distant metastasis-free survival. Furthermore, in some embodiments the

method comprises correlating an increased expression level of the *PGR* gene to an increased likelihood of response to hormonal treatment. In some embodiments the method comprises correlating a decreased expression level of the *PGR* gene to a decreased likelihood of response to hormonal treatment.

[0042] The present invention further provides a method for determining in a patient the prognosis of breast cancer or the likelihood of breast cancer recurrence, which comprises: determining the expression of a plurality of test genes comprising (1) at least 2, 3, 5, 4, 6, 8, 10 or 15 or more cell-cycle genes (e.g., CCGs in Panel F in Table 9 or any of Panels H, I, J, L, M, N & O (including 2, 3, 4, 5, or 6 genes in a sub-panel of Panel O in Tables 30 to 34)), and/or (2) at least one of the *ABCC5* gene and the *PGR* gene or both, together or separately in one or more samples from the patient, and using the expression of said plurality of test genes in determining the prognosis of the breast cancer in the patient, or predicting the breast cancer outcome, the likelihood of breast cancer recurrence or probability of post-surgery distant metastasis-free survival. In some embodiments, the method comprises correlating an overall increased expression level of cell-cycle genes, i.e., CCGs, to poor prognosis of the breast cancer in the patient, poor breast cancer outcome, and increased likelihood of breast cancer recurrence, and decreased probability of post-surgery distant metastasis-free survival. In some embodiments, the method comprises correlating an increased level of *ABCC5* gene expression to poor prognosis of the breast cancer in the patient, poor breast cancer outcome, and increased likelihood of breast cancer recurrence, and decreased probability of post-surgery distant metastasis-free survival. In contrast, in some embodiments, the method comprises correlating an increased level of *PGR* gene expression, in patients who have received hormonal therapy, to better prognosis of the breast cancer in the patient, better breast cancer outcome, and decreased likelihood of breast cancer recurrence, and increased probability of post-surgery distant metastasis-free survival. Conversely, in some embodiments, the method comprises correlating an increased level of *PGR* gene expression, in patients who have not received hormonal therapy, to better prognosis of the breast cancer in the patient, better breast cancer outcome, and decreased likelihood of breast cancer recurrence, and increased probability of post-surgery distant metastasis-free survival.

[0043] In some embodiments of the methods described above, the patient is *ER*⁺ and node negative. In some embodiments, the patient is *ER*⁺ and node negative, has undergone surgery

to remove the tumor in her breast, and is placed on hormone therapy. In some embodiments of the methods described above, the patient is *ER*⁺ and node positive.

[0044] The prognosis and treatment methods that involve determining a test value may further include a step of comparing the test value to one or more reference values, and correlating the test value to, e.g., a good or poor prognosis, an increased or decreased likelihood of recurrence, an increased or decreased likelihood of recurrence or metastasis-free survival, an increased or decreased likelihood of response to the particular treatment regimen, etc. In some embodiments, the CCP expression data are combined with *ABCC5* and/or *PGR* expression data into one test value, which may then be compared against a reference value for the combined score. In other embodiments, the CCP expression data are used to provide a discrete CCP test value, which is then combined with *ABCC5* and/or *PGR* expression data. In some embodiments a test value greater than the reference value is correlated to an increased likelihood of response to treatment comprising chemotherapy. In some embodiments the test value is correlated to an increased likelihood of response to treatment (e.g., treatment comprising chemotherapy), poor prognosis, an increased likelihood of recurrence, and/or a decreased likelihood of recurrence or metastasis-free survival if the test value exceeds the reference value by at least some amount (e.g., at least 0.5, 0.75, 0.85, 0.90, 0.95, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 or more fold or standard deviations).

[0045] In some embodiments, the method of determining the likelihood of response to a particular treatment regimen comprises (1) determining in a tumor sample from a patient having breast cancer the expression of a panel of genes in said tumor sample including at least 4 or at least 8 cell-cycle genes; (2) providing a test value by (a) weighting the determined expression of each of a plurality of test genes selected from the panel of genes with a predefined coefficient, and (b) combining the weighted expression to provide the test value, wherein the cell-cycle genes are weighted to contribute at least 50%, at least 75% or at least 85% of the test value; (3) determining in a tumor sample from the patient the expression of *ABCC5* and/or *PGR*; and (4)(a) correlating a test value that is greater than some reference and/or *ABCC5* expression that is greater than some reference and/or *PGR* expression that is greater than some reference to an increased likelihood of response to the particular treatment regimen (e.g., a treatment regimen comprising chemotherapy, a treatment regimen comprising hormonal therapy), or (b) correlating a test value that is not greater than some reference and/or *ABCC5* expression that is not greater than some reference and/or *PGR*

expression that is not greater than some reference to no increased likelihood of response to the particular treatment regimen (*e.g.*, a treatment regimen comprising chemotherapy, a treatment regimen comprising hormonal therapy).

[0046] In some embodiments, the panel of genes includes at least 2, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100 or more cell-cycle genes. In some embodiments the test genes are weighted such that the cell-cycle genes are weighted to contribute at least 50%, at least 55%, at least 60%, at least 65%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 99% or 100% of the test value. In some embodiments 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 75%, 80%, 85%, 90%, 95%, or at least 99% or 100% of the plurality of test genes are cell-cycle genes.

[0047] As used herein, “determining the status” of a gene (or panel of genes) refers to determining the presence, absence, or extent/level of some physical, chemical, or genetic characteristic of the gene or its expression product(s). Such characteristics include, but are not limited to, expression levels, activity levels, mutations, copy number, methylation status, etc.

[0048] In the context of CCGs as used to determine likelihood of response to a particular treatment regimen (*e.g.*, a treatment regimen comprising chemotherapy), particularly useful characteristics include expression levels (*e.g.*, mRNA, cDNA or protein levels) and activity levels. Characteristics may be assayed directly (*e.g.*, by assaying a CCG’s expression level) or determined indirectly (*e.g.*, assaying the level of a gene or genes whose expression level is correlated to the expression level of the CCG).

[0049] “Abnormal status” means a marker’s status in a particular sample differs from the status generally found in average samples (*e.g.*, healthy samples, average diseased samples). Examples include mutated, elevated, decreased, present, absent, etc. An “elevated status” means that one or more of the above characteristics (*e.g.*, expression or mRNA level) is higher than normal levels. Generally this means an increase in the characteristic (*e.g.*, expression or mRNA level) as compared to an index value as discussed below. Conversely a “low status” means that one or more of the above characteristics (*e.g.*, gene expression or mRNA level) is lower than normal levels. Generally this means a decrease in the characteristic (*e.g.*, expression) as compared to an index value as discussed below. In this context, a “negative status” generally means the characteristic is absent

or undetectable or, in the case of sequence analysis, there is a deleterious sequence variant (including full or partial gene deletion).

[0050] Gene expression can be determined either at the RNA level (*i.e.*, mRNA or noncoding RNA (ncRNA)) (*e.g.*, miRNA, tRNA, rRNA, snoRNA, siRNA and piRNA) or at the protein level. Measuring gene expression at the mRNA level includes measuring levels of cDNA corresponding to mRNA. Levels of proteins in a tumor sample can be determined by any known technique in the art, *e.g.*, HPLC, mass spectrometry, or using antibodies specific to selected proteins (*e.g.*, IHC, ELISA, etc.).

[0051] In some embodiments, the amount of RNA transcribed from the panel of genes including test genes is measured in the tumor sample. In addition, the amount of RNA of one or more housekeeping genes in the tumor sample is also measured, and used to normalize or calibrate the expression of the test genes. The terms “normalizing genes” and “housekeeping genes” are defined herein below.

[0052] In any embodiment of the invention involving a “plurality of test genes,” the plurality of test genes may include at least 2, 3 or 4 cell-cycle genes, which constitute at least 50%, 75% or 80% of the plurality of test genes, and preferably 100% of the plurality of test genes. In other such embodiments, the plurality of test genes includes at least 5, 6, 7, or at least 8 cell-cycle genes, which constitute at least 20%, 25%, 30%, 40%, 50%, 60%, 70%, 75%, 80% or 90% of the plurality of test genes, and preferably 100% of the plurality of test genes. As will be clear from the context of this document, a panel of genes is a plurality of genes. In some embodiments these genes are assayed together in one or more samples from a patient.

[0053] In some embodiments, the plurality of test genes includes at least 8, 10, 12, 15, 20, 25 or 30 cell-cycle genes, which constitute at least 20%, 25%, 30%, 40%, 50%, 60%, 70%, 75%, 80% or 90% of the plurality of test genes, and preferably 100% of the plurality of test genes.

[0054] As will be apparent to a skilled artisan apprised of the present invention and the disclosure herein, “tumor sample” means any biological sample containing one or more tumor cells, or one or more tumor-derived RNA or protein, and obtained from a cancer patient. For example, a tissue sample obtained from a tumor tissue of a cancer patient is a useful tumor sample in the present invention. The tissue sample can be an FFPE sample, or fresh frozen sample, and preferably contain largely tumor cells. A single malignant cell from a cancer patient’s tumor is also

a useful tumor sample. Such a malignant cell can be obtained directly from the patient's tumor, or purified from the patient's bodily fluid (e.g., blood, urine). Thus, a bodily fluid such as blood, urine, sputum and saliva containing one or tumor cells, or tumor-derived RNA or proteins, can also be useful as a tumor sample for purposes of practicing the present invention.

[0055] In some embodiments the patient has (e.g., has been diagnosed with) a particular subtype of breast cancer. Thus, in some embodiments the patient has (e.g., has been diagnosed with) a subtype of breast cancer chosen from the group consisting of: triple negative breast cancer (TNBC); ER+ breast cancer; node negative breast cancer; ER+/node negative breast cancer; invasive breast cancer; invasive ductal carcinoma; inflammatory breast cancer; medullary carcinoma; metaplastic breast cancer; Paget's disease of the nipple; tubular carcinoma; ductal carcinoma; ductal carcinoma *in situ* (DCIS); papillary carcinoma; lobular carcinoma; invasive lobular carcinoma; and lobular carcinoma *in situ* (LCIS). In some embodiments the patient has (e.g., has been diagnosed with) DCIS.

[0056] Those skilled in the art are familiar with various techniques for determining the expression of a gene in a tissue or cell sample, which can be measured as the level of the mRNA transcribed from, or the protein encoded by, the gene. Useful techniques include, but are not limited to, microarray analysis (e.g., for assaying mRNA or microRNA expression, copy number, etc.), quantitative real-time PCRTM ("qRT-PCRTM", e.g., TaqManTM), immunoanalysis (e.g., ELISA, immunohistochemistry), etc. The activity level of a polypeptide encoded by a gene may be used in much the same way as the expression level of the gene or polypeptide. Often higher activity levels indicate higher expression levels and while lower activity levels indicate lower expression levels. Thus, in some embodiments, the invention provides any of the methods discussed above, wherein the activity level of a polypeptide encoded by the CCG is determined rather than or in addition to the expression level of the CCG. Those skilled in the art are familiar with techniques for measuring the activity of various such proteins, including those encoded by the genes listed in Exemplary CCGs are listed in Tables 1, 2, 3, 5, 6, 7, 8 & 9, as well as those encoded by *ABCC5* and *PGR*. The methods of the invention may be practiced independent of the particular technique used.

[0057] In preferred embodiments, the expression of one or more normalizing (often called "housekeeping") genes is also obtained for use in normalizing the expression of test genes. As used herein, "normalizing genes" referred to the genes whose expression is used to calibrate or

normalize the measured expression of the gene of interest (*e.g.*, test genes). Importantly, the expression of normalizing genes should be independent of cancer outcome/prognosis, and the expression of the normalizing genes is very similar among all the tumor samples. The normalization ensures accurate comparison of expression of a test gene between different samples. For this purpose, housekeeping genes known in the art can be used. Housekeeping genes are well known in the art, with examples including, but are not limited to, *GUSB* (glucuronidase, beta), *HMBS* (hydroxymethylbilane synthase), *SDHA* (succinate dehydrogenase complex, subunit A, flavoprotein), *UBC* (ubiquitin C) and *YWHAZ* (tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide). One or more housekeeping genes can be used. Preferably, at least 2, 5, 10 or 15 housekeeping genes are used to provide a combined normalizing gene set. The amount of gene expression of such normalizing genes can be averaged, combined together by straight additions or by a defined algorithm. Some examples of particularly useful housekeeper genes for use in the methods and compositions of the invention include those listed in Table A below.

Table A

Gene Symbol	Entrez GeneID	Applied Biosystems Assay ID	RefSeq Accession Nos.
<i>CLTC</i> *	1213	Hs00191535_m1	NM_004859.3
<i>GUSB</i>	2990	Hs99999908_m1	NM_000181.2
<i>HMBS</i>	3145	Hs00609297_m1	NM_000190.3
<i>MMADHC</i> *	27249	Hs00739517_g1	NM_015702.2
<i>MRFAP1</i> *	93621	Hs00738144_g1	NM_033296.1
<i>PPP2CA</i> *	5515	Hs00427259_m1	NM_002715.2
<i>PSMA1</i> *	5682	Hs00267631_m1	
<i>PSMC1</i> *	5700	Hs02386942_g1	NM_002802.2
<i>RPL13A</i> *	23521	Hs03043885_g1	NM_012423.2
<i>RPL37</i> *	6167	Hs02340038_g1	NM_000997.4
<i>RPL38</i> *	6169	Hs00605263_g1	NM_000999.3
<i>RPL4</i> *	6124	Hs03044647_g1	NM_000968.2
<i>RPL8</i> *	6132	Hs00361285_g1	NM_033301.1; NM_000973.3
<i>RPS29</i> *	6235	Hs03004310_g1	NM_001030001.1; NM_001032.3
<i>SDHA</i>	6389	Hs00188166_m1	NM_004168.2

<i>SLC25A3</i> *	6515	Hs00358082_m1	NM_213611.1; NM_002635.2; NM_005888.2
<i>TXNLI</i> *	9352	Hs00355488_m1	NR_024546.1; NM_004786.2
<i>UBA52</i> *	7311	Hs03004332_g1	NM_001033930.1; NM_003333.3
<i>UBC</i>	7316	Hs00824723_m1	NM_021009.4
<i>YWHAZ</i>	7534	Hs00237047_m1	NM_003406.3

* Subset of housekeeping genes used in normalizing CCGs and generating the CCP Score in Example 1.

[0058] In the case of measuring RNA levels for the genes, one convenient and sensitive approach is real-time quantitative PCRTM (qPCR) assay, following a reverse transcription reaction. Typically, a cycle threshold (C_t) is determined for each test gene and each normalizing gene, *i.e.*, the number of cycles at which the fluorescence from a qPCR reaction above background is detectable.

[0059] The overall expression of the one or more normalizing genes can be represented by a “normalizing value” which can be generated by combining the expression of all normalizing genes, either weighted equally (straight addition or averaging) or by different predefined coefficients. For example, in a simplest manner, the normalizing value C_{tH} can be the cycle threshold (C_t) of one single normalizing gene, or an average of the C_t values of 2 or more, preferably 10 or more, or 15 or more normalizing genes, in which case, the predefined coefficient is $1/N$, where N is the total number of normalizing genes used. Thus, $C_{tH} = (C_{tH1} + C_{tH2} + \dots + C_{tHn})/N$. As will be apparent to skilled artisans, depending on the normalizing genes used, and the weight desired to be given to each normalizing gene, any coefficients (from $0/N$ to N/N) can be given to the normalizing genes in weighting the expression of such normalizing genes. That is, $C_{tH} = xC_{tH1} + yC_{tH2} + \dots + zC_{tHn}$, wherein $x + y + \dots + z = 1$.

[0060] As discussed above, the methods of the invention generally involve determining the level of expression of a panel of CCGs, and the *ABCC5* and/or *PGR* genes and, optionally, deriving from these determined expression levels a score or value that can predict prognosis, therapy response, etc. With modern high-throughput techniques, it is often possible to determine the expression level of tens, hundreds or thousands of genes. Indeed, it is possible to determine the level of expression of the entire transcriptome (*i.e.*, each transcribed sequence in the

genome). Once such a global assay has been performed, one may then informatically analyze one or more subsets of transcripts (*i.e.*, panels or, as often used herein, pluralities of test genes). After measuring the expression of hundreds or thousands of transcripts in a sample, for example, one may analyze (*e.g.*, informatically) the expression of a panel or plurality of test genes comprising primarily CCGs and *ABCC5* and/or *PGR* according to the present invention by combining the expression level values of the individual test genes to obtain a test value.

[0061] As will be apparent to a skilled artisan, the CCP value provided in the present invention represents the overall expression level of the plurality of test genes composed substantially of (or weighted to be represented substantially by) cell-cycle genes. In one embodiment, to provide a CCP value in the methods of the invention, the normalized expression for a test gene can be obtained by normalizing the measured C_t for the test gene against the C_{tH} , *i.e.*, $\Delta C_{t1} = (C_{t1} - C_{tH})$. Thus, the CCP value representing the overall expression of the plurality of test genes can be provided by combining the normalized expression of all test genes, either by straight addition or averaging (*i.e.*, weighted equally) or by a different predefined coefficient. For example, the simplest approach is averaging the normalized expression of all test genes: $CCP \text{ value} = (\Delta C_{t1} + \Delta C_{t2} + \dots + \Delta C_{tn})/n$. As will be apparent to skilled artisans, depending on the test genes used, different weight can also be given to different test genes in the present invention. In each case where this document discloses using the expression of a plurality of genes (*e.g.*, “determining [in a tumor sample from the patient] the expression of a plurality of test genes” or “correlating increased expression of said plurality of test genes to an increased likelihood of response”), this includes in some embodiments using a test value representing or corresponding to the overall expression of this plurality of genes (*e.g.*, “determining [in a tumor sample from the patient] a test value representing the expression of a plurality of test genes” or “correlating an increased test value [or a test value above some reference value] representing the expression of said plurality of test genes to an increased likelihood of response”).

[0062] Similarly, the normalized expression for the *ABCC5* gene can be obtained by normalizing the measured C_t for the *ABCC5* gene against the C_{tH} , *i.e.*, $\Delta C_{t(ABCC5)} = (C_{t(ABCC5)} - C_{tH})$. Likewise, the normalized expression for the *PGR* gene can be obtained by normalizing the measured C_t for the *PGR* gene against the C_{tH} , *i.e.*, $\Delta C_{t(PGR)} = (C_{t(PGR)} - C_{tH})$. The normalized expression for the *ABCC5* gene and/or *PGR* gene can be combined with the CCP value described above to provide a

test value. Same or different weight can be given to these three components using predefined coefficients.

[0063] It has been determined that, once the CCP phenomenon reported herein is appreciated, the choice of individual CCGs for a test panel can, in some embodiments, be somewhat arbitrary. In other words, many CCGs have been found to be very good surrogates for each other. Thus any CCG (or panel of CCGs) can be used in the various embodiments of the invention. In other embodiments of the invention, optimized CCGs are used. One way of assessing whether particular CCGs will serve well in the methods and compositions of the invention is by assessing their correlation with the mean expression of CCGs (*e.g.*, all known CCGs, a specific set of CCGs, etc.). Those CCGs that correlate particularly well with the mean are expected to perform well in assays of the invention, *e.g.*, because these will reduce noise in the assay.

[0064] Some CCGs do not correlate well with the mean (*e.g.*, *ABCC5*'s correlation to the mean is 0.097). In some embodiments of the present invention, such genes may be grouped, tested, analyzed, etc. separately from those that correlate well. This is especially useful if these non-correlated genes are independently associated with the clinical feature of interest (*e.g.*, prognosis, therapy response, etc.). Again, *ABCC5* is a good example, as it does not correlate with the CCG mean at all but it correlates well with prognosis. As shown in the example below, where *ABCC5* remains a significant predictor of prognosis even in multivariate analysis with correlated CCP genes, *ABCC5* adds prognostic information beyond CCGs that correlate well with the mean (*e.g.*, Panel F). Thus, in some preferred embodiments of the invention, non-correlated genes are analyzed together with correlated genes. In some embodiments, a CCG is non-correlated if its correlation to the CCG mean is less than 0.5, 0.4, 0.3, 0.2, 0.10, 0.09, 0.08, 0.07, 0.06, 0.05, 0.04, 0.03, 0.02, 0.01 or less.

[0065] 126 CCGs and 47 housekeeping genes had their expression compared to the CCG and housekeeping mean in order to determine preferred genes for use in some embodiments of the invention. Rankings of select CCGs according to their correlation with the mean CCG expression as well as their ranking according to predictive value are given in Tables 2, 3, 5, 6, 7 & 12-20.

[0066] Assays of 126 CCGs and 47 HK (housekeeping) genes were run against 96 commercially obtained, anonymous tumor FFPE samples without outcome or other clinical data. The working hypothesis was that the assays would measure with varying degrees of accuracy the

same underlying phenomenon (cell cycle proliferation within the tumor for the CCGs, and sample concentration for the HK genes). Assays were ranked by the Pearson's correlation coefficient between the individual gene and the mean of all the candidate genes, that being the best available estimate of biological activity. Rankings for these 126 CCGs according to their correlation to the overall CCG mean are reported in Table 2.

Table 2

Gene #	Gene Symbol	Correl. w/ Mean	Gene #	Gene Symbol	Correl. w/ Mean	Gene #	Gene Symbol	Correl. w/ Mean
1	<i>TPX2</i>	0.931	44	<i>PBK</i>	0.805	87	<i>KIF18A</i>	0.6987
2	<i>CCNB2</i>	0.9287	45	<i>ESPL1</i>	0.805	88	<i>DONSON</i>	0.688
3	<i>KIF4A</i>	0.9163	46	<i>MKI67</i>	0.7993	89	<i>MCM4</i>	0.686
4	<i>KIF2C</i>	0.9147	47	<i>SPAG5</i>	0.7993	90	<i>RAD54B</i>	0.679
5	<i>BIRC5</i>	0.9077	48	<i>MCM10</i>	0.7963	91	<i>RNASEH2A</i>	0.6733
6	<i>BIRC5</i>	0.9077	49	<i>MCM6</i>	0.7957	92	<i>TUBA1C</i>	0.6697
7	<i>RACGAP1</i>	0.9073	50	<i>OIP5</i>	0.7943	93	<i>C18orf24</i>	0.6697
8	<i>CDC2</i>	0.906	51	<i>CDC45L</i>	0.7937	94	<i>SMC2</i>	0.6697
9	<i>PRC1</i>	0.9053	52	<i>KIF23</i>	0.7927	95	<i>CENPI</i>	0.6697
10	<i>DLGAP5/</i> <i>DLG7</i>	0.9033	53	<i>EZH2</i>	0.789	96	<i>GMPS</i>	0.6683
11	<i>CEP55</i>	0.903	54	<i>SPC25</i>	0.7887	97	<i>DDX39</i>	0.6673
12	<i>CCNB1</i>	0.9	55	<i>STIL</i>	0.7843	98	<i>POLE2</i>	0.6583
13	<i>TOP2A</i>	0.8967	56	<i>CENPN</i>	0.783	99	<i>APOBEC3B</i>	0.6513
14	<i>CDC20</i>	0.8953	57	<i>GTSE1</i>	0.7793	100	<i>RFC2</i>	0.648
15	<i>KIF20A</i>	0.8927	58	<i>RAD51</i>	0.779	101	<i>PSMA7</i>	0.6473
16	<i>BUB1B</i>	0.8927	59	<i>CDCA3</i>	0.7783	102	<i>MPHOSPH1/</i> <i>kif20b</i>	0.6457
17	<i>CDKN3</i>	0.8887	60	<i>TACC3</i>	0.778	103	<i>CDT1</i>	0.645
18	<i>NUSAP1</i>	0.8873	61	<i>PLK4</i>	0.7753	104	<i>H2AFX</i>	0.6387
19	<i>CCNA2</i>	0.8853	62	<i>ASF1B</i>	0.7733	105	<i>ORC6L</i>	0.634
20	<i>KIF11</i>	0.8723	63	<i>DTL</i>	0.769	106	<i>C1orf135</i>	0.6333
21	<i>CDCA8</i>	0.8713	64	<i>CHEK1</i>	0.7673	107	<i>PSRC1</i>	0.633
22	<i>NCAPG</i>	0.8707	65	<i>NCAPG2</i>	0.7667	108	<i>VRK1</i>	0.6323
23	<i>ASPM</i>	0.8703	66	<i>PLK1</i>	0.7657	109	<i>CKAP2</i>	0.6307
24	<i>FOXMI</i>	0.87	67	<i>TIMELESS</i>	0.762	110	<i>CCDC99</i>	0.6303
25	<i>NEK2</i>	0.869	68	<i>E2F8</i>	0.7587	111	<i>CCNE1</i>	0.6283
26	<i>ZWINT</i>	0.8683	69	<i>EXO1</i>	0.758	112	<i>LMNB2</i>	0.625
27	<i>PTTG1</i>	0.8647	70	<i>ECT2</i>	0.744	113	<i>GPSM2</i>	0.625

28	<i>RRM2</i>	0.8557	71	<i>STMN1</i>	0.737	114	<i>PAICS</i>	0.6243
29	<i>TTK</i>	0.8483	72	<i>STMN1</i>	0.737	115	<i>MCAM</i>	0.6227
30	<i>TRIP13</i>	0.841	73	<i>RFC4</i>	0.737	116	<i>DSN1</i>	0.622
31	<i>GINSI</i>	0.841	74	<i>CDC6</i>	0.7363	117	<i>NCAPD2</i>	0.6213
32	<i>CENPF</i>	0.8397	75	<i>CENPM</i>	0.7267	118	<i>RAD54L</i>	0.6213
33	<i>HMMR</i>	0.8367	76	<i>MYBL2</i>	0.725	119	<i>PDSS1</i>	0.6203
34	<i>NCAPH</i>	0.8353	77	<i>SHCBP1</i>	0.723	120	<i>HN1</i>	0.62
35	<i>NDC80</i>	0.8313	78	<i>ATAD2</i>	0.723	121	<i>C21orf45</i>	0.6193
36	<i>KIF15</i>	0.8307	79	<i>KIFC1</i>	0.7183	122	<i>CTSL2</i>	0.619
37	<i>CENPE</i>	0.8287	80	<i>DBF4</i>	0.718	123	<i>CTPS</i>	0.6183
38	<i>TYMS</i>	0.8283	81	<i>CKS1B</i>	0.712	124	<i>MCM7</i>	0.618
39	<i>KIAA0101</i>	0.8203	82	<i>PCNA</i>	0.7103	125	<i>ZWILCH</i>	0.618
40	<i>FANCI</i>	0.813	83	<i>FBXO5</i>	0.7053	126	<i>RFC5</i>	0.6177
41	<i>RAD51AP1</i>	0.8107	84	<i>C12orf48</i>	0.7027			
42	<i>CKS2</i>	0.81	85	<i>TK1</i>	0.7017			
43	<i>MCM2</i>	0.8063	86	<i>BLM</i>	0.701			

[0067] After excluding CCGs with low average expression, assays that produced sample failures, CCGs with correlations less than 0.58, and HK genes with correlations less than 0.95, a subset of 56 CCGs (Panel G) and 36 HK candidate genes were left. Correlation coefficients were recalculated on these subsets, with the rankings shown in Tables 3 and 4, respectively.

Table 3 ("Panel G")

Gene #	Gene Symbol	Correl. w/ CCG mean	Gene #	Gene Symbol	Correl. w/ CCG mean	Gene #	Gene Symbol	Correl. w/ CCG mean
1	<i>FOXM1</i>	0.908	20	<i>C18orf24</i>	0.817	39	<i>FANCI</i>	0.702
2	<i>CDC20</i>	0.907	21	<i>RAD54L</i>	0.816	40	<i>KIF15</i>	0.701
3	<i>CDKN3</i>	0.9	22	<i>PTTG1</i>	0.814	41	<i>PLK4</i>	0.688
4	<i>CDC2</i>	0.899	23	<i>KIF4A</i>	0.814	42	<i>APOBEC3B</i>	0.67
5	<i>KIF11</i>	0.898	24	<i>CDCA3</i>	0.811	43	<i>NCAPG</i>	0.667
6	<i>KIAA0101</i>	0.89	25	<i>MCM10</i>	0.802	44	<i>TRIP13</i>	0.653
7	<i>NUSAP1</i>	0.887	26	<i>PRC1</i>	0.79	45	<i>KIF23</i>	0.652
8	<i>CENPF</i>	0.882	27	<i>DTL</i>	0.788	46	<i>NCAPH</i>	0.649
9	<i>ASPM</i>	0.879	28	<i>CEP55</i>	0.787	47	<i>TYMS</i>	0.648
10	<i>BUB1B</i>	0.879	29	<i>RAD51</i>	0.783	48	<i>GINSI</i>	0.639
11	<i>RRM2</i>	0.876	30	<i>CENPM</i>	0.781	49	<i>STMN1</i>	0.63
12	<i>DLGAP5</i>	0.875	31	<i>CDCA8</i>	0.774	50	<i>ZWINT</i>	0.621
13	<i>BIRC5</i>	0.864	32	<i>OIP5</i>	0.773	51	<i>BLM</i>	0.62

14	<i>KIF20A</i>	0.86	33	<i>SHCBP1</i>	0.762	52	<i>TTK</i>	0.62
15	<i>PLK1</i>	0.86	34	<i>ORC6L</i>	0.736	53	<i>CDC6</i>	0.619
16	<i>TOP2A</i>	0.851	35	<i>CCNB1</i>	0.727	54	<i>KIF2C</i>	0.596
17	<i>TK1</i>	0.837	36	<i>CHEK1</i>	0.723	55	<i>RAD51API</i>	0.567
18	<i>PBK</i>	0.831	37	<i>TACC3</i>	0.722	56	<i>NCAPG2</i>	0.535
19	<i>ASF1B</i>	0.827	38	<i>MCM4</i>	0.703			

Table 4

Gene #	Gene Symbol	Correlation with HK Mean
1	<i>RPL38</i>	0.989
2	<i>UBA52</i>	0.986
3	<i>PSMC1</i>	0.985
4	<i>RPL4</i>	0.984
5	<i>RPL37</i>	0.983
6	<i>RPS29</i>	0.983
7	<i>SLC25A3</i>	0.982
8	<i>CLTC</i>	0.981
9	<i>TXNLI</i>	0.98
10	<i>PSMA1</i>	0.98
11	<i>RPL8</i>	0.98
12	<i>MMADHC</i>	0.979
13	<i>RPL13A; LOC728658</i>	0.979
14	<i>PPP2CA</i>	0.978
15	<i>MRFAP1</i>	0.978

[0068] The CCGs in Panel F were likewise ranked according to correlation to the CCG mean as shown in Table 5 below.

Table 5

Gene #	Gene Symbol	Correl. w/ CCG mean	Gene #	Gene Symbol	Correl. w/ CCG mean	Gene #	Gene Symbol	Correl. w/ CCG mean
1	<i>DLGAP5</i>	0.931	12	<i>C18orf24</i>	0.885	22	<i>TOP2A</i>	0.852
2	<i>ASPM</i>	0.931	13	<i>PLK1</i>	0.879	23	<i>KIF20A</i>	0.851
3	<i>KIF11</i>	0.926	14	<i>CDKN3</i>	0.874	24	<i>KIAA0101</i>	0.839
4	<i>BIRC5</i>	0.916	15	<i>RRM2</i>	0.871	25	<i>CDCA3</i>	0.835
5	<i>CDCA8</i>	0.902	16	<i>RAD51</i>	0.864	26	<i>ASF1B</i>	0.797

6	<i>CDC20</i>	0.9	17	<i>CEP55</i>	0.862	27	<i>CENPM</i>	0.786
7	<i>MCM10</i>	0.899	18	<i>ORC6L</i>	0.86	28	<i>TK1</i>	0.783
8	<i>PRC1</i>	0.895	19	<i>RAD54L</i>	0.86	29	<i>PBK</i>	0.775
9	<i>BUB1B</i>	0.892	20	<i>CDC2</i>	0.858	30	<i>PTTG1</i>	0.751
10	<i>FOXMI</i>	0.889	21	<i>CENPF</i>	0.855	31	<i>DTL</i>	0.737
11	<i>NUSAPI</i>	0.888						

[0069] When choosing specific CCGs for inclusion in any embodiment of the invention, the individual predictive power of each gene may be used to rank them in importance. The inventors have determined that the CCGs in Panel C can be ranked as shown in Table 6 below according to the predictive power of each individual gene. The CCGs in Panel F can be similarly ranked as shown in Table 7 below.

Table 6

Gene #	Gene	p-value	Gene #	Gene	p-value	Gene #	Gene	p-value
1	<i>NUSAPI</i>	2.8E-07	12	<i>BUB1</i>	8.3E-05	23	<i>KPNA2</i>	2.0E-02
2	<i>DLG7</i>	5.9E-07	13	<i>PBK</i>	1.2E-04	24	<i>UBE2C</i>	2.2E-02
3	<i>CDC2</i>	6.0E-07	14	<i>TTK</i>	3.2E-04	25	<i>MELK</i>	2.5E-02
4	<i>FOXMI</i>	1.1E-06	15	<i>CDC45L</i>	7.7E-04	26	<i>CENPA</i>	2.9E-02
5	<i>MYBL2</i>	1.1E-06	16	<i>PRC1</i>	1.2E-03	27	<i>CKS2</i>	5.7E-02
6	<i>CDCA8</i>	3.3E-06	17	<i>DTL</i>	1.4E-03	28	<i>MAD2L1</i>	1.7E-01
7	<i>CDC20</i>	3.8E-06	18	<i>CCNB1</i>	1.5E-03	29	<i>UBE2S</i>	2.0E-01
8	<i>RRM2</i>	7.2E-06	19	<i>TPX2</i>	1.9E-03	30	<i>AURKA</i>	4.8E-01
9	<i>PTTG1</i>	1.8E-05	20	<i>ZWINT</i>	9.3E-03	31	<i>TIMELESS</i>	4.8E-01
10	<i>CCNB2</i>	5.2E-05	21	<i>KIF23</i>	1.1E-02			
11	<i>HMMR</i>	5.2E-05	22	<i>TRIP13</i>	1.7E-02			

Table 7

Gene #	Gene Symbol	p-value	Gene #	Gene Symbol	p-value	Gene #	Gene Symbol	p-value
1	<i>MCM10</i>	8.60E-10	12	<i>BUB1B</i>	1.10E-05	23	<i>C18orf24</i>	0.0011
2	<i>ASPM</i>	2.30E-09	13	<i>RAD54L</i>	1.40E-05	24	<i>BIRC5</i>	0.00118
3	<i>DLGAP5</i>	1.20E-08	14	<i>CEP55</i>	2.60E-05	25	<i>RRM2</i>	0.00255
4	<i>CENPF</i>	1.40E-08	15	<i>CDCA8</i>	3.10E-05	26	<i>CENPM</i>	0.0027
5	<i>CDC20</i>	2.10E-08	16	<i>TK1</i>	3.30E-05	27	<i>RAD51</i>	0.0028
6	<i>FOXMI</i>	3.40E-07	17	<i>DTL</i>	3.60E-05	28	<i>KIAA0101</i>	0.00348
7	<i>TOP2A</i>	4.30E-07	18	<i>PRC1</i>	3.90E-05	29	<i>CDCA3</i>	0.00863
8	<i>NUSAPI</i>	4.70E-07	19	<i>PTTG1</i>	4.10E-05	30	<i>PBK</i>	0.00923

9	<i>CDKN3</i>	5.50E-07	20	<i>CDC2</i>	0.00013	31	<i>ASF1B</i>	0.00936
10	<i>KIF11</i>	6.30E-06	21	<i>ORC6L</i>	0.00017			
11	<i>KIF20A</i>	6.50E-06	22	<i>PLK1</i>	0.0005			

[0070] Thus, in some embodiments of each of the various aspects of the invention the plurality of test genes comprises the top 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 25, 30, 35, 40 or more CCGs listed in Table 2, 3, 5, 6, or 7. In some embodiments the plurality of test genes comprises at least some number of CCGs (*e.g.*, at least 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50 or more CCGs) and this plurality of CCGs comprises at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, or 20 of the following genes: *ASPM*, *BIRC5*, *BUB1B*, *CCNB2*, *CDC2*, *CDC20*, *CDCA8*, *CDKN3*, *CENPF*, *DLGAP5*, *FOXMI*, *KIAA0101*, *KIF11*, *KIF2C*, *KIF4A*, *MCM10*, *NUSAP1*, *PRC1*, *RACGAP1*, and *TPX2*. In some embodiments the plurality of test genes comprises at least some number of CCGs (*e.g.*, at least 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50 or more CCGs) and this plurality of CCGs comprises at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, or 20 of the following genes: *TPX2*, *CCNB2*, *KIF4A*, *KIF2C*, *BIRC5*, *RACGAP1*, *CDC2*, *PRC1*, *DLGAP5/DLG7*, *CEP55*, *CCNB1*, *TOP2A*, *CDC20*, *KIF20A*, *BUB1B*, *CDKN3*, *NUSAP1*, *CCNA2*, *KIF11*, and *CDCA8*. In some embodiments the plurality of test genes comprises at least some number of CCGs (*e.g.*, at least 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50 or more CCGs) and this plurality of CCGs comprises any one, two, three, four, five, six, seven, eight, nine, or ten or all of gene numbers 1 & 2, 1 to 3, 1 to 4, 1 to 5, 1 to 6, 1 to 7, 1 to 8, 1 to 9, or 1 to 10 of any of Table 2, 3, 5, 6, or 7. In some embodiments the plurality of test genes comprises at least some number of CCGs (*e.g.*, at least 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50 or more CCGs) and this plurality of CCGs comprises any one, two, three, four, five, six, seven, eight, or nine or all of gene numbers 2 & 3, 2 to 4, 2 to 5, 2 to 6, 2 to 7, 2 to 8, 2 to 9, or 2 to 10 of any of Table 2, 3, 5, 6, or 7. In some embodiments the plurality of test genes comprises at least some number of CCGs (*e.g.*, at least 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50 or more CCGs) and this plurality of CCGs comprises any one, two, three, four, five, six, seven, or eight or all of gene numbers 3 & 4, 3 to 5, 3 to 6, 3 to 7, 3 to 8, 3 to 9, or 3 to 10 of any of Table 2, 3, 5, 6, or 7. In some embodiments the plurality of test genes comprises at least some number of CCGs (*e.g.*, at least 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50 or more CCGs) and this plurality of CCGs comprises any one, two, three, four, five, six, or seven or all of gene numbers 4 & 5, 4 to 6, 4 to 7, 4 to 8, 4 to 9, or 4 to 10 of any of Table 2, 3, 5, 6, or 7. In some embodiments the plurality of test genes comprises at least some number of CCGs (*e.g.*, at least

3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50 or more CCGs) and this plurality of CCGs comprises any one, two, three, four, five, six, seven, eight, nine, 10, 11, 12, 13, 14, or 15 or all of gene numbers 1 & 2, 1 to 3, 1 to 4, 1 to 5, 1 to 6, 1 to 7, 1 to 8, 1 to 9, 1 to 10, 1 to 11, 1 to 12, 1 to 13, 1 to 14, or 1 to 15 of any of Table 2, 3, 5, 6, or 7.

[0071] In preferred embodiments, the test value representing the overall expression of the plurality of test genes is compared to one or more reference values (or index values), and optionally correlated to breast cancer prognosis, or an increased or no increased likelihood of breast cancer recurrence or post-surgery metastasis-free survival. In some cases such values are called “scores,” especially in the Examples below. In some embodiments a test value greater than the reference value(s) can be correlated to increased likelihood of poor prognosis or decreased probability of post-surgery metastasis-free survival. In some embodiments the test value is deemed “greater than” the reference value (e.g., the threshold index value), and thus correlated to an increased likelihood of poor prognosis or decreased probability of post-surgery metastasis-free survival, if the test value exceeds the reference value by at least some amount (*e.g.*, at least 0.5, 0.75, 0.85, 0.90, 0.95, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 or more fold or standard deviations).

[0072] For example, the index value may represent the gene expression levels found in a normal sample obtained from the patient of interest (including tissue surrounding the cancerous tissue in a biopsy), in which case an expression level in the tumor sample significantly higher than this index value would indicate, *e.g.*, increased likelihood of response to a particular treatment regimen (*e.g.*, a treatment regimen comprising chemotherapy).

[0073] Alternatively, the index value may represent the average expression level for a set of individuals from a diverse cancer population or a subset of the population. For example, one may determine the average expression level of a gene or gene panel in a random sampling of patients with cancer (*e.g.*, breast cancer). This average expression level may be termed the “threshold index value”.

[0074] Alternatively, the index value may represent the average expression level of a particular gene or gene panel in a plurality of training patients (*e.g.*, breast cancer patients) with similar outcomes whose clinical and follow-up data are available and sufficient to define and categorize the patients by disease outcome. *See, e.g.*, Examples, *infra*. For example, a “good prognosis index value” can be generated from a plurality of training cancer patients characterized as

having “good prognosis” after breast cancer surgery and hormone deprivation therapy. A “poor prognosis index value” can be generated from a plurality of training cancer patients defined as having “poor prognosis” breast cancer surgery and hormone deprivation therapy. Thus, a good prognosis index value of a particular gene or gene panel may represent the average level of expression of the particular gene or gene panel in patients having a “good prognosis,” whereas a poor prognosis index value of a particular gene or gene panel represents the average level of expression of the particular gene or gene panel in patients having a “poor prognosis.” Thus, if the determined level of expression of a relevant gene or gene panel is closer to the good prognosis index value of the gene or gene panel than to the poor prognosis index value of the gene or gene panel, then it can be concluded that the patient is more likely to have a good prognosis. On the other hand, if the determined level of expression of a relevant gene or gene panel is closer to the poor prognosis index value of the gene or gene panel than to the good prognosis index value of the gene or gene panel, then it can be concluded that the patient is more likely to have a poor prognosis.

[0075] Alternatively index values may be determined thusly: In order to assign patients to risk groups, a threshold value may be set for the cell cycle mean combined with the *ABCC5* mean, and optionally *PGR* mean. The optimal threshold value is selected based on the receiver operating characteristic (ROC) curve, which plots sensitivity vs (1 – specificity). For each increment of the combined mean, the sensitivity and specificity of the test is calculated using that value as a threshold. The actual threshold will be the value that optimizes these metrics according to the artisan’s requirements (*e.g.*, what degree of sensitivity or specificity is desired, etc.).

[0076] Those skilled in the art are familiar with various ways of determining the expression of a panel of genes (*i.e.*, a plurality of genes). One may determine the expression of a panel of genes by determining the average expression level (normalized or absolute) of all panel genes in a sample obtained from a particular patient (either throughout the sample or in a subset of cells or a single cell from the sample). Increased expression in this context will mean the average expression is higher than the average expression level of these genes in some reference (*e.g.*, higher than in normal patients; higher than some index value that has been determined to represent the average expression level in a reference population, such as patients with the same cancer; etc.). Alternatively, one may determine the expression of a panel of genes by determining the average expression level (normalized or absolute) of at least a certain number (*e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10,

15, 20, 25, 30 or more) or at least a certain proportion (*e.g.*, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 99%, 100%) of the genes in the panel. Alternatively, one may determine the expression of a panel of genes by determining the absolute copy number of the analyte representing each gene in the panel (*e.g.*, mRNA, cDNA, protein) and either total or average these across the genes.

[0077] Panels of CCGs (*e.g.*, 2, 3, 4, 5, or 6 CCGs) can accurately predict breast cancer prognosis. But addition of the *ABCC5* and *PGR* genes significantly increases the prediction power. In some embodiments the panel comprises at least 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50, 70, 80, 90, 100, 200, or more CCGs. In some embodiments the panel comprises at least 10, 15, 20, or more CCGs. In some embodiments the panel comprises between 5 and 100 CCGs, between 7 and 40 CCGs, between 5 and 25 CCGs, between 10 and 20 CCGs, or between 10 and 15 CCGs. In some embodiments CCGs comprise at least a certain proportion of the panel. Thus in some embodiments the panel comprises at least 25%, 30%, 40%, 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% CCGs. In some preferred embodiments the panel comprises at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 70, 80, 90, 100, 200, or more CCGs, and such CCGs constitute of at least 50%, 60%, 70%, preferably at least 75%, 80%, 85%, more preferably at least 90%, 95%, 96%, 97%, 98%, or 99% or more of the total number of genes in the panel. In some embodiments the panel of CCGs comprises the genes in Table 1, 2, 3, 5, 6, 7, 8, or 9 or Panel A, B, C, D, E, F, or G. In some embodiments the panel comprises at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 25, 30, or more of the genes in Table 1, 2, 3, 5, 6, 7, 8, or 9 or Panel A, B, C, D, E, F, or G. In some embodiments the invention provides a method of determining the prognosis in a breast cancer patient comprising determining the status of the CCGs in any one of Table 1, 2, 3, 5, 6, 7, 8, or 9 or Panel A, B, C, D, E, F, or G, determining the status of the *ABCC5* gene or the *PGR* gene or both, and using the combined expression to determine the prognosis of the breast cancer.

[0078] Several panels of (or comprising) CCGs (shown in Tables 1, 2, 3, 5, 6, 7, 8, 9, 10, 11 & 25 and Panels A, B, C, D, E, F, G, H, I, J, L, M, N & O (including sub-panels of Panel O in Tables 30 to 34)) are useful in this regard.

Table 8: “Panel C”

Gene Symbol	Entrez GeneID	Gene Symbol	Entrez GeneID	Gene Symbol	Entrez GeneID
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<i>AURKA</i>	6790	<i>DTL</i> *	51514	<i>PTTGI</i> *	9232
<i>BUB1</i> *	699	<i>FOXMI</i> *	2305	<i>RRM2</i> *	6241
<i>CCNB1</i> *	891	<i>HMMR</i> *	3161	<i>TIMELESS</i> *	8914
<i>CCNB2</i> *	9133	<i>KIF23</i> *	9493	<i>TPX2</i> *	22974
<i>CDC2</i> *	983	<i>KPNA2</i>	3838	<i>TRIP13</i> *	9319
<i>CDC20</i> *	991	<i>MAD2L1</i> *	4085	<i>TTK</i> *	7272
<i>CDC45L</i> *	8318	<i>MELK</i>	9833	<i>UBE2C</i>	11065
<i>CDC48</i> *	55143	<i>MYBL2</i> *	4605	<i>UBE2S</i> *	27338
<i>CENPA</i>	1058	<i>NUSAPI</i> *	51203	<i>ZWINT</i> *	11130
<i>CKS2</i> *	1164	<i>PBK</i> *	55872		
<i>DLG7</i> *	9787	<i>PRCI</i> *	9055		

* These genes can be used as a 26-gene subset panel ("Panel D") in some embodiments of the invention.

Table 9: "Panel E"

Name	GeneID	Name	GeneID	Name	GeneID
<i>ASF1B</i> *	55723	<i>CENPM</i> *	79019	<i>ORC6L</i> *	23594
<i>ASPM</i> *	259266	<i>CEP55</i> *	55165	<i>PBK</i> *	55872
<i>BIRC5</i> *	332	<i>DLGAP5</i> *	9787	<i>PLK1</i> *	5347
<i>BUB1B</i> *	701	<i>DTL</i> *	51514	<i>PRCI</i> *	9055
<i>C18orf24</i> *	220134	<i>FOXMI</i> *	2305	<i>PTTGI</i> *	9232
<i>CDC2</i> *	983	<i>KIAA0101</i> *	9768	<i>RAD51</i> *	5888
<i>CDC20</i> *	991	<i>KIF11</i> *	3832	<i>RAD54L</i> *	8438
<i>CDC43</i> *	83461	<i>KIF20A</i> *	10112	<i>RRM2</i> *	6241
<i>CDC48</i> *	55143	<i>KIF4A</i>	24137	<i>TK1</i> *	7083
<i>CDKN3</i> *	1033	<i>MCM10</i> *	55388	<i>TOP2A</i> *	7153
<i>CENPF</i> *	1063	<i>NUSAPI</i> *	51203		

* These genes can be used as a 31-gene subset panel ("Panel F") in some embodiments of the invention.

Table 10: "Panel H"

ASF1B*#	Hs00216780_m1	RRM2*#	Hs00357247_g1
ASPM*#	Hs00411505_m1	TK1*#	Hs01062125_m1
BUB1B*#	Hs01084828_m1	TOP2A*#	Hs00172214_m1
C18orf24*#	Hs00536843_m1	GAPDH^	Hs99999905_m1
CDC2*#	Hs00364293_m1	CLTC**	Hs00191535_m1
CDKN3*#	Hs00193192_m1	MMADHC**	Hs00739517_g1

CENPF*#	Hs00193201_m1	PPP2CA**	Hs00427259_m1
CENPM*#	Hs00608780_m1	PSMA1**	Hs00267631_m1
DTL*#	Hs00978565_m1	PSMC1**	Hs02386942_g1
CDCA3*#	Hs00229905_m1	RPL13A**	Hs03043885_g1
KIAA0101*#	Hs00207134_m1	RPL37**	Hs02340038_g1
KIF11*#	Hs00189698_m1	RPL38**	Hs00605263_g1
KIF20A*#	Hs00993573_m1	RPL4**	Hs03044647_g1
KIF4A*#	Hs01020169_m1	RPL8**	Hs00361285_g1
MCM10*#	Hs00960349_m1	RPS29**	Hs03004310_g1
NUSAP1*#	Hs01006195_m1	SLC25A3**	Hs00358082_m1
PBK*#	Hs00218544_m1	TXNL1**	Hs00355488_m1
PLK1*#	Hs00153444_m1	UBA52**	Hs03004332_g1
PRC1*#	Hs00187740_m1	ESR1# ¹	Hs01046815_m1; Hs00174860_m1
PTTG1*#	Hs00851754_u1	ABCC5#	Hs00981085_m1
RAD51*#	Hs00153418_m1	PGR#	Hs00172183_m1
RAD54L*#	Hs00269177_m1		

* CCP genes (Panel I)

CCP genes plus *ESR1*, *ABCC5*, and *PGR* (Panel J). ¹ Note that in some embodiments utilizing Panel J, *ESR1* is optional and is analyzed primarily as a confirmation of the tumor's ER+ status. Thus, in some embodiments Panel J lacks *ESR1*.

** Housekeeping genes (Panel K)

Table 11: "Panel L"

Gene Symbol	ABI Assay ID	Entrez GeneID	Gene Symbol	ABI Assay ID	Entrez GeneID
<i>ASF1B</i> *#	Hs00216780_m1	55723	<i>RRM2</i> *#	Hs00357247_g1	6241
<i>ASPM</i> *#	Hs00411505_m1	259266	<i>TK1</i> *#	Hs01062125_m1	7083
<i>BUB1B</i> *#	Hs01084828_m1	701	<i>TOP2A</i> *#	Hs00172214_m1	7153
<i>C18orf24</i> *#	Hs00536843_m1	220134	<i>GAPDH</i> [^]	Hs99999905_m1	2597
<i>CDC2</i> *#	Hs00364293_m1	983	<i>CLTC</i> **	Hs00191535_m1	1213
<i>CDKN3</i> *#	Hs00193192_m1	83461	<i>MMADHC</i> **	Hs00739517_g1	27249
<i>CENPF</i> *#	Hs00193201_m1	1033	<i>PPP2CA</i> **	Hs00427259_m1	5515
<i>CENPM</i> *#	Hs00608780_m1	1063	<i>PSMA1</i> **	Hs00267631_m1	5682
<i>DTL</i> *#	Hs00978565_m1	79019	<i>PSMC1</i> **	Hs02386942_g1	5700
<i>CDCA3</i> *#	Hs00229905_m1	51514	<i>RPL13A</i> **	Hs03043885_g1	23521
<i>KIAA0101</i> *#	Hs00207134_m1	9768	<i>RPL37</i> **	Hs02340038_g1	6167
<i>KIF11</i> *#	Hs00189698_m1	3832	<i>RPL38</i> **	Hs00605263_g1	6169
<i>KIF20A</i> *#	Hs00993573_m1	10112	<i>RPL4</i> **	Hs03044647_g1	6124

<i>MCM10</i> *#	Hs00960349_m1	55388	<i>RPL8</i> **	Hs00361285_g1	6132
<i>NUSAP1</i> *#	Hs01006195_m1	51203	<i>RPS29</i> **	Hs03004310_g1	6235
<i>PBK</i> *#	Hs00218544_m1	55872	<i>SLC25A3</i> **	Hs00358082_m1	6515
<i>PLK1</i> *#	Hs00153444_m1	5347	<i>TXNL1</i> **	Hs00355488_m1	9352
<i>PRC1</i> *#	Hs00187740_m1	9055	<i>UBA52</i> **	Hs03004332_g1	7311
<i>PTTG1</i> *#	Hs00851754_u1	9232	<i>ESR1</i> ¹	Hs01046815_m1; Hs00174860_m1	2099
<i>RAD51</i> *#	Hs00153418_m1	5888	<i>ABCC5</i> #	Hs00981085_m1	10057
<i>RAD54L</i> *#	Hs00269177_m1	8438	<i>PGR</i> #	Hs00172183_m1	5241

* CCP genes (Panel M)

CCP genes plus *ESR1*, *ABCC5*, and *PGR* (Panel N). ¹ Note that in some embodiments utilizing Panel N, *ESR1* is optional and is analyzed primarily as a confirmation of the tumor's ER+ status. Thus, in some embodiments Panel N lacks *ESR1*.

** Housekeeping genes

^ Internal control gene

[0079] Similar to Tables 2 to 7 above, the CCP genes in Tables 10 & 11 were ranked according to correlation to the CCP mean and according to independent predictive value (p-value). Rankings according to correlation to the mean are shown in Tables 12 to 14 below. Rankings according to p-value are shown in Tables 15 & 16 below.

Table 12

Gene #	Gene Symbol	Gene #	Gene Symbol
1	<i>KIF4A</i>	14	<i>KIAA0101</i>
2	<i>CDC2</i>	15	<i>PBK</i>
3	<i>PRC1</i>	16	<i>MCM10</i>
4	<i>TOP2A</i>	17	<i>RAD51</i>
5	<i>KIF20A</i>	18	<i>CDCA3</i>
6	<i>BUB1B</i>	19	<i>ASF1B</i>
7	<i>CDKN3</i>	20	<i>DTL</i>
8	<i>PTTG1</i>	21	<i>PLK1</i>
9	<i>NUSAP1</i>	22	<i>CENPM</i>
10	<i>KIF11</i>	23	<i>TK1</i>
11	<i>ASPM</i>	24	<i>C18orf24</i>
12	<i>RRM2</i>	25	<i>RAD54L</i>
13	<i>CENPF</i>		

Table 13

Gene #	Gene Symbol	Gene #	Gene Symbol
1	<i>CDKN3</i>	14	<i>PBK</i>
2	<i>CDC2</i>	15	<i>ASF1B</i>
3	<i>KIF11</i>	16	<i>C18orf24</i>
4	<i>KIAA0101</i>	17	<i>RAD54L</i>
5	<i>NUSAP1</i>	18	<i>PTTG1</i>
6	<i>CENPF</i>	19	<i>KIF4A</i>
7	<i>ASPM</i>	20	<i>CDCA3</i>
8	<i>BUB1B</i>	21	<i>MCM10</i>
9	<i>RRM2</i>	22	<i>PRC1</i>
10	<i>KIF20A</i>	23	<i>DTL</i>
11	<i>PLK1</i>	24	<i>RAD51</i>
12	<i>TOP2A</i>	25	<i>CENPM</i>
13	<i>TK1</i>		

Table 14

Gene #	Gene Symbol	Gene #	Gene Symbol
1	<i>ASPM</i>	14	<i>CENPF</i>
2	<i>KIF11</i>	15	<i>TOP2A</i>
3	<i>MCM10</i>	16	<i>KIF20A</i>
4	<i>PRC1</i>	17	<i>KIAA0101</i>
5	<i>BUB1B</i>	18	<i>CDCA3</i>
6	<i>NUSAP1</i>	19	<i>ASF1B</i>
7	<i>C18orf24</i>	20	<i>CENPM</i>
8	<i>PLK1</i>	21	<i>TK1</i>
9	<i>CDKN3</i>	22	<i>PBK</i>
10	<i>RRM2</i>	23	<i>PTTG1</i>
11	<i>RAD51</i>	24	<i>DTL</i>
12	<i>RAD54L</i>	25	<i>KIF4A</i>
13	<i>CDC2</i>		

Table 15

Gene #	Gene Symbol	Gene #	Gene Symbol
1	<i>NUSAP1</i>	14	<i>CENPF</i>

2	<i>CDC2</i>	15	<i>CENPM</i>
3	<i>RRM2</i>	16	<i>KIAA0101</i>
4	<i>PTTG1</i>	17	<i>KIF11</i>
5	<i>PBK</i>	18	<i>KIF20A</i>
6	<i>PRC1</i>	19	<i>KIF4A</i>
7	<i>DTL</i>	20	<i>MCM10</i>
8	<i>ASF1B</i>	21	<i>PLK1</i>
9	<i>ASPM</i>	22	<i>RAD51</i>
10	<i>BUB1B</i>	23	<i>RAD54L</i>
11	<i>C18orf24</i>	24	<i>TK1</i>
12	<i>CDCA3</i>	25	<i>TOP2A</i>
13	<i>CDKN3</i>		

Table 16

Gene #	Gene Symbol	Gene #	Gene Symbol
1	<i>MCM10</i>	14	<i>PTTG1</i>
2	<i>ASPM</i>	15	<i>CDC2</i>
3	<i>CENPF</i>	16	<i>PLK1</i>
4	<i>TOP2A</i>	17	<i>C18orf24</i>
5	<i>NUSAP1</i>	18	<i>RRM2</i>
6	<i>CDKN3</i>	19	<i>CENPM</i>
7	<i>KIF11</i>	20	<i>RAD51</i>
8	<i>KIF20A</i>	21	<i>KIAA0101</i>
9	<i>BUB1B</i>	22	<i>CDCA3</i>
10	<i>RAD54L</i>	23	<i>PBK</i>
11	<i>TK1</i>	24	<i>ASF1B</i>
12	<i>DTL</i>	25	<i>KIF4A</i>
13	<i>PRC1</i>		

[0080] The rankings of each gene according to correlation to the mean (Tables 2, 3 & 5) and p-value (Tables 6 & 7) were used to derive two different combination rankings. Table 17 ranks the CCP genes of Table 10 according to the highest unweighted combination score calculated by the following formula: Combination score for each gene = $(1/(\text{correlation in Table 2})) + (1/(\text{correlation in Table 3})) + (1/(\text{correlation in Table 5})) + (1/(\text{p-value in Table 6})) + (1/(\text{p-value in Table 7}))$. Table 18 ranks the CCP genes of Table 10 according to the highest weighted combination score (which gives greater weight to p-value over correlation to the mean) calculated by the

following formula: Combination score for each gene = $(2/(\text{correlation in Table 2})) + (3/(\text{correlation in Table 3})) + (5/(\text{correlation in Table 5})) + (7/(\text{p-value in Table 6})) + (10/(\text{p-value in Table 7}))$.

Table 17

Gene #	Gene Symbol	Gene #	Gene Symbol
1	<i>NUSAP1</i>	14	<i>KIF20A</i>
2	<i>MCM10</i>	15	<i>KIAA0101</i>
3	<i>ASPM</i>	16	<i>PLK1</i>
4	<i>CDC2</i>	17	<i>PBK</i>
5	<i>KIF11</i>	18	<i>C18orf24</i>
6	<i>CDKN3</i>	19	<i>RAD54L</i>
7	<i>CENPF</i>	20	<i>DTL</i>
8	<i>KIF4A</i>	21	<i>TK1</i>
9	<i>PRC1</i>	22	<i>RAD51</i>
10	<i>BUB1B</i>	23	<i>ASF1B</i>
11	<i>RRM2</i>	24	<i>CDCA3</i>
12	<i>TOP2A</i>	25	<i>CENPM</i>
13	<i>PTTG1</i>		

Table 18

Gene #	Gene Symbol	Gene #	Gene Symbol
1	<i>NUSAP1</i>	14	<i>KIAA0101</i>
2	<i>CDC2</i>	15	<i>PBK</i>
3	<i>KIF11</i>	16	<i>PLK1</i>
4	<i>ASPM</i>	17	<i>DTL</i>
5	<i>CDKN3</i>	18	<i>KIF4A</i>
6	<i>BUB1B</i>	19	<i>RAD51</i>
7	<i>PRC1</i>	20	<i>C18orf24</i>
8	<i>RRM2</i>	21	<i>ASF1B</i>
9	<i>CENPF</i>	22	<i>CDCA3</i>
10	<i>TOP2A</i>	23	<i>TK1</i>
11	<i>KIF20A</i>	24	<i>RAD54L</i>
12	<i>PTTG1</i>	25	<i>CENPM</i>
13	<i>MCM10</i>		

[0081] Similar to above, the rankings of each gene in Panel O of Example 3 according to correlation to the mean (Table 25) and p-value (Table 26) were used to derive two

different combination rankings. Table 19 ranks the genes of Panel O according to the lowest unweighted combination score calculated by the following formula: Combination score for each gene = (gene's rank in Table 25)+(gene's rank in Table 26). Table 20 ranks the genes of Panel O according to the lowest weighted combination score (which gives greater weight to p-value over correlation to the mean) calculated by the following formula: Combination score for each gene = (gene's rank in Table 25)+(0.5*(gene's rank in Table 26)).

Table 19

Gene #	Gene Symbol	Gene #	Gene Symbol	Gene #	Gene Symbol	Gene #	Gene Symbol
1	<i>BUB1B</i>	7	<i>MCM10</i>	13	<i>RAD54L</i>	19	<i>CDK1</i>
2	<i>SKA1</i>	8	<i>CENPM</i>	14	<i>TK1</i>	20	<i>DTL</i>
3	<i>ASPM</i>	9	<i>RAD51</i>	15	<i>PTTG1</i>	21	<i>KIF20A</i>
4	<i>KIAA0101</i>	10	<i>PBK</i>	16	<i>KIF11</i>	22	<i>ASF1B</i>
5	<i>PRC1</i>	11	<i>RRM2</i>	17	<i>NUSAP1</i>	23	<i>CDKN3</i>
6	<i>CDCA3</i>	12	<i>PLK1</i>	18	<i>CENPF</i>		

Table 20

Gene #	Gene Symbol	Gene #	Gene Symbol	Gene #	Gene Symbol	Gene #	Gene Symbol
1	<i>ASPM</i>	7	<i>CENPM</i>	13	<i>MCM10</i>	19	<i>ASF1B</i>
2	<i>KIAA0101</i>	8	<i>PLK1</i>	14	<i>DTL</i>	20	<i>RAD54L</i>
3	<i>BUB1B</i>	9	<i>KIF11</i>	15	<i>NUSAP1</i>	21	<i>KIF20A</i>
4	<i>PTTG1</i>	10	<i>RRM2</i>	16	<i>PRC1</i>	22	<i>CDK1</i>
5	<i>CDCA3</i>	11	<i>RAD51</i>	17	<i>TK1</i>	23	<i>CDKN3</i>
6	<i>SKA1</i>	12	<i>PBK</i>	18	<i>CENPF</i>		

[0082] In CCG signatures the particular CCGs assayed is often not as important as the total number of CCGs. The number of CCGs assayed can vary depending on many factors, *e.g.*, technical constraints, cost considerations, the classification being made, the cancer being tested, the desired level of predictive power, etc. Increasing the number of CCGs assayed in a panel according to the invention is, as a general matter, advantageous because, *e.g.*, a larger pool of mRNAs to be assayed means less “noise” caused by outliers and less chance of an assay error throwing off the

overall predictive power of the test. However, cost and other considerations will generally limit this number and finding the optimal number of CCGs for a signature is desirable.

[0083] It has been discovered that the predictive power of a CCG signature often ceases to increase significantly beyond a certain number of CCGs. In order to determine the optimal number of cell cycle genes for the signature, the predictive power of the mean was tested for randomly selected sets of from 1 to 30 of the CCGs in Panel C. This demonstrates, for some embodiments of the invention, a threshold number of CCGs in a panel (10, 15, or between 10 and 15) that provides significantly improved predictive power. In some embodiments even smaller panels of CCGs are sufficient to prognose disease outcome and/or predict therapy response/benefit. To evaluate how even smaller subsets of a larger CCG set (*i.e.*, smaller CCG subpanels) performed, the inventors compared how well the CCGs from Panel C predicted outcome as a function of the number of CCGs included in the signature. As shown in Table 21 below, small CCG signatures (*e.g.*, 2, 3, 4, 5, 6 CCGs, etc.) are significant predictors.

Table 21

# of CCGs	Mean of log10 (p-value)*
1	-3.579
2	-4.279
3	-5.049
4	-5.473
5	-5.877
6	-6.228

* For 1000 randomly drawn subsets, size 1 through 6, of CCGs.

[0084] Tables 30 to 34 further illustrate this feature of the invention by showing the predictive power (both univariate and multivariate p-value) of numerous sub-panels chosen from Panel O. As can be seen, each 2-gene and 3-gene sub-panel chosen from Panel O is significantly predictive of breast cancer prognosis and recurrence in the cohort described in Examples 1 & 3. The same is true for all 4-gene, 5-gene and 6-gene sub-panels chosen from the top 10 genes in Panel O (*i.e.*, from the genes in Panel O ranked according to p-value as in Table 26). Thus, in each embodiment of the invention described in this document, there is a further embodiment in which the panel of genes (or the plurality of test genes, etc.) comprises a sub-panel of any of Tables 30 to 34. By way of non-limiting example, the invention provides a method of determining the prognosis of a

patient having breast cancer or the likelihood of cancer recurrence in said patient, comprising: (1) obtaining a sample from said patient; (2) determining the expression levels of a panel of genes in said sample, wherein said panel comprises a sub-panel of Panel O chosen from any of Tables 30 to 34 and optionally includes *ABCC5* or *PGR* or both; (3) providing a test value by (i) weighting the determined expression of each of a plurality of test genes selected from said panel of genes with a predefined coefficient, and (ii) combining the weighted expression to provide said test value, wherein the genes of said sub-panel are weighted to contribute at least 25% of the test value and wherein said plurality of test genes optionally includes *ABCC5* or *PGR* or both; and (4) classifying said patient as having a poor or a good prognosis or a an increased or not increased likelihood of cancer recurrence based at least in part on said test value.

[0085] In some embodiments, the optimal number of CCGs in a signature (n_0) can be found wherever the following is true

$$(P_{n+1} - P_n) < C_0,$$

wherein P is the predictive power (*i.e.*, P_n is the predictive power of a signature with n genes and P_{n+1} is the predictive power of a signature with n genes plus one) and C_0 is some optimization constant. Predictive power can be defined in many ways known to those skilled in the art including, but not limited to, the signature's p-value. C_0 can be chosen by the artisan based on his or her specific constraints. For example, if cost is not a critical factor and extremely high levels of sensitivity and specificity are desired, C_0 can be set very low such that only trivial increases in predictive power are disregarded. On the other hand, if cost is decisive and moderate levels of sensitivity and specificity are acceptable, C_0 can be set higher such that only significant increases in predictive power warrant increasing the number of genes in the signature.

[0086] Alternatively, a graph of predictive power as a function of gene number may be plotted and the second derivative of this plot taken. The point at which the second derivative decreases to some predetermined value (C_0') may be the optimal number of genes in the signature. It has been shown that p-values ceased to improve significantly between about 10 and about 15 CCGs, thus indicating that an optimal number of CCGs in a prognostic panel is from about 10 to about 15. Thus in some preferred embodiments of the invention between about 10 and about 15 CCGs are used in addition to the *ABCC5* gene or the *PGR* gene or both. In some embodiments the panel comprises between about 10 and about 15 CCGs and the CCGs constitute at least 80% of the

panel (or are weighted to contribute at least 75%). In other embodiments the panel comprises CCGs plus one or more additional markers that significantly increase the predictive power of the panel (*i.e.*, make the predictive power significantly better than if the panel consisted of only the CCGs). Any other combination of CCGs (including any of those listed in Table 1, 2, 3, 5, 6, 7, 8, or 9 or Panel A, B, C, D, E, F, or G) can be used to practice the invention.

[0087] In some embodiments the panel comprises at least 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50 or more CCGs. In some embodiments the panel comprises between 5 and 100 CCGs, between 7 and 40 CCGs, between 5 and 25 CCGs, between 10 and 20 CCGs, or between 10 and 15 CCGs. In some embodiments CCGs comprise at least a certain proportion of the panel. Thus in some embodiments the panel comprises at least 25%, 30%, 40%, 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% CCGs. In some embodiments the CCGs are any of the genes listed in Table 1, 2, 3, 5, 6, 7, 8, or 9 or Panel A, B, C, D, E, F, or G. In some embodiments the panel comprises at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50 or more genes in any of Table 1, 2, 3, 5, 6, 7, 8, or 9 or Panel A, B, C, D, E, F, or G. In some embodiments the panel comprises all of the genes in any of Table 1, 2, 3, 5, 6, 7, 8, or 9 or Panel A, B, C, D, E, F, or G.

[0088] As mentioned above, many of the CCGs of the invention have been analyzed to determine their correlation to the CCG mean and also, for the genes, to determine their relative predictive value within a panel (see Tables 1, 2, 3, 5, 6, 7, 8, 9, 10, 11 & 25 and Panels A, B, C, D, E, F, G, H, I, J, L, M, N & O (including sub-panels of Panel O in Tables 30 to 34)). Thus in some embodiments the plurality of test genes comprises at least some number of CCGs (*e.g.*, at least 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50 or more CCGs from Table 1, 2, 3, 5, 6, 7, 8, 9, 10, 11 or 25 or Panel A, B, C, D, E, F, G, H, I, J, L, M, N or O (including sub-panels of Panel O in Tables 30 to 34)) and this plurality of CCGs comprises the top 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 25, 30, 35, 40 or more CCGs listed in Table 2, 3, 5, 6, 7, or 12-20. In some embodiments the plurality of test genes comprises at least some number of CCGs (*e.g.*, at least 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50 or more CCGs from Tables 1, 2, 3, 5, 6, 7, 8, 9, 10, 11 or 25 or Panels A, B, C, D, E, F, G, H, I, J, L, M, N or O (including sub-panels of Panel O in Tables 30 to 34)) and this plurality of CCGs comprises at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, or 20 of the following genes: *ASPM*, *BIRC5*, *BUB1B*, *CCNB2*, *CDC2*, *CDC20*, *CDCA8*, *CDKN3*, *CENPF*, *DLGAP5*, *FOXMI*,

KIAA0101, KIF11, KIF2C, KIF4A, MCM10, NUSAP1, PRC1, RACGAP1, and TPX2. In some embodiments the plurality of test genes comprises at least some number of CCGs (*e.g.*, at least 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50 or more CCGs from Table 1, 2, 3, 5, 6, 7, 8, 9, 10, 11 or 25 or Panel A, B, C, D, E, F, G, H, I, J, L, M, N or O (including sub-panels of Panel O in Tables 30 to 34)) and this plurality of CCGs comprises any one, two, three, four, five, six, seven, eight, nine, or ten or all of gene numbers 1 & 2, 1 to 3, 1 to 4, 1 to 5, 1 to 6, 1 to 7, 1 to 8, 1 to 9, or 1 to 10 of any of Table 2, 3, 5, 6, 7, or 12-20. In some embodiments the plurality of test genes comprises at least some number of CCGs (*e.g.*, at least 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50 or more CCGs from Table 1, 2, 3, 5, 6, 7, 8, 9, 10, 11 or 25 or Panel A, B, C, D, E, F, G, H, I, J, L, M, N or O (including sub-panels of Panel O in Tables 30 to 34)) and this plurality of CCGs comprises any one, two, three, four, five, six, seven, eight, or nine or all of gene numbers 2 & 3, 2 to 4, 2 to 5, 2 to 6, 2 to 7, 2 to 8, 2 to 9, or 2 to 10 of any of Table 2, 3, 5, 6, 7, or 12-20. In some embodiments the plurality of test genes comprises at least some number of CCGs (*e.g.*, at least 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50 or more CCGs from Table 1, 2, 3, 5, 6, 7, 8, 9, 10, 11 or 25 or Panel A, B, C, D, E, F, G, H, I, J, L, M, N or O (including sub-panels of Panel O in Tables 30 to 34)) and this plurality of CCGs comprises any one, two, three, four, five, six, seven, or eight or all of gene numbers 3 & 4, 3 to 5, 3 to 6, 3 to 7, 3 to 8, 3 to 9, or 3 to 10 of any of Table 2, 3, 5, 6, 7, or 12-20. In some embodiments the plurality of test genes comprises at least some number of CCGs (*e.g.*, at least 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50 or more CCGs from Table 1, 2, 3, 5, 6, 7, 8, 9, 10, 11 or 25 or Panel A, B, C, D, E, F, G, H, I, J, L, M, N or O (including sub-panels of Panel O in Tables 30 to 34)) and this plurality of CCGs comprises any one, two, three, four, five, six, or seven or all of gene numbers 4 & 5, 4 to 6, 4 to 7, 4 to 8, 4 to 9, or 4 to 10 of any of Table 2, 3, 5, 6, 7, or 12-20. In some embodiments the plurality of test genes comprises at least some number of CCGs (*e.g.*, at least 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50 or more CCGs from Table 1, 2, 3, 5, 6, 7, 8, 9, 10, 11 or 25 or Panel A, B, C, D, E, F, G, H, I, J, L, M, N or O (including sub-panels of Panel O in Tables 30 to 34)) and this plurality of CCGs comprises any one, two, three, four, five, six, seven, eight, nine, 10, 11, 12, 13, 14, or 15 or all of gene numbers 1 & 2, 1 to 3, 1 to 4, 1 to 5, 1 to 6, 1 to 7, 1 to 8, 1 to 9, 1 to 10, 1 to 11, 1 to 12, 1 to 13, 1 to 14, or 1 to 15 of any of Table 2, 3, 5, 6, 7, or 12-20.

[0089] For many breast cancer patients and their physicians surgery to remove the tumor (sometimes including surrounding healthy tissue) is the standard of care. Because surgery can

cure some patients and adjuvant chemotherapy is debilitating and expensive, the decision whether to undertake adjuvant chemotherapy is more difficult. For patients identified according to the methods described above as having a poor prognosis or decreased probability of post-surgery distant metastasis-free survival, aggressive treatment should be provided. Such aggressive treatment may include any treatment regimen beside surgery and hormone deprivation therapy (using blockers of estrogen receptor, or aromatase inhibitors). Thus, in one aspect, the present invention provides a method for treating breast cancer, which comprises determining the prognosis of breast cancer in a patient as described herein, and recommending, prescribing or administering a particular treatment regimen (*e.g.*, a treatment regimen comprising chemotherapy) based at least in part on the determined prognosis.

[0090] For many breast cancer patients neoadjuvant chemotherapy is administered. In such cases, chemotherapy is given to the patient before any resection, generally in the hope that the tumor will shrink without the need for surgery. Neoadjuvant chemotherapy can cure some patients but the toxic drugs can be debilitating and expensive, making the decision whether to undertake neoadjuvant chemotherapy difficult. For patients identified according to the methods described above as having a poor prognosis (*e.g.*, increased probability of recurrence or decreased probability of post-surgery distant metastasis-free survival), aggressive treatment comprising neoadjuvant chemotherapy may be provided. See Example 2, below. Thus, in one aspect, the present invention provides a method for treating breast cancer, which comprises determining the prognosis of breast cancer in a patient who has not yet had surgical resection of the tumor as described herein, and recommending, prescribing or administering a treatment regimen comprising neoadjuvant chemotherapy based at least in part on the determined prognosis.

[0091] Unless stated otherwise (or unless context clearly indicates otherwise), “chemotherapy” as used herein means adjuvant and/or neoadjuvant chemotherapy.

[0092] In one embodiment, the breast cancer treatment method includes: determining in a tumor sample from the patient the expression of a plurality of test genes comprising at least 6, 8, 10 or 15 or more cell-cycle genes, determining in the same or different sample from the patient the expression of the *ABCC5* gene or the *PGR* gene or both, and recommending, prescribing or administering a particular treatment regimen (*e.g.*, a treatment regimen comprising chemotherapy) based in part on the determined expression of the plurality of test genes, as well as the determined

ABCC5 and/or *PGR* expression. In some embodiments, the method further comprises administering to the patient a non-hormone-blocking therapy agent or radiotherapy. “Hormone-blocking therapy” as generally understood in the art means drugs that block the estrogen receptor, e.g. tamoxifen, or block the production of estrogen, e.g., using aromatase inhibitors such as anastrozole (Arimidex) or letrozole (Femara). Non-hormone-blocking therapy agents suitable for breast cancer adjuvant therapy are known in the art and may include, e.g., cyclophosphamide, doxorubicin (Adriamycin), taxane, methotrexate, fluorouracil, and monoclonal antibodies such as Trastuzumab.

[0093] As used herein, a patient has an “increased likelihood” of some clinical feature or outcome (e.g., response) if the probability of the patient having the feature or outcome exceeds some reference probability or value. The reference probability may be the probability of the feature or outcome across the general relevant patient population. For example, if the probability of cancer recurrence after surgery in the general breast cancer patient population (or some specific subpopulation) is X% and a particular patient has been determined by the methods of the present invention to have a probability of recurrence of Y%, and if $Y > X$, then the patient has an “increased likelihood” of response. Alternatively, as discussed above, a threshold or reference value may be determined and a particular patient’s probability of response may be compared to that threshold or reference. Because predicting outcome is a prognostic endeavor, “predicting prognosis” will sometimes be used herein to refer to predicting recurrence or survival.

[0094] The results of any analyses according to the invention will often be communicated to physicians, genetic counselors and/or patients (or other interested parties such as researchers) in a transmittable form that can be communicated or transmitted to any of the above parties. Such a form can vary and can be tangible or intangible. The results can be embodied in descriptive statements, diagrams, photographs, charts, images or any other visual forms. For example, graphs showing expression or activity level or sequence variation information for various genes can be used in explaining the results. Diagrams showing such information for additional target gene(s) are also useful in indicating some testing results. The statements and visual forms can be recorded on a tangible medium such as papers, computer readable media such as floppy disks, compact disks, *etc.*, or on an intangible medium, e.g., an electronic medium in the form of email or website on internet or intranet. In addition, results can also be recorded in a sound form and

transmitted through any suitable medium, *e.g.*, analog or digital cable lines, fiber optic cables, *etc.*, via telephone, facsimile, wireless mobile phone, internet phone and the like.

[0095] Thus, the information and data on a test result can be produced anywhere in the world and transmitted to a different location. As an illustrative example, when an expression level, activity level, or sequencing (or genotyping) assay is conducted outside the United States, the information and data on a test result may be generated, cast in a transmittable form as described above, and then imported into the United States. Accordingly, the present invention also encompasses a method for producing a transmittable form of information on at least one of (a) expression level or (b) activity level for at least one patient sample. The method comprises the steps of (1) determining at least one of (a) or (b) above according to methods of the present invention; and (2) embodying the result of the determining step in a transmittable form. The transmittable form is a product of such a method.

[0096] Several embodiments of the invention described herein involve a step of correlating high CCP gene expression according to the present invention (*e.g.*, high expression of a panel of CCP genes as described in various embodiments throughout this application; a test value derived from or reflecting high expression; *etc.*) to a particular clinical feature (*e.g.*, a poor prognosis; an increased likelihood of breast cancer recurrence; *etc.*) if the CCP gene expression is greater than some reference (or optionally to another feature if the expression is less than some reference). Throughout this document, wherever such an embodiment is described, a further, related embodiment of the invention may involve, in addition to or instead of a correlating step, one or both of the following steps: (a) concluding that the patient has (or classifying the patient as having) the clinical feature based at least in part on high CCP expression (or a test value derived from or reflecting such); or (b) communicating that the patient has the clinical feature based at least in part on high CCP expression (or a test value derived from or reflecting such).

[0097] By way of illustration, but not limitation, one embodiment described in this document is a method for determining in a patient the prognosis of breast cancer or the likelihood of breast cancer recurrence, comprising: (1) determining the expression of a plurality of test genes comprising (a) at least 4, 6, 8, 10 or 15 or more cell-cycle genes (*e.g.*, CCGs in Panel F in Table 9; in any of Panels H, I, J, L, M, N & O; or in any sub-panel of Panel O in any of Tables 30 through 34; *etc.*), and/or (b) at least one of the *ABCC5* gene and the *PGR* gene or both, together or separately in

one or more samples from the patient, and (2) correlating high expression of said plurality of test genes to poor prognosis of the breast cancer in the patient, increased likelihood of poor breast cancer outcome, an increased likelihood of breast cancer recurrence, and/or a decreased probability of post-surgery distant metastasis-free survival. According to the preceding paragraph, this description of this embodiment is understood to include a description of two further, related embodiments, *i.e.*, a method for determining in a patient the prognosis of breast cancer or the likelihood of breast cancer recurrence, comprising: (1) determining the expression of a plurality of test genes comprising (a) at least 2, 3, 4, 5, 6, 8, 10 or 15 or more cell-cycle genes (e.g., CCGs in Panel F in Table 9 or any of Panels H, I, J, L, M, N & O (at least 2, 3, 4, 5, or 6 of which are in a sub-panel of Panel O in Tables 30 to 34)), and/or (b) at least one of the *ABCC5* gene and the *PGR* gene or both, together or separately in one or more samples from the patient, and (2)(a) concluding that said patient has a poor prognosis of the breast cancer, an increased likelihood of poor breast cancer outcome, an increased likelihood of breast cancer recurrence, and/or a decreased probability of post-surgery distant metastasis-free survival based at least in part on high expression of said plurality of test genes; or (2)(b) communicating that said patient has a poor prognosis of the breast cancer, an increased likelihood of poor breast cancer outcome, an increased likelihood of breast cancer recurrence, and/or a decreased probability of post-surgery distant metastasis-free survival based at least in part on high expression of said plurality of test genes.

[0098] In each embodiment described in this document involving correlating a particular assay or analysis output (e.g., high CCP gene expression, etc.) to some likelihood (e.g., increased, not increased, decreased, etc.) of some clinical feature (e.g., poor prognosis, breast cancer recurrence, etc.), or additionally or alternatively concluding or communicating such clinical feature based at least in part on such particular assay or analysis output, such correlating, concluding or communicating may comprise assigning a risk or likelihood of the clinical feature occurring based at least in part on the particular assay or analysis output. In some embodiments, such risk is a percentage probability of the event or outcome occurring (e.g., at least 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 99% probability). In some embodiments, the patient is assigned to a risk group (e.g., low risk, intermediate risk, high risk, etc.). In some embodiments “low risk” is any percentage probability below 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, or 50%. In some embodiments “intermediate risk” is any percentage probability above 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%,

45%, or 50% and below 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, or 75%. In some embodiments “high risk” is any percentage probability above 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 99%.

[0099] As used herein, “communicating” a particular piece of information means to make such information known to another person or to transfer such information to a thing (*e.g.*, a computer). In some methods of the invention, a patient’s prognosis or likelihood of recurrence or response to a particular treatment is communicated. In some embodiments, the information used to arrive at such a prognosis or response prediction (*e.g.*, high CCP gene expression according to the present invention, etc.) is communicated. This communication may be auditory (*e.g.*, verbal), visual (*e.g.*, written), electronic (*e.g.*, data transferred from one computer system to another), etc. In some embodiments, communicating a cancer classification (*e.g.*, prognosis, likelihood of response, appropriate treatment, etc.) comprises generating a report that communicates the cancer classification. In some embodiments the report is a paper report, an auditory report, or an electronic record. In some embodiments the report is displayed and/or stored on a computing device (*e.g.*, handheld device, desktop computer, smart device, website, etc.). In some embodiments the cancer classification is communicated to a physician (*e.g.*, a report communicating the classification is provided to the physician). In some embodiments the cancer classification is communicated to a patient (*e.g.*, a report communicating the classification is provided to the patient). Communicating a cancer classification can also be accomplished by transferring information (*e.g.*, data) embodying the classification to a server computer and allowing an intermediary or end-user to access such information (*e.g.*, by viewing the information as displayed from the server, by downloading the information in the form of one or more files transferred from the server to the intermediary or end-user’s device, etc.).

[00100] Wherever an embodiment of the invention comprises concluding some fact (*e.g.*, a patient’s prognosis or a patient’s likelihood of recurrence or response to a particular treatment regimen), this may include in some embodiments a computer program concluding such fact, typically after performing an algorithm that applies information on CCP gene expression according to the present invention.

[00101] In each embodiment described herein involving CCP gene expression levels, the present invention encompasses a further, related embodiment involving a test value or score

(e.g., CCP score, etc.) derived from, incorporating, and/or, at least to some degree, reflecting such expression levels. In other words, the bare CCP gene expressions data or levels need not be used in the various methods, systems, etc. of the invention; a test value or score derived from such numbers or lengths may be used. Typically, such test value will be compared to a reference value (as described at length in this document) and the method will end by correlating a high test value (or a test value derived from, incorporating, and/or, at least to some degree, reflecting high CCP gene expression) to a poor prognosis. The invention encompasses, *mutatis mutandis*, corresponding embodiments where the test value or score is used to determine the patient's prognosis, the patient's likelihood of response to a particular treatment regimen, the patient's or patient's sample's likelihood of having a breast cancer recurrence, etc.

[00102] Techniques for analyzing such expression, activity, and/or sequence data (indeed any data obtained according to the invention) will often be implemented using hardware, software or a combination thereof in one or more computer systems or other processing systems capable of effectuating such analysis.

[00103] Thus, the present invention further provides a system for determining gene expression in a tumor sample, comprising: (1) a sample analyzer for determining the expression levels of a panel of genes in a sample (e.g., a tumor sample) including at least 2, 4, 6, 8 or 10 cell-cycle genes, wherein the sample analyzer contains the sample which is from a patient having breast cancer, or mRNA molecules from the patient sample or cDNA molecules from mRNA expressed from the panel of genes; (2) a first computer program for (a) receiving gene expression data on at least 4 test genes selected from the panel of genes, (b) weighting the determined expression of each of the test genes, and (c) combining the weighted expression to provide a test value, wherein at least 20%, 50%, at least 75% or at least 90% of the test genes are cell-cycle genes (or wherein the cell-cycle genes are weighted to contribute at least 50%, 60%, 70%, 80%, 90%, 95% or 100% of the test value), and wherein the test genes include *ABCC5* or *PGR* or both; and (3) a second computer program for comparing the test value to one or more reference values each associated with (a) a predetermined degree of risk of cancer recurrence or progression of cancer and/or (b) a predetermined degree of likelihood of response to a particular treatment regimen (e.g., treatment regimen comprising chemotherapy). In some embodiments, the system further comprises a display

module displaying the comparison between the test value to the one or more reference values, or displaying a result of the comparing step.

[00104] In some embodiments, the amount of RNA transcribed from the panel of genes including test genes is measured in the sample. In addition, the amount of RNA of one or more housekeeping genes in the sample is also measured, and used to normalize or calibrate the expression of the test genes, as described above.

[00105] In some embodiments, the plurality of test genes includes at least 2, 3 or 4 cell-cycle genes, which constitute at least 50%, 75% or 80% of the plurality of test genes, and preferably 100% of the plurality of test genes. In some embodiments, the plurality of test genes includes at least 5, 6 or 7, or at least 8 cell-cycle genes, which constitute at least 20%, 25%, 30%, 40%, 50%, 60%, 70%, 75%, 80% or 90% of the plurality of test genes, and preferably 100% of the plurality of test genes.

[00106] In some other embodiments, the plurality of test genes includes at least 8, 10, 12, 15, 20, 25 or 30 cell-cycle genes, which constitute at least 20%, 25%, 30%, 40%, 50%, 60%, 70%, 75%, 80% or 90% of the plurality of test genes, and preferably 100% of the plurality of test genes.

[00107] The sample analyzer can be any instrument useful in determining gene expression, including, *e.g.*, a sequencing machine, a real-time PCR machine, and a microarray instrument.

[00108] The computer-based analysis function can be implemented in any suitable language and/or browsers. For example, it may be implemented with C language and preferably using object-oriented high-level programming languages such as Visual Basic, SmallTalk, C++, and the like. The application can be written to suit environments such as the Microsoft WindowsTM environment including WindowsTM 98, WindowsTM 2000, WindowsTM NT, and the like. In addition, the application can also be written for the MacIntoshTM, SUNTM, UNIX or LINUX environment. In addition, the functional steps can also be implemented using a universal or platform-independent programming language. Examples of such multi-platform programming languages include, but are not limited to, hypertext markup language (HTML), JAVATM, JavaScriptTM, Flash programming language, common gateway interface/structured query language (CGI/SQL), practical extraction report language (PERL), AppleScriptTM and other system script languages, programming

language/structured query language (PL/SQL), and the like. Java™- or JavaScript™-enabled browsers such as HotJava™, Microsoft™ Explorer™, or Netscape™ can be used. When active content web pages are used, they may include Java™ applets or ActiveX™ controls or other active content technologies.

[00109] The analysis function can also be embodied in computer program products and used in the systems described above or other computer- or internet-based systems. Accordingly, another aspect of the present invention relates to a computer program product comprising a computer-usable medium having computer-readable program codes or instructions embodied thereon for enabling a processor to carry out gene status analysis. These computer program instructions may be loaded onto a computer or other programmable apparatus to produce a machine, such that the instructions which execute on the computer or other programmable apparatus create means for implementing the functions or steps described above. These computer program instructions may also be stored in a computer-readable memory or medium that can direct a computer or other programmable apparatus to function in a particular manner, such that the instructions stored in the computer-readable memory or medium produce an article of manufacture including instruction means which implement the analysis. The computer program instructions may also be loaded onto a computer or other programmable apparatus to cause a series of operational steps to be performed on the computer or other programmable apparatus to produce a computer implemented process such that the instructions which execute on the computer or other programmable apparatus provide steps for implementing the functions or steps described above.

[00110] Thus one aspect of the present invention provides a system for determining whether a patient has increased likelihood of response to a particular treatment regimen. Generally speaking, the system comprises (1) computer program for receiving, storing, and/or retrieving a patient's CCG status data (*e.g.*, expression level, activity level, variants), *ABCC5* status data, *PGR* status data, and optionally clinical parameter data (*e.g.*, age, tumor size, node status); (2) computer program for querying this patient data; (3) computer program for concluding whether there is an increased likelihood of recurrence based on this patient data; and optionally (4) computer program for outputting/displaying this conclusion. In some embodiments this means for outputting the conclusion may comprise a computer program for informing a health care professional of the conclusion.

[00111] One example of such a computer system is the computer system [400] illustrated in **Figure 4**. Computer system [400] may include at least one input module [430] for entering patient data into the computer system [400]. The computer system [400] may include at least one output module [424] for indicating whether a patient has an increased or decreased likelihood of response and/or indicating suggested treatments determined by the computer system [400]. Computer system [400] may include at least one memory module [406] in communication with the at least one input module [430] and the at least one output module [424].

[00112] The at least one memory module [406] may include, *e.g.*, a removable storage drive [408], which can be in various forms, including but not limited to, a magnetic tape drive, a floppy disk drive, a VCD drive, a DVD drive, an optical disk drive, *etc.* The removable storage drive [408] may be compatible with a removable storage unit [410] such that it can read from and/or write to the removable storage unit [410]. Removable storage unit [410] may include a computer usable storage medium having stored therein computer-readable program codes or instructions and/or computer readable data. For example, removable storage unit [410] may store patient data. Example of removable storage unit [410] are well known in the art, including, but not limited to, floppy disks, magnetic tapes, optical disks, and the like. The at least one memory module [406] may also include a hard disk drive [412], which can be used to store computer readable program codes or instructions, and/or computer readable data.

[00113] In addition, as shown in **Figure 4**, the at least one memory module [406] may further include an interface [414] and a removable storage unit [416] that is compatible with interface [414] such that software, computer readable codes or instructions can be transferred from the removable storage unit [416] into computer system [400]. Examples of interface [414] and removable storage unit [416] pairs include, *e.g.*, removable memory chips (*e.g.*, EPROMs or PROMs) and sockets associated therewith, program cartridges and cartridge interface, and the like. Computer system [400] may also include a secondary memory module [418], such as random access memory (RAM).

[00114] Computer system [400] may include at least one processor module [402]. It should be understood that the at least one processor module [402] may consist of any number of devices. The at least one processor module [402] may include a data processing device, such as a microprocessor or microcontroller or a central processing unit. The at least one processor module

[402] may include another logic device such as a DMA (Direct Memory Access) processor, an integrated communication processor device, a custom VLSI (Very Large Scale Integration) device or an ASIC (Application Specific Integrated Circuit) device. In addition, the at least one processor module [402] may include any other type of analog or digital circuitry that is designed to perform the processing functions described herein.

[00115] As shown in **Figure 4**, in computer system [400], the at least one memory module [404], the at least one processor module [402], and secondary memory module [418] are all operably linked together through communication infrastructure [420], which may be a communications bus, system board, cross-bar, *etc.*). Through the communication infrastructure [420], computer program codes or instructions or computer readable data can be transferred and exchanged. Input interface [426] may operably connect the at least one input module [426] to the communication infrastructure [420]. Likewise, output interface [422] may operably connect the at least one output module [424] to the communication infrastructure [420].

[00116] The at least one input module [430] may include, for example, a keyboard, mouse, touch screen, scanner, and other input devices known in the art. The at least one output module [424] may include, for example, a display screen, such as a computer monitor, TV monitor, or the touch screen of the at least one input module [430]; a printer; and audio speakers. Computer system [400] may also include, modems, communication ports, network cards such as Ethernet cards, and newly developed devices for accessing intranets or the internet.

[00117] The at least one memory module [406] may be configured for storing patient data entered via the at least one input module [430] and processed via the at least one processor module [402]. Patient data relevant to the present invention may include expression level, activity level, copy number and/or sequence information for *ABCC5*, *PGR*, and/or a CCG. Patient data relevant to the present invention may also include clinical parameters relevant to the patient's disease (e.g., age, tumor size, node status, tumor stage). Any other patient data a physician might find useful in making treatment decisions/recommendations may also be entered into the system, including but not limited to age, gender, and race/ethnicity and lifestyle data such as diet information. Other possible types of patient data include symptoms currently or previously experienced, patient's history of illnesses, medications, and medical procedures.

[00118] The at least one memory module [406] may include a computer-implemented method stored therein. The at least one processor module [402] may be used to execute software or computer-readable instruction codes of the computer-implemented method. The computer-implemented method may be configured to, based upon the patient data, indicate whether the patient has an increased likelihood of recurrence, progression or response to any particular treatment, generate a list of possible treatments, etc.

[00119] In certain embodiments, the computer-implemented method may be configured to identify a patient as having or not having an increased likelihood of recurrence or progression. For example, the computer-implemented method may be configured to inform a physician that a particular patient has an increased likelihood of recurrence. Alternatively or additionally, the computer-implemented method may be configured to actually suggest a particular course of treatment based on the answers to/results for various queries.

[00120] **Figure 3** illustrates one embodiment of a computer-implemented method [300] of the invention that may be implemented with the computer system [400] of the invention. The method [300] begins with one of three queries ([310], [311], [312]), either sequentially or substantially simultaneously. If the answer to/result for **any** of these queries is “Yes” [320], the method concludes [330] that the patient has an increased likelihood of recurrence or of response to a particular treatment regimen (e.g., treatment comprising chemotherapy). If the answer to/result for **all** of these queries is “No” [321], the method concludes [331] that the patient does not have an increased likelihood of recurrence or of response to a particular treatment regimen (e.g., treatment comprising chemotherapy). The method [300] may then proceed with more queries, make a particular treatment recommendation ([340], [341]), or simply end.

[00121] When the queries are performed sequentially, they may be made in the order suggested by **Figure 3** or in any other order. Whether subsequent queries are made can also be dependent on the results/answers for preceding queries. In some embodiments of the method illustrated in **Figure 3**, for example, the method asks about CCP [311] first and, if the patient has increased CCP gene expression then the method concludes such [330] or optionally confirms by *ABCC5* status [311], and/or *PGR* status [312]. Optionally, the method may query clinical parameters (e.g., tumor size, age, tumor stage) before or after querying any of the molecular characteristics of CCP [310], *ABCC5* [311], and/or *PGR* [312]. As mentioned above, the preceding

order of queries may be modified. In some embodiments an answer of “yes” to one query (*e.g.*, [310]) prompts one or more of the remaining queries to confirm that the patient has, *e.g.*, increased risk of recurrence.

[00122] In some embodiments, the computer-implemented method of the invention [300] is open-ended. In other words, the apparent first step [310] in **Figure 3** may actually form part of a larger process and, within this larger process, need not be the first step/query. Additional steps may also be added onto the core methods discussed above. These additional steps include, but are not limited to, informing a health care professional (or the patient itself) of the conclusion reached; combining the conclusion reached by the illustrated method [300] with other facts or conclusions to reach some additional or refined conclusion regarding the patient’s diagnosis, prognosis, treatment, etc.; making a recommendation for treatment (*e.g.*, “patient should/should not undergo adjuvant chemotherapy”); additional queries about additional biomarkers, clinical parameters (*e.g.*, age, tumor size, node status, tumor stage), or other useful patient information (*e.g.*, age at diagnosis, general patient health, etc.).

[00123] Regarding the above computer-implemented method [300], the answers to the queries may be determined by the method instituting a search of patient data for the answer. For example, to answer the respective queries ([310], [311], [312]), patient data may be searched for CCG status (*e.g.*, CCG expression level data), ABCC5 status, PGR status (and optionally clinical parameters, *e.g.*, age, tumor size, node status, tumor stage, nomogram score, etc.). If such a comparison has not already been performed, the method may compare these data to some reference in order to determine if the patient has an abnormal (*e.g.*, elevated, low, negative) status. Additionally or alternatively, the method may present one or more of the queries ([310], [311], [312]) to a user (*e.g.*, a physician) of the computer system [400]. For example, the questions ([310], [311], [312]) may be presented via an output module [424]. The user may then answer “Yes” or “No” or provide some other value (*e.g.*, numerical or qualitative value representing CCG status) via an input module [430]. The method may then proceed based upon the answer received. Likewise, the conclusions [330, 331] may be presented to a user of the computer-implemented method via an output module [424].

[00124] Thus in some embodiments the invention provides a method comprising: accessing information on a patient’s CCG status and the status of *ABCC5* or *PGR* or both stored in a

computer-readable medium; querying this information to determine whether a sample obtained from the patient shows increased expression of a plurality of test genes comprising at least 2 CCGs (e.g., a test value representing the expression of this plurality of test genes that is weighted such that CCGs contribute at least 50% to the test value, such test value being higher than some reference value), *ABCC5* and/or *PGR*; outputting [or displaying] the quantitative or qualitative (e.g., “increased”) likelihood that the patient will respond to a particular treatment regimen. As used herein in the context of computer-implemented embodiments of the invention, “displaying” means communicating any information by any sensory means. Examples include, but are not limited to, visual displays, e.g., on a computer screen or on a sheet of paper printed at the command of the computer, and auditory displays, e.g., computer generated or recorded auditory expression of a patient’s genotype.

[00125] The practice of the present invention may also employ conventional biology methods, software and systems. Computer software products of the invention typically include computer readable media having computer-executable instructions for performing the logic steps of the method of the invention. Suitable computer readable medium include floppy disk, CD-ROM/DVD/DVD-ROM, hard-disk drive, flash memory, ROM/RAM, magnetic tapes and etc. Basic computational biology methods are described in, for example, Setubal *et al.*, INTRODUCTION TO COMPUTATIONAL BIOLOGY METHODS (PWS Publishing Company, Boston, 1997); Salzberg *et al.* (Ed.), COMPUTATIONAL METHODS IN MOLECULAR BIOLOGY, (Elsevier, Amsterdam, 1998); Rashidi & Buehler, BIOINFORMATICS BASICS: APPLICATION IN BIOLOGICAL SCIENCE AND MEDICINE (CRC Press, London, 2000); and Ouelette & Bzevanis, BIOINFORMATICS: A PRACTICAL GUIDE FOR ANALYSIS OF GENE AND PROTEINS (Wiley & Sons, Inc., 2nd ed., 2001); *see also*, U.S. Pat. No. 6,420,108.

[00126] The present invention may also make use of various computer program products and software for a variety of purposes, such as probe design, management of data, analysis, and instrument operation. *See* U.S. Pat. Nos. 5,593,839; 5,795,716; 5,733,729; 5,974,164; 6,066,454; 6,090,555; 6,185,561; 6,188,783; 6,223,127; 6,229,911 and 6,308,170. Additionally, the present invention may have embodiments that include methods for providing genetic information over networks such as the Internet as shown in U.S. Ser. Nos. 10/197,621 (U.S. Pub. No. 20030097222); 10/063,559 (U.S. Pub. No. 20020183936), 10/065,856 (U.S. Pub. No.

20030100995); 10/065,868 (U.S. Pub. No. 20030120432); 10/423,403 (U.S. Pub. No. 20040049354).

[00127] Techniques for analyzing such expression, activity, and/or sequence data (indeed any data obtained according to the invention) will often be implemented using hardware, software or a combination thereof in one or more computer systems or other processing systems capable of effectuating such analysis.

[00128] Thus one aspect of the present invention provides systems related to the above methods of the invention. In one embodiment the invention provides a system for determining a patient's prognosis and/or whether a patient will respond to a particular treatment regimen, comprising:

- (1) a sample analyzer for determining the expression levels in a sample of a plurality of test genes including at least 4 CCGs, and *ABCC5* or *PGR* or both, wherein the sample analyzer contains the sample, RNA from the sample and expressed from the panel of genes, or DNA synthesized from said RNA;
- (2) a first computer program for
 - (a) receiving gene expression data on said plurality of test genes,
 - (b) weighting the determined expression of each of the test genes with a predefined coefficient, and
 - (c) combining the weighted expression to provide a test value, wherein the combined weight given to said at least 4 CCGs, and *ABCC5* or *PGR* or both, is at least 40% (or 50%, 60%, 70%, 80%, 90%) of the total weight given to the expression of all of said plurality of test genes; and
- (3) a second computer program for comparing the test value to one or more reference values each associated with a predetermined likelihood of recurrence or progression or a predetermined likelihood of response to a particular treatment regimen.

In some embodiments at least 20%, 50%, 75%, or 90% of said plurality of test genes are CCGs. In some embodiments the sample analyzer contains reagents for determining the expression levels in the sample of said panel of genes including at least 4 CCGs and *ABCC5* or *PGR* or both.

[00129] In another embodiment the invention provides a system for determining gene expression in a sample (e.g., tumor sample), comprising: (1) a sample analyzer for determining the

expression levels of a panel of genes in a sample including at least 4 CCGs and *ABCC5* or *PGR* or both, wherein the sample analyzer contains the sample which is from a patient having breast cancer, RNA from the sample and expressed from the panel of genes, or DNA synthesized from said RNA; (2) a first computer program for (a) receiving gene expression data on at least 4 test genes selected from the panel of genes, (b) weighting the determined expression of each of the test genes with a predefined coefficient, and (c) combining the weighted expression to provide a test value, wherein the combined weight given to said at least 4 CCGs is at least 40% (or 50%, 60%, 70%, 80%, 90%) of the total weight given to the expression of all of said plurality of test genes; and (3) a second computer program for comparing the test value to one or more reference values each associated with a predetermined degree of risk of cancer recurrence or progression of breast cancer. In some embodiments at least 20%, 50%, 75%, or 90% of said plurality of test genes are CCGs. In some embodiments the system comprises a computer program for determining the patient's prognosis and/or determining (including quantifying) the patient's degree of risk of cancer recurrence or progression based at least in part on the comparison of the test value with said one or more reference values.

[00130] In some embodiments, the system further comprises a display module displaying the comparison between the test value and the one or more reference values, or displaying a result of the comparing step, or displaying the patient's prognosis and/or degree of risk of cancer recurrence or progression.

[00131] In a preferred embodiment, the amount of RNA transcribed from the panel of genes including test genes (and/or DNA reverse transcribed therefrom) is measured in the sample. In addition, the amount of RNA of one or more housekeeping genes in the sample (and/or DNA reverse transcribed therefrom) is also measured, and used to normalize or calibrate the expression of the test genes, as described above.

[00132] In some embodiments, the plurality of test genes includes at least 2, 3 or 4 CCGs and *ABCC5* or *PGR* or both, which constitute at least 50%, 75%, 80%, 90% or 95% of the plurality of test genes of the plurality of test genes. In some embodiments, the plurality of test genes includes at least 5, 6 or 7, or at least 8 CCGs and *ABCC5* or *PGR* or both, which constitute at least 20%, 25%, 30%, 40%, 50%, 60%, 70%, 75%, 80% or 90% of the plurality of test genes. Thus in some embodiments the plurality of test genes comprises in addition to *ABCC5* or *PGR* or both, at

least some number of CCGs (*e.g.*, at least 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50 or more CCGs) and this plurality of CCGs comprises the top 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 25, 30, 35, 40 or more CCGs listed in Table 2, 3, 5, 6, or 7. In some embodiments the plurality of test genes comprises in addition to *ABCC5* or *PGR* or both, at least some number of CCGs (*e.g.*, at least 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50 or more CCGs) and this plurality of CCGs comprises at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, or 20 of the following genes: *ASPM*, *BIRC5*, *BUB1B*, *CCNB2*, *CDC2*, *CDC20*, *CDCA8*, *CDKN3*, *CENPF*, *DLGAP5*, *FOXMI*, *KIAA0101*, *KIF11*, *KIF2C*, *KIF4A*, *MCM10*, *NUSAP1*, *PRC1*, *RACGAP1*, and *TPX2*. In some embodiments the plurality of test genes comprises beside *ABCC5* or *PGR* or both, at least some number of CCGs (*e.g.*, at least 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50 or more CCGs) and this plurality of CCGs comprises any one, two, three, four, five, six, seven, eight, nine, or ten or all of gene numbers 1 & 2, 1 to 3, 1 to 4, 1 to 5, 1 to 6, 1 to 7, 1 to 8, 1 to 9, or 1 to 10 of any of Table 2, 3, 5, 6, or 7. In some embodiments the plurality of test genes comprises in addition to *ABCC5* or *PGR* or both, at least some number of CCGs (*e.g.*, at least 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50 or more CCGs) and this plurality of CCGs comprises any one, two, three, four, five, six, seven, eight, or nine or all of gene numbers 2 & 3, 2 to 4, 2 to 5, 2 to 6, 2 to 7, 2 to 8, 2 to 9, or 2 to 10 of any of Table 2, 3, 5, 6, or 7. In some embodiments the plurality of test genes comprises in addition to *ABCC5* or *PGR* or both, at least some number of CCGs (*e.g.*, at least 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50 or more CCGs) and this plurality of CCGs comprises any one, two, three, four, five, six, seven, or eight or all of gene numbers 3 & 4, 3 to 5, 3 to 6, 3 to 7, 3 to 8, 3 to 9, or 3 to 10 of any of Table 2, 3, 5, 6, or 7. In some embodiments the plurality of test genes comprises in addition to *ABCC5* or *PGR* or both, at least some number of CCGs (*e.g.*, at least 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50 or more CCGs) and this plurality of CCGs comprises any one, two, three, four, five, six, or seven or all of gene numbers 4 & 5, 4 to 6, 4 to 7, 4 to 8, 4 to 9, or 4 to 10 of any of Table 2, 3, 5, 6, or 7. In some embodiments the plurality of test genes comprises in addition to *ABCC5* or *PGR* or both, at least some number of CCGs (*e.g.*, at least 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50 or more CCGs) and this plurality of CCGs comprises any one, two, three, four, five, six, seven, eight, nine, 10, 11, 12, 13, 14, or 15 or all of gene numbers 1 & 2, 1 to 3, 1 to 4, 1 to 5, 1 to 6, 1 to 7, 1 to 8, 1 to 9, 1 to 10, 1 to 11, 1 to 12, 1 to 13, 1 to 14, or 1 to 15 of any of Table 2, 3, 5, 6, or 7.

[00133] In some other embodiments, the plurality of test genes includes in addition to *ABCC5* or *PGR* or both, at least 8, 10, 12, 15, 20, 25 or 30 CCGs, which constitute at least 20%, 25%, 30%, 40%, 50%, 60%, 70%, 75%, 80% or 90% of the plurality of test genes, and preferably 100% of the plurality of test genes.

[00134] The sample analyzer can be any instrument useful in determining gene expression, including, *e.g.*, a sequencing machine (*e.g.*, Illumina HiSeqTM, Ion Torrent PGM, ABI SOLiDTM sequencer, PacBio RS, Helicos HeliscopeTM, etc.), a real-time PCR machine (*e.g.*, ABI 7900, Fluidigm BioMarkTM, etc.), a microarray instrument, etc.

[00135] In one aspect, the present invention provides methods of treating a cancer patient comprising obtaining CCG status information (*e.g.*, the CCGs in Table 1, 2, 3, 5, 6, 7, 8, or 9 or Panel A, B, C, D, E, F, or G), and recommending, prescribing or administering a treatment for the cancer patient based on the CCG status. For example, the invention provides a method of treating a cancer patient comprising:

- (1) determining the expression of a plurality of test genes, wherein said plurality of test genes comprises in addition to *ABCC5* or *PGR* or both, at least 4 (or 5, 6, 7, 8, 9, 10, 15, 20, 30 or more) CCGs;
- (2) based at least in part on the determination in step (1), recommending, prescribing or administering either
 - (a) a treatment regimen comprising chemotherapy (*e.g.*, adjuvant chemotherapy) if the patient has increased expression of the plurality of test genes (*e.g.*, and CCGs are weighted to contribute at least 50% to the determination of increased expression of the plurality of test genes), or
 - (b) a treatment regimen not comprising chemotherapy if the patient does not have increased expression of the plurality of test genes (*e.g.*, and CCGs are weighted to contribute at least 50% to the determination of increased expression of the plurality of test genes).

[00136] In one aspect, the invention provides compositions for use in the above methods. Such compositions include, but are not limited to, nucleic acid probes hybridizing to, *ABCC5* or *PGR* or both, and a CCG including but not limited to a CCG listed in any of Table 1, 2, 3, 5, 6, 7, 8, 9, 10, 11 or 25 or Panel A, B, C, D, E, F, G, H, I, J, L, M, N or O (or to any nucleic acids

encoded thereby or complementary thereto); nucleic acid primers and primer pairs suitable for selectively amplifying all or a portion of *ABCC5* or *PGR* or both, and the CCG or any nucleic acids encoded thereby; antibodies binding immunologically to a polypeptide encoded by *ABCC5* or *PGR* or both, and by CCG; probe sets comprising a plurality of said nucleic acid probes, nucleic acid primers, antibodies, and/or polypeptides; microarrays comprising any of these; kits comprising any of these; *etc.* In some aspects, the invention provides computer methods, systems, software and/or modules for use in the above methods.

[00137] In some embodiments the invention provides a probe comprising an isolated oligonucleotide capable of selectively hybridizing to *ABCC5* or *PGR* or both, and at least one of the genes in any of Table 1, 2, 3, 5, 6, 7, 8, 9, 10, 11 or 25 or Panel A, B, C, D, E, F, G, H, I, J, L, M, N or O. The terms “probe” and “oligonucleotide” (also “oligo”), when used in the context of nucleic acids, interchangeably refer to a relatively short nucleic acid fragment or sequence. The invention also provides primers useful in the methods of the invention. “Primers” are probes capable, under the right conditions and with the right companion reagents, of selectively amplifying a target nucleic acid (*e.g.*, a target gene). In the context of nucleic acids, “probe” is used herein to encompass “primer” since primers can generally also serve as probes.

[00138] The probe can generally be of any suitable size/length. In some embodiments the probe has a length from about 8 to 200, 15 to 150, 15 to 100, 15 to 75, 15 to 60, or 20 to 55 bases in length. They can be labeled with detectable markers with any suitable detection marker including but not limited to, radioactive isotopes, fluorophores, biotin, enzymes (*e.g.*, alkaline phosphatase), enzyme substrates, ligands and antibodies, *etc.* See Jablonski *et al.*, NUCLEIC ACIDS RES. (1986) 14:6115-6128; Nguyen *et al.*, BIOTECHNIQUES (1992) 13:116-123; Rigby *et al.*, J. MOL. BIOL. (1977) 113:237-251. Indeed, probes may be modified in any conventional manner for various molecular biological applications. Techniques for producing and using such oligonucleotide probes are conventional in the art.

[00139] Probes according to the invention can be used in the hybridization/ amplification/ detection techniques discussed above. Thus, some embodiments of the invention comprise probe sets suitable for use in a microarray in detecting, amplifying and/or quantitating *ABCC5* or *PGR* or both, and a plurality of CCGs. In some embodiments the probe sets have a certain proportion of their probes directed to CCGs—*e.g.*, a probe set consisting of 10%, 20%, 30%,

40%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% probes specific for CCGs. In some embodiments the probe set comprises probes directed to at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 40, 45, 50, 60, 70, 80, 90, 100, 125, 150, 175, 200, 250, 300, 350, 400, 450, 500, 600, 700, or 800 or more, or all, of the genes in Table 1, 2, 3, 5, 6, 7, 8, or 9 or Panel A, B, C, D, E, F, or G. Such probe sets can be incorporated into high-density arrays comprising 5,000, 10,000, 20,000, 50,000, 100,000, 200,000, 300,000, 400,000, 500,000, 600,000, 700,000, 800,000, 900,000, or 1,000,000 or more different probes. In other embodiments the probe sets comprise primers (*e.g.*, primer pairs) for amplifying nucleic acids comprising at least a portion of one or more of the CCGs in Table 1, 2, 3, 5, 6, 7, 8, or 9 or Panel A, B, C, D, E, F, or G.

[00140] In another aspect of the present invention, a kit is provided for practicing the prognosis of the present invention. The kit may include a carrier for the various components of the kit. The carrier can be a container or support, in the form of, *e.g.*, bag, box, tube, rack, and is optionally compartmentalized. The carrier may define an enclosed confinement for safety purposes during shipment and storage. The kit includes various components useful in determining the status of *ABCC5* or *PGR* or both, and one or more CCGs and one or more housekeeping gene markers, using the above-discussed detection techniques. For example, the kit may include oligonucleotides specifically hybridizing under high stringency to mRNA or cDNA of the genes in Table 1, 2, 3, 5, 6, 7, 8, or 9 or Panel A, B, C, D, E, F, or G. Such oligonucleotides can be used as PCR primers in RT-PCR reactions, or hybridization probes. In some embodiments the kit comprises reagents (*e.g.*, probes, primers, and or antibodies) for determining the expression level of a panel of genes, where said panel comprises at least 25%, 30%, 40%, 50%, 60%, 75%, 80%, 90%, 95%, 99%, or 100% CCGs (*e.g.*, CCGs in Table 1, 2, 3, 5, 6, 7, 8, or 9 or Panel A, B, C, D, E, F, or G). In some embodiments the kit consists of reagents (*e.g.*, probes, primers, and or antibodies) for determining the expression level of no more than 2500 genes, wherein at least 5, 10, 15, 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 150, 200, 250, or more of these genes are CCGs (*e.g.*, CCGs in Table 1, 2, 3, 5, 6, 7, 8, or 9 or Panel A, B, C, D, E, F, or G).

[00141] The oligonucleotides in the detection kit can be labeled with any suitable detection marker including but not limited to, radioactive isotopes, fluorophores, biotin, enzymes (*e.g.*, alkaline phosphatase), enzyme substrates, ligands and antibodies, etc. See Jablonski *et al.*,

Nucleic Acids Res., 14:6115-6128 (1986); Nguyen *et al.*, *Biotechniques*, 13:116-123 (1992); Rigby *et al.*, *J. Mol. Biol.*, 113:237-251 (1977). Alternatively, the oligonucleotides included in the kit are not labeled, and instead, one or more markers are provided in the kit so that users may label the oligonucleotides at the time of use.

[00142] In another embodiment of the invention, the detection kit contains one or more antibodies selectively immunoreactive with one or more proteins encoded by *ABCC5* or *PGR* or both, and by one or more CCGs or optionally any additional markers. Examples include antibodies that bind immunologically to a protein encoded by a gene in Table 1, 2, 3, 5, 6, 7, 8, or 9 or Panel A, B, C, D, E, F, or G. Methods for producing and using such antibodies are well-known in the art.

[00143] Various other components useful in the detection techniques may also be included in the detection kit of this invention. Examples of such components include, but are not limited to, Taq polymerase, deoxyribonucleotides, dideoxyribonucleotides, other primers suitable for the amplification of a target DNA sequence, RNase A, and the like. In addition, the detection kit preferably includes instructions on using the kit for practice the prognosis method of the present invention using human samples.

EXAMPLE 1

[00144] The expression of the genes in Panel L was evaluated for its ability to determine prognosis of breast cancer patients. Panel L includes 24 CCP genes (Panel M), *ESR1*, *ABCC5*, and *PGR* (which together with Panel M form Panel N (note that *ESR1* is optional and in this study was analyzed primarily to confirm ER+ status)), and 14 housekeeping genes (Panel K). Table 11 illustrates these panels and how they interact.

Clinical Data

[00145] This study initially involved 537 breast cancer patients. All patients were ER+ and node negative. For each patient, dates were recorded for the following events: surgery; Tamoxifen start and end; breast, axillary, sub-clavicular fossa, and distant metastatic relapse; loss to follow-up; and death. The cause of death and disease status at death were also included.

[00146] The primary outcome of interest, distant metastasis-free survival (DMFS), was calculated as the time in years from surgery to distant metastasis. DMFS was censored for patients that were lost to follow-up before experiencing distant metastasis or that experienced distant metastasis after 10 years. Using this definition, 63 distant metastasis events were observed.

[00147] Other clinical data for each patient included age (mean = 56.6, sd = 10.6) and type of adjuvant therapy status (414 tamoxifen, 39 hormone therapy other than tamoxifen, and 84 none). Information on each tumor included ER and PR status (both on a scale from 0 to 8), size (mm), histologic type, and grade (148 poorly differentiated, 255 moderately differentiated, 133 well differentiated, and 1 missing). Patients that received tamoxifen or another hormone therapy were treated the same throughout the analysis.

qPCR Data

qPCR Assay Details and CCP Score

[00148] The CCP score was calculated from RNA expression of 24 CCP genes (Panel M) normalized by 14 housekeeper genes (HK) (Panel K). The relative numbers of CCP genes (24) and HK genes (14) were optimized in order to minimize the variance of the CCP score. The CCP score is the unweighted mean of C_T values for CCP gene expression, normalized by the unweighted mean of the HK genes so that higher values indicate higher expression. One unit is equivalent to a two-fold change in expression. The CCP scores were centered by the mean value, again determined in the training set.

[00149] A dilution experiment was performed on four of the commercial prostate samples to estimate the measurement error of the CCP score ($se = 0.10$) and the effect of missing values. It was found that the CCP score remained stable as concentration decreased to the point of 10 failures out of the total 24 CCP genes. Based on this result, samples with more than 9 missing values were not assigned a CCP score.

[00150] From each FFPE sample block one 5 μ m section was cut and stained with haematoxylin and eosin. Tumor areas were marked by a pathologist. Additional two 10 μ m sections were cut directly adjacent to the H&E stained section. Tumor areas on the unstained sections were identified by alignment with the marked areas on the H&E stain and macro-dissected manually into Eppendorff tubes. Sections were deparaffinized by xylene extractions followed by washes with

ethanol. After an overnight incubation with proteinase K, deparaffinized tissue was subjected to RNA extraction using the Qiagen miRNAeasy kit according to manufacturer's instructions. Total RNA was treated with DNASE I to remove potential genomic DNA contamination. Final RNA yield was determined on a Nanodrop spectrophotometer.

[00151] For each sample 500ng RNA was converted to cDNA using the high capacity cDNA archive kit (Applied Biosystems). Newly synthesized cDNA served as template for replicate pre-amplification reactions. Each of the reactions contained 3µl cDNA and a pool of Taqman™ assays for all 38 genes in the signature (14 housekeeping genes, 24 cell cycle genes). Preamplification was run for 14 cycles to generate sufficient total copies even from a low copy sample to inoculate individual PCR reactions for 38 genes. Preamplification reactions were diluted 1:20 before loading on Taqman™ low density arrays (TLDA, Applied Biosystems). Raw data for the calculation of the CCP score were the C_t values of the 46 genes from the TLDA arrays. The CCP score was the unweighted mean of C_t values for cell cycle gene expression, normalized by the unweighted mean of the house keeper genes so that higher values indicate higher expression. One unit is equivalent to a two-fold change in expression. The CCP scores were centered by the mean value determined in the commercial training set.

[00152] CCP scores were unusable for 36 samples: 21 for too many missing housekeeper genes (12 were required), 14 for too many missing CCP genes (18 were required), and 1 because the standard deviation of the by-card CCP scores was greater than 0.5. Therefore, 498 (93%) samples received passing CCP scores.

Other qPCR Expression

[00153] In addition to the CCP genes, *ABCC5*, *PGR* and *ESR1* were also measured via the same process described above. For *ABCC5*, the Hs00981085_m1 was used. 506 patients had acceptable measurements for *ABCC5*. For *PGR*, the Hs00172183_m1 was used. 449 patients had acceptable measurements for *PGR*. Two assays for *ESR1* were run: Hs01046815_m1 and Hs00174860_m1. Both had the same number of missing values and their measurements correlated well. The expression for the two assays was averaged and 513 patients had acceptable values.

Relationship between IHC and qPCR

[00154] Figure 1 shows the relationship between PR IHC and *PGR* qPCR expression. Missing values for *PGR* qPCR occurred mainly in samples with low PR IHC. Therefore, they were imputed using the predicted value from a linear regression model predicting *PGR* qPCR from PR IHC fit to all samples whose PR IHC was greater than 2.

Associations with DMFS

Univariate

[00155] Table 22 summarizes the results of univariate prediction of DMFS for each variable. Figure 2 illustrates the relationship between CCP score and DMFS.

Table 22

Variable	HR (95% CI)	p-value	n
Age of Patient	0.99 (0.97, 1.02)	0.63	537
Grade of Tumor	1.51 (1.07, 2.13)	0.019	536
Tumor Size (mm)	1.07 (1.03, 1.11)	0.00066	508
Hormone Therapy	0.82 (0.43, 1.57)	0.55	537
ER Expression by IHC	0.89 (0.75, 1.07)	0.22	521
PR Expression by IHC	0.87 (0.79, 0.96)	0.006	522
<i>ABCC5</i> Expression by qPCR	1.46 (1.09, 1.96)	0.012	506
<i>ESR1</i> Expression by qPCR	0.94 (0.82, 1.07)	0.33	513
<i>PGR</i> Expression by qPCR	0.83 (0.75, 0.92)	0.00072	534
CCP Score	1.82 (1.39, 2.38)	9.20×10^{-6}	498

Interactions

[00156] The interaction between *PGR* qPCR expression and hormone therapy status is a significant predictor of DMFS (p-value = 0.0012, n = 534). The HR for *PGR* is 0.76 (0.68, 0.86) in patients treated with hormone therapy and 1.18 (0.92, 1.52) in patients that did not receive hormone therapy. Likewise, the interaction between PR IHC expression and hormone therapy status is a significant predictor of DMFS (p-value = 0.0033, n = 522). The HR for PR is 0.82 (0.74, 0.9) in patients treated with hormone therapy and 1.22 (0.91, 1.64) in patients that did not receive hormone therapy.

[00157] The relationship between log hazards of distant metastasis and CCP appears to be non-linear as squared CCP is a significant predictor of DMFS (p-value = 0.022, n = 498). The

HR for CCP is smaller for high CCP scores. The p-value for CCP and squared CCP combined is 3.9×10^{-6} .

Multivariate

[00158] A multivariate model for DMFS was fit with the following predictors: age of patient, grade of tumor, size of tumor, interaction of hormone therapy status and PR IHC expression, CCP score, and squared CCP score. *ABCC5* qPCR expression was added to the model to assess its significance. CCP, PR IHC and *ABCC5* qPCR expression remained significant in the expanded model. A summary of the final model (n = 453) including *ABCC5* qPCR expression is given in Table 23. From this analysis, Panels M and N emerged as very good predictors of DMFS.

Table 23

Variable		HR (95% CI)	p-value
Age of Patient		0.98 (0.95, 1.01)	0.22
Grade of Tumor		1.1 (0.71, 1.72)	0.66
Tumor Size (mm)		1.05 (1, 1.09)	0.048
<i>ABCC5</i> Expression by qPCR		1.47 (1.07, 2.02)	0.016
Hormone Therapy/ PR Interaction	Hormone	10.79 (0.98,	
	PR IHC in	0.87 (0.77, 0.99)	0.0016
	PR IHC in	1.45 (1, 2.09)	
CCP Score	CCP Score	1.86 (1.15, 3.03)	0.00052
	Squared CCP Score	0.63 (0.42, 0.94)	

Relationship between Estrogen and Progesterone Receptor Expression

[00159] Although all patients were ER+ by IHC (i.e., they had ER IHC greater than 1), some patients had very low *ESR1* qPCR expression. All patients with low *ESR1* qPCR expression also had low progesterone receptor expression. However, there were a large number of patients that had very low progesterone receptor expression by qPCR and/or IHC and normal *ESR1* qPCR expression. This may explain why the interaction between progesterone receptor expression and hormone treatment status is a significant predictor of DMFS while the interaction between estrogen receptor expression and hormone treatment status is not.

EXAMPLE 2

[00160] Panel K was further evaluated for predictive value in the neoadjuvant setting. Response and gene expression data were studied from three publicly available microarray datasets as shown in Table 24 below.

Table 24

Study Identifier	Reference	Neoadjuvant Chemotherapy Regimen
GSE16716, breast cancer subset in GSE20194	Popovici et al., Breast Cancer Res. (2010) 12(1):R5	T/FAC = T (Paclitaxel) + FAC (5-fluoro-uracil, doxorubicin, cyclophosphamide)
GSE20271	Tabchy et al., Clin. Cancer Res. (2010) 16(21):5351-5361	T/FAC = T (Paclitaxel) + FAC (5-fluoro-uracil, doxorubicin, cyclophosphamide) or FAC alone (5-fluoro-uracil, doxorubicin, cyclophosphamide)
GSE32646	Miyake et al., Cancer Sci. (2012) 103(5):913-920	P-FEC = P (Paclitaxel) + FEC (5-fluoro-uracil, epirubicin, cyclophosphamide)

[00161] In these datasets, there were 287 ER+ patients treated with neoadjuvant chemotherapy as shown in Table 24. 23 of these (8.0%) showed complete response with neoadjuvant treatment. Panel M significantly predicted complete response (p-value = 0.003) as shown in Figure 7.

EXAMPLE 3

[00162] The samples analyzed in Example 1 were combined with 181 additional samples from patients with positive nodes. This combined cohort was analyzed as described in Example 1 with the following distinctions and as further noted below: (a) use of hormone therapy as a time dependent covariate was introduced and (b) expression was measured for an altered gene panel ("Panel O", as shown in Tables 25 & 26 below, together with an altered list of housekeeper genes, as shown in Table 27). Two assays were selected to measure the expression of each of *ABCC5* (Assay ID nos. Hs00981085_m1 and Hs00981087_m1) and *PGR* (Assay ID nos. Hs01556702_m1 and Hs01556707_m1).

Table 25: Genes of Panel O Ranked by Correlation to CCP Mean

Gene #	Gene	Assay	Correlation to CCP Mean
1	<i>ASPM</i>	Hs00411505_m1	0.89

2	<i>MCM10</i>	Hs00960349_m1	0.89
3	<i>BUB1B</i>	Hs01084828_m1	0.88
4	<i>KIF20A</i>	Hs00993573_m1	0.88
5	<i>SKA1</i>	Hs00536843_m1	0.88
6	<i>CDKN3</i>	Hs00193192_m1	0.87
7	<i>PRC1</i>	Hs00187740_m1	0.87
8	<i>RAD54L</i>	Hs00269177_m1	0.87
9	<i>RRM2</i>	Hs00357247_g1	0.87
10	<i>PTTG1</i>	Hs00851754_u1	0.86
11	<i>NUSAP1</i>	Hs01006195_m1	0.85
12	<i>RAD51</i>	Hs00153418_m1	0.84
13	<i>CDK1</i>	Hs00364293_m1	0.83
14	<i>KIAA0101</i>	Hs00207134_m1	0.81
15	<i>KIF11</i>	Hs00189698_m1	0.81
16	<i>PBK</i>	Hs00218544_m1	0.81
17	<i>CDCA3</i>	Hs00229905_m1	0.78
18	<i>CENPF</i>	Hs00193201_m1	0.78
19	<i>DTL</i>	Hs00978565_m1	0.77
20	<i>TK1</i>	Hs01062125_m1	0.76
21	<i>ASF1B</i>	Hs00216780_m1	0.74
22	<i>PLK1</i>	Hs00153444_m1	0.7
23	<i>CENPM</i>	Hs00608780_m1	0.66

Table 26: CCP Genes Ranked by Univariate P-Value

Gene #	Gene Symbol	Assay ID	Univariate p-value
1	<i>CDKN3</i>	Hs00193192_m1	1.00E-08
2	<i>SKA1</i>	Hs00536843_m1	2.30E-07
3	<i>BUB1B</i>	Hs01084828_m1	3.50E-07
4	<i>KIF20A</i>	Hs00993573_m1	7.10E-07
5	<i>RRM2</i>	Hs00357247_g1	9.00E-07
6	<i>ASPM</i>	Hs00411505_m1	2.70E-06
7	<i>NUSAP1</i>	Hs01006195_m1	4.60E-06
8	<i>DTL</i>	Hs00978565_m1	9.50E-06
9	<i>PLK1</i>	Hs00153444_m1	1.20E-05
10	<i>CDK1</i>	Hs00364293_m1	1.60E-05
11	<i>PRC1</i>	Hs00187740_m1	2.30E-05
12	<i>PTTG1</i>	Hs00851754_u1	2.30E-05
13	<i>MCM10</i>	Hs00960349_m1	3.60E-05

14	<i>CENPM</i>	Hs00608780_m1	7.90E-05
15	<i>CENPF</i>	Hs00193201_m1	1.30E-04
16	<i>KIF11</i>	Hs00189698_m1	2.50E-04
17	<i>RAD51</i>	Hs00153418_m1	8.00E-04
18	<i>PBK</i>	Hs00218544_m1	8.70E-04
19	<i>TK1</i>	Hs01062125_m1	1.00E-03
20	<i>RAD54L</i>	Hs00269177_m1	2.00E-03
21	<i>CDC43</i>	Hs00229905_m1	3.70E-03
22	<i>KIAA0101</i>	Hs00207134_m1	1.90E-02
23	<i>ASF1B</i>	Hs00216780_m1	4.40E-02

Table 27: Housekeeper Genes

Gene Symbol	Assay
<i>CLTC</i>	Hs00191535_m1
<i>PPP2CA</i>	Hs00427259_m1
<i>PSMA1</i>	Hs00267631_m1
<i>PSMC1</i>	Hs02386942_g1
<i>RPL13A (RPL13AP5)</i>	Hs03043885_g1
<i>RPL8</i>	Hs00361285_g1
<i>RPS29</i>	Hs03004310_g1
<i>SLC25A3</i>	Hs00358082_m1
<i>TXNL1</i>	Hs00355488_m1

[00163] As previously described for the node-negative samples, gene expression data was collected for the new node-positive samples and CCP scores and average ABCC5 and PGR expression were calculated. CCP scores were considered acceptable if at least 17 CCP genes were adequately measured and the standard deviation of the replicate CCP scores was less than 0.5. Both assays for ABCC5 were required to yield quality values while only one of the two PGR assays was considered sufficient. After removing samples that did not meet the quality requirements, 595 patients from the combined cohort remained. The correlation with the CCP score as well as the p-value from univariate analysis of DMFS for each CCP gene is given in Tables 23 & 24.

[00164] In contrast to Example 1, hormone therapy was included as a time dependent covariate instead of a binary indicator of treatment. The effect of hormone therapy was only estimated in recipients during the time while it was being administered. When the exact dates of the

beginning and end of therapy were unknown it was assumed that the patient received hormone therapy for the first five years after surgery (which is the standard of care).

[00165] Univariate analysis of DMFS and clinical and molecular variables was conducted on 565 patients with complete clinical and molecular data using Cox proportional hazards regression. The results are summarized in Table 28.

Table 28: Univariate Results

Variable	p-value	HR (95% CI)
Age	0.87	1 (0.98, 1.02)
Grade	6.49E-05	1.84 (1.36, 2.5)
Tumor Size (cm)	2.71E-06	2.07 (1.56, 2.74)
Node Positive	5.05E-05	2.61 (1.68, 4.06)
CCP Score	1.34E-07	1.91 (1.5, 2.44)
ABCC5 Expression	1.53E-03	1.51 (1.17, 1.95)
PGR Expression	0.07	0.92 (0.84, 1.01)
Hormone Therapy	0.77	1.1 (0.6, 2.02)

[00166] While neither hormone therapy nor PGR expression is significant in univariate analysis in this cohort, their interaction is highly predictive of DMFS (p-value = 0.00016). In the interaction, the HR for hormone therapy when PGR is zero is 1.12 (0.59, 2.12), the HR for PGR while patients are untreated is 1.11 (0.96, 1.27), and the HR for PGR during treatment is 0.71 (0.59, 0.85).

[00167] Grade, tumor size, node status, CCP score, ABCC5 expression, and the interaction between PGR and hormone therapy were included together in a Cox model. Summarized results are in Table 29.

Table 29: Multivariate Results

Variable	p-value	HR (95% CI)
Age	0.87	1 (0.98, 1.02)
Grade	6.49E-05	1.84 (1.36, 2.5)
Tumor Size (cm)	2.71E-06	2.07 (1.56, 2.74)
Node Positive	5.05E-05	2.61 (1.68, 4.06)
CCP Score	1.34E-07	1.91 (1.5, 2.44)
ABCC5	1.53E-03	1.51 (1.17, 1.95)

Expression		
PGR Expression	0.07	0.92 (0.84, 1.01)
Hormone Therapy	0.77	1.1 (0.6, 2.02)

[00168] Tables 30 through 34 below illustrate further embodiments of the invention involving 2-gene, 3-gene, 4-gene, 5-gene and 6-gene sub-panels chosen from Panel O.

Table 30: Predictive power (both univariate and multivariate) for all 2-gene sub-panels chosen from Panel O.

Sub-Panel #	Genes in Sub-Panel	uni pval	multi pval
1	CDKN3, SKA1	1.13E-08	6.47E-05
2	CDKN3, BUB1B	1.11E-08	2.56E-04
3	CDKN3, KIF20A	2.18E-08	9.18E-04
4	CDKN3, RRM2	1.35E-08	2.44E-04
5	CDKN3, ASPM	5.74E-08	3.25E-04
6	CDKN3, NUSAP1	4.10E-08	2.69E-04
7	CDKN3, DTL	3.06E-08	2.67E-04
8	CDKN3, PLK1	3.24E-08	5.94E-03
9	CDKN3, CDK1	1.04E-07	3.62E-03
10	CDKN3, PRC1	1.07E-07	1.18E-03
11	CDKN3, PTTG1	1.73E-07	9.97E-04
12	CDKN3, MCM10	3.39E-07	1.07E-03
13	CDKN3, CENPM	2.96E-08	7.39E-04
14	CDKN3, CENPF	3.64E-07	5.41E-04
15	CDKN3, KIF11	6.52E-07	6.80E-03
16	CDKN3, RAD51	2.69E-06	3.93E-02
17	CDKN3, PBK	4.41E-06	3.32E-02
18	CDKN3, TK1	9.58E-07	1.30E-03
19	CDKN3, RAD54L	2.22E-06	7.57E-03
20	CDKN3, CDCA3	4.38E-05	4.16E-02
21	CDKN3, KIAA0101	1.27E-05	1.06E-02
22	CDKN3, ASF1B	3.90E-05	7.30E-02
23	SKA1, BUB1B	5.59E-08	3.04E-04
24	SKA1, KIF20A	6.31E-08	7.58E-04
25	SKA1, RRM2	7.19E-08	2.52E-04
26	SKA1, ASPM	2.30E-07	3.16E-04
27	SKA1, NUSAP1	2.40E-07	3.75E-04
28	SKA1, DTL	5.63E-08	1.10E-04

Sub-Panel #	Genes in Sub-Panel	uni pval	multi pval
29	SKA1, PLK1	2.50E-07	5.67E-03
30	SKA1, CDK1	2.34E-07	1.63E-03
31	SKA1, PRC1	3.73E-07	1.18E-03
32	SKA1, PTTG1	5.72E-07	7.85E-04
33	SKA1, MCM10	5.78E-07	4.84E-04
34	SKA1, CENPM	1.92E-07	7.67E-04
35	SKA1, CENPF	2.22E-06	6.50E-04
36	SKA1, KIF11	3.14E-06	6.36E-03
37	SKA1, RAD51	4.50E-06	2.20E-02
38	SKA1, PBK	6.58E-06	1.95E-02
39	SKA1, TK1	2.67E-06	9.87E-04
40	SKA1, RAD54L	6.93E-06	7.35E-03
41	SKA1, CDCA3	8.91E-05	2.94E-02
42	SKA1, KIAA0101	2.74E-05	7.43E-03
43	SKA1, ASF1B	1.56E-04	7.03E-02
44	BUB1B, KIF20A	1.32E-07	2.52E-03
45	BUB1B, RRM2	4.63E-08	7.80E-04
46	BUB1B, ASPM	3.85E-07	1.24E-03
47	BUB1B, NUSAP1	1.67E-07	9.00E-04
48	BUB1B, DTL	2.61E-07	8.44E-04
49	BUB1B, PLK1	1.56E-07	1.23E-02
50	BUB1B, CDK1	2.34E-07	5.11E-03
51	BUB1B, PRC1	1.17E-06	4.39E-03
52	BUB1B, PTTG1	5.87E-07	2.63E-03
53	BUB1B, MCM10	1.73E-06	2.95E-03
54	BUB1B, CENPM	4.15E-08	1.32E-03
55	BUB1B, CENPF	1.74E-06	1.63E-03
56	BUB1B, KIF11	1.24E-06	9.88E-03

Sub-Panel #	Genes in Sub-Panel	uni pval	multi pval
57	BUB1B, RAD51	1.65E-05	7.40E-02
58	BUB1B, PBK	8.01E-06	3.54E-02
59	BUB1B, TK1	2.94E-06	2.77E-03
60	BUB1B, RAD54L	8.61E-06	1.65E-02
61	BUB1B, CDCA3	2.05E-04	8.10E-02
62	BUB1B, KIAA0101	5.01E-05	2.14E-02
63	BUB1B, ASF1B	9.48E-05	1.00E-01
64	KIF20A, RRM2	6.57E-08	1.96E-03
65	KIF20A, ASPM	3.65E-07	2.68E-03
66	KIF20A, NUSAP1	3.26E-07	4.25E-03
67	KIF20A, DTL	3.45E-07	3.56E-03
68	KIF20A, PLK1	1.77E-07	3.30E-02
69	KIF20A, CDK1	9.55E-07	2.64E-02
70	KIF20A, PRC1	8.24E-07	7.91E-03
71	KIF20A, PTTG1	1.38E-06	1.06E-02
72	KIF20A, MCM10	1.60E-06	6.23E-03
73	KIF20A, CENPM	9.11E-08	5.32E-03
74	KIF20A, CENPF	2.14E-06	5.19E-03
75	KIF20A, KIF11	3.23E-06	4.03E-02
76	KIF20A, RAD51	2.12E-05	2.08E-01
77	KIF20A, PBK	2.19E-05	1.10E-01
78	KIF20A, TK1	4.04E-06	8.21E-03
79	KIF20A, RAD54L	1.06E-05	3.83E-02
80	KIF20A, CDCA3	1.01E-04	1.07E-01
81	KIF20A, KIAA0101	6.91E-05	6.24E-02
82	KIF20A, ASF1B	7.69E-05	1.90E-01
83	RRM2, ASPM	1.97E-07	1.05E-03
84	RRM2, NUSAP1	4.53E-07	1.50E-03
85	RRM2, DTL	2.56E-07	1.12E-03
86	RRM2, PLK1	4.53E-07	2.20E-02
87	RRM2, CDK1	7.15E-07	9.79E-03
88	RRM2, PRC1	8.13E-07	4.77E-03
89	RRM2, PTTG1	7.76E-07	3.21E-03
90	RRM2, MCM10	1.61E-06	3.52E-03
91	RRM2, CENPM	2.01E-06	7.95E-03
92	RRM2, CENPF	1.36E-06	1.37E-03
93	RRM2, KIF11	4.06E-06	1.86E-02
94	RRM2, RAD51	3.10E-05	1.25E-01

Sub-Panel #	Genes in Sub-Panel	uni pval	multi pval
95	RRM2, PBK	1.68E-05	5.07E-02
96	RRM2, TK1	5.32E-06	4.61E-03
97	RRM2, RAD54L	1.45E-05	2.62E-02
98	RRM2, CDCA3	2.14E-04	9.09E-02
99	RRM2, KIAA0101	5.28E-05	2.99E-02
100	RRM2, ASF1B	2.11E-04	1.29E-01
101	ASPM, NUSAP1	6.17E-07	1.03E-03
102	ASPM, DTL	1.12E-06	1.46E-03
103	ASPM, PLK1	2.88E-07	1.02E-02
104	ASPM, CDK1	1.37E-06	8.38E-03
105	ASPM, PRC1	2.40E-06	4.24E-03
106	ASPM, PTTG1	2.28E-06	3.10E-03
107	ASPM, MCM10	4.44E-06	3.25E-03
108	ASPM, CENPM	2.75E-07	1.65E-03
109	ASPM, CENPF	7.35E-06	2.33E-03
110	ASPM, KIF11	6.04E-06	1.25E-02
111	ASPM, RAD51	3.41E-05	6.90E-02
112	ASPM, PBK	4.20E-05	5.71E-02
113	ASPM, TK1	8.90E-06	3.10E-03
114	ASPM, RAD54L	2.22E-05	1.84E-02
115	ASPM, CDCA3	1.71E-04	4.78E-02
116	ASPM, KIAA0101	1.10E-04	2.37E-02
117	ASPM, ASF1B	1.19E-04	8.17E-02
118	NUSAP1, DTL	7.09E-07	1.14E-03
119	NUSAP1, PLK1	4.60E-07	2.00E-02
120	NUSAP1, CDK1	2.01E-06	1.17E-02
121	NUSAP1, PRC1	1.55E-06	4.23E-03
122	NUSAP1, PTTG1	2.60E-06	4.04E-03
123	NUSAP1, MCM10	3.06E-06	2.94E-03
124	NUSAP1, CENPM	3.07E-06	7.09E-03
125	NUSAP1, CENPF	6.31E-06	2.20E-03
126	NUSAP1, KIF11	1.38E-05	2.57E-02
127	NUSAP1, RAD51	4.82E-05	1.16E-01
128	NUSAP1, PBK	1.38E-05	2.80E-02
129	NUSAP1, TK1	1.71E-05	4.95E-03
130	NUSAP1, RAD54L	3.35E-05	2.71E-02
131	NUSAP1, CDCA3	1.92E-04	7.16E-02
132	NUSAP1, KIAA0101	2.29E-04	4.36E-02

Sub-Panel #	Genes in Sub-Panel	uni pval	multi pval
133	NUSAP1, ASF1B	4.12E-04	1.59E-01
134	DTL, PLK1	2.24E-06	2.09E-02
135	DTL, CDK1	1.25E-06	1.33E-02
136	DTL, PRC1	2.19E-06	3.45E-03
137	DTL, PTTG1	1.57E-06	3.25E-03
138	DTL, MCM10	4.74E-06	3.70E-03
139	DTL, CENPM	2.18E-06	4.78E-03
140	DTL, CENPF	7.34E-06	1.82E-03
141	DTL, KIF11	8.86E-06	2.52E-02
142	DTL, RAD51	3.56E-05	8.07E-02
143	DTL, PBK	1.37E-04	1.22E-01
144	DTL, TK1	2.06E-05	5.33E-03
145	DTL, RAD54L	6.14E-05	2.89E-02
146	DTL, CDCA3	5.52E-05	3.75E-02
147	DTL, KIAA0101	3.11E-04	4.67E-02
148	DTL, ASF1B	3.32E-04	1.48E-01
149	PLK1, CDK1	1.44E-06	8.43E-02
150	PLK1, PRC1	1.50E-06	4.64E-02
151	PLK1, PTTG1	1.08E-06	3.61E-02
152	PLK1, MCM10	1.35E-06	2.32E-02
153	PLK1, CENPM	3.03E-06	6.10E-02
154	PLK1, CENPF	8.40E-06	3.08E-02
155	PLK1, KIF11	2.01E-05	1.93E-01
156	PLK1, RAD51	1.23E-05	3.20E-01
157	PLK1, PBK	4.18E-06	7.77E-02
158	PLK1, TK1	6.06E-06	4.40E-02
159	PLK1, RAD54L	3.99E-05	2.31E-01
160	PLK1, CDCA3	1.29E-04	1.62E-01
161	PLK1, KIAA0101	4.96E-05	1.97E-01
162	PLK1, ASF1B	3.74E-04	4.93E-01
163	CDK1, PRC1	2.88E-06	2.26E-02
164	CDK1, PTTG1	5.73E-06	3.24E-02
165	CDK1, MCM10	1.10E-05	2.42E-02
166	CDK1, CENPM	5.43E-06	3.72E-02
167	CDK1, CENPF	4.23E-06	6.90E-03
168	CDK1, KIF11	3.00E-05	1.32E-01
169	CDK1, RAD51	8.39E-05	3.38E-01
170	CDK1, PBK	2.31E-04	2.54E-01
171	CDK1, TK1	2.84E-05	3.46E-02

Sub-Panel #	Genes in Sub-Panel	uni pval	multi pval
172	CDK1, RAD54L	5.79E-05	1.17E-01
173	CDK1, CDCA3	2.43E-04	2.57E-01
174	CDK1, KIAA0101	4.31E-04	1.64E-01
175	CDK1, ASF1B	4.73E-04	3.92E-01
176	PRC1, PTTG1	4.09E-06	9.94E-03
177	PRC1, MCM10	1.15E-05	1.04E-02
178	PRC1, CENPM	1.45E-06	1.04E-02
179	PRC1, CENPF	7.47E-06	4.29E-03
180	PRC1, KIF11	1.05E-05	3.73E-02
181	PRC1, RAD51	1.81E-04	2.31E-01
182	PRC1, PBK	6.05E-05	8.52E-02
183	PRC1, TK1	3.71E-05	1.33E-02
184	PRC1, RAD54L	8.25E-05	6.00E-02
185	PRC1, CDCA3	5.96E-04	1.50E-01
186	PRC1, KIAA0101	3.72E-04	6.90E-02
187	PRC1, ASF1B	6.22E-04	2.16E-01
188	PTTG1, MCM10	8.74E-06	7.19E-03
189	PTTG1, CENPM	2.72E-06	1.07E-02
190	PTTG1, CENPF	1.51E-05	4.77E-03
191	PTTG1, KIF11	3.24E-05	5.57E-02
192	PTTG1, RAD51	8.25E-05	1.98E-01
193	PTTG1, PBK	7.52E-05	1.05E-01
194	PTTG1, TK1	3.84E-05	1.20E-02
195	PTTG1, RAD54L	7.61E-05	5.59E-02
196	PTTG1, CDCA3	5.33E-04	1.58E-01
197	PTTG1, KIAA0101	4.59E-04	8.02E-02
198	PTTG1, ASF1B	7.93E-04	3.07E-01
199	MCM10, CENPM	2.48E-06	5.75E-03
200	MCM10, CENPF	1.05E-05	2.88E-03
201	MCM10, KIF11	3.64E-05	3.61E-02
202	MCM10, RAD51	2.99E-04	1.84E-01
203	MCM10, PBK	2.89E-04	1.64E-01
204	MCM10, TK1	5.60E-05	1.03E-02
205	MCM10, RAD54L	1.10E-04	4.08E-02
206	MCM10, CDCA3	5.26E-04	1.08E-01
207	MCM10, KIAA0101	4.05E-04	4.94E-02
208	MCM10, ASF1B	4.39E-04	1.34E-01
209	CENPM, CENPF	4.44E-06	3.83E-03

Sub-Panel #	Genes in Sub-Panel	uni pval	multi pval
210	CENPM, KIF11	4.74E-05	8.82E-02
211	CENPM, RAD51	3.50E-05	1.86E-01
212	CENPM, PBK	3.20E-05	8.32E-02
213	CENPM, TK1	3.00E-05	1.68E-02
214	CENPM, RAD54L	4.90E-05	6.42E-02
215	CENPM, CDCA3	4.24E-04	1.33E-01
216	CENPM, KIAA0101	2.02E-04	7.55E-02
217	CENPM, ASF1B	1.12E-03	2.76E-01
218	CENPF, KIF11	5.06E-05	2.49E-02
219	CENPF, RAD51	1.10E-04	6.54E-02
220	CENPF, PBK	8.77E-05	3.56E-02
221	CENPF, TK1	5.21E-05	4.90E-03
222	CENPF, RAD54L	9.28E-05	2.52E-02
223	CENPF, CDCA3	4.87E-04	5.35E-02
224	CENPF, KIAA0101	5.19E-04	3.14E-02
225	CENPF, ASF1B	6.89E-04	1.24E-01
226	KIF11, RAD51	3.23E-04	5.88E-01
227	KIF11, PBK	3.04E-04	2.76E-01
228	KIF11, TK1	1.83E-04	7.24E-02
229	KIF11, RAD54L	3.17E-04	2.14E-01
230	KIF11, CDCA3	5.46E-04	2.35E-01
231	KIF11, KIAA0101	2.11E-03	2.97E-01

Sub-Panel #	Genes in Sub-Panel	uni pval	multi pval
232	KIF11, ASF1B	9.80E-04	4.35E-01
233	RAD51, PBK	6.99E-04	5.41E-01
234	RAD51, TK1	6.09E-04	2.46E-01
235	RAD51, RAD54L	1.30E-03	6.20E-01
236	RAD51, CDCA3	2.36E-03	7.62E-01
237	RAD51, KIAA0101	6.61E-03	7.11E-01
238	RAD51, ASF1B	1.22E-02	7.89E-01
239	PBK, TK1	6.68E-04	2.03E-01
240	PBK, RAD54L	2.53E-04	2.28E-01
241	PBK, CDCA3	1.44E-03	5.24E-01
242	PBK, KIAA0101	3.26E-03	3.97E-01
243	PBK, ASF1B	1.57E-02	9.42E-01
244	TK1, RAD54L	5.99E-04	7.01E-02
245	TK1, CDCA3	1.37E-03	1.42E-01
246	TK1, KIAA0101	2.54E-03	8.93E-02
247	TK1, ASF1B	3.19E-03	2.98E-01
248	RAD54L, CDCA3	5.76E-03	5.38E-01
249	RAD54L, KIAA0101	2.87E-03	2.39E-01
250	RAD54L, ASF1B	6.08E-03	6.60E-01
251	CDCA3, KIAA0101	9.95E-03	5.41E-01
252	CDCA3, ASF1B	9.54E-03	8.40E-01
253	KIAA0101, ASF1B	1.42E-02	6.77E-01

Table 31: Predictive power (both univariate and multivariate) for all 3-gene sub-panels chosen from Panel O.

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
1	CDKN3, SKA1, BUB1B	1.14E-08	1.18E-04
2	CDKN3, SKA1, KIF20A	1.51E-08	2.41E-04
3	CDKN3, SKA1, RRM2	1.26E-08	8.62E-05
4	CDKN3, SKA1, ASPM	3.81E-08	1.31E-04
5	CDKN3, SKA1, NUSAP1	3.14E-08	1.22E-04
6	CDKN3, SKA1, DTL	1.27E-08	5.68E-05
7	CDKN3, SKA1, PLK1	2.30E-08	1.02E-03
8	CDKN3, SKA1, CDK1	4.07E-08	4.27E-04
9	CDKN3, SKA1, PRC1	4.23E-08	3.03E-04

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
10	CDKN3, SKA1, PTTG1	6.54E-08	2.32E-04
11	CDKN3, SKA1, MCM10	7.11E-08	1.75E-04
12	CDKN3, SKA1, CENPM	1.39E-08	1.41E-04
13	CDKN3, SKA1, CENPF	1.49E-07	1.82E-04
14	CDKN3, SKA1, KIF11	2.84E-07	1.24E-03
15	CDKN3, SKA1, RAD51	4.39E-07	4.71E-03
16	CDKN3, SKA1, PBK	6.57E-07	4.70E-03
17	CDKN3, SKA1, TK1	1.64E-07	2.53E-04

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
18	CDKN3, SKA1, RAD54L	3.33E-07	1.25E-03
19	CDKN3, SKA1, CDCA3	1.43E-05	1.04E-02
20	CDKN3, SKA1, KIAA0101	9.31E-07	1.19E-03
21	CDKN3, SKA1, ASF1B	6.33E-06	1.01E-02
22	CDKN3, BUB1B, KIF20A	1.82E-08	6.21E-04
23	CDKN3, BUB1B, RRM2	8.01E-09	2.23E-04
24	CDKN3, BUB1B, ASPM	4.21E-08	3.69E-04
25	CDKN3, BUB1B, NUSAP1	2.08E-08	2.62E-04
26	CDKN3, BUB1B, DTL	2.91E-08	2.77E-04
27	CDKN3, BUB1B, PLK1	1.33E-08	2.29E-03
28	CDKN3, BUB1B, CDK1	3.85E-08	1.20E-03
29	CDKN3, BUB1B, PRC1	7.01E-08	8.95E-04
30	CDKN3, BUB1B, PTTG1	5.97E-08	6.39E-04
31	CDKN3, BUB1B, MCM10	1.39E-07	7.83E-04
32	CDKN3, BUB1B, CENPM	4.35E-09	2.53E-04
33	CDKN3, BUB1B, CENPF	1.08E-07	4.31E-04
34	CDKN3, BUB1B, KIF11	1.44E-07	2.01E-03
35	CDKN3, BUB1B, RAD51	1.06E-06	1.55E-02
36	CDKN3, BUB1B, PBK	7.69E-07	8.70E-03
37	CDKN3, BUB1B, TK1	1.45E-07	6.18E-04
38	CDKN3, BUB1B, RAD54L	3.20E-07	2.66E-03
39	CDKN3, BUB1B, CDCA3	2.43E-05	2.64E-02
40	CDKN3, BUB1B, KIAA0101	1.24E-06	3.18E-03
41	CDKN3, BUB1B, ASF1B	3.27E-06	1.34E-02
42	CDKN3, KIF20A, RRM2	1.13E-08	4.40E-04
43	CDKN3, KIF20A, ASPM	4.78E-08	6.82E-04
44	CDKN3, KIF20A, NUSAP1	3.83E-08	8.36E-04
45	CDKN3, KIF20A, DTL	4.23E-08	7.98E-04
46	CDKN3, KIF20A, PLK1	1.98E-08	5.46E-03

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
47	CDKN3, KIF20A, CDK1	1.10E-07	4.46E-03
48	CDKN3, KIF20A, PRC1	6.62E-08	1.46E-03
49	CDKN3, KIF20A, PTTG1	1.21E-07	1.84E-03
50	CDKN3, KIF20A, MCM10	1.51E-07	1.44E-03
51	CDKN3, KIF20A, CENPM	8.98E-09	7.35E-04
52	CDKN3, KIF20A, CENPF	1.58E-07	1.13E-03
53	CDKN3, KIF20A, KIF11	3.04E-07	6.25E-03
54	CDKN3, KIF20A, RAD51	1.50E-06	4.02E-02
55	CDKN3, KIF20A, PBK	1.89E-06	2.43E-02
56	CDKN3, KIF20A, TK1	2.12E-07	1.42E-03
57	CDKN3, KIF20A, RAD54L	4.56E-07	5.42E-03
58	CDKN3, KIF20A, CDCA3	1.50E-05	3.35E-02
59	CDKN3, KIF20A, KIAA0101	1.88E-06	8.33E-03
60	CDKN3, KIF20A, ASF1B	3.01E-06	2.52E-02
61	CDKN3, RRM2, ASPM	2.73E-08	2.89E-04
62	CDKN3, RRM2, NUSAP1	3.32E-08	2.91E-04
63	CDKN3, RRM2, DTL	2.51E-08	2.64E-04
64	CDKN3, RRM2, PLK1	2.92E-08	3.22E-03
65	CDKN3, RRM2, CDK1	6.72E-08	1.63E-03
66	CDKN3, RRM2, PRC1	5.25E-08	8.25E-04
67	CDKN3, RRM2, PTTG1	6.67E-08	6.13E-04
68	CDKN3, RRM2, MCM10	1.29E-07	7.85E-04
69	CDKN3, RRM2, CENPM	4.46E-08	8.03E-04
70	CDKN3, RRM2, CENPF	8.94E-08	3.29E-04
71	CDKN3, RRM2, KIF11	2.73E-07	2.73E-03
72	CDKN3, RRM2, RAD51	1.63E-06	2.15E-02
73	CDKN3, RRM2, PBK	1.13E-06	1.02E-02
74	CDKN3, RRM2, TK1	1.93E-07	7.29E-04
75	CDKN3, RRM2, RAD54L	4.49E-07	3.37E-03
76	CDKN3, RRM2, CDCA3	2.27E-05	2.58E-02

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
77	CDKN3, RRM2, KIAA0101	1.23E-06	3.62E-03
78	CDKN3, RRM2, ASF1B	4.99E-06	1.57E-02
79	CDKN3, ASPM, NUSAP1	6.35E-08	3.00E-04
80	CDKN3, ASPM, DTL	9.99E-08	4.13E-04
81	CDKN3, ASPM, PLK1	2.91E-08	2.09E-03
82	CDKN3, ASPM, CDK1	1.51E-07	1.78E-03
83	CDKN3, ASPM, PRC1	1.55E-07	9.21E-04
84	CDKN3, ASPM, PTTG1	1.87E-07	7.45E-04
85	CDKN3, ASPM, MCM10	3.43E-07	8.74E-04
86	CDKN3, ASPM, CENPM	2.14E-08	3.20E-04
87	CDKN3, ASPM, CENPF	3.81E-07	5.82E-04
88	CDKN3, ASPM, KIF11	5.12E-07	2.46E-03
89	CDKN3, ASPM, RAD51	2.28E-06	1.48E-02
90	CDKN3, ASPM, PBK	3.34E-06	1.36E-02
91	CDKN3, ASPM, TK1	4.06E-07	7.03E-04
92	CDKN3, ASPM, RAD54L	8.30E-07	3.05E-03
93	CDKN3, ASPM, CDCA3	2.34E-05	1.73E-02
94	CDKN3, ASPM, KIAA0101	2.89E-06	3.60E-03
95	CDKN3, ASPM, ASF1B	4.58E-06	1.15E-02
96	CDKN3, NUSAP1, DTL	5.13E-08	2.70E-04
97	CDKN3, NUSAP1, PLK1	3.08E-08	2.90E-03
98	CDKN3, NUSAP1, CDK1	1.35E-07	1.81E-03
99	CDKN3, NUSAP1, PRC1	9.29E-08	7.81E-04
100	CDKN3, NUSAP1, PTTG1	1.63E-07	7.49E-04
101	CDKN3, NUSAP1, MCM10	2.17E-07	7.13E-04
102	CDKN3, NUSAP1, CENPM	6.19E-08	7.03E-04
103	CDKN3, NUSAP1, CENPF	2.63E-07	4.70E-04
104	CDKN3, NUSAP1, KIF11	6.35E-07	3.47E-03
105	CDKN3, NUSAP1, RAD51	2.11E-06	1.92E-02
106	CDKN3, NUSAP1, PBK	9.82E-07	5.88E-03

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
107	CDKN3, NUSAP1, TK1	4.59E-07	7.96E-04
108	CDKN3, NUSAP1, RAD54L	8.60E-07	3.37E-03
109	CDKN3, NUSAP1, CDCA3	2.01E-05	2.08E-02
110	CDKN3, NUSAP1, KIAA0101	3.62E-06	4.85E-03
111	CDKN3, NUSAP1, ASF1B	7.98E-06	1.78E-02
112	CDKN3, DTL, PLK1	8.81E-08	3.34E-03
113	CDKN3, DTL, CDK1	5.60E-08	1.63E-03
114	CDKN3, DTL, PRC1	1.19E-07	7.40E-04
115	CDKN3, DTL, PTTG1	1.32E-07	7.10E-04
116	CDKN3, DTL, MCM10	3.29E-07	9.45E-04
117	CDKN3, DTL, CENPM	4.38E-08	5.58E-04
118	CDKN3, DTL, CENPF	2.70E-07	4.17E-04
119	CDKN3, DTL, KIF11	2.60E-07	2.72E-03
120	CDKN3, DTL, RAD51	1.73E-06	1.57E-02
121	CDKN3, DTL, PBK	6.50E-06	2.64E-02
122	CDKN3, DTL, TK1	5.33E-07	9.21E-04
123	CDKN3, DTL, RAD54L	1.35E-06	3.92E-03
124	CDKN3, DTL, CDCA3	5.08E-06	1.05E-02
125	CDKN3, DTL, KIAA0101	4.73E-06	5.76E-03
126	CDKN3, DTL, ASF1B	3.91E-06	1.40E-02
127	CDKN3, PLK1, CDK1	9.97E-08	1.31E-02
128	CDKN3, PLK1, PRC1	6.86E-08	6.71E-03
129	CDKN3, PLK1, PTTG1	6.87E-08	5.17E-03
130	CDKN3, PLK1, MCM10	1.04E-07	4.63E-03
131	CDKN3, PLK1, CENPM	6.28E-08	6.50E-03
132	CDKN3, PLK1, CENPF	2.68E-07	4.70E-03
133	CDKN3, PLK1, KIF11	7.65E-07	2.53E-02
134	CDKN3, PLK1, RAD51	4.78E-07	5.09E-02
135	CDKN3, PLK1, PBK	2.64E-07	1.55E-02
136	CDKN3, PLK1, TK1	1.83E-07	5.92E-03
137	CDKN3, PLK1, RAD54L	8.24E-07	3.04E-02
138	CDKN3, PLK1, CDCA3	1.16E-05	4.02E-02
139	CDKN3, PLK1, KIAA0101	1.04E-06	2.54E-02
140	CDKN3, PLK1, ASF1B	6.89E-06	6.94E-02
141	CDKN3, CDK1, PRC1	1.99E-07	3.69E-03

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
142	CDKN3, CDK1, PTTG1	3.84E-07	4.67E-03
143	CDKN3, CDK1, MCM10	7.85E-07	4.77E-03
144	CDKN3, CDK1, CENPM	1.44E-07	3.96E-03
145	CDKN3, CDK1, CENPF	2.62E-07	1.37E-03
146	CDKN3, CDK1, KIF11	8.72E-07	1.49E-02
147	CDKN3, CDK1, RAD51	4.47E-06	6.83E-02
148	CDKN3, CDK1, PBK	1.27E-05	6.04E-02
149	CDKN3, CDK1, TK1	9.66E-07	4.85E-03
150	CDKN3, CDK1, RAD54L	1.78E-06	1.55E-02
151	CDKN3, CDK1, CDCA3	2.11E-05	6.36E-02
152	CDKN3, CDK1, KIAA0101	8.50E-06	2.25E-02
153	CDKN3, CDK1, ASF1B	7.61E-06	4.96E-02
154	CDKN3, PRC1, PTTG1	2.25E-07	1.67E-03
155	CDKN3, PRC1, MCM10	5.58E-07	2.07E-03
156	CDKN3, PRC1, CENPM	4.29E-08	1.20E-03
157	CDKN3, PRC1, CENPF	3.20E-07	9.08E-04
158	CDKN3, PRC1, KIF11	6.08E-07	5.48E-03
159	CDKN3, PRC1, RAD51	6.18E-06	4.29E-02
160	CDKN3, PRC1, PBK	3.21E-06	1.82E-02
161	CDKN3, PRC1, TK1	8.49E-07	1.97E-03
162	CDKN3, PRC1, RAD54L	1.67E-06	7.74E-03
163	CDKN3, PRC1, CDCA3	5.02E-05	4.27E-02
164	CDKN3, PRC1, KIAA0101	5.76E-06	8.61E-03
165	CDKN3, PRC1, ASF1B	1.24E-05	2.76E-02
166	CDKN3, PTTG1, MCM10	5.52E-07	1.56E-03
167	CDKN3, PTTG1, CENPM	8.71E-08	1.14E-03
168	CDKN3, PTTG1, CENPF	5.98E-07	9.44E-04
169	CDKN3, PTTG1, KIF11	1.53E-06	7.20E-03
170	CDKN3, PTTG1, RAD51	3.92E-06	3.29E-02
171	CDKN3, PTTG1, PBK	4.44E-06	2.07E-02
172	CDKN3, PTTG1, TK1	1.06E-06	1.79E-03
173	CDKN3, PTTG1, RAD54L	1.90E-06	6.69E-03
174	CDKN3, PTTG1,	4.91E-05	4.19E-02

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
	CDCA3		
175	CDKN3, PTTG1, KIAA0101	7.53E-06	9.01E-03
176	CDKN3, PTTG1, ASF1B	1.64E-05	3.56E-02
177	CDKN3, MCM10, CENPM	1.09E-07	9.21E-04
178	CDKN3, MCM10, CENPF	5.69E-07	7.64E-04
179	CDKN3, MCM10, KIF11	2.22E-06	6.59E-03
180	CDKN3, MCM10, RAD51	1.37E-05	4.06E-02
181	CDKN3, MCM10, PBK	1.73E-05	3.92E-02
182	CDKN3, MCM10, TK1	1.84E-06	1.95E-03
183	CDKN3, MCM10, RAD54L	3.34E-06	6.69E-03
184	CDKN3, MCM10, CDCA3	5.88E-05	3.54E-02
185	CDKN3, MCM10, KIAA0101	9.84E-06	7.78E-03
186	CDKN3, MCM10, ASF1B	1.45E-05	2.12E-02
187	CDKN3, CENPM, CENPF	1.07E-07	5.34E-04
188	CDKN3, CENPM, KIF11	8.23E-07	8.42E-03
189	CDKN3, CENPM, RAD51	7.51E-07	2.36E-02
190	CDKN3, CENPM, PBK	1.05E-06	1.36E-02
191	CDKN3, CENPM, TK1	3.27E-07	1.55E-03
192	CDKN3, CENPM, RAD54L	5.60E-07	5.62E-03
193	CDKN3, CENPM, CDCA3	2.06E-05	2.88E-02
194	CDKN3, CENPM, KIAA0101	1.71E-06	6.52E-03
195	CDKN3, CENPM, ASF1B	9.80E-06	2.81E-02
196	CDKN3, CENPF, KIF11	1.87E-06	4.05E-03
197	CDKN3, CENPF, RAD51	4.46E-06	1.29E-02
198	CDKN3, CENPF, PBK	4.81E-06	8.62E-03
199	CDKN3, CENPF, TK1	1.26E-06	9.36E-04
200	CDKN3, CENPF, RAD54L	2.04E-06	3.67E-03
201	CDKN3, CENPF, CDCA3	4.10E-05	1.66E-02

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
202	CDKN3, CENPF, KIAA0101	8.21E-06	4.24E-03
203	CDKN3, CENPF, ASF1B	1.44E-05	1.56E-02
204	CDKN3, KIF11, RAD51	1.29E-05	1.18E-01
205	CDKN3, KIF11, PBK	1.48E-05	5.97E-02
206	CDKN3, KIF11, TK1	4.33E-06	9.00E-03
207	CDKN3, KIF11, RAD54L	7.01E-06	2.58E-02
208	CDKN3, KIF11, CDCA3	3.87E-05	4.92E-02
209	CDKN3, KIF11, KIAA0101	3.34E-05	3.89E-02
210	CDKN3, KIF11, ASF1B	1.29E-05	4.93E-02
211	CDKN3, RAD51, PBK	3.88E-05	1.51E-01
212	CDKN3, RAD51, TK1	1.43E-05	4.20E-02
213	CDKN3, RAD51, RAD54L	2.79E-05	1.19E-01
214	CDKN3, RAD51, CDCA3	1.79E-04	2.69E-01
215	CDKN3, RAD51, KIAA0101	1.16E-04	1.52E-01
216	CDKN3, RAD51, ASF1B	2.31E-04	3.21E-01
217	CDKN3, PBK, TK1	2.02E-05	3.86E-02
218	CDKN3, PBK, RAD54L	9.18E-06	4.51E-02
219	CDKN3, PBK, CDCA3	1.11E-04	1.80E-01
220	CDKN3, PBK, KIAA0101	8.12E-05	8.36E-02
221	CDKN3, PBK, ASF1B	4.80E-04	3.09E-01
222	CDKN3, TK1, RAD54L	7.72E-06	8.17E-03
223	CDKN3, TK1, CDCA3	8.54E-05	3.83E-02
224	CDKN3, TK1, KIAA0101	2.60E-05	1.01E-02
225	CDKN3, TK1, ASF1B	4.25E-05	3.68E-02
226	CDKN3, RAD54L, CDCA3	2.89E-04	1.42E-01
227	CDKN3, RAD54L, KIAA0101	3.17E-05	2.84E-02
228	CDKN3, RAD54L, ASF1B	8.14E-05	1.00E-01
229	CDKN3, CDCA3, KIAA0101	4.90E-04	1.46E-01
230	CDKN3, CDCA3, ASF1B	4.19E-04	2.33E-01
231	CDKN3, KIAA0101, ASF1B	1.92E-04	1.09E-01

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
232	SKA1, BUB1B, KIF20A	4.45E-08	5.98E-04
233	SKA1, BUB1B, RRM2	2.84E-08	2.48E-04
234	SKA1, BUB1B, ASPM	1.20E-07	3.86E-04
235	SKA1, BUB1B, NUSAP1	7.82E-08	3.41E-04
236	SKA1, BUB1B, DTL	4.47E-08	1.68E-04
237	SKA1, BUB1B, PLK1	6.25E-08	2.30E-03
238	SKA1, BUB1B, CDK1	7.41E-08	7.38E-04
239	SKA1, BUB1B, PRC1	1.69E-07	9.17E-04
240	SKA1, BUB1B, PTTG1	1.44E-07	5.75E-04
241	SKA1, BUB1B, MCM10	2.15E-07	4.79E-04
242	SKA1, BUB1B, CENPM	2.23E-08	2.85E-04
243	SKA1, BUB1B, CENPF	3.99E-07	4.74E-04
244	SKA1, BUB1B, KIF11	5.26E-07	2.13E-03
245	SKA1, BUB1B, RAD51	1.53E-06	1.05E-02
246	SKA1, BUB1B, PBK	1.06E-06	6.29E-03
247	SKA1, BUB1B, TK1	3.66E-07	5.78E-04
248	SKA1, BUB1B, RAD54L	8.14E-07	2.87E-03
249	SKA1, BUB1B, CDCA3	4.21E-05	2.10E-02
250	SKA1, BUB1B, KIAA0101	2.44E-06	2.65E-03
251	SKA1, BUB1B, ASF1B	1.20E-05	1.50E-02
252	SKA1, KIF20A, RRM2	3.57E-08	4.60E-04
253	SKA1, KIF20A, ASPM	1.12E-07	6.01E-04
254	SKA1, KIF20A, NUSAP1	9.86E-08	7.84E-04
255	SKA1, KIF20A, DTL	4.68E-08	3.68E-04
256	SKA1, KIF20A, PLK1	6.21E-08	4.21E-03
257	SKA1, KIF20A, CDK1	1.39E-07	2.06E-03
258	SKA1, KIF20A, PRC1	1.40E-07	1.34E-03
259	SKA1, KIF20A, PTTG1	2.24E-07	1.39E-03
260	SKA1, KIF20A, MCM10	2.05E-07	7.85E-04
261	SKA1, KIF20A, CENPM	2.97E-08	5.88E-04
262	SKA1, KIF20A, CENPF	4.17E-07	9.44E-04
263	SKA1, KIF20A, KIF11	8.16E-07	5.54E-03
264	SKA1, KIF20A, RAD51	1.59E-06	2.41E-02
265	SKA1, KIF20A, PBK	2.17E-06	1.63E-02
266	SKA1, KIF20A, TK1	4.33E-07	1.15E-03

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
267	SKA1, KIF20A, RAD54L	9.58E-07	5.11E-03
268	SKA1, KIF20A, CDCA3	2.33E-05	2.45E-02
269	SKA1, KIF20A, KIAA0101	3.00E-06	6.08E-03
270	SKA1, KIF20A, ASF1B	1.21E-05	2.95E-02
271	SKA1, RRM2, ASPM	9.03E-08	2.87E-04
272	SKA1, RRM2, NUSAP1	1.31E-07	3.58E-04
273	SKA1, RRM2, DTL	4.17E-08	1.40E-04
274	SKA1, RRM2, PLK1	1.00E-07	2.48E-03
275	SKA1, RRM2, CDK1	1.28E-07	8.92E-04
276	SKA1, RRM2, PRC1	1.34E-07	7.67E-04
277	SKA1, RRM2, PTTG1	1.72E-07	5.01E-04
278	SKA1, RRM2, MCM10	2.07E-07	4.15E-04
279	SKA1, RRM2, CENPM	1.46E-07	6.76E-04
280	SKA1, RRM2, CENPF	3.48E-07	3.42E-04
281	SKA1, RRM2, KIF11	8.76E-07	2.49E-03
282	SKA1, RRM2, RAD51	1.82E-06	1.09E-02
283	SKA1, RRM2, PBK	1.54E-06	6.56E-03
284	SKA1, RRM2, TK1	4.85E-07	5.82E-04
285	SKA1, RRM2, RAD54L	1.13E-06	3.21E-03
286	SKA1, RRM2, CDCA3	4.58E-05	2.18E-02
287	SKA1, RRM2, KIAA0101	2.43E-06	2.56E-03
288	SKA1, RRM2, ASF1B	2.11E-05	1.89E-02
289	SKA1, ASPM, NUSAP1	2.17E-07	3.53E-04
290	SKA1, ASPM, DTL	1.45E-07	2.24E-04
291	SKA1, ASPM, PLK1	1.35E-07	2.12E-03
292	SKA1, ASPM, CDK1	2.51E-07	9.70E-04
293	SKA1, ASPM, PRC1	3.73E-07	8.93E-04
294	SKA1, ASPM, PTTG1	4.15E-07	6.01E-04
295	SKA1, ASPM, MCM10	5.35E-07	5.09E-04
296	SKA1, ASPM, CENPM	7.87E-08	3.04E-04
297	SKA1, ASPM, CENPF	1.19E-06	5.62E-04
298	SKA1, ASPM, KIF11	1.59E-06	2.44E-03
299	SKA1, ASPM, RAD51	3.03E-06	9.39E-03
300	SKA1, ASPM, PBK	4.40E-06	9.41E-03
301	SKA1, ASPM, TK1	9.64E-07	5.99E-04
302	SKA1, ASPM, RAD54L	2.04E-06	3.10E-03
303	SKA1, ASPM, CDCA3	4.47E-05	1.43E-02

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
304	SKA1, ASPM, KIAA0101	5.31E-06	2.72E-03
305	SKA1, ASPM, ASF1B	1.90E-05	1.38E-02
306	SKA1, NUSAP1, DTL	8.72E-08	1.65E-04
307	SKA1, NUSAP1, PLK1	1.50E-07	2.91E-03
308	SKA1, NUSAP1, CDK1	2.47E-07	1.08E-03
309	SKA1, NUSAP1, PRC1	2.82E-07	9.03E-04
310	SKA1, NUSAP1, PTTG1	4.39E-07	7.24E-04
311	SKA1, NUSAP1, MCM10	3.82E-07	4.53E-04
312	SKA1, NUSAP1, CENPM	2.38E-07	7.51E-04
313	SKA1, NUSAP1, CENPF	1.08E-06	5.66E-04
314	SKA1, NUSAP1, KIF11	2.10E-06	3.77E-03
315	SKA1, NUSAP1, RAD51	3.29E-06	1.34E-02
316	SKA1, NUSAP1, PBK	1.53E-06	4.42E-03
317	SKA1, NUSAP1, TK1	1.24E-06	7.91E-04
318	SKA1, NUSAP1, RAD54L	2.41E-06	3.84E-03
319	SKA1, NUSAP1, CDCA3	3.73E-05	1.59E-02
320	SKA1, NUSAP1, KIAA0101	7.61E-06	4.16E-03
321	SKA1, NUSAP1, ASF1B	3.32E-05	2.20E-02
322	SKA1, DTL, PLK1	2.70E-07	2.52E-03
323	SKA1, DTL, CDK1	5.47E-08	5.02E-04
324	SKA1, DTL, PRC1	1.47E-07	4.05E-04
325	SKA1, DTL, PTTG1	1.47E-07	2.93E-04
326	SKA1, DTL, MCM10	2.58E-07	2.93E-04
327	SKA1, DTL, CENPM	6.94E-08	2.56E-04
328	SKA1, DTL, CENPF	7.84E-07	3.63E-04
329	SKA1, DTL, KIF11	5.82E-07	1.83E-03
330	SKA1, DTL, RAD51	1.74E-06	7.91E-03
331	SKA1, DTL, PBK	4.19E-06	1.11E-02
332	SKA1, DTL, TK1	6.03E-07	4.15E-04
333	SKA1, DTL, RAD54L	1.63E-06	2.27E-03
334	SKA1, DTL, CDCA3	9.68E-06	7.75E-03
335	SKA1, DTL, KIAA0101	4.17E-06	2.39E-03
336	SKA1, DTL, ASF1B	1.07E-05	1.25E-02

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
337	SKA1, PLK1, CDK1	3.17E-07	8.32E-03
338	SKA1, PLK1, PRC1	2.02E-07	5.08E-03
339	SKA1, PLK1, PTTG1	2.68E-07	4.63E-03
340	SKA1, PLK1, MCM10	2.01E-07	2.34E-03
341	SKA1, PLK1, CENPM	2.01E-07	4.21E-03
342	SKA1, PLK1, CENPF	1.15E-06	4.51E-03
343	SKA1, PLK1, KIF11	2.01E-06	1.86E-02
344	SKA1, PLK1, RAD51	1.32E-06	4.11E-02
345	SKA1, PLK1, PBK	6.30E-07	1.23E-02
346	SKA1, PLK1, TK1	5.18E-07	4.21E-03
347	SKA1, PLK1, RAD54L	2.14E-06	2.34E-02
348	SKA1, PLK1, CDCA3	2.67E-05	3.29E-02
349	SKA1, PLK1, KIAA0101	2.52E-06	1.70E-02
350	SKA1, PLK1, ASF1B	2.38E-05	6.86E-02
351	SKA1, CDK1, PRC1	2.97E-07	2.03E-03
352	SKA1, CDK1, PTTG1	4.91E-07	2.06E-03
353	SKA1, CDK1, MCM10	6.83E-07	1.61E-03
354	SKA1, CDK1, CENPM	2.44E-07	1.93E-03
355	SKA1, CDK1, CENPF	7.98E-07	1.06E-03
356	SKA1, CDK1, KIF11	1.75E-06	9.04E-03
357	SKA1, CDK1, RAD51	4.40E-06	3.38E-02
358	SKA1, CDK1, PBK	8.80E-06	2.66E-02
359	SKA1, CDK1, TK1	1.27E-06	2.27E-03
360	SKA1, CDK1, RAD54L	2.51E-06	8.94E-03
361	SKA1, CDK1, CDCA3	4.16E-05	4.80E-02
362	SKA1, CDK1, KIAA0101	9.30E-06	1.10E-02
363	SKA1, CDK1, ASF1B	2.37E-05	4.37E-02
364	SKA1, PRC1, PTTG1	4.59E-07	1.38E-03
365	SKA1, PRC1, MCM10	7.11E-07	1.16E-03
366	SKA1, PRC1, CENPM	1.43E-07	1.06E-03
367	SKA1, PRC1, CENPF	9.15E-07	8.64E-04
368	SKA1, PRC1, KIF11	1.77E-06	5.04E-03
369	SKA1, PRC1, RAD51	5.35E-06	2.30E-02
370	SKA1, PRC1, PBK	3.58E-06	1.22E-02
371	SKA1, PRC1, TK1	1.67E-06	1.63E-03
372	SKA1, PRC1, RAD54L	3.23E-06	7.26E-03
373	SKA1, PRC1, CDCA3	8.33E-05	3.38E-02

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
374	SKA1, PRC1, KIAA0101	8.55E-06	6.23E-03
375	SKA1, PRC1, ASF1B	4.16E-05	3.12E-02
376	SKA1, PTTG1, MCM10	6.83E-07	7.35E-04
377	SKA1, PTTG1, CENPM	2.51E-07	8.54E-04
378	SKA1, PTTG1, CENPF	1.81E-06	8.99E-04
379	SKA1, PTTG1, KIF11	3.63E-06	5.75E-03
380	SKA1, PTTG1, RAD51	5.22E-06	2.03E-02
381	SKA1, PTTG1, PBK	4.44E-06	1.20E-02
382	SKA1, PTTG1, TK1	1.98E-06	1.25E-03
383	SKA1, PTTG1, RAD54L	3.76E-06	5.70E-03
384	SKA1, PTTG1, CDCA3	8.54E-05	3.12E-02
385	SKA1, PTTG1, KIAA0101	1.12E-05	5.68E-03
386	SKA1, PTTG1, ASF1B	5.11E-05	3.46E-02
387	SKA1, MCM10, CENPM	1.82E-07	4.56E-04
388	SKA1, MCM10, CENPF	1.11E-06	4.60E-04
389	SKA1, MCM10, KIF11	3.46E-06	3.73E-03
390	SKA1, MCM10, RAD51	9.57E-06	1.66E-02
391	SKA1, MCM10, PBK	1.30E-05	1.86E-02
392	SKA1, MCM10, TK1	2.31E-06	9.67E-04
393	SKA1, MCM10, RAD54L	4.33E-06	4.01E-03
394	SKA1, MCM10, CDCA3	8.91E-05	2.45E-02
395	SKA1, MCM10, KIAA0101	1.00E-05	3.66E-03
396	SKA1, MCM10, ASF1B	4.08E-05	1.96E-02
397	SKA1, CENPM, CENPF	5.38E-07	5.93E-04
398	SKA1, CENPM, KIF11	2.22E-06	6.67E-03
399	SKA1, CENPM, RAD51	1.12E-06	1.25E-02
400	SKA1, CENPM, PBK	1.28E-06	7.44E-03
401	SKA1, CENPM, TK1	7.93E-07	1.10E-03
402	SKA1, CENPM, RAD54L	1.48E-06	4.70E-03
403	SKA1, CENPM, CDCA3	4.65E-05	2.35E-02
404	SKA1, CENPM, KIAA0101	3.57E-06	4.34E-03
405	SKA1, CENPM, ASF1B	3.64E-05	3.04E-02
406	SKA1, CENPF, KIF11	5.62E-06	3.52E-03
407	SKA1, CENPF, RAD51	8.01E-06	9.58E-03
408	SKA1, CENPF, PBK	7.68E-06	6.21E-03

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
409	SKA1, CENPF, TK1	3.42E-06	8.22E-04
410	SKA1, CENPF, RAD54L	5.89E-06	3.77E-03
411	SKA1, CENPF, CDCA3	9.22E-05	1.56E-02
412	SKA1, CENPF, KIAA0101	1.77E-05	3.57E-03
413	SKA1, CENPF, ASF1B	5.89E-05	1.82E-02
414	SKA1, KIF11, RAD51	1.55E-05	6.95E-02
415	SKA1, KIF11, PBK	2.15E-05	4.13E-02
416	SKA1, KIF11, TK1	1.00E-05	7.24E-03
417	SKA1, KIF11, RAD54L	1.72E-05	2.38E-02
418	SKA1, KIF11, CDCA3	8.48E-05	4.27E-02
419	SKA1, KIF11, KIAA0101	6.12E-05	2.81E-02
420	SKA1, KIF11, ASF1B	6.89E-05	6.69E-02
421	SKA1, RAD51, PBK	2.68E-05	8.24E-02
422	SKA1, RAD51, TK1	1.34E-05	2.18E-02
423	SKA1, RAD51, RAD54L	2.56E-05	7.06E-02
424	SKA1, RAD51, CDCA3	2.53E-04	2.15E-01
425	SKA1, RAD51, KIAA0101	9.59E-05	8.17E-02
426	SKA1, RAD51, ASF1B	3.17E-04	2.44E-01
427	SKA1, PBK, TK1	2.29E-05	2.41E-02
428	SKA1, PBK, RAD54L	9.91E-06	3.13E-02
429	SKA1, PBK, CDCA3	1.14E-04	1.18E-01
430	SKA1, PBK, KIAA0101	7.74E-05	4.88E-02
431	SKA1, PBK, ASF1B	6.79E-04	2.53E-01
432	SKA1, TK1, RAD54L	1.46E-05	6.89E-03
433	SKA1, TK1, CDCA3	1.33E-04	2.83E-02
434	SKA1, TK1, KIAA0101	3.67E-05	6.46E-03
435	SKA1, TK1, ASF1B	1.41E-04	4.01E-02
436	SKA1, RAD54L, CDCA3	4.03E-04	1.09E-01
437	SKA1, RAD54L, KIAA0101	4.75E-05	2.15E-02
438	SKA1, RAD54L, ASF1B	2.37E-04	1.11E-01
439	SKA1, CDCA3, KIAA0101	7.58E-04	1.15E-01
440	SKA1, CDCA3, ASF1B	6.27E-04	1.76E-01
441	SKA1, KIAA0101, ASF1B	4.96E-04	1.03E-01
442	BUB1B, KIF20A,	3.17E-08	9.52E-04

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
	RRM2		
443	BUB1B, KIF20A, ASPM	1.67E-07	1.48E-03
444	BUB1B, KIF20A, NUSAP1	1.08E-07	1.67E-03
445	BUB1B, KIF20A, DTL	1.60E-07	1.56E-03
446	BUB1B, KIF20A, PLK1	5.61E-08	9.03E-03
447	BUB1B, KIF20A, CDK1	2.27E-07	5.94E-03
448	BUB1B, KIF20A, PRC1	2.86E-07	3.18E-03
449	BUB1B, KIF20A, PTTG1	3.00E-07	3.28E-03
450	BUB1B, KIF20A, MCM10	4.72E-07	2.74E-03
451	BUB1B, KIF20A, CENPM	1.51E-08	1.21E-03
452	BUB1B, KIF20A, CENPF	4.80E-07	2.20E-03
453	BUB1B, KIF20A, KIF11	5.37E-07	8.66E-03
454	BUB1B, KIF20A, RAD51	5.27E-06	6.15E-02
455	BUB1B, KIF20A, PBK	2.95E-06	2.57E-02
456	BUB1B, KIF20A, TK1	5.47E-07	2.46E-03
457	BUB1B, KIF20A, RAD54L	1.21E-06	9.28E-03
458	BUB1B, KIF20A, CDCA3	4.95E-05	5.58E-02
459	BUB1B, KIF20A, KIAA0101	5.40E-06	1.35E-02
460	BUB1B, KIF20A, ASF1B	7.77E-06	3.56E-02
461	BUB1B, RRM2, ASPM	8.31E-08	7.16E-04
462	BUB1B, RRM2, NUSAP1	6.64E-08	6.29E-04
463	BUB1B, RRM2, DTL	7.03E-08	5.49E-04
464	BUB1B, RRM2, PLK1	5.83E-08	5.38E-03
465	BUB1B, RRM2, CDK1	9.90E-08	2.25E-03
466	BUB1B, RRM2, PRC1	1.86E-07	1.94E-03
467	BUB1B, RRM2, PTTG1	1.29E-07	1.23E-03
468	BUB1B, RRM2, MCM10	3.37E-07	1.60E-03
469	BUB1B, RRM2, CENPM	4.31E-08	1.17E-03
470	BUB1B, RRM2, CENPF	2.29E-07	7.69E-04
471	BUB1B, RRM2, KIF11	3.46E-07	3.79E-03
472	BUB1B, RRM2, RAD51	4.67E-06	3.61E-02

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
473	BUB1B, RRM2, PBK	1.58E-06	1.17E-02
474	BUB1B, RRM2, TK1	3.72E-07	1.30E-03
475	BUB1B, RRM2, RAD54L	9.41E-07	5.99E-03
476	BUB1B, RRM2, CDCA3	6.19E-05	4.42E-02
477	BUB1B, RRM2, KIAA0101	3.01E-06	6.49E-03
478	BUB1B, RRM2, ASF1B	9.14E-06	2.20E-02
479	BUB1B, ASPM, NUSAP1	1.96E-07	7.50E-04
480	BUB1B, ASPM, DTL	3.81E-07	9.29E-04
481	BUB1B, ASPM, PLK1	9.43E-08	3.99E-03
482	BUB1B, ASPM, CDK1	3.44E-07	2.78E-03
483	BUB1B, ASPM, PRC1	6.72E-07	2.28E-03
484	BUB1B, ASPM, PTTG1	5.04E-07	1.61E-03
485	BUB1B, ASPM, MCM10	1.07E-06	1.88E-03
486	BUB1B, ASPM, CENPM	4.23E-08	6.43E-04
487	BUB1B, ASPM, CENPF	1.13E-06	1.29E-03
488	BUB1B, ASPM, KIF11	9.68E-07	3.87E-03
489	BUB1B, ASPM, RAD51	8.10E-06	2.68E-02
490	BUB1B, ASPM, PBK	5.77E-06	1.61E-02
491	BUB1B, ASPM, TK1	1.11E-06	1.45E-03
492	BUB1B, ASPM, RAD54L	2.30E-06	5.97E-03
493	BUB1B, ASPM, CDCA3	7.65E-05	3.16E-02
494	BUB1B, ASPM, KIAA0101	8.59E-06	6.93E-03
495	BUB1B, ASPM, ASF1B	1.25E-05	1.84E-02
496	BUB1B, NUSAP1, DTL	1.53E-07	5.62E-04
497	BUB1B, NUSAP1, PLK1	7.35E-08	5.07E-03
498	BUB1B, NUSAP1, CDK1	2.11E-07	2.42E-03
499	BUB1B, NUSAP1, PRC1	3.65E-07	1.94E-03
500	BUB1B, NUSAP1, PTTG1	3.27E-07	1.47E-03
501	BUB1B, NUSAP1, MCM10	6.04E-07	1.52E-03
502	BUB1B, NUSAP1, CENPM	6.89E-08	1.06E-03
503	BUB1B, NUSAP1, CENPF	6.61E-07	1.02E-03

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
504	BUB1B, NUSAP1, KIF11	8.79E-07	4.70E-03
505	BUB1B, NUSAP1, RAD51	6.50E-06	3.27E-02
506	BUB1B, NUSAP1, PBK	1.41E-06	6.75E-03
507	BUB1B, NUSAP1, TK1	9.15E-07	1.42E-03
508	BUB1B, NUSAP1, RAD54L	1.90E-06	6.11E-03
509	BUB1B, NUSAP1, CDCA3	6.02E-05	3.67E-02
510	BUB1B, NUSAP1, KIAA0101	8.65E-06	8.35E-03
511	BUB1B, NUSAP1, ASF1B	1.57E-05	2.48E-02
512	BUB1B, DTL, PLK1	2.61E-07	5.44E-03
513	BUB1B, DTL, CDK1	1.35E-07	2.28E-03
514	BUB1B, DTL, PRC1	6.46E-07	1.83E-03
515	BUB1B, DTL, PTTG1	3.62E-07	1.34E-03
516	BUB1B, DTL, MCM10	1.13E-06	1.86E-03
517	BUB1B, DTL, CENPM	6.77E-08	8.00E-04
518	BUB1B, DTL, CENPF	8.66E-07	8.51E-04
519	BUB1B, DTL, KIF11	5.19E-07	3.91E-03
520	BUB1B, DTL, RAD51	6.84E-06	2.66E-02
521	BUB1B, DTL, PBK	1.01E-05	2.59E-02
522	BUB1B, DTL, TK1	1.42E-06	1.56E-03
523	BUB1B, DTL, RAD54L	3.69E-06	6.70E-03
524	BUB1B, DTL, CDCA3	2.31E-05	2.12E-02
525	BUB1B, DTL, KIAA0101	1.40E-05	9.37E-03
526	BUB1B, DTL, ASF1B	1.11E-05	2.10E-02
527	BUB1B, PLK1, CDK1	1.76E-07	1.60E-02
528	BUB1B, PLK1, PRC1	2.68E-07	1.22E-02
529	BUB1B, PLK1, PTTG1	1.52E-07	8.23E-03
530	BUB1B, PLK1, MCM10	3.01E-07	7.74E-03
531	BUB1B, PLK1, CENPM	9.75E-08	8.88E-03
532	BUB1B, PLK1, CENPF	6.83E-07	7.74E-03
533	BUB1B, PLK1, KIF11	9.94E-07	2.80E-02
534	BUB1B, PLK1, RAD51	1.75E-06	7.76E-02
535	BUB1B, PLK1, PBK	4.73E-07	1.81E-02
536	BUB1B, PLK1, TK1	3.77E-07	8.65E-03
537	BUB1B, PLK1, RAD54L	1.78E-06	4.14E-02

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
538	BUB1B, PLK1, CDCA3	3.32E-05	6.47E-02
539	BUB1B, PLK1, KIAA0101	2.83E-06	3.65E-02
540	BUB1B, PLK1, ASF1B	1.46E-05	8.63E-02
541	BUB1B, CDK1, PRC1	5.78E-07	5.91E-03
542	BUB1B, CDK1, PTTG1	5.72E-07	5.88E-03
543	BUB1B, CDK1, MCM10	1.59E-06	6.55E-03
544	BUB1B, CDK1, CENPM	1.19E-07	4.00E-03
545	BUB1B, CDK1, CENPF	5.28E-07	2.06E-03
546	BUB1B, CDK1, KIF11	9.95E-07	1.58E-02
547	BUB1B, CDK1, RAD51	1.05E-05	8.74E-02
548	BUB1B, CDK1, PBK	1.30E-05	5.26E-02
549	BUB1B, CDK1, TK1	1.47E-06	5.81E-03
550	BUB1B, CDK1, RAD54L	2.97E-06	1.95E-02
551	BUB1B, CDK1, CDCA3	5.82E-05	9.33E-02
552	BUB1B, CDK1, KIAA0101	1.54E-05	2.71E-02
553	BUB1B, CDK1, ASF1B	1.34E-05	5.98E-02
554	BUB1B, PRC1, PTTG1	8.02E-07	3.71E-03
555	BUB1B, PRC1, MCM10	1.96E-06	4.24E-03
556	BUB1B, PRC1, CENPM	1.18E-07	2.44E-03
557	BUB1B, PRC1, CENPF	1.33E-06	2.27E-03
558	BUB1B, PRC1, KIF11	1.42E-06	8.72E-03
559	BUB1B, PRC1, RAD51	2.33E-05	6.92E-02
560	BUB1B, PRC1, PBK	6.14E-06	2.16E-02
561	BUB1B, PRC1, TK1	2.70E-06	3.93E-03
562	BUB1B, PRC1, RAD54L	5.21E-06	1.42E-02
563	BUB1B, PRC1, CDCA3	1.96E-04	7.57E-02
564	BUB1B, PRC1, KIAA0101	1.89E-05	1.56E-02
565	BUB1B, PRC1, ASF1B	3.56E-05	4.19E-02
566	BUB1B, PTTG1, MCM10	1.38E-06	2.97E-03
567	BUB1B, PTTG1, CENPM	9.55E-08	1.71E-03
568	BUB1B, PTTG1, CENPF	1.39E-06	1.86E-03
569	BUB1B, PTTG1, KIF11	1.95E-06	9.14E-03
570	BUB1B, PTTG1, RAD51	1.08E-05	5.16E-02

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
571	BUB1B, PTTG1, PBK	6.06E-06	2.17E-02
572	BUB1B, PTTG1, TK1	1.96E-06	2.93E-03
573	BUB1B, PTTG1, RAD54L	3.87E-06	1.11E-02
574	BUB1B, PTTG1, CDCA3	1.35E-04	6.78E-02
575	BUB1B, PTTG1, KIAA0101	1.66E-05	1.44E-02
576	BUB1B, PTTG1, ASF1B	3.15E-05	4.72E-02
577	BUB1B, MCM10, CENPM	1.90E-07	1.52E-03
578	BUB1B, MCM10, CENPF	1.71E-06	1.66E-03
579	BUB1B, MCM10, KIF11	3.80E-06	9.00E-03
580	BUB1B, MCM10, RAD51	3.88E-05	6.14E-02
581	BUB1B, MCM10, PBK	2.71E-05	4.20E-02
582	BUB1B, MCM10, TK1	4.26E-06	3.35E-03
583	BUB1B, MCM10, RAD54L	7.77E-06	1.11E-02
584	BUB1B, MCM10, CDCA3	1.75E-04	5.84E-02
585	BUB1B, MCM10, KIAA0101	2.47E-05	1.27E-02
586	BUB1B, MCM10, ASF1B	3.41E-05	3.03E-02
587	BUB1B, CENPM, CENPF	1.69E-07	9.19E-04
588	BUB1B, CENPM, KIF11	6.49E-07	8.41E-03
589	BUB1B, CENPM, RAD51	1.47E-06	3.42E-02
590	BUB1B, CENPM, PBK	8.44E-07	1.28E-02
591	BUB1B, CENPM, TK1	3.57E-07	2.03E-03
592	BUB1B, CENPM, RAD54L	7.21E-07	7.91E-03
593	BUB1B, CENPM, CDCA3	4.52E-05	4.46E-02
594	BUB1B, CENPM, KIAA0101	2.61E-06	9.10E-03
595	BUB1B, CENPM, ASF1B	1.14E-05	3.18E-02
596	BUB1B, CENPF, KIF11	3.13E-06	5.88E-03
597	BUB1B, CENPF, RAD51	1.52E-05	2.40E-02
598	BUB1B, CENPF, PBK	8.03E-06	1.04E-02
599	BUB1B, CENPF, TK1	3.03E-06	1.77E-03

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
600	BUB1B, CENPF, RAD54L	5.08E-06	6.87E-03
601	BUB1B, CENPF, CDCA3	1.27E-04	2.99E-02
602	BUB1B, CENPF, KIAA0101	2.18E-05	7.81E-03
603	BUB1B, CENPF, ASF1B	3.55E-05	2.37E-02
604	BUB1B, KIF11, RAD51	2.67E-05	1.50E-01
605	BUB1B, KIF11, PBK	1.61E-05	5.57E-02
606	BUB1B, KIF11, TK1	5.50E-06	1.06E-02
607	BUB1B, KIF11, RAD54L	9.64E-06	3.16E-02
608	BUB1B, KIF11, CDCA3	8.73E-05	7.40E-02
609	BUB1B, KIF11, KIAA0101	4.93E-05	4.62E-02
610	BUB1B, KIF11, ASF1B	2.19E-05	6.23E-02
611	BUB1B, RAD51, PBK	5.55E-05	1.50E-01
612	BUB1B, RAD51, TK1	3.79E-05	6.23E-02
613	BUB1B, RAD51, RAD54L	7.02E-05	1.62E-01
614	BUB1B, RAD51, CDCA3	5.54E-04	3.86E-01
615	BUB1B, RAD51, KIAA0101	3.04E-04	2.00E-01
616	BUB1B, RAD51, ASF1B	5.08E-04	4.01E-01
617	BUB1B, PBK, TK1	2.57E-05	3.84E-02
618	BUB1B, PBK, RAD54L	1.23E-05	4.64E-02
619	BUB1B, PBK, CDCA3	2.22E-04	2.06E-01
620	BUB1B, PBK, KIAA0101	1.18E-04	8.44E-02
621	BUB1B, PBK, ASF1B	6.61E-04	3.08E-01
622	BUB1B, TK1, RAD54L	1.46E-05	1.24E-02
623	BUB1B, TK1, CDCA3	2.34E-04	6.04E-02
624	BUB1B, TK1, KIAA0101	5.32E-05	1.51E-02
625	BUB1B, TK1, ASF1B	7.74E-05	4.72E-02
626	BUB1B, RAD54L, CDCA3	7.02E-04	2.01E-01
627	BUB1B, RAD54L, KIAA0101	6.72E-05	4.14E-02
628	BUB1B, RAD54L, ASF1B	1.50E-04	1.26E-01
629	BUB1B, CDCA3, KIAA0101	1.33E-03	2.07E-01

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
630	BUB1B, CDCA3, ASF1B	8.71E-04	2.95E-01
631	BUB1B, KIAA0101, ASF1B	3.91E-04	1.37E-01
632	KIF20A, RRM2, ASPM	7.90E-08	1.08E-03
633	KIF20A, RRM2, NUSAP1	1.01E-07	1.58E-03
634	KIF20A, RRM2, DTL	8.05E-08	1.22E-03
635	KIF20A, RRM2, PLK1	8.40E-08	1.13E-02
636	KIF20A, RRM2, CDK1	2.12E-07	6.35E-03
637	KIF20A, RRM2, PRC1	1.44E-07	2.57E-03
638	KIF20A, RRM2, PTTG1	2.16E-07	2.82E-03
639	KIF20A, RRM2, MCM10	2.98E-07	2.37E-03
640	KIF20A, RRM2, CENPM	6.24E-08	2.38E-03
641	KIF20A, RRM2, CENPF	3.19E-07	1.87E-03
642	KIF20A, RRM2, KIF11	5.95E-07	9.45E-03
643	KIF20A, RRM2, RAD51	5.54E-06	7.67E-02
644	KIF20A, RRM2, PBK	3.27E-06	2.74E-02
645	KIF20A, RRM2, TK1	4.46E-07	2.34E-03
646	KIF20A, RRM2, RAD54L	1.04E-06	9.66E-03
647	KIF20A, RRM2, CDCA3	3.73E-05	5.52E-02
648	KIF20A, RRM2, KIAA0101	3.74E-06	1.34E-02
649	KIF20A, RRM2, ASF1B	6.59E-06	3.36E-02
650	KIF20A, ASPM, NUSAP1	2.47E-07	1.76E-03
651	KIF20A, ASPM, DTL	3.79E-07	1.90E-03
652	KIF20A, ASPM, PLK1	1.03E-07	8.24E-03
653	KIF20A, ASPM, CDK1	5.86E-07	7.25E-03
654	KIF20A, ASPM, PRC1	5.16E-07	3.13E-03
655	KIF20A, ASPM, PTTG1	6.87E-07	3.47E-03
656	KIF20A, ASPM, MCM10	9.04E-07	2.82E-03
657	KIF20A, ASPM, CENPM	5.38E-08	1.37E-03
658	KIF20A, ASPM, CENPF	1.24E-06	2.58E-03
659	KIF20A, ASPM, KIF11	1.42E-06	9.69E-03
660	KIF20A, ASPM, RAD51	9.23E-06	5.87E-02
661	KIF20A, ASPM, PBK	9.42E-06	3.50E-02
662	KIF20A, ASPM, TK1	1.16E-06	2.55E-03

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
663	KIF20A, ASPM, RAD54L	2.46E-06	9.92E-03
664	KIF20A, ASPM, CDCA3	4.06E-05	3.75E-02
665	KIF20A, ASPM, KIAA0101	9.83E-06	1.42E-02
666	KIF20A, ASPM, ASF1B	9.07E-06	2.99E-02
667	KIF20A, NUSAP1, DTL	2.34E-07	1.94E-03
668	KIF20A, NUSAP1, PLK1	1.07E-07	1.25E-02
669	KIF20A, NUSAP1, CDK1	5.82E-07	9.79E-03
670	KIF20A, NUSAP1, PRC1	3.88E-07	3.96E-03
671	KIF20A, NUSAP1, PTTG1	6.96E-07	5.09E-03
672	KIF20A, NUSAP1, MCM10	7.34E-07	3.45E-03
673	KIF20A, NUSAP1, CENPM	1.45E-07	3.65E-03
674	KIF20A, NUSAP1, CENPF	9.90E-07	3.05E-03
675	KIF20A, NUSAP1, KIF11	1.81E-06	1.50E-02
676	KIF20A, NUSAP1, RAD51	9.19E-06	8.77E-02
677	KIF20A, NUSAP1, PBK	3.85E-06	2.37E-02
678	KIF20A, NUSAP1, TK1	1.44E-06	4.04E-03
679	KIF20A, NUSAP1, RAD54L	2.85E-06	1.46E-02
680	KIF20A, NUSAP1, CDCA3	3.43E-05	4.62E-02
681	KIF20A, NUSAP1, KIAA0101	1.34E-05	2.35E-02
682	KIF20A, NUSAP1, ASF1B	1.58E-05	5.17E-02
683	KIF20A, DTL, PLK1	2.83E-07	1.24E-02
684	KIF20A, DTL, CDK1	3.90E-07	9.61E-03
685	KIF20A, DTL, PRC1	5.16E-07	3.34E-03
686	KIF20A, DTL, PTTG1	6.36E-07	4.28E-03
687	KIF20A, DTL, MCM10	1.11E-06	3.75E-03
688	KIF20A, DTL, CENPM	1.07E-07	2.53E-03
689	KIF20A, DTL, CENPF	1.06E-06	2.34E-03
690	KIF20A, DTL, KIF11	1.06E-06	1.32E-02
691	KIF20A, DTL, RAD51	8.26E-06	6.76E-02
692	KIF20A, DTL, PBK	1.87E-05	6.51E-02

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
693	KIF20A, DTL, TK1	1.74E-06	3.86E-03
694	KIF20A, DTL, RAD54L	4.42E-06	1.44E-02
695	KIF20A, DTL, CDCA3	1.32E-05	2.84E-02
696	KIF20A, DTL, KIAA0101	1.80E-05	2.37E-02
697	KIF20A, DTL, ASF1B	1.03E-05	4.41E-02
698	KIF20A, PLK1, CDK1	4.33E-07	4.45E-02
699	KIF20A, PLK1, PRC1	2.47E-07	2.22E-02
700	KIF20A, PLK1, PTTG1	2.71E-07	2.09E-02
701	KIF20A, PLK1, MCM10	3.34E-07	1.52E-02
702	KIF20A, PLK1, CENPM	1.42E-07	2.10E-02
703	KIF20A, PLK1, CENPF	6.98E-07	1.49E-02
704	KIF20A, PLK1, KIF11	1.88E-06	6.87E-02
705	KIF20A, PLK1, RAD51	2.15E-06	1.69E-01
706	KIF20A, PLK1, PBK	9.81E-07	4.62E-02
707	KIF20A, PLK1, TK1	5.60E-07	1.98E-02
708	KIF20A, PLK1, RAD54L	2.32E-06	7.76E-02
709	KIF20A, PLK1, CDCA3	2.13E-05	8.14E-02
710	KIF20A, PLK1, KIAA0101	4.40E-06	7.93E-02
711	KIF20A, PLK1, ASF1B	1.35E-05	1.46E-01
712	KIF20A, CDK1, PRC1	8.64E-07	1.36E-02
713	KIF20A, CDK1, PTTG1	1.69E-06	2.04E-02
714	KIF20A, CDK1, MCM10	2.25E-06	1.51E-02
715	KIF20A, CDK1, CENPM	3.58E-07	1.38E-02
716	KIF20A, CDK1, CENPF	1.22E-06	7.56E-03
717	KIF20A, CDK1, KIF11	3.34E-06	5.34E-02
718	KIF20A, CDK1, RAD51	1.95E-05	2.06E-01
719	KIF20A, CDK1, PBK	3.73E-05	1.30E-01
720	KIF20A, CDK1, TK1	3.03E-06	1.67E-02
721	KIF20A, CDK1, RAD54L	5.94E-06	4.69E-02
722	KIF20A, CDK1, CDCA3	4.16E-05	1.22E-01
723	KIF20A, CDK1, KIAA0101	2.84E-05	6.59E-02
724	KIF20A, CDK1, ASF1B	1.84E-05	1.24E-01
725	KIF20A, PRC1, PTTG1	9.43E-07	7.07E-03
726	KIF20A, PRC1, MCM10	1.48E-06	5.85E-03
727	KIF20A, PRC1, CENPM	1.10E-07	4.29E-03

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
728	KIF20A, PRC1, CENPF	1.38E-06	4.53E-03
729	KIF20A, PRC1, KIF11	1.84E-06	1.90E-02
730	KIF20A, PRC1, RAD51	2.18E-05	1.27E-01
731	KIF20A, PRC1, PBK	9.38E-06	4.43E-02
732	KIF20A, PRC1, TK1	2.35E-06	6.07E-03
733	KIF20A, PRC1, RAD54L	4.70E-06	2.11E-02
734	KIF20A, PRC1, CDCA3	9.64E-05	8.50E-02
735	KIF20A, PRC1, KIAA0101	1.84E-05	2.79E-02
736	KIF20A, PRC1, ASF1B	2.24E-05	6.03E-02
737	KIF20A, PTTG1, MCM10	1.76E-06	6.17E-03
738	KIF20A, PTTG1, CENPM	2.39E-07	5.49E-03
739	KIF20A, PTTG1, CENPF	2.36E-06	5.42E-03
740	KIF20A, PTTG1, KIF11	4.25E-06	2.66E-02
741	KIF20A, PTTG1, RAD51	1.79E-05	1.29E-01
742	KIF20A, PTTG1, PBK	1.59E-05	5.94E-02
743	KIF20A, PTTG1, TK1	3.31E-06	7.45E-03
744	KIF20A, PTTG1, RAD54L	6.47E-06	2.47E-02
745	KIF20A, PTTG1, CDCA3	8.49E-05	8.58E-02
746	KIF20A, PTTG1, KIAA0101	2.78E-05	3.69E-02
747	KIF20A, PTTG1, ASF1B	3.35E-05	8.91E-02
748	KIF20A, MCM10, CENPM	2.20E-07	3.06E-03
749	KIF20A, MCM10, CENPF	2.03E-06	3.61E-03
750	KIF20A, MCM10, KIF11	5.01E-06	2.02E-02
751	KIF20A, MCM10, RAD51	3.83E-05	1.15E-01
752	KIF20A, MCM10, PBK	3.92E-05	8.06E-02
753	KIF20A, MCM10, TK1	4.02E-06	5.59E-03
754	KIF20A, MCM10, RAD54L	7.65E-06	1.77E-02
755	KIF20A, MCM10, CDCA3	9.70E-05	6.83E-02
756	KIF20A, MCM10, KIAA0101	2.53E-05	2.39E-02
757	KIF20A, MCM10,	2.43E-05	4.55E-02

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
	ASF1B		
758	KIF20A, CENPM, CENPF	3.06E-07	2.93E-03
759	KIF20A, CENPM, KIF11	1.52E-06	2.61E-02
760	KIF20A, CENPM, RAD51	2.15E-06	9.04E-02
761	KIF20A, CENPM, PBK	2.23E-06	3.78E-02
762	KIF20A, CENPM, TK1	5.72E-07	4.89E-03
763	KIF20A, CENPM, RAD54L	1.07E-06	1.69E-02
764	KIF20A, CENPM, CDCA3	2.57E-05	5.57E-02
765	KIF20A, CENPM, KIAA0101	4.25E-06	2.30E-02
766	KIF20A, CENPM, ASF1B	1.14E-05	6.22E-02
767	KIF20A, CENPF, KIF11	4.75E-06	1.51E-02
768	KIF20A, CENPF, RAD51	1.83E-05	5.98E-02
769	KIF20A, CENPF, PBK	1.60E-05	3.03E-02
770	KIF20A, CENPF, TK1	4.22E-06	4.56E-03
771	KIF20A, CENPF, RAD54L	7.34E-06	1.60E-02
772	KIF20A, CENPF, CDCA3	7.22E-05	3.71E-02
773	KIF20A, CENPF, KIAA0101	3.24E-05	2.21E-02
774	KIF20A, CENPF, ASF1B	3.59E-05	5.15E-02
775	KIF20A, KIF11, RAD51	3.87E-05	2.96E-01
776	KIF20A, KIF11, PBK	3.98E-05	1.31E-01
777	KIF20A, KIF11, TK1	9.64E-06	2.77E-02
778	KIF20A, KIF11, RAD54L	1.69E-05	7.01E-02
779	KIF20A, KIF11, CDCA3	7.09E-05	1.09E-01
780	KIF20A, KIF11, KIAA0101	7.96E-05	1.01E-01
781	KIF20A, KIF11, ASF1B	2.52E-05	1.20E-01
782	KIF20A, RAD51, PBK	8.82E-05	2.88E-01
783	KIF20A, RAD51, TK1	4.30E-05	1.27E-01
784	KIF20A, RAD51, RAD54L	8.21E-05	2.87E-01
785	KIF20A, RAD51, CDCA3	3.38E-04	4.62E-01
786	KIF20A, RAD51, KIAA0101	3.52E-04	3.65E-01

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
787	KIF20A, RAD51, ASF1B	4.59E-04	5.86E-01
788	KIF20A, PBK, TK1	5.10E-05	8.48E-02
789	KIF20A, PBK, RAD54L	2.51E-05	1.00E-01
790	KIF20A, PBK, CDCA3	1.96E-04	2.92E-01
791	KIF20A, PBK, KIAA0101	2.22E-04	1.79E-01
792	KIF20A, PBK, ASF1B	7.26E-04	4.55E-01
793	KIF20A, TK1, RAD54L	1.75E-05	2.23E-02
794	KIF20A, TK1, CDCA3	1.33E-04	7.40E-02
795	KIF20A, TK1, KIAA0101	6.42E-05	3.18E-02
796	KIF20A, TK1, ASF1B	6.13E-05	7.45E-02
797	KIF20A, RAD54L, CDCA3	4.28E-04	2.28E-01
798	KIF20A, RAD54L, KIAA0101	8.41E-05	7.88E-02
799	KIF20A, RAD54L, ASF1B	1.21E-04	1.83E-01
800	KIF20A, CDCA3, KIAA0101	7.75E-04	2.41E-01
801	KIF20A, CDCA3, ASF1B	5.20E-04	3.37E-01
802	KIF20A, KIAA0101, ASF1B	3.25E-04	2.14E-01
803	RRM2, ASPM, NUSAP1	1.84E-07	7.56E-04
804	RRM2, ASPM, DTL	2.11E-07	8.10E-04
805	RRM2, ASPM, PLK1	1.22E-07	5.14E-03
806	RRM2, ASPM, CDK1	3.36E-07	3.28E-03
807	RRM2, ASPM, PRC1	3.86E-07	2.08E-03
808	RRM2, ASPM, PTTG1	3.76E-07	1.49E-03
809	RRM2, ASPM, MCM10	7.75E-07	1.84E-03
810	RRM2, ASPM, CENPM	1.60E-07	1.47E-03
811	RRM2, ASPM, CENPF	7.74E-07	1.09E-03
812	RRM2, ASPM, KIF11	1.13E-06	4.75E-03
813	RRM2, ASPM, RAD51	9.35E-06	3.61E-02
814	RRM2, ASPM, PBK	6.31E-06	1.81E-02
815	RRM2, ASPM, TK1	9.53E-07	1.54E-03
816	RRM2, ASPM, RAD54L	2.19E-06	6.97E-03
817	RRM2, ASPM, CDCA3	5.64E-05	2.99E-02
818	RRM2, ASPM, KIAA0101	6.48E-06	7.51E-03
819	RRM2, ASPM, ASF1B	1.17E-05	1.96E-02

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
820	RRM2, NUSAP1, DTL	2.12E-07	7.22E-04
821	RRM2, NUSAP1, PLK1	2.28E-07	8.46E-03
822	RRM2, NUSAP1, CDK1	5.04E-07	3.92E-03
823	RRM2, NUSAP1, PRC1	3.97E-07	2.22E-03
824	RRM2, NUSAP1, PTTG1	5.40E-07	1.85E-03
825	RRM2, NUSAP1, MCM10	7.55E-07	1.84E-03
826	RRM2, NUSAP1, CENPM	8.20E-07	3.58E-03
827	RRM2, NUSAP1, CENPF	8.46E-07	1.08E-03
828	RRM2, NUSAP1, KIF11	2.32E-06	7.61E-03
829	RRM2, NUSAP1, RAD51	1.31E-05	5.03E-02
830	RRM2, NUSAP1, PBK	2.90E-06	9.16E-03
831	RRM2, NUSAP1, TK1	1.70E-06	2.10E-03
832	RRM2, NUSAP1, RAD54L	3.52E-06	9.02E-03
833	RRM2, NUSAP1, CDCA3	6.90E-05	3.97E-02
834	RRM2, NUSAP1, KIAA0101	1.14E-05	1.11E-02
835	RRM2, NUSAP1, ASF1B	2.85E-05	3.11E-02
836	RRM2, DTL, PLK1	4.54E-07	8.12E-03
837	RRM2, DTL, CDK1	2.62E-07	3.87E-03
838	RRM2, DTL, PRC1	3.97E-07	1.78E-03
839	RRM2, DTL, PTTG1	3.36E-07	1.43E-03
840	RRM2, DTL, MCM10	8.92E-07	1.98E-03
841	RRM2, DTL, CENPM	5.22E-07	2.48E-03
842	RRM2, DTL, CENPF	6.56E-07	7.75E-04
843	RRM2, DTL, KIF11	1.20E-06	6.79E-03
844	RRM2, DTL, RAD51	9.42E-06	3.89E-02
845	RRM2, DTL, PBK	1.25E-05	3.04E-02
846	RRM2, DTL, TK1	1.58E-06	2.01E-03
847	RRM2, DTL, RAD54L	4.38E-06	8.78E-03
848	RRM2, DTL, CDCA3	2.30E-05	2.39E-02
849	RRM2, DTL, KIAA0101	1.19E-05	1.11E-02
850	RRM2, DTL, ASF1B	1.85E-05	2.84E-02
851	RRM2, PLK1, CDK1	5.44E-07	2.74E-02
852	RRM2, PLK1, PRC1	4.07E-07	1.71E-02
853	RRM2, PLK1, PTTG1	3.38E-07	1.24E-02

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
854	RRM2, PLK1, MCM10	5.17E-07	1.11E-02
855	RRM2, PLK1, CENPM	9.11E-07	2.26E-02
856	RRM2, PLK1, CENPF	8.97E-07	8.93E-03
857	RRM2, PLK1, KIF11	3.41E-06	5.07E-02
858	RRM2, PLK1, RAD51	3.75E-06	1.16E-01
859	RRM2, PLK1, PBK	1.32E-06	2.80E-02
860	RRM2, PLK1, TK1	1.05E-06	1.45E-02
861	RRM2, PLK1, RAD54L	4.48E-06	6.76E-02
862	RRM2, PLK1, CDCA3	5.78E-05	8.15E-02
863	RRM2, PLK1, KIAA0101	5.62E-06	5.64E-02
864	RRM2, PLK1, ASF1B	3.20E-05	1.13E-01
865	RRM2, CDK1, PRC1	6.43E-07	7.39E-03
866	RRM2, CDK1, PTTG1	9.59E-07	8.23E-03
867	RRM2, CDK1, MCM10	1.95E-06	8.52E-03
868	RRM2, CDK1, CENPM	1.21E-06	1.14E-02
869	RRM2, CDK1, CENPF	7.01E-07	2.60E-03
870	RRM2, CDK1, KIF11	3.32E-06	2.88E-02
871	RRM2, CDK1, RAD51	2.09E-05	1.33E-01
872	RRM2, CDK1, PBK	2.42E-05	6.72E-02
873	RRM2, CDK1, TK1	2.67E-06	8.88E-03
874	RRM2, CDK1, RAD54L	5.50E-06	2.90E-02
875	RRM2, CDK1, CDCA3	7.36E-05	1.11E-01
876	RRM2, CDK1, KIAA0101	1.91E-05	3.53E-02
877	RRM2, CDK1, ASF1B	2.90E-05	8.01E-02
878	RRM2, PRC1, PTTG1	6.62E-07	3.85E-03
879	RRM2, PRC1, MCM10	1.58E-06	4.57E-03
880	RRM2, PRC1, CENPM	5.42E-07	5.43E-03
881	RRM2, PRC1, CENPF	8.70E-07	1.95E-03
882	RRM2, PRC1, KIF11	1.96E-06	1.15E-02
883	RRM2, PRC1, RAD51	2.96E-05	9.46E-02
884	RRM2, PRC1, PBK	8.04E-06	2.56E-02
885	RRM2, PRC1, TK1	2.68E-06	4.66E-03
886	RRM2, PRC1, RAD54L	5.68E-06	1.77E-02
887	RRM2, PRC1, CDCA3	1.49E-04	7.49E-02
888	RRM2, PRC1, KIAA0101	1.58E-05	1.81E-02
889	RRM2, PRC1, ASF1B	3.89E-05	4.54E-02
890	RRM2, PTTG1, MCM10	1.39E-06	3.29E-03

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
891	RRM2, PTTG1, CENPM	7.92E-07	4.90E-03
892	RRM2, PTTG1, CENPF	1.35E-06	1.74E-03
893	RRM2, PTTG1, KIF11	3.75E-06	1.33E-02
894	RRM2, PTTG1, RAD51	1.79E-05	7.61E-02
895	RRM2, PTTG1, PBK	9.68E-06	2.73E-02
896	RRM2, PTTG1, TK1	2.72E-06	3.80E-03
897	RRM2, PTTG1, RAD54L	5.56E-06	1.50E-02
898	RRM2, PTTG1, CDCA3	1.31E-04	7.16E-02
899	RRM2, PTTG1, KIAA0101	1.77E-05	1.78E-02
900	RRM2, PTTG1, ASF1B	4.49E-05	5.52E-02
901	RRM2, MCM10, CENPM	8.48E-07	3.68E-03
902	RRM2, MCM10, CENPF	1.44E-06	1.55E-03
903	RRM2, MCM10, KIF11	5.63E-06	1.23E-02
904	RRM2, MCM10, RAD51	5.63E-05	8.65E-02
905	RRM2, MCM10, PBK	3.78E-05	5.10E-02
906	RRM2, MCM10, TK1	4.76E-06	4.15E-03
907	RRM2, MCM10, RAD54L	9.53E-06	1.44E-02
908	RRM2, MCM10, CDCA3	1.50E-04	6.03E-02
909	RRM2, MCM10, KIAA0101	2.36E-05	1.54E-02
910	RRM2, MCM10, ASF1B	3.81E-05	3.41E-02
911	RRM2, CENPM, CENPF	8.22E-07	2.09E-03
912	RRM2, CENPM, KIF11	6.99E-06	2.42E-02
913	RRM2, CENPM, RAD51	1.12E-05	7.85E-02
914	RRM2, CENPM, PBK	6.50E-06	2.73E-02
915	RRM2, CENPM, TK1	3.06E-06	6.21E-03
916	RRM2, CENPM, RAD54L	5.48E-06	2.07E-02
917	RRM2, CENPM, CDCA3	1.19E-04	6.57E-02
918	RRM2, CENPM, KIAA0101	1.23E-05	2.04E-02
919	RRM2, CENPM, ASF1B	6.02E-05	5.73E-02
920	RRM2, CENPF, KIF11	4.43E-06	7.05E-03
921	RRM2, CENPF, RAD51	1.63E-05	2.69E-02
922	RRM2, CENPF, PBK	9.16E-06	1.08E-02

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
923	RRM2, CENPF, TK1	3.17E-06	1.81E-03
924	RRM2, CENPF, RAD54L	5.83E-06	7.95E-03
925	RRM2, CENPF, CDCA3	1.08E-04	2.86E-02
926	RRM2, CENPF, KIAA0101	1.98E-05	8.40E-03
927	RRM2, CENPF, ASF1B	3.92E-05	2.51E-02
928	RRM2, KIF11, RAD51	5.87E-05	2.20E-01
929	RRM2, KIF11, PBK	3.29E-05	7.07E-02
930	RRM2, KIF11, TK1	1.17E-05	1.65E-02
931	RRM2, KIF11, RAD54L	2.16E-05	4.92E-02
932	RRM2, KIF11, CDCA3	1.49E-04	9.92E-02
933	RRM2, KIF11, KIAA0101	7.59E-05	6.43E-02
934	RRM2, KIF11, ASF1B	5.49E-05	8.60E-02
935	RRM2, RAD51, PBK	1.08E-04	2.03E-01
936	RRM2, RAD51, TK1	6.62E-05	9.37E-02
937	RRM2, RAD51, RAD54L	1.30E-04	2.37E-01
938	RRM2, RAD51, CDCA3	5.18E-04	3.99E-01
939	RRM2, RAD51, KIAA0101	4.30E-04	2.78E-01
940	RRM2, RAD51, ASF1B	7.52E-04	4.52E-01
941	RRM2, PBK, TK1	4.77E-05	5.02E-02
942	RRM2, PBK, RAD54L	2.44E-05	6.27E-02
943	RRM2, PBK, CDCA3	2.14E-04	1.87E-01
944	RRM2, PBK, KIAA0101	1.75E-04	1.07E-01
945	RRM2, PBK, ASF1B	8.95E-04	3.09E-01
946	RRM2, TK1, RAD54L	2.30E-05	1.80E-02
947	RRM2, TK1, CDCA3	2.43E-04	6.62E-02
948	RRM2, TK1, KIAA0101	6.02E-05	1.99E-02
949	RRM2, TK1, ASF1B	1.15E-04	5.70E-02
950	RRM2, RAD54L, CDCA3	7.81E-04	2.28E-01
951	RRM2, RAD54L, KIAA0101	8.55E-05	5.61E-02
952	RRM2, RAD54L, ASF1B	2.26E-04	1.46E-01
953	RRM2, CDCA3, KIAA0101	1.15E-03	2.21E-01
954	RRM2, CDCA3, ASF1B	1.34E-03	3.54E-01
955	RRM2, KIAA0101, ASF1B	4.40E-04	1.51E-01

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
956	ASPM, NUSAP1, DTL	4.30E-07	7.66E-04
957	ASPM, NUSAP1, PLK1	1.47E-07	4.53E-03
958	ASPM, NUSAP1, CDK1	6.54E-07	3.26E-03
959	ASPM, NUSAP1, PRC1	7.08E-07	1.92E-03
960	ASPM, NUSAP1, PTTG1	8.76E-07	1.62E-03
961	ASPM, NUSAP1, MCM10	1.32E-06	1.62E-03
962	ASPM, NUSAP1, CENPM	2.49E-07	1.22E-03
963	ASPM, NUSAP1, CENPF	1.96E-06	1.30E-03
964	ASPM, NUSAP1, KIF11	2.54E-06	5.40E-03
965	ASPM, NUSAP1, RAD51	1.21E-05	3.08E-02
966	ASPM, NUSAP1, PBK	5.81E-06	1.06E-02
967	ASPM, NUSAP1, TK1	2.16E-06	1.53E-03
968	ASPM, NUSAP1, RAD54L	4.19E-06	6.68E-03
969	ASPM, NUSAP1, CDCA3	5.26E-05	2.33E-02
970	ASPM, NUSAP1, KIAA0101	1.70E-05	9.04E-03
971	ASPM, NUSAP1, ASF1B	1.92E-05	2.06E-02
972	ASPM, DTL, PLK1	4.87E-07	5.52E-03
973	ASPM, DTL, CDK1	5.51E-07	3.77E-03
974	ASPM, DTL, PRC1	1.25E-06	2.11E-03
975	ASPM, DTL, PTTG1	1.06E-06	1.80E-03
976	ASPM, DTL, MCM10	2.47E-06	2.27E-03
977	ASPM, DTL, CENPM	2.75E-07	1.16E-03
978	ASPM, DTL, CENPF	2.63E-06	1.29E-03
979	ASPM, DTL, KIF11	1.95E-06	5.47E-03
980	ASPM, DTL, RAD51	1.32E-05	2.71E-02
981	ASPM, DTL, PBK	3.59E-05	4.01E-02
982	ASPM, DTL, TK1	3.38E-06	1.98E-03
983	ASPM, DTL, RAD54L	8.16E-06	8.28E-03
984	ASPM, DTL, CDCA3	2.27E-05	1.48E-02
985	ASPM, DTL, KIAA0101	2.74E-05	1.12E-02
986	ASPM, DTL, ASF1B	1.56E-05	1.97E-02
987	ASPM, PLK1, CDK1	4.16E-07	1.69E-02
988	ASPM, PLK1, PRC1	4.16E-07	1.06E-02
989	ASPM, PLK1, PTTG1	3.18E-07	7.44E-03

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
990	ASPM, PLK1, MCM10	5.82E-07	7.13E-03
991	ASPM, PLK1, CENPM	2.11E-07	8.18E-03
992	ASPM, PLK1, CENPF	1.46E-06	7.65E-03
993	ASPM, PLK1, KIF11	1.97E-06	2.59E-02
994	ASPM, PLK1, RAD51	3.18E-06	7.23E-02
995	ASPM, PLK1, PBK	1.48E-06	2.31E-02
996	ASPM, PLK1, TK1	7.34E-07	7.63E-03
997	ASPM, PLK1, RAD54L	3.21E-06	3.96E-02
998	ASPM, PLK1, CDCA3	2.34E-05	3.76E-02
999	ASPM, PLK1, KIAA0101	5.03E-06	3.43E-02
1000	ASPM, PLK1, ASF1B	1.50E-05	6.74E-02
1001	ASPM, CDK1, PRC1	1.34E-06	7.00E-03
1002	ASPM, CDK1, PTTG1	1.81E-06	7.78E-03
1003	ASPM, CDK1, MCM10	3.77E-06	8.02E-03
1004	ASPM, CDK1, CENPM	5.16E-07	5.59E-03
1005	ASPM, CDK1, CENPF	1.99E-06	3.21E-03
1006	ASPM, CDK1, KIF11	3.79E-06	2.10E-02
1007	ASPM, CDK1, RAD51	2.17E-05	8.96E-02
1008	ASPM, CDK1, PBK	4.92E-05	7.75E-02
1009	ASPM, CDK1, TK1	4.06E-06	7.46E-03
1010	ASPM, CDK1, RAD54L	7.70E-06	2.42E-02
1011	ASPM, CDK1, CDCA3	5.94E-05	6.90E-02
1012	ASPM, CDK1, KIAA0101	3.29E-05	3.17E-02
1013	ASPM, CDK1, ASF1B	2.01E-05	5.65E-02
1014	ASPM, PRC1, PTTG1	1.62E-06	3.74E-03
1015	ASPM, PRC1, MCM10	3.44E-06	4.27E-03
1016	ASPM, PRC1, CENPM	3.10E-07	2.50E-03
1017	ASPM, PRC1, CENPF	3.14E-06	2.61E-03
1018	ASPM, PRC1, KIF11	3.37E-06	9.19E-03
1019	ASPM, PRC1, RAD51	3.58E-05	6.41E-02
1020	ASPM, PRC1, PBK	1.83E-05	2.96E-02
1021	ASPM, PRC1, TK1	4.92E-06	3.92E-03
1022	ASPM, PRC1, RAD54L	9.11E-06	1.46E-02
1023	ASPM, PRC1, CDCA3	1.50E-04	4.96E-02
1024	ASPM, PRC1, KIAA0101	3.07E-05	1.60E-02
1025	ASPM, PRC1, ASF1B	3.71E-05	3.41E-02
1026	ASPM, PTTG1, MCM10	3.03E-06	3.19E-03

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
1027	ASPM, PTTG1, CENPM	3.95E-07	2.02E-03
1028	ASPM, PTTG1, CENPF	4.21E-06	2.39E-03
1029	ASPM, PTTG1, KIF11	6.03E-06	1.07E-02
1030	ASPM, PTTG1, RAD51	2.10E-05	4.89E-02
1031	ASPM, PTTG1, PBK	2.30E-05	3.20E-02
1032	ASPM, PTTG1, TK1	4.72E-06	3.19E-03
1033	ASPM, PTTG1, RAD54L	8.75E-06	1.22E-02
1034	ASPM, PTTG1, CDCA3	1.22E-04	4.53E-02
1035	ASPM, PTTG1, KIAA0101	3.31E-05	1.57E-02
1036	ASPM, PTTG1, ASF1B	4.01E-05	4.01E-02
1037	ASPM, MCM10, CENPM	5.98E-07	1.75E-03
1038	ASPM, MCM10, CENPF	4.37E-06	2.04E-03
1039	ASPM, MCM10, KIF11	9.26E-06	1.00E-02
1040	ASPM, MCM10, RAD51	6.50E-05	5.85E-02
1041	ASPM, MCM10, PBK	7.94E-05	5.68E-02
1042	ASPM, MCM10, TK1	8.28E-06	3.53E-03
1043	ASPM, MCM10, RAD54L	1.48E-05	1.20E-02
1044	ASPM, MCM10, CDCA3	1.48E-04	3.95E-02
1045	ASPM, MCM10, KIAA0101	4.32E-05	1.36E-02
1046	ASPM, MCM10, ASF1B	3.82E-05	2.54E-02
1047	ASPM, CENPM, CENPF	7.90E-07	1.29E-03
1048	ASPM, CENPM, KIF11	2.45E-06	1.02E-02
1049	ASPM, CENPM, RAD51	3.89E-06	3.44E-02
1050	ASPM, CENPM, PBK	4.58E-06	2.04E-02
1051	ASPM, CENPM, TK1	1.22E-06	2.33E-03
1052	ASPM, CENPM, RAD54L	2.27E-06	9.16E-03
1053	ASPM, CENPM, CDCA3	4.51E-05	2.88E-02
1054	ASPM, CENPM, KIAA0101	7.14E-06	1.01E-02
1055	ASPM, CENPM, ASF1B	1.75E-05	2.87E-02
1056	ASPM, CENPF, KIF11	9.86E-06	7.37E-03
1057	ASPM, CENPF, RAD51	3.14E-05	2.39E-02
1058	ASPM, CENPF, PBK	3.30E-05	1.69E-02

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
1059	ASPM, CENPF, TK1	8.32E-06	2.20E-03
1060	ASPM, CENPF, RAD54L	1.31E-05	8.44E-03
1061	ASPM, CENPF, CDCA3	1.31E-04	2.12E-02
1062	ASPM, CENPF, KIAA0101	5.04E-05	9.55E-03
1063	ASPM, CENPF, ASF1B	5.32E-05	2.22E-02
1064	ASPM, KIF11, RAD51	5.18E-05	1.41E-01
1065	ASPM, KIF11, PBK	6.06E-05	7.74E-02
1066	ASPM, KIF11, TK1	1.45E-05	1.18E-02
1067	ASPM, KIF11, RAD54L	2.41E-05	3.55E-02
1068	ASPM, KIF11, CDCA3	8.76E-05	4.96E-02
1069	ASPM, KIF11, KIAA0101	1.04E-04	5.05E-02
1070	ASPM, KIF11, ASF1B	3.17E-05	5.40E-02
1071	ASPM, RAD51, PBK	1.66E-04	1.88E-01
1072	ASPM, RAD51, TK1	6.50E-05	5.81E-02
1073	ASPM, RAD51, RAD54L	1.18E-04	1.58E-01
1074	ASPM, RAD51, CDCA3	4.32E-04	2.69E-01
1075	ASPM, RAD51, KIAA0101	4.62E-04	1.95E-01
1076	ASPM, RAD51, ASF1B	5.27E-04	3.32E-01
1077	ASPM, PBK, TK1	8.76E-05	5.41E-02
1078	ASPM, PBK, RAD54L	4.05E-05	6.51E-02
1079	ASPM, PBK, CDCA3	3.00E-04	1.87E-01
1080	ASPM, PBK, KIAA0101	3.33E-04	1.15E-01
1081	ASPM, PBK, ASF1B	1.05E-03	3.17E-01
1082	ASPM, TK1, RAD54L	2.88E-05	1.34E-02
1083	ASPM, TK1, CDCA3	1.97E-04	3.93E-02
1084	ASPM, TK1, KIAA0101	9.38E-05	1.60E-02
1085	ASPM, TK1, ASF1B	8.86E-05	3.92E-02
1086	ASPM, RAD54L, CDCA3	6.05E-04	1.48E-01
1087	ASPM, RAD54L, KIAA0101	1.19E-04	4.51E-02
1088	ASPM, RAD54L, ASF1B	1.71E-04	1.10E-01
1089	ASPM, CDCA3, KIAA0101	1.07E-03	1.49E-01
1090	ASPM, CDCA3, ASF1B	7.99E-04	2.24E-01
1091	ASPM, KIAA0101, ASF1B	4.16E-04	1.19E-01

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
1092	NUSAP1, DTL, PLK1	4.32E-07	6.51E-03
1093	NUSAP1, DTL, CDK1	5.49E-07	4.28E-03
1094	NUSAP1, DTL, PRC1	6.23E-07	1.52E-03
1095	NUSAP1, DTL, PTTG1	7.05E-07	1.53E-03
1096	NUSAP1, DTL, MCM10	1.30E-06	1.64E-03
1097	NUSAP1, DTL, CENPM	7.03E-07	2.14E-03
1098	NUSAP1, DTL, CENPF	1.54E-06	9.05E-04
1099	NUSAP1, DTL, KIF11	2.86E-06	8.37E-03
1100	NUSAP1, DTL, RAD51	9.86E-06	3.00E-02
1101	NUSAP1, DTL, PBK	9.80E-06	1.71E-02
1102	NUSAP1, DTL, TK1	3.21E-06	1.95E-03
1103	NUSAP1, DTL, RAD54L	7.26E-06	8.05E-03
1104	NUSAP1, DTL, CDCA3	1.90E-05	1.77E-02
1105	NUSAP1, DTL, KIAA0101	2.98E-05	1.32E-02
1106	NUSAP1, DTL, ASF1B	2.99E-05	3.13E-02
1107	NUSAP1, PLK1, CDK1	5.02E-07	2.37E-02
1108	NUSAP1, PLK1, PRC1	3.90E-07	1.48E-02
1109	NUSAP1, PLK1, PTTG1	3.94E-07	1.18E-02
1110	NUSAP1, PLK1, MCM10	4.81E-07	9.26E-03
1111	NUSAP1, PLK1, CENPM	7.18E-07	1.88E-02
1112	NUSAP1, PLK1, CENPF	1.62E-06	1.08E-02
1113	NUSAP1, PLK1, KIF11	3.85E-06	4.84E-02
1114	NUSAP1, PLK1, RAD51	3.96E-06	1.20E-01
1115	NUSAP1, PLK1, PBK	6.84E-07	1.62E-02
1116	NUSAP1, PLK1, TK1	1.18E-06	1.34E-02
1117	NUSAP1, PLK1, RAD54L	4.73E-06	6.25E-02
1118	NUSAP1, PLK1, CDCA3	2.84E-05	5.13E-02
1119	NUSAP1, PLK1, KIAA0101	8.36E-06	5.97E-02
1120	NUSAP1, PLK1, ASF1B	2.87E-05	1.13E-01
1121	NUSAP1, CDK1, PRC1	1.00E-06	7.06E-03
1122	NUSAP1, CDK1, PTTG1	1.97E-06	9.29E-03
1123	NUSAP1, CDK1, MCM10	3.01E-06	8.04E-03
1124	NUSAP1, CDK1,	1.75E-06	1.12E-02

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
	CENPM		
1125	NUSAP1, CDK1, CENPF	1.55E-06	3.00E-03
1126	NUSAP1, CDK1, KIF11	8.20E-06	3.63E-02
1127	NUSAP1, CDK1, RAD51	2.25E-05	1.13E-01
1128	NUSAP1, CDK1, PBK	1.97E-05	4.34E-02
1129	NUSAP1, CDK1, TK1	5.53E-06	9.53E-03
1130	NUSAP1, CDK1, RAD54L	9.31E-06	2.90E-02
1131	NUSAP1, CDK1, CDCA3	7.00E-05	9.54E-02
1132	NUSAP1, CDK1, KIAA0101	4.71E-05	4.27E-02
1133	NUSAP1, CDK1, ASF1B	5.04E-05	9.31E-02
1134	NUSAP1, PRC1, PTTG1	1.24E-06	3.92E-03
1135	NUSAP1, PRC1, MCM10	2.33E-06	4.03E-03
1136	NUSAP1, PRC1, CENPM	6.10E-07	4.49E-03
1137	NUSAP1, PRC1, CENPF	2.08E-06	2.29E-03
1138	NUSAP1, PRC1, KIF11	3.64E-06	1.25E-02
1139	NUSAP1, PRC1, RAD51	3.46E-05	8.44E-02
1140	NUSAP1, PRC1, PBK	6.17E-06	1.50E-02
1141	NUSAP1, PRC1, TK1	4.99E-06	4.48E-03
1142	NUSAP1, PRC1, RAD54L	9.16E-06	1.70E-02
1143	NUSAP1, PRC1, CDCA3	1.26E-04	5.95E-02
1144	NUSAP1, PRC1, KIAA0101	3.62E-05	2.11E-02
1145	NUSAP1, PRC1, ASF1B	5.43E-05	4.85E-02
1146	NUSAP1, PTTG1, MCM10	2.43E-06	3.19E-03
1147	NUSAP1, PTTG1, CENPM	1.27E-06	4.80E-03
1148	NUSAP1, PTTG1, CENPF	3.68E-06	2.39E-03
1149	NUSAP1, PTTG1, KIF11	8.82E-06	1.66E-02
1150	NUSAP1, PTTG1, RAD51	2.43E-05	7.08E-02
1151	NUSAP1, PTTG1, PBK	8.79E-06	1.71E-02
1152	NUSAP1, PTTG1, TK1	6.49E-06	4.33E-03

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
1153	NUSAP1, PTTG1, RAD54L	1.10E-05	1.59E-02
1154	NUSAP1, PTTG1, CDCA3	1.16E-04	5.82E-02
1155	NUSAP1, PTTG1, KIAA0101	5.00E-05	2.38E-02
1156	NUSAP1, PTTG1, ASF1B	7.66E-05	6.46E-02
1157	NUSAP1, MCM10, CENPM	1.03E-06	2.97E-03
1158	NUSAP1, MCM10, CENPF	2.88E-06	1.66E-03
1159	NUSAP1, MCM10, KIF11	1.00E-05	1.31E-02
1160	NUSAP1, MCM10, RAD51	6.33E-05	7.50E-02
1161	NUSAP1, MCM10, PBK	3.06E-05	3.26E-02
1162	NUSAP1, MCM10, TK1	8.62E-06	3.92E-03
1163	NUSAP1, MCM10, RAD54L	1.49E-05	1.34E-02
1164	NUSAP1, MCM10, CDCA3	1.30E-04	4.68E-02
1165	NUSAP1, MCM10, KIAA0101	4.94E-05	1.72E-02
1166	NUSAP1, MCM10, ASF1B	5.37E-05	3.50E-02
1167	NUSAP1, CENPM, CENPF	1.71E-06	2.37E-03
1168	NUSAP1, CENPM, KIF11	1.16E-05	2.70E-02
1169	NUSAP1, CENPM, RAD51	1.01E-05	6.84E-02
1170	NUSAP1, CENPM, PBK	4.19E-06	1.54E-02
1171	NUSAP1, CENPM, TK1	4.95E-06	5.88E-03
1172	NUSAP1, CENPM, RAD54L	7.55E-06	1.94E-02
1173	NUSAP1, CENPM, CDCA3	8.59E-05	4.93E-02
1174	NUSAP1, CENPM, KIAA0101	2.67E-05	2.41E-02
1175	NUSAP1, CENPM, ASF1B	8.14E-05	6.39E-02
1176	NUSAP1, CENPF, KIF11	1.13E-05	9.37E-03
1177	NUSAP1, CENPF, RAD51	3.13E-05	3.11E-02
1178	NUSAP1, CENPF, PBK	1.03E-05	6.96E-03
1179	NUSAP1, CENPF, TK1	8.92E-06	2.40E-03
1180	NUSAP1, CENPF,	1.36E-05	9.30E-03

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
	RAD54L		
1181	NUSAP1, CENPF, CDCA3	1.10E-04	2.41E-02
1182	NUSAP1, CENPF, KIAA0101	6.14E-05	1.23E-02
1183	NUSAP1, CENPF, ASF1B	7.70E-05	3.10E-02
1184	NUSAP1, KIF11, RAD51	7.11E-05	2.02E-01
1185	NUSAP1, KIF11, PBK	2.87E-05	4.76E-02
1186	NUSAP1, KIF11, TK1	2.75E-05	2.00E-02
1187	NUSAP1, KIF11, RAD54L	4.11E-05	5.43E-02
1188	NUSAP1, KIF11, CDCA3	1.46E-04	8.46E-02
1189	NUSAP1, KIF11, KIAA0101	2.02E-04	8.22E-02
1190	NUSAP1, KIF11, ASF1B	9.73E-05	1.05E-01
1191	NUSAP1, RAD51, PBK	8.08E-05	1.44E-01
1192	NUSAP1, RAD51, TK1	9.00E-05	8.53E-02
1193	NUSAP1, RAD51, RAD54L	1.57E-04	2.18E-01
1194	NUSAP1, RAD51, CDCA3	4.15E-04	3.30E-01
1195	NUSAP1, RAD51, KIAA0101	6.86E-04	2.77E-01
1196	NUSAP1, RAD51, ASF1B	8.47E-04	4.45E-01
1197	NUSAP1, PBK, TK1	4.48E-05	3.29E-02
1198	NUSAP1, PBK, RAD54L	2.00E-05	4.00E-02
1199	NUSAP1, PBK, CDCA3	1.47E-04	1.36E-01
1200	NUSAP1, PBK, KIAA0101	1.98E-04	8.15E-02
1201	NUSAP1, PBK, ASF1B	7.73E-04	2.49E-01
1202	NUSAP1, TK1, RAD54L	4.57E-05	1.85E-02
1203	NUSAP1, TK1, CDCA3	2.29E-04	5.39E-02
1204	NUSAP1, TK1, KIAA0101	1.67E-04	2.52E-02
1205	NUSAP1, TK1, ASF1B	1.97E-04	6.44E-02
1206	NUSAP1, RAD54L, CDCA3	7.18E-04	1.94E-01
1207	NUSAP1, RAD54L, KIAA0101	1.96E-04	6.57E-02
1208	NUSAP1, RAD54L, ASF1B	3.46E-04	1.63E-01

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
1209	NUSAP1, CDCA3, KIAA0101	1.28E-03	2.03E-01
1210	NUSAP1, CDCA3, ASF1B	1.33E-03	3.29E-01
1211	NUSAP1, KIAA0101, ASF1B	8.71E-04	1.84E-01
1212	DTL, PLK1, CDK1	6.30E-07	2.41E-02
1213	DTL, PLK1, PRC1	1.23E-06	1.49E-02
1214	DTL, PLK1, PTTG1	7.98E-07	1.15E-02
1215	DTL, PLK1, MCM10	1.59E-06	1.17E-02
1216	DTL, PLK1, CENPM	1.66E-06	1.80E-02
1217	DTL, PLK1, CENPF	5.03E-06	1.19E-02
1218	DTL, PLK1, KIF11	3.93E-06	4.10E-02
1219	DTL, PLK1, RAD51	9.09E-06	1.13E-01
1220	DTL, PLK1, PBK	7.04E-06	4.89E-02
1221	DTL, PLK1, TK1	3.34E-06	1.48E-02
1222	DTL, PLK1, RAD54L	1.60E-05	6.85E-02
1223	DTL, PLK1, CDCA3	1.96E-05	3.95E-02
1224	DTL, PLK1, KIAA0101	2.26E-05	6.59E-02
1225	DTL, PLK1, ASF1B	3.82E-05	1.07E-01
1226	DTL, CDK1, PRC1	7.70E-07	7.01E-03
1227	DTL, CDK1, PTTG1	1.01E-06	8.90E-03
1228	DTL, CDK1, MCM10	2.24E-06	8.32E-03
1229	DTL, CDK1, CENPM	9.52E-07	1.01E-02
1230	DTL, CDK1, CENPF	1.07E-06	2.74E-03
1231	DTL, CDK1, KIF11	4.97E-06	3.71E-02
1232	DTL, CDK1, RAD51	1.19E-05	9.55E-02
1233	DTL, CDK1, PBK	6.37E-05	1.22E-01
1234	DTL, CDK1, TK1	3.81E-06	9.86E-03
1235	DTL, CDK1, RAD54L	8.35E-06	3.04E-02
1236	DTL, CDK1, CDCA3	2.27E-05	6.15E-02
1237	DTL, CDK1, KIAA0101	3.97E-05	4.47E-02
1238	DTL, CDK1, ASF1B	3.30E-05	8.92E-02
1239	DTL, PRC1, PTTG1	1.25E-06	3.24E-03
1240	DTL, PRC1, MCM10	4.01E-06	4.47E-03
1241	DTL, PRC1, CENPM	5.58E-07	3.17E-03
1242	DTL, PRC1, CENPF	2.44E-06	1.70E-03
1243	DTL, PRC1, KIF11	2.48E-06	1.10E-02
1244	DTL, PRC1, RAD51	3.59E-05	6.76E-02
1245	DTL, PRC1, PBK	3.39E-05	4.61E-02

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
1246	DTL, PRC1, TK1	7.24E-06	4.46E-03
1247	DTL, PRC1, RAD54L	1.65E-05	1.72E-02
1248	DTL, PRC1, CDCA3	5.30E-05	3.66E-02
1249	DTL, PRC1, KIAA0101	5.48E-05	2.18E-02
1250	DTL, PRC1, ASF1B	4.47E-05	4.37E-02
1251	DTL, PTTG1, MCM10	2.95E-06	3.53E-03
1252	DTL, PTTG1, CENPM	7.15E-07	3.33E-03
1253	DTL, PTTG1, CENPF	3.03E-06	1.78E-03
1254	DTL, PTTG1, KIF11	4.40E-06	1.43E-02
1255	DTL, PTTG1, RAD51	1.60E-05	5.29E-02
1256	DTL, PTTG1, PBK	4.11E-05	5.67E-02
1257	DTL, PTTG1, TK1	6.16E-06	4.21E-03
1258	DTL, PTTG1, RAD54L	1.38E-05	1.59E-02
1259	DTL, PTTG1, CDCA3	3.65E-05	3.37E-02
1260	DTL, PTTG1, KIAA0101	5.37E-05	2.42E-02
1261	DTL, PTTG1, ASF1B	4.46E-05	5.51E-02
1262	DTL, MCM10, CENPM	1.12E-06	2.82E-03
1263	DTL, MCM10, CENPF	3.77E-06	1.66E-03
1264	DTL, MCM10, KIF11	6.81E-06	1.23E-02
1265	DTL, MCM10, RAD51	7.16E-05	7.02E-02
1266	DTL, MCM10, PBK	1.61E-04	1.02E-01
1267	DTL, MCM10, TK1	1.35E-05	4.94E-03
1268	DTL, MCM10, RAD54L	2.84E-05	1.65E-02
1269	DTL, MCM10, CDCA3	5.35E-05	2.94E-02
1270	DTL, MCM10, KIAA0101	8.02E-05	2.15E-02
1271	DTL, MCM10, ASF1B	3.91E-05	3.12E-02
1272	DTL, CENPM, CENPF	1.28E-06	1.52E-03
1273	DTL, CENPM, KIF11	6.58E-06	2.30E-02
1274	DTL, CENPM, RAD51	7.08E-06	4.72E-02
1275	DTL, CENPM, PBK	1.78E-05	4.44E-02
1276	DTL, CENPM, TK1	4.39E-06	4.98E-03
1277	DTL, CENPM, RAD54L	9.26E-06	1.71E-02
1278	DTL, CENPM, CDCA3	2.74E-05	2.81E-02
1279	DTL, CENPM, KIAA0101	2.58E-05	2.10E-02
1280	DTL, CENPM, ASF1B	5.44E-05	5.50E-02
1281	DTL, CENPF, KIF11	7.54E-06	7.42E-03
1282	DTL, CENPF, RAD51	3.14E-05	2.41E-02

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
1283	DTL, CENPF, PBK	4.48E-05	2.10E-02
1284	DTL, CENPF, TK1	9.49E-06	2.10E-03
1285	DTL, CENPF, RAD54L	1.78E-05	8.08E-03
1286	DTL, CENPF, CDCA3	5.69E-05	1.66E-02
1287	DTL, CENPF, KIAA0101	6.82E-05	1.08E-02
1288	DTL, CENPF, ASF1B	5.19E-05	2.37E-02
1289	DTL, KIF11, RAD51	3.66E-05	1.66E-01
1290	DTL, KIF11, PBK	8.99E-05	1.31E-01
1291	DTL, KIF11, TK1	1.86E-05	1.89E-02
1292	DTL, KIF11, RAD54L	3.50E-05	5.21E-02
1293	DTL, KIF11, CDCA3	3.78E-05	4.68E-02
1294	DTL, KIF11, KIAA0101	1.64E-04	8.32E-02
1295	DTL, KIF11, ASF1B	6.21E-05	9.59E-02
1296	DTL, RAD51, PBK	2.28E-04	2.58E-01
1297	DTL, RAD51, TK1	8.39E-05	7.03E-02
1298	DTL, RAD51, RAD54L	1.87E-04	1.94E-01
1299	DTL, RAD51, CDCA3	2.50E-04	2.63E-01
1300	DTL, RAD51, KIAA0101	7.18E-04	2.55E-01
1301	DTL, RAD51, ASF1B	6.93E-04	3.93E-01
1302	DTL, PBK, TK1	2.28E-04	1.04E-01
1303	DTL, PBK, RAD54L	1.15E-04	1.17E-01
1304	DTL, PBK, CDCA3	2.50E-04	2.38E-01
1305	DTL, PBK, KIAA0101	9.18E-04	2.12E-01
1306	DTL, PBK, ASF1B	1.90E-03	4.75E-01
1307	DTL, TK1, RAD54L	7.54E-05	2.09E-02
1308	DTL, TK1, CDCA3	9.13E-05	3.27E-02
1309	DTL, TK1, KIAA0101	2.38E-04	2.87E-02
1310	DTL, TK1, ASF1B	1.50E-04	5.80E-02
1311	DTL, RAD54L, CDCA3	3.77E-04	1.36E-01
1312	DTL, RAD54L, KIAA0101	3.30E-04	7.43E-02
1313	DTL, RAD54L, ASF1B	3.27E-04	1.53E-01
1314	DTL, CDCA3, KIAA0101	6.36E-04	1.44E-01
1315	DTL, CDCA3, ASF1B	6.04E-04	2.39E-01
1316	DTL, KIAA0101, ASF1B	7.55E-04	1.78E-01
1317	PLK1, CDK1, PRC1	1.05E-06	4.47E-02
1318	PLK1, CDK1, PTTG1	1.14E-06	4.37E-02

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
1319	PLK1, CDK1, MCM10	2.14E-06	3.85E-02
1320	PLK1, CDK1, CENPM	1.65E-06	5.00E-02
1321	PLK1, CDK1, CENPF	2.61E-06	2.73E-02
1322	PLK1, CDK1, KIF11	6.38E-06	1.29E-01
1323	PLK1, CDK1, RAD51	1.07E-05	2.93E-01
1324	PLK1, CDK1, PBK	7.20E-06	9.90E-02
1325	PLK1, CDK1, TK1	3.21E-06	4.78E-02
1326	PLK1, CDK1, RAD54L	1.20E-05	1.68E-01
1327	PLK1, CDK1, CDCA3	5.16E-05	1.60E-01
1328	PLK1, CDK1, KIAA0101	2.52E-05	1.61E-01
1329	PLK1, CDK1, ASF1B	3.93E-05	2.50E-01
1330	PLK1, PRC1, PTTG1	7.01E-07	2.25E-02
1331	PLK1, PRC1, MCM10	1.43E-06	2.03E-02
1332	PLK1, PRC1, CENPM	7.57E-07	2.95E-02
1333	PLK1, PRC1, CENPF	2.07E-06	1.63E-02
1334	PLK1, PRC1, KIF11	4.47E-06	7.02E-02
1335	PLK1, PRC1, RAD51	9.63E-06	1.78E-01
1336	PLK1, PRC1, PBK	2.30E-06	3.94E-02
1337	PLK1, PRC1, TK1	2.61E-06	2.58E-02
1338	PLK1, PRC1, RAD54L	9.99E-06	1.03E-01
1339	PLK1, PRC1, CDCA3	6.31E-05	9.53E-02
1340	PLK1, PRC1, KIAA0101	1.58E-05	9.17E-02
1341	PLK1, PRC1, ASF1B	6.20E-05	1.70E-01
1342	PLK1, PTTG1, MCM10	9.91E-07	1.46E-02
1343	PLK1, PTTG1, CENPM	8.41E-07	2.58E-02
1344	PLK1, PTTG1, CENPF	3.00E-06	1.64E-02
1345	PLK1, PTTG1, KIF11	8.91E-06	8.46E-02
1346	PLK1, PTTG1, RAD51	5.26E-06	1.55E-01
1347	PLK1, PTTG1, PBK	1.82E-06	3.41E-02
1348	PLK1, PTTG1, TK1	2.15E-06	2.09E-02
1349	PLK1, PTTG1, RAD54L	8.37E-06	8.95E-02
1350	PLK1, PTTG1, CDCA3	7.42E-05	1.11E-01
1351	PLK1, PTTG1, KIAA0101	1.40E-05	8.38E-02
1352	PLK1, PTTG1, ASF1B	5.36E-05	1.81E-01
1353	PLK1, MCM10, CENPM	8.49E-07	1.75E-02
1354	PLK1, MCM10, CENPF	2.12E-06	1.00E-02

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
1355	PLK1, MCM10, KIF11	7.79E-06	5.59E-02
1356	PLK1, MCM10, RAD51	1.47E-05	1.41E-01
1357	PLK1, MCM10, PBK	8.33E-06	6.62E-02
1358	PLK1, MCM10, TK1	3.37E-06	1.75E-02
1359	PLK1, MCM10, RAD54L	1.19E-05	7.05E-02
1360	PLK1, MCM10, CDCA3	6.61E-05	7.52E-02
1361	PLK1, MCM10, KIAA0101	1.82E-05	6.35E-02
1362	PLK1, MCM10, ASF1B	4.80E-05	1.14E-01
1363	PLK1, CENPM, CENPF	2.39E-06	1.82E-02
1364	PLK1, CENPM, KIF11	1.36E-05	1.12E-01
1365	PLK1, CENPM, RAD51	6.05E-06	1.87E-01
1366	PLK1, CENPM, PBK	2.27E-06	4.16E-02
1367	PLK1, CENPM, TK1	3.17E-06	3.13E-02
1368	PLK1, CENPM, RAD54L	1.16E-05	1.16E-01
1369	PLK1, CENPM, CDCA3	7.13E-05	9.75E-02
1370	PLK1, CENPM, KIAA0101	1.38E-05	9.47E-02
1371	PLK1, CENPM, ASF1B	9.65E-05	2.00E-01
1372	PLK1, CENPF, KIF11	1.43E-05	4.64E-02
1373	PLK1, CENPF, RAD51	1.61E-05	1.05E-01
1374	PLK1, CENPF, PBK	5.24E-06	2.40E-02
1375	PLK1, CENPF, TK1	5.29E-06	1.52E-02
1376	PLK1, CENPF, RAD54L	1.70E-05	6.46E-02
1377	PLK1, CENPF, CDCA3	8.18E-05	4.78E-02
1378	PLK1, CENPF, KIAA0101	3.10E-05	5.59E-02
1379	PLK1, CENPF, ASF1B	7.85E-05	1.06E-01
1380	PLK1, KIF11, RAD51	3.24E-05	3.79E-01
1381	PLK1, KIF11, PBK	1.96E-05	1.28E-01
1382	PLK1, KIF11, TK1	2.19E-05	9.62E-02
1383	PLK1, KIF11, RAD54L	5.79E-05	2.51E-01
1384	PLK1, KIF11, CDCA3	1.09E-04	1.61E-01
1385	PLK1, KIF11, KIAA0101	1.12E-04	2.55E-01
1386	PLK1, KIF11, ASF1B	1.92E-04	3.75E-01
1387	PLK1, RAD51, PBK	1.57E-05	2.04E-01
1388	PLK1, RAD51, TK1	1.78E-05	1.71E-01
1389	PLK1, RAD51, RAD54L	6.37E-05	4.74E-01

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
1390	PLK1, RAD51, CDCA3	1.87E-04	4.37E-01
1391	PLK1, RAD51, KIAA0101	1.31E-04	4.85E-01
1392	PLK1, RAD51, ASF1B	3.49E-04	6.90E-01
1393	PLK1, PBK, TK1	1.00E-05	7.09E-02
1394	PLK1, PBK, RAD54L	9.80E-06	1.19E-01
1395	PLK1, PBK, CDCA3	7.46E-05	1.64E-01
1396	PLK1, PBK, KIAA0101	3.97E-05	1.57E-01
1397	PLK1, PBK, ASF1B	3.61E-04	3.76E-01
1398	PLK1, TK1, RAD54L	3.24E-05	1.02E-01
1399	PLK1, TK1, CDCA3	1.03E-04	8.97E-02
1400	PLK1, TK1, KIAA0101	5.10E-05	9.20E-02
1401	PLK1, TK1, ASF1B	1.46E-04	1.89E-01
1402	PLK1, RAD54L, CDCA3	4.85E-04	3.13E-01
1403	PLK1, RAD54L, KIAA0101	1.21E-04	2.72E-01
1404	PLK1, RAD54L, ASF1B	4.59E-04	4.89E-01
1405	PLK1, CDCA3, KIAA0101	5.30E-04	2.89E-01
1406	PLK1, CDCA3, ASF1B	9.08E-04	4.84E-01
1407	PLK1, KIAA0101, ASF1B	6.36E-04	4.72E-01
1408	CDK1, PRC1, PTTG1	2.36E-06	1.52E-02
1409	CDK1, PRC1, MCM10	6.20E-06	1.58E-02
1410	CDK1, PRC1, CENPM	1.10E-06	1.49E-02
1411	CDK1, PRC1, CENPF	1.84E-06	5.04E-03
1412	CDK1, PRC1, KIF11	5.32E-06	4.26E-02
1413	CDK1, PRC1, RAD51	5.75E-05	1.95E-01
1414	CDK1, PRC1, PBK	4.94E-05	9.22E-02
1415	CDK1, PRC1, TK1	8.55E-06	1.69E-02
1416	CDK1, PRC1, RAD54L	1.52E-05	4.90E-02
1417	CDK1, PRC1, CDCA3	1.38E-04	1.52E-01
1418	CDK1, PRC1, KIAA0101	6.38E-05	5.96E-02
1419	CDK1, PRC1, ASF1B	5.71E-05	1.15E-01
1420	CDK1, PTTG1, MCM10	7.21E-06	1.68E-02
1421	CDK1, PTTG1, CENPM	2.41E-06	1.94E-02
1422	CDK1, PTTG1, CENPF	3.54E-06	6.37E-03
1423	CDK1, PTTG1, KIF11	1.45E-05	6.24E-02
1424	CDK1, PTTG1, RAD51	4.29E-05	1.91E-01

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
1425	CDK1, PTTG1, PBK	8.15E-05	1.22E-01
1426	CDK1, PTTG1, TK1	1.18E-05	2.04E-02
1427	CDK1, PTTG1, RAD54L	2.00E-05	5.67E-02
1428	CDK1, PTTG1, CDCA3	1.36E-04	1.62E-01
1429	CDK1, PTTG1, KIAA0101	9.26E-05	7.57E-02
1430	CDK1, PTTG1, ASF1B	8.41E-05	1.60E-01
1431	CDK1, MCM10, CENPM	3.09E-06	1.40E-02
1432	CDK1, MCM10, CENPF	4.60E-06	5.50E-03
1433	CDK1, MCM10, KIF11	1.67E-05	4.51E-02
1434	CDK1, MCM10, RAD51	1.49E-04	1.99E-01
1435	CDK1, MCM10, PBK	2.71E-04	1.81E-01
1436	CDK1, MCM10, TK1	2.19E-05	1.89E-02
1437	CDK1, MCM10, RAD54L	3.66E-05	4.90E-02
1438	CDK1, MCM10, CDCA3	1.56E-04	1.25E-01
1439	CDK1, MCM10, KIAA0101	1.22E-04	5.96E-02
1440	CDK1, MCM10, ASF1B	6.33E-05	8.84E-02
1441	CDK1, CENPM, CENPF	1.45E-06	5.62E-03
1442	CDK1, CENPM, KIF11	1.71E-05	8.24E-02
1443	CDK1, CENPM, RAD51	1.72E-05	1.64E-01
1444	CDK1, CENPM, PBK	3.71E-05	1.00E-01
1445	CDK1, CENPM, TK1	7.98E-06	2.18E-02
1446	CDK1, CENPM, RAD54L	1.23E-05	5.70E-02
1447	CDK1, CENPM, CDCA3	1.00E-04	1.35E-01
1448	CDK1, CENPM, KIAA0101	5.05E-05	7.39E-02
1449	CDK1, CENPM, ASF1B	8.51E-05	1.43E-01
1450	CDK1, CENPF, KIF11	1.04E-05	2.42E-02
1451	CDK1, CENPF, RAD51	3.58E-05	7.54E-02
1452	CDK1, CENPF, PBK	4.63E-05	4.21E-02
1453	CDK1, CENPF, TK1	8.18E-06	6.60E-03
1454	CDK1, CENPF, RAD54L	1.25E-05	2.12E-02
1455	CDK1, CENPF, CDCA3	1.20E-04	6.86E-02
1456	CDK1, CENPF, KIAA0101	6.58E-05	2.90E-02
1457	CDK1, CENPF, ASF1B	5.15E-05	6.23E-02

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
1458	CDK1, KIF11, RAD51	1.01E-04	4.23E-01
1459	CDK1, KIF11, PBK	1.79E-04	2.36E-01
1460	CDK1, KIF11, TK1	3.68E-05	6.79E-02
1461	CDK1, KIF11, RAD54L	5.28E-05	1.45E-01
1462	CDK1, KIF11, CDCA3	1.61E-04	2.05E-01
1463	CDK1, KIF11, KIAA0101	2.82E-04	1.92E-01
1464	CDK1, KIF11, ASF1B	1.13E-04	2.30E-01
1465	CDK1, RAD51, PBK	3.94E-04	4.27E-01
1466	CDK1, RAD51, TK1	1.47E-04	2.17E-01
1467	CDK1, RAD51, RAD54L	2.53E-04	4.41E-01
1468	CDK1, RAD51, CDCA3	6.71E-04	6.64E-01
1469	CDK1, RAD51, KIAA0101	1.09E-03	4.91E-01
1470	CDK1, RAD51, ASF1B	1.10E-03	7.12E-01
1471	CDK1, PBK, TK1	3.32E-04	1.90E-01
1472	CDK1, PBK, RAD54L	1.45E-04	2.05E-01
1473	CDK1, PBK, CDCA3	4.00E-04	4.30E-01
1474	CDK1, PBK, KIAA0101	1.18E-03	3.08E-01
1475	CDK1, PBK, ASF1B	2.30E-03	6.29E-01
1476	CDK1, TK1, RAD54L	7.45E-05	6.23E-02
1477	CDK1, TK1, CDCA3	2.27E-04	1.40E-01
1478	CDK1, TK1, KIAA0101	2.77E-04	7.82E-02
1479	CDK1, TK1, ASF1B	1.91E-04	1.49E-01
1480	CDK1, RAD54L, CDCA3	7.22E-04	3.91E-01
1481	CDK1, RAD54L, KIAA0101	3.26E-04	1.63E-01
1482	CDK1, RAD54L, ASF1B	3.33E-04	3.10E-01
1483	CDK1, CDCA3, KIAA0101	1.44E-03	4.12E-01
1484	CDK1, CDCA3, ASF1B	1.52E-03	5.94E-01
1485	CDK1, KIAA0101, ASF1B	8.95E-04	3.29E-01
1486	PRC1, PTTG1, MCM10	4.75E-06	7.15E-03
1487	PRC1, PTTG1, CENPM	7.26E-07	6.64E-03
1488	PRC1, PTTG1, CENPF	3.89E-06	3.87E-03
1489	PRC1, PTTG1, KIF11	7.06E-06	2.23E-02
1490	PRC1, PTTG1, RAD51	5.32E-05	1.25E-01
1491	PRC1, PTTG1, PBK	2.08E-05	4.12E-02

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
1492	PRC1, PTTG1, TK1	9.34E-06	8.27E-03
1493	PRC1, PTTG1, RAD54L	1.66E-05	2.83E-02
1494	PRC1, PTTG1, CDCA3	2.64E-04	1.06E-01
1495	PRC1, PTTG1, KIAA0101	6.23E-05	3.38E-02
1496	PRC1, PTTG1, ASF1B	9.88E-05	8.56E-02
1497	PRC1, MCM10, CENPM	1.49E-06	5.85E-03
1498	PRC1, MCM10, CENPF	5.11E-06	3.62E-03
1499	PRC1, MCM10, KIF11	1.40E-05	2.11E-02
1500	PRC1, MCM10, RAD51	1.59E-04	1.31E-01
1501	PRC1, MCM10, PBK	8.30E-05	7.27E-02
1502	PRC1, MCM10, TK1	1.83E-05	8.76E-03
1503	PRC1, MCM10, RAD54L	3.02E-05	2.62E-02
1504	PRC1, MCM10, CDCA3	3.56E-04	9.21E-02
1505	PRC1, MCM10, KIAA0101	8.62E-05	2.83E-02
1506	PRC1, MCM10, ASF1B	1.01E-04	5.43E-02
1507	PRC1, CENPM, CENPF	8.65E-07	2.84E-03
1508	PRC1, CENPM, KIF11	4.97E-06	2.85E-02
1509	PRC1, CENPM, RAD51	1.67E-05	1.13E-01
1510	PRC1, CENPM, PBK	6.42E-06	3.32E-02
1511	PRC1, CENPM, TK1	4.16E-06	8.79E-03
1512	PRC1, CENPM, RAD54L	7.03E-06	2.87E-02
1513	PRC1, CENPM, CDCA3	1.25E-04	7.98E-02
1514	PRC1, CENPM, KIAA0101	2.18E-05	3.02E-02
1515	PRC1, CENPM, ASF1B	6.92E-05	7.57E-02
1516	PRC1, CENPF, KIF11	9.15E-06	1.25E-02
1517	PRC1, CENPF, RAD51	5.34E-05	5.18E-02
1518	PRC1, CENPF, PBK	2.32E-05	1.91E-02
1519	PRC1, CENPF, TK1	1.16E-05	4.24E-03
1520	PRC1, CENPF, RAD54L	1.80E-05	1.59E-02
1521	PRC1, CENPF, CDCA3	2.13E-04	4.29E-02
1522	PRC1, CENPF, KIAA0101	7.19E-05	1.72E-02
1523	PRC1, CENPF, ASF1B	9.25E-05	4.15E-02
1524	PRC1, KIF11, RAD51	1.32E-04	3.13E-01
1525	PRC1, KIF11, PBK	5.82E-05	9.92E-02
1526	PRC1, KIF11, TK1	2.87E-05	2.85E-02

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
1527	PRC1, KIF11, RAD54L	4.49E-05	7.60E-02
1528	PRC1, KIF11, CDCA3	1.91E-04	1.22E-01
1529	PRC1, KIF11, KIAA0101	1.98E-04	1.00E-01
1530	PRC1, KIF11, ASF1B	8.78E-05	1.20E-01
1531	PRC1, RAD51, PBK	2.23E-04	2.57E-01
1532	PRC1, RAD51, TK1	2.14E-04	1.51E-01
1533	PRC1, RAD51, RAD54L	3.47E-04	3.29E-01
1534	PRC1, RAD51, CDCA3	1.15E-03	5.25E-01
1535	PRC1, RAD51, KIAA0101	1.26E-03	3.79E-01
1536	PRC1, RAD51, ASF1B	1.73E-03	6.01E-01
1537	PRC1, PBK, TK1	1.11E-04	7.40E-02
1538	PRC1, PBK, RAD54L	5.05E-05	8.77E-02
1539	PRC1, PBK, CDCA3	4.61E-04	2.70E-01
1540	PRC1, PBK, KIAA0101	3.90E-04	1.44E-01
1541	PRC1, PBK, ASF1B	1.62E-03	3.87E-01
1542	PRC1, TK1, RAD54L	7.67E-05	3.36E-02
1543	PRC1, TK1, CDCA3	5.39E-04	9.86E-02
1544	PRC1, TK1, KIAA0101	2.40E-04	3.78E-02
1545	PRC1, TK1, ASF1B	2.97E-04	8.97E-02
1546	PRC1, RAD54L, CDCA3	1.52E-03	2.99E-01
1547	PRC1, RAD54L, KIAA0101	2.82E-04	9.26E-02
1548	PRC1, RAD54L, ASF1B	5.12E-04	2.10E-01
1549	PRC1, CDCA3, KIAA0101	2.65E-03	2.98E-01
1550	PRC1, CDCA3, ASF1B	2.19E-03	4.36E-01
1551	PRC1, KIAA0101, ASF1B	1.18E-03	2.20E-01
1552	PTTG1, MCM10, CENPM	1.50E-06	4.52E-03
1553	PTTG1, MCM10, CENPF	5.80E-06	2.91E-03
1554	PTTG1, MCM10, KIF11	2.10E-05	2.35E-02
1555	PTTG1, MCM10, RAD51	1.00E-04	1.09E-01
1556	PTTG1, MCM10, PBK	9.92E-05	7.95E-02
1557	PTTG1, MCM10, TK1	1.67E-05	7.24E-03
1558	PTTG1, MCM10, RAD54L	2.78E-05	2.24E-02
1559	PTTG1, MCM10, CDCA3	2.65E-04	8.15E-02

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
1560	PTTG1, MCM10, KIAA0101	8.74E-05	2.77E-02
1561	PTTG1, MCM10, ASF1B	9.89E-05	6.14E-02
1562	PTTG1, CENPM, CENPF	2.01E-06	3.15E-03
1563	PTTG1, CENPM, KIF11	1.41E-05	3.93E-02
1564	PTTG1, CENPM, RAD51	1.11E-05	9.68E-02
1565	PTTG1, CENPM, PBK	1.03E-05	3.96E-02
1566	PTTG1, CENPM, TK1	5.74E-06	8.69E-03
1567	PTTG1, CENPM, RAD54L	8.80E-06	2.77E-02
1568	PTTG1, CENPM, CDCA3	1.34E-04	8.18E-02
1569	PTTG1, CENPM, KIAA0101	3.11E-05	3.28E-02
1570	PTTG1, CENPM, ASF1B	9.97E-05	1.01E-01
1571	PTTG1, CENPF, KIF11	2.17E-05	1.61E-02
1572	PTTG1, CENPF, RAD51	4.88E-05	4.73E-02
1573	PTTG1, CENPF, PBK	3.67E-05	2.13E-02
1574	PTTG1, CENPF, TK1	1.63E-05	4.22E-03
1575	PTTG1, CENPF, RAD54L	2.42E-05	1.50E-02
1576	PTTG1, CENPF, CDCA3	2.33E-04	4.53E-02
1577	PTTG1, CENPF, KIAA0101	1.04E-04	1.90E-02
1578	PTTG1, CENPF, ASF1B	1.34E-04	5.39E-02
1579	PTTG1, KIF11, RAD51	1.30E-04	3.12E-01
1580	PTTG1, KIF11, PBK	1.03E-04	1.25E-01
1581	PTTG1, KIF11, TK1	5.16E-05	3.58E-02
1582	PTTG1, KIF11, RAD54L	7.72E-05	9.06E-02
1583	PTTG1, KIF11, CDCA3	2.86E-04	1.49E-01
1584	PTTG1, KIF11, KIAA0101	3.57E-04	1.30E-01
1585	PTTG1, KIF11, ASF1B	1.54E-04	1.70E-01
1586	PTTG1, RAD51, PBK	1.82E-04	2.53E-01
1587	PTTG1, RAD51, TK1	1.35E-04	1.29E-01
1588	PTTG1, RAD51, RAD54L	2.35E-04	3.06E-01
1589	PTTG1, RAD51, CDCA3	9.45E-04	5.48E-01
1590	PTTG1, RAD51,	9.99E-04	3.77E-01

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
	KIAA0101		
1591	PTTG1, RAD51, ASF1B	1.60E-03	6.64E-01
1592	PTTG1, PBK, TK1	1.47E-04	8.70E-02
1593	PTTG1, PBK, RAD54L	6.39E-05	9.86E-02
1594	PTTG1, PBK, CDCA3	3.92E-04	2.86E-01
1595	PTTG1, PBK, KIAA0101	5.54E-04	1.77E-01
1596	PTTG1, PBK, ASF1B	2.22E-03	5.02E-01
1597	PTTG1, TK1, RAD54L	7.91E-05	3.17E-02
1598	PTTG1, TK1, CDCA3	4.55E-04	9.66E-02
1599	PTTG1, TK1, KIAA0101	2.74E-04	4.10E-02
1600	PTTG1, TK1, ASF1B	3.42E-04	1.13E-01
1601	PTTG1, RAD54L, CDCA3	1.41E-03	3.10E-01
1602	PTTG1, RAD54L, KIAA0101	3.18E-04	9.97E-02
1603	PTTG1, RAD54L, ASF1B	5.96E-04	2.60E-01
1604	PTTG1, CDCA3, KIAA0101	2.44E-03	3.15E-01
1605	PTTG1, CDCA3, ASF1B	1.97E-03	4.68E-01
1606	PTTG1, KIAA0101, ASF1B	1.43E-03	2.85E-01
1607	MCM10, CENPM, CENPF	1.35E-06	1.80E-03
1608	MCM10, CENPM, KIF11	1.18E-05	2.45E-02
1609	MCM10, CENPM, RAD51	2.96E-05	8.84E-02
1610	MCM10, CENPM, PBK	2.95E-05	5.85E-02
1611	MCM10, CENPM, TK1	6.76E-06	6.30E-03
1612	MCM10, CENPM, RAD54L	1.07E-05	1.92E-02
1613	MCM10, CENPM, CDCA3	1.31E-04	6.16E-02
1614	MCM10, CENPM, KIAA0101	2.81E-05	2.07E-02
1615	MCM10, CENPM, ASF1B	5.64E-05	4.79E-02
1616	MCM10, CENPF, KIF11	1.97E-05	1.22E-02
1617	MCM10, CENPF, RAD51	8.54E-05	4.55E-02
1618	MCM10, CENPF, PBK	9.10E-05	3.82E-02
1619	MCM10, CENPF, TK1	1.67E-05	3.54E-03

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
1620	MCM10, CENPF, RAD54L	2.47E-05	1.18E-02
1621	MCM10, CENPF, CDCA3	2.17E-04	3.47E-02
1622	MCM10, CENPF, KIAA0101	8.32E-05	1.33E-02
1623	MCM10, CENPF, ASF1B	8.31E-05	2.86E-02
1624	MCM10, KIF11, RAD51	3.44E-04	3.16E-01
1625	MCM10, KIF11, PBK	3.49E-04	2.03E-01
1626	MCM10, KIF11, TK1	6.83E-05	2.98E-02
1627	MCM10, KIF11, RAD54L	1.02E-04	7.23E-02
1628	MCM10, KIF11, CDCA3	2.50E-04	1.04E-01
1629	MCM10, KIF11, KIAA0101	3.54E-04	9.49E-02
1630	MCM10, KIF11, ASF1B	1.05E-04	9.51E-02
1631	MCM10, RAD51, PBK	7.36E-04	3.60E-01
1632	MCM10, RAD51, TK1	3.45E-04	1.33E-01
1633	MCM10, RAD51, RAD54L	5.47E-04	2.86E-01
1634	MCM10, RAD51, CDCA3	1.42E-03	4.84E-01
1635	MCM10, RAD51, KIAA0101	1.68E-03	3.29E-01
1636	MCM10, RAD51, ASF1B	1.88E-03	5.02E-01
1637	MCM10, PBK, TK1	4.13E-04	1.29E-01
1638	MCM10, PBK, RAD54L	2.09E-04	1.48E-01
1639	MCM10, PBK, CDCA3	7.76E-04	3.57E-01
1640	MCM10, PBK, KIAA0101	1.20E-03	2.25E-01
1641	MCM10, PBK, ASF1B	3.19E-03	5.04E-01
1642	MCM10, TK1, RAD54L	1.09E-04	2.74E-02
1643	MCM10, TK1, CDCA3	5.25E-04	8.07E-02
1644	MCM10, TK1, KIAA0101	2.92E-04	3.17E-02
1645	MCM10, TK1, ASF1B	2.62E-04	6.59E-02
1646	MCM10, RAD54L, CDCA3	1.40E-03	2.38E-01
1647	MCM10, RAD54L, KIAA0101	3.53E-04	7.45E-02
1648	MCM10, RAD54L, ASF1B	4.60E-04	1.55E-01
1649	MCM10, CDCA3, KIAA0101	2.18E-03	2.38E-01

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
1650	MCM10, CDCA3, ASF1B	1.72E-03	3.38E-01
1651	MCM10, KIAA0101, ASF1B	9.50E-04	1.64E-01
1652	CENPM, CENPF, KIF11	1.41E-05	1.87E-02
1653	CENPM, CENPF, RAD51	1.12E-05	3.38E-02
1654	CENPM, CENPF, PBK	9.00E-06	1.38E-02
1655	CENPM, CENPF, TK1	5.79E-06	3.72E-03
1656	CENPM, CENPF, RAD54L	8.27E-06	1.30E-02
1657	CENPM, CENPF, CDCA3	1.12E-04	3.24E-02
1658	CENPM, CENPF, KIAA0101	3.10E-05	1.43E-02
1659	CENPM, CENPF, ASF1B	7.24E-05	4.22E-02
1660	CENPM, KIF11, RAD51	8.00E-05	3.26E-01
1661	CENPM, KIF11, PBK	6.97E-05	1.28E-01
1662	CENPM, KIF11, TK1	4.91E-05	4.96E-02
1663	CENPM, KIF11, RAD54L	6.78E-05	1.13E-01
1664	CENPM, KIF11, CDCA3	2.24E-04	1.31E-01
1665	CENPM, KIF11, KIAA0101	2.60E-04	1.41E-01
1666	CENPM, KIF11, ASF1B	2.13E-04	1.84E-01
1667	CENPM, RAD51, PBK	6.50E-05	2.17E-01
1668	CENPM, RAD51, TK1	5.55E-05	1.23E-01
1669	CENPM, RAD51, RAD54L	9.02E-05	2.84E-01
1670	CENPM, RAD51, CDCA3	3.51E-04	3.88E-01
1671	CENPM, RAD51, KIAA0101	3.37E-04	3.25E-01
1672	CENPM, RAD51, ASF1B	8.81E-04	5.50E-01
1673	CENPM, PBK, TK1	6.48E-05	7.48E-02
1674	CENPM, PBK, RAD54L	2.39E-05	8.45E-02
1675	CENPM, PBK, CDCA3	2.30E-04	2.15E-01
1676	CENPM, PBK, KIAA0101	1.94E-04	1.38E-01
1677	CENPM, PBK, ASF1B	1.24E-03	3.76E-01
1678	CENPM, TK1, RAD54L	4.80E-05	3.51E-02
1679	CENPM, TK1, CDCA3	2.85E-04	7.91E-02
1680	CENPM, TK1,	1.32E-04	3.82E-02

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
	KIAA0101		
1681	CENPM, TK1, ASF1B	3.04E-04	1.05E-01
1682	CENPM, RAD54L, CDCA3	8.58E-04	2.52E-01
1683	CENPM, RAD54L, KIAA0101	1.39E-04	9.11E-02
1684	CENPM, RAD54L, ASF1B	4.83E-04	2.30E-01
1685	CENPM, CDCA3, KIAA0101	1.35E-03	2.58E-01
1686	CENPM, CDCA3, ASF1B	2.14E-03	4.36E-01
1687	CENPM, KIAA0101, ASF1B	9.39E-04	2.35E-01
1688	CENPF, KIF11, RAD51	9.83E-05	1.28E-01
1689	CENPF, KIF11, PBK	9.57E-05	5.92E-02
1690	CENPF, KIF11, TK1	5.23E-05	1.85E-02
1691	CENPF, KIF11, RAD54L	7.07E-05	5.11E-02
1692	CENPF, KIF11, CDCA3	1.93E-04	5.40E-02
1693	CENPF, KIF11, KIAA0101	3.17E-04	6.65E-02
1694	CENPF, KIF11, ASF1B	1.30E-04	8.44E-02
1695	CENPF, RAD51, PBK	2.38E-04	1.42E-01
1696	CENPF, RAD51, TK1	1.20E-04	5.01E-02
1697	CENPF, RAD51, RAD54L	1.95E-04	1.45E-01
1698	CENPF, RAD51, CDCA3	7.31E-04	2.40E-01
1699	CENPF, RAD51, KIAA0101	8.58E-04	1.79E-01
1700	CENPF, RAD51, ASF1B	1.01E-03	3.13E-01
1701	CENPF, PBK, TK1	1.45E-04	3.95E-02
1702	CENPF, PBK, RAD54L	5.29E-05	4.74E-02
1703	CENPF, PBK, CDCA3	3.91E-04	1.32E-01
1704	CENPF, PBK, KIAA0101	5.41E-04	8.57E-02
1705	CENPF, PBK, ASF1B	1.70E-03	2.77E-01
1706	CENPF, TK1, RAD54L	7.75E-05	1.70E-02
1707	CENPF, TK1, CDCA3	3.68E-04	4.00E-02
1708	CENPF, TK1, KIAA0101	2.89E-04	2.00E-02
1709	CENPF, TK1, ASF1B	2.94E-04	5.41E-02
1710	CENPF, RAD54L, CDCA3	9.67E-04	1.46E-01

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
1711	CENPF, RAD54L, KIAA0101	3.00E-04	5.38E-02
1712	CENPF, RAD54L, ASF1B	4.61E-04	1.45E-01
1713	CENPF, CDCA3, KIAA0101	1.94E-03	1.51E-01
1714	CENPF, CDCA3, ASF1B	1.58E-03	2.33E-01
1715	CENPF, KIAA0101, ASF1B	1.23E-03	1.52E-01
1716	KIF11, RAD51, PBK	5.38E-04	5.32E-01
1717	KIF11, RAD51, TK1	4.27E-04	3.65E-01
1718	KIF11, RAD51, RAD54L	6.63E-04	6.61E-01
1719	KIF11, RAD51, CDCA3	6.14E-04	5.62E-01
1720	KIF11, RAD51, KIAA0101	2.85E-03	7.52E-01
1721	KIF11, RAD51, ASF1B	1.54E-03	8.20E-01
1722	KIF11, PBK, TK1	5.16E-04	2.20E-01
1723	KIF11, PBK, RAD54L	1.97E-04	2.29E-01
1724	KIF11, PBK, CDCA3	6.53E-04	4.39E-01
1725	KIF11, PBK, KIAA0101	1.85E-03	3.77E-01
1726	KIF11, PBK, ASF1B	1.78E-03	5.54E-01
1727	KIF11, TK1, RAD54L	3.05E-04	1.10E-01
1728	KIF11, TK1, CDCA3	5.04E-04	1.44E-01
1729	KIF11, TK1, KIAA0101	1.12E-03	1.46E-01
1730	KIF11, TK1, ASF1B	3.86E-04	1.73E-01
1731	KIF11, RAD54L, CDCA3	1.24E-03	3.57E-01
1732	KIF11, RAD54L, KIAA0101	1.15E-03	2.73E-01
1733	KIF11, RAD54L, ASF1B	6.06E-04	3.44E-01
1734	KIF11, CDCA3, KIAA0101	2.34E-03	3.77E-01
1735	KIF11, CDCA3, ASF1B	2.46E-03	5.65E-01
1736	KIF11, KIAA0101, ASF1B	1.72E-03	3.93E-01
1737	RAD51, PBK, TK1	8.59E-04	4.09E-01
1738	RAD51, PBK, RAD54L	4.96E-04	4.87E-01
1739	RAD51, PBK, CDCA3	1.37E-03	7.25E-01
1740	RAD51, PBK, KIAA0101	3.44E-03	6.42E-01
1741	RAD51, PBK, ASF1B	1.03E-02	9.18E-01
1742	RAD51, TK1, RAD54L	9.78E-04	3.55E-01

Sub-Panel #	Genes in Sub-Panel	Uni pval	Multi pval
1743	RAD51, TK1, CDCA3	1.78E-03	4.80E-01
1744	RAD51, TK1, KIAA0101	3.15E-03	4.10E-01
1745	RAD51, TK1, ASF1B	4.35E-03	6.63E-01
1746	RAD51, RAD54L, CDCA3	4.28E-03	9.49E-01
1747	RAD51, RAD54L, KIAA0101	3.76E-03	6.98E-01
1748	RAD51, RAD54L, ASF1B	6.44E-03	9.58E-01
1749	RAD51, CDCA3, KIAA0101	9.20E-03	9.83E-01
1750	RAD51, CDCA3, ASF1B	7.34E-03	8.41E-01
1751	RAD51, KIAA0101, ASF1B	1.65E-02	9.19E-01
1752	PBK, TK1, RAD54L	3.71E-04	1.69E-01
1753	PBK, TK1, CDCA3	1.04E-03	3.48E-01
1754	PBK, TK1, KIAA0101	2.34E-03	2.65E-01
1755	PBK, TK1, ASF1B	6.81E-03	6.41E-01
1756	PBK, RAD54L, CDCA3	1.59E-03	5.99E-01
1757	PBK, RAD54L, KIAA0101	9.29E-04	2.83E-01
1758	PBK, RAD54L, ASF1B	4.10E-03	7.01E-01
1759	PBK, CDCA3, KIAA0101	4.58E-03	6.96E-01
1760	PBK, CDCA3, ASF1B	8.00E-03	9.42E-01
1761	PBK, KIAA0101, ASF1B	1.53E-02	8.53E-01
1762	TK1, RAD54L, CDCA3	2.98E-03	2.90E-01
1763	TK1, RAD54L, KIAA0101	1.21E-03	1.10E-01
1764	TK1, RAD54L, ASF1B	1.74E-03	2.63E-01
1765	TK1, CDCA3, KIAA0101	4.45E-03	2.84E-01
1766	TK1, CDCA3, ASF1B	4.04E-03	4.34E-01
1767	TK1, KIAA0101, ASF1B	3.50E-03	2.75E-01
1768	RAD54L, CDCA3, KIAA0101	9.04E-03	6.34E-01
1769	RAD54L, CDCA3, ASF1B	8.91E-03	8.60E-01
1770	RAD54L, KIAA0101, ASF1B	4.48E-03	4.96E-01
1771	CDCA3, KIAA0101, ASF1B	1.44E-02	8.55E-01

Table 32: Predictive power (both univariate and multivariate) for all 4-gene sub-panels chosen from the top 10 genes (ranked by p-value) of Panel O.

Sub-Panel #	Genes in Sub-Panel	uni pval	multi pval	Sub-Panel #	Genes in Sub-Panel	uni pval	multi pval
1	CDKN3, SKA1, BUB1B, KIF20A	1.59E-08	2.69E-04		DTL		
2	CDKN3, SKA1, BUB1B, RRM2	1.03E-08	1.21E-04	24	CDKN3, SKA1, NUSAP1, PLK1	3.31E-08	9.26E-04
3	CDKN3, SKA1, BUB1B, ASPM	3.42E-08	1.90E-04	25	CDKN3, SKA1, NUSAP1, CDK1	6.91E-08	4.29E-04
4	CDKN3, SKA1, BUB1B, NUSAP1	2.29E-08	1.61E-04	26	CDKN3, SKA1, DTL, PLK1	6.09E-08	9.39E-04
5	CDKN3, SKA1, BUB1B, DTL	1.84E-08	1.08E-04	27	CDKN3, SKA1, DTL, CDK1	1.71E-08	2.01E-04
6	CDKN3, SKA1, BUB1B, PLK1	1.60E-08	8.09E-04	28	CDKN3, SKA1, PLK1, CDK1	8.11E-08	2.74E-03
7	CDKN3, SKA1, BUB1B, CDK1	3.01E-08	3.59E-04	29	CDKN3, BUB1B, KIF20A, RRM2	9.93E-09	3.73E-04
8	CDKN3, SKA1, KIF20A, RRM2	1.36E-08	2.03E-04	30	CDKN3, BUB1B, KIF20A, ASPM	3.93E-08	5.82E-04
9	CDKN3, SKA1, KIF20A, ASPM	3.71E-08	2.81E-04	31	CDKN3, BUB1B, KIF20A, NUSAP1	2.69E-08	6.10E-04
10	CDKN3, SKA1, KIF20A, NUSAP1	3.07E-08	3.19E-04	32	CDKN3, BUB1B, KIF20A, DTL	4.32E-08	6.51E-04
11	CDKN3, SKA1, KIF20A, DTL	2.18E-08	2.02E-04	33	CDKN3, BUB1B, KIF20A, PLK1	1.49E-08	2.96E-03
12	CDKN3, SKA1, KIF20A, PLK1	1.89E-08	1.40E-03	34	CDKN3, BUB1B, KIF20A, CDK1	6.51E-08	2.06E-03
13	CDKN3, SKA1, KIF20A, CDK1	5.23E-08	8.11E-04	35	CDKN3, BUB1B, RRM2, ASPM	2.19E-08	3.03E-04
14	CDKN3, SKA1, RRM2, ASPM	2.82E-08	1.42E-04	36	CDKN3, BUB1B, RRM2, NUSAP1	1.66E-08	2.51E-04
15	CDKN3, SKA1, RRM2, NUSAP1	3.12E-08	1.47E-04	37	CDKN3, BUB1B, RRM2, DTL	2.14E-08	2.62E-04
16	CDKN3, SKA1, RRM2, DTL	1.66E-08	8.33E-05	38	CDKN3, BUB1B, RRM2, PLK1	1.39E-08	1.75E-03
17	CDKN3, SKA1, RRM2, PLK1	2.29E-08	7.90E-04	39	CDKN3, BUB1B, RRM2, CDK1	3.19E-08	8.62E-04
18	CDKN3, SKA1, RRM2, CDK1	4.14E-08	3.67E-04	40	CDKN3, BUB1B, ASPM, NUSAP1	4.36E-08	3.23E-04
19	CDKN3, SKA1, ASPM, NUSAP1	5.65E-08	1.72E-04	41	CDKN3, BUB1B, ASPM, DTL	8.59E-08	4.32E-04
20	CDKN3, SKA1, ASPM, DTL	4.97E-08	1.37E-04	42	CDKN3, BUB1B, ASPM, PLK1	2.25E-08	1.49E-03
21	CDKN3, SKA1, ASPM, PLK1	3.45E-08	7.95E-04	43	CDKN3, BUB1B, ASPM, CDK1	9.21E-08	1.12E-03
22	CDKN3, SKA1, ASPM, CDK1	8.31E-08	4.51E-04	44	CDKN3, BUB1B, NUSAP1, DTL	3.92E-08	2.72E-04
23	CDKN3, SKA1, NUSAP1,	2.95E-08	9.67E-05	45	CDKN3, BUB1B, NUSAP1, PLK1	1.72E-08	1.68E-03

Sub-Panel #	Genes in Sub-Panel	uni pval	multi pval	Sub-Panel #	Genes in Sub-Panel	uni pval	multi pval
46	CDKN3, BUB1B, NUSAP1, CDK1	5.66E-08	9.10E-04	71	CDKN3, RRM2, NUSAP1, CDK1	9.56E-08	1.18E-03
47	CDKN3, BUB1B, DTL, PLK1	5.08E-08	2.00E-03	72	CDKN3, RRM2, DTL, PLK1	7.85E-08	2.57E-03
48	CDKN3, BUB1B, DTL, CDK1	3.11E-08	7.74E-04	73	CDKN3, RRM2, DTL, CDK1	4.63E-08	1.05E-03
49	CDKN3, BUB1B, PLK1, CDK1	4.73E-08	5.39E-03	74	CDKN3, RRM2, PLK1, CDK1	1.09E-07	8.00E-03
50	CDKN3, KIF20A, RRM2, ASPM	2.29E-08	4.23E-04	75	CDKN3, ASPM, NUSAP1, DTL	9.58E-08	3.47E-04
51	CDKN3, KIF20A, RRM2, NUSAP1	2.44E-08	5.20E-04	76	CDKN3, ASPM, NUSAP1, PLK1	3.48E-08	1.58E-03
52	CDKN3, KIF20A, RRM2, DTL	2.56E-08	4.84E-04	77	CDKN3, ASPM, NUSAP1, CDK1	1.47E-07	1.16E-03
53	CDKN3, KIF20A, RRM2, PLK1	2.10E-08	3.33E-03	78	CDKN3, ASPM, DTL, PLK1	9.92E-08	2.09E-03
54	CDKN3, KIF20A, RRM2, CDK1	5.90E-08	1.98E-03	79	CDKN3, ASPM, DTL, CDK1	1.00E-07	1.17E-03
55	CDKN3, KIF20A, ASPM, NUSAP1	5.80E-08	6.52E-04	80	CDKN3, ASPM, PLK1, CDK1	1.06E-07	5.81E-03
56	CDKN3, KIF20A, ASPM, DTL	9.53E-08	7.76E-04	81	CDKN3, NUSAP1, DTL, PLK1	7.64E-08	2.13E-03
57	CDKN3, KIF20A, ASPM, PLK1	2.85E-08	2.84E-03	82	CDKN3, NUSAP1, DTL, CDK1	7.90E-08	1.11E-03
58	CDKN3, KIF20A, ASPM, CDK1	1.51E-07	2.47E-03	83	CDKN3, NUSAP1, PLK1, CDK1	1.03E-07	6.94E-03
59	CDKN3, KIF20A, NUSAP1, DTL	5.99E-08	7.25E-04	84	CDKN3, DTL, PLK1, CDK1	8.84E-08	6.36E-03
60	CDKN3, KIF20A, NUSAP1, PLK1	2.67E-08	3.68E-03	85	SKA1, BUB1B, KIF20A, RRM2	2.64E-08	4.13E-04
61	CDKN3, KIF20A, NUSAP1, CDK1	1.31E-07	2.88E-03	86	SKA1, BUB1B, KIF20A, ASPM	8.52E-08	5.70E-04
62	CDKN3, KIF20A, DTL, PLK1	6.45E-08	4.11E-03	87	SKA1, BUB1B, KIF20A, NUSAP1	6.26E-08	6.22E-04
63	CDKN3, KIF20A, DTL, CDK1	7.56E-08	2.56E-03	88	SKA1, BUB1B, KIF20A, DTL	5.24E-08	4.00E-04
64	CDKN3, KIF20A, PLK1, CDK1	1.07E-07	1.34E-02	89	SKA1, BUB1B, KIF20A, PLK1	3.88E-08	2.49E-03
65	CDKN3, RRM2, ASPM, NUSAP1	4.10E-08	2.96E-04	90	SKA1, BUB1B, KIF20A, CDK1	8.64E-08	1.19E-03
66	CDKN3, RRM2, ASPM, DTL	5.55E-08	3.58E-04	91	SKA1, BUB1B, RRM2, ASPM	5.89E-08	3.21E-04
67	CDKN3, RRM2, ASPM, PLK1	2.92E-08	1.74E-03	92	SKA1, BUB1B, RRM2, NUSAP1	5.29E-08	3.11E-04
68	CDKN3, RRM2, ASPM, CDK1	8.88E-08	1.18E-03	93	SKA1, BUB1B, RRM2, DTL	3.35E-08	1.79E-04
69	CDKN3, RRM2, NUSAP1, DTL	4.44E-08	2.81E-04	94	SKA1, BUB1B, RRM2, PLK1	3.95E-08	1.46E-03
70	CDKN3, RRM2, NUSAP1, PLK1	3.92E-08	2.34E-03	95	SKA1, BUB1B, RRM2, CDK1	5.72E-08	5.73E-04

Sub-Panel #	Genes in Sub-Panel	uni pval	multi pval	Sub-Panel #	Genes in Sub-Panel	uni pval	multi pval
96	SKA1, BUB1B, ASPM, NUSAP1	1.21E-07	3.84E-04		NUSAP1		
97	SKA1, BUB1B, ASPM, DTL	1.22E-07	2.97E-04	122	SKA1, RRM2, ASPM, DTL	8.73E-08	2.29E-04
98	SKA1, BUB1B, ASPM, PLK1	7.59E-08	1.53E-03	123	SKA1, RRM2, ASPM, PLK1	8.39E-08	1.47E-03
99	SKA1, BUB1B, ASPM, CDK1	1.46E-07	7.43E-04	124	SKA1, RRM2, ASPM, CDK1	1.51E-07	7.29E-04
100	SKA1, BUB1B, NUSAP1, DTL	6.36E-08	2.05E-04	125	SKA1, RRM2, NUSAP1, DTL	7.69E-08	1.99E-04
101	SKA1, BUB1B, NUSAP1, PLK1	6.29E-08	1.72E-03	126	SKA1, RRM2, NUSAP1, PLK1	1.11E-07	1.95E-03
102	SKA1, BUB1B, NUSAP1, CDK1	1.01E-07	6.56E-04	127	SKA1, RRM2, NUSAP1, CDK1	1.73E-07	7.92E-04
103	SKA1, BUB1B, DTL, PLK1	1.28E-07	1.66E-03	128	SKA1, RRM2, DTL, PLK1	1.56E-07	1.68E-03
104	SKA1, BUB1B, DTL, CDK1	3.29E-08	3.36E-04	129	SKA1, RRM2, DTL, CDK1	5.06E-08	4.20E-04
105	SKA1, BUB1B, PLK1, CDK1	1.25E-07	3.88E-03	130	SKA1, RRM2, PLK1, CDK1	2.14E-07	4.57E-03
106	SKA1, KIF20A, RRM2, ASPM	5.97E-08	4.39E-04	131	SKA1, ASPM, NUSAP1, DTL	1.52E-07	2.44E-04
107	SKA1, KIF20A, RRM2, NUSAP1	6.69E-08	5.67E-04	132	SKA1, ASPM, NUSAP1, PLK1	1.26E-07	1.64E-03
108	SKA1, KIF20A, RRM2, DTL	3.74E-08	3.08E-04	133	SKA1, ASPM, NUSAP1, CDK1	2.45E-07	7.76E-04
109	SKA1, KIF20A, RRM2, PLK1	4.99E-08	2.53E-03	134	SKA1, ASPM, DTL, PLK1	2.51E-07	1.74E-03
110	SKA1, KIF20A, RRM2, CDK1	8.94E-08	1.16E-03	135	SKA1, ASPM, DTL, CDK1	1.01E-07	4.79E-04
111	SKA1, KIF20A, ASPM, NUSAP1	1.32E-07	6.29E-04	136	SKA1, ASPM, PLK1, CDK1	2.66E-07	4.13E-03
112	SKA1, KIF20A, ASPM, DTL	1.17E-07	4.52E-04	137	SKA1, NUSAP1, DTL, PLK1	1.99E-07	1.72E-03
113	SKA1, KIF20A, ASPM, PLK1	7.47E-08	2.38E-03	138	SKA1, NUSAP1, DTL, CDK1	8.34E-08	4.72E-04
114	SKA1, KIF20A, ASPM, CDK1	1.93E-07	1.35E-03	139	SKA1, NUSAP1, PLK1, CDK1	2.58E-07	4.76E-03
115	SKA1, KIF20A, NUSAP1, DTL	7.41E-08	4.18E-04	140	SKA1, DTL, PLK1, CDK1	1.95E-07	3.79E-03
116	SKA1, KIF20A, NUSAP1, PLK1	7.13E-08	2.99E-03	141	BUB1B, KIF20A, RRM2, ASPM	5.38E-08	7.91E-04
117	SKA1, KIF20A, NUSAP1, CDK1	1.70E-07	1.56E-03	142	BUB1B, KIF20A, RRM2, NUSAP1	4.67E-08	9.00E-04
118	SKA1, KIF20A, DTL, PLK1	1.22E-07	2.73E-03	143	BUB1B, KIF20A, RRM2, DTL	5.83E-08	8.18E-04
119	SKA1, KIF20A, DTL, CDK1	5.91E-08	8.86E-04	144	BUB1B, KIF20A, RRM2, PLK1	3.76E-08	4.94E-03
120	SKA1, KIF20A, PLK1, CDK1	1.92E-07	7.63E-03	145	BUB1B, KIF20A, RRM2, CDK1	9.19E-08	2.60E-03
121	SKA1, RRM2, ASPM,	1.26E-07	3.45E-04	146	BUB1B, KIF20A, ASPM, NUSAP1	1.34E-07	1.16E-03
				147	BUB1B, KIF20A, ASPM, DTL	2.46E-07	1.31E-03
				148	BUB1B, KIF20A, ASPM, PLK1	6.47E-08	4.40E-03

Sub-Panel #	Genes in Sub-Panel	uni pval	multi pval	Sub-Panel #	Genes in Sub-Panel	uni pval	multi pval
149	BUB1B, KIF20A, ASPM, CDK1	2.84E-07	3.35E-03	174	BUB1B, NUSAP1, PLK1, CDK1	1.40E-07	8.15E-03
150	BUB1B, KIF20A, NUSAP1, DTL	1.36E-07	1.17E-03	175	BUB1B, DTL, PLK1, CDK1	1.55E-07	7.71E-03
151	BUB1B, KIF20A, NUSAP1, PLK1	5.11E-08	5.42E-03	176	KIF20A, RRM2, ASPM, NUSAP1	9.71E-08	9.88E-04
152	BUB1B, KIF20A, NUSAP1, CDK1	2.07E-07	3.62E-03	177	KIF20A, RRM2, ASPM, DTL	1.23E-07	9.87E-04
153	BUB1B, KIF20A, DTL, PLK1	1.40E-07	5.78E-03	178	KIF20A, RRM2, ASPM, PLK1	7.03E-08	4.85E-03
154	BUB1B, KIF20A, DTL, CDK1	1.53E-07	3.35E-03	179	KIF20A, RRM2, ASPM, CDK1	2.03E-07	3.14E-03
155	BUB1B, KIF20A, PLK1, CDK1	1.65E-07	1.57E-02	180	KIF20A, RRM2, NUSAP1, DTL	1.06E-07	1.04E-03
156	BUB1B, RRM2, ASPM, NUSAP1	8.40E-08	5.77E-04	181	KIF20A, RRM2, NUSAP1, PLK1	8.94E-08	6.82E-03
157	BUB1B, RRM2, ASPM, DTL	1.31E-07	6.51E-04	182	KIF20A, RRM2, NUSAP1, CDK1	2.31E-07	3.92E-03
158	BUB1B, RRM2, ASPM, PLK1	5.70E-08	2.77E-03	183	KIF20A, RRM2, DTL, PLK1	1.67E-07	6.65E-03
159	BUB1B, RRM2, ASPM, CDK1	1.49E-07	1.70E-03	184	KIF20A, RRM2, DTL, CDK1	1.43E-07	3.66E-03
160	BUB1B, RRM2, NUSAP1, DTL	8.18E-08	4.71E-04	185	KIF20A, RRM2, PLK1, CDK1	2.76E-07	2.03E-02
161	BUB1B, RRM2, NUSAP1, PLK1	5.94E-08	3.45E-03	186	KIF20A, ASPM, NUSAP1, DTL	2.75E-07	1.34E-03
162	BUB1B, RRM2, NUSAP1, CDK1	1.22E-07	1.52E-03	187	KIF20A, ASPM, NUSAP1, PLK1	9.23E-08	5.11E-03
163	BUB1B, RRM2, DTL, PLK1	1.36E-07	3.59E-03	188	KIF20A, ASPM, NUSAP1, CDK1	4.32E-07	4.17E-03
164	BUB1B, RRM2, DTL, CDK1	7.60E-08	1.40E-03	189	KIF20A, ASPM, DTL, PLK1	2.41E-07	5.79E-03
165	BUB1B, RRM2, PLK1, CDK1	1.36E-07	9.31E-03	190	KIF20A, ASPM, DTL, CDK1	3.64E-07	4.26E-03
166	BUB1B, ASPM, NUSAP1, DTL	2.26E-07	6.28E-04	191	KIF20A, ASPM, PLK1, CDK1	3.07E-07	1.61E-02
167	BUB1B, ASPM, NUSAP1, PLK1	7.33E-08	2.59E-03	192	KIF20A, NUSAP1, DTL, PLK1	1.84E-07	6.49E-03
168	BUB1B, ASPM, NUSAP1, CDK1	2.48E-07	1.65E-03	193	KIF20A, NUSAP1, DTL, CDK1	3.22E-07	5.13E-03
169	BUB1B, ASPM, DTL, PLK1	2.26E-07	3.15E-03	194	KIF20A, NUSAP1, PLK1, CDK1	3.00E-07	2.02E-02
170	BUB1B, ASPM, DTL, CDK1	2.13E-07	1.69E-03	195	KIF20A, DTL, PLK1, CDK1	3.21E-07	1.97E-02
171	BUB1B, ASPM, PLK1, CDK1	1.81E-07	7.32E-03	196	RRM2, ASPM, NUSAP1, DTL	1.87E-07	6.06E-04
172	BUB1B, NUSAP1, DTL, PLK1	1.46E-07	3.07E-03	197	RRM2, ASPM, NUSAP1, PLK1	1.15E-07	3.36E-03
173	BUB1B, NUSAP1, DTL, CDK1	1.34E-07	1.45E-03	198	RRM2, ASPM, NUSAP1, CDK1	2.93E-07	1.96E-03

Sub-Panel #	Genes in Sub-Panel	uni pval	multi pval	Sub-Panel #	Genes in Sub-Panel	uni pval	multi pval
199	RRM2, ASPM, DTL, PLK1	2.51E-07	3.77E-03	205	RRM2, DTL, PLK1, CDK1	3.67E-07	1.27E-02
200	RRM2, ASPM, DTL, CDK1	2.16E-07	2.06E-03	206	ASPM, NUSAP1, DTL, PLK1	2.67E-07	3.11E-03
201	RRM2, ASPM, PLK1, CDK1	2.84E-07	1.00E-02	207	ASPM, NUSAP1, DTL, CDK1	3.60E-07	2.02E-03
202	RRM2, NUSAP1, DTL, PLK1	2.79E-07	4.38E-03	208	ASPM, NUSAP1, PLK1, CDK1	2.87E-07	8.49E-03
203	RRM2, NUSAP1, DTL, CDK1	2.49E-07	2.22E-03	209	ASPM, DTL, PLK1, CDK1	3.42E-07	8.78E-03
204	RRM2, NUSAP1, PLK1, CDK1	3.79E-07	1.29E-02	210	NUSAP1, DTL, PLK1, CDK1	3.49E-07	1.09E-02

Table 33: Predictive power (both univariate and multivariate) for all 5-gene sub-panels chosen from the top 10 genes (ranked by p-value) of Panel O.

Sub-Panel #	Genes in Sub-Panel	uni pval	multi pval	Sub-Panel #	Genes in Sub-Panel	uni pval	multi pval
1	CDKN3, SKA1, BUB1B, KIF20A, RRM2	1.30E-08	2.26E-04		NUSAP1, DTL		
2	CDKN3, SKA1, BUB1B, KIF20A, ASPM	3.56E-08	3.13E-04	17	CDKN3, SKA1, BUB1B, NUSAP1, PLK1	2.36E-08	7.92E-04
3	CDKN3, SKA1, BUB1B, KIF20A, NUSAP1	2.67E-08	3.23E-04	18	CDKN3, SKA1, BUB1B, NUSAP1, CDK1	4.78E-08	3.74E-04
4	CDKN3, SKA1, BUB1B, KIF20A, DTL	2.89E-08	2.57E-04	19	CDKN3, SKA1, BUB1B, DTL, PLK1	5.13E-08	8.77E-04
5	CDKN3, SKA1, BUB1B, KIF20A, PLK1	1.69E-08	1.15E-03	20	CDKN3, SKA1, BUB1B, DTL, CDK1	1.69E-08	1.99E-04
6	CDKN3, SKA1, BUB1B, KIF20A, CDK1	4.53E-08	6.49E-04	21	CDKN3, SKA1, BUB1B, PLK1, CDK1	5.53E-08	1.89E-03
7	CDKN3, SKA1, BUB1B, RRM2, ASPM	2.50E-08	1.84E-04	22	CDKN3, SKA1, KIF20A, RRM2, ASPM	2.73E-08	2.44E-04
8	CDKN3, SKA1, BUB1B, RRM2, NUSAP1	2.13E-08	1.68E-04	23	CDKN3, SKA1, KIF20A, RRM2, NUSAP1	2.75E-08	2.81E-04
9	CDKN3, SKA1, BUB1B, RRM2, DTL	1.88E-08	1.25E-04	24	CDKN3, SKA1, KIF20A, RRM2, DTL	2.21E-08	1.97E-04
10	CDKN3, SKA1, BUB1B, RRM2, PLK1	1.57E-08	6.76E-04	25	CDKN3, SKA1, KIF20A, RRM2, PLK1	2.10E-08	1.11E-03
11	CDKN3, SKA1, BUB1B, RRM2, CDK1	3.01E-08	3.33E-04	26	CDKN3, SKA1, KIF20A, RRM2, CDK1	4.52E-08	5.97E-04
12	CDKN3, SKA1, BUB1B, ASPM, NUSAP1	4.55E-08	2.17E-04	27	CDKN3, SKA1, KIF20A, ASPM, NUSAP1	5.33E-08	3.35E-04
13	CDKN3, SKA1, BUB1B, ASPM, DTL	5.59E-08	2.00E-04	28	CDKN3, SKA1, KIF20A, ASPM, DTL	5.93E-08	2.89E-04
14	CDKN3, SKA1, BUB1B, ASPM, PLK1	2.90E-08	7.52E-04	29	CDKN3, SKA1, KIF20A, ASPM, PLK1	3.21E-08	1.14E-03
15	CDKN3, SKA1, BUB1B, ASPM, CDK1	6.88E-08	4.40E-04	30	CDKN3, SKA1, KIF20A, ASPM, CDK1	9.28E-08	7.29E-04
16	CDKN3, SKA1, BUB1B,	3.16E-08	1.42E-04	31	CDKN3, SKA1, KIF20A, NUSAP1, DTL	3.90E-08	2.57E-04

Sub-Panel #	Genes in Sub-Panel	uni pval	multi pval
32	CDKN3, SKA1, KIF20A, NUSAP1, PLK1	2.91E-08	1.31E-03
33	CDKN3, SKA1, KIF20A, NUSAP1, CDK1	7.69E-08	7.69E-04
34	CDKN3, SKA1, KIF20A, DTL, PLK1	5.57E-08	1.38E-03
35	CDKN3, SKA1, KIF20A, DTL, CDK1	2.89E-08	4.42E-04
36	CDKN3, SKA1, KIF20A, PLK1, CDK1	8.51E-08	3.44E-03
37	CDKN3, SKA1, RRM2, ASPM, NUSAP1	4.67E-08	1.88E-04
38	CDKN3, SKA1, RRM2, ASPM, DTL	4.33E-08	1.55E-04
39	CDKN3, SKA1, RRM2, ASPM, PLK1	3.22E-08	7.02E-04
40	CDKN3, SKA1, RRM2, ASPM, CDK1	6.97E-08	4.10E-04
41	CDKN3, SKA1, RRM2, NUSAP1, DTL	3.47E-08	1.26E-04
42	CDKN3, SKA1, RRM2, NUSAP1, PLK1	3.65E-08	8.23E-04
43	CDKN3, SKA1, RRM2, NUSAP1, CDK1	6.84E-08	3.99E-04
44	CDKN3, SKA1, RRM2, DTL, PLK1	5.98E-08	8.37E-04
45	CDKN3, SKA1, RRM2, DTL, CDK1	2.24E-08	2.17E-04
46	CDKN3, SKA1, RRM2, PLK1, CDK1	8.31E-08	2.05E-03
47	CDKN3, SKA1, ASPM, NUSAP1, DTL	6.80E-08	1.65E-04
48	CDKN3, SKA1, ASPM, NUSAP1, PLK1	4.62E-08	7.86E-04
49	CDKN3, SKA1, ASPM, NUSAP1, CDK1	1.04E-07	4.34E-04
50	CDKN3, SKA1, ASPM, DTL, PLK1	9.81E-08	9.34E-04
51	CDKN3, SKA1, ASPM, DTL, CDK1	4.36E-08	2.66E-04
52	CDKN3, SKA1, ASPM, PLK1, CDK1	1.11E-07	2.03E-03
53	CDKN3, SKA1, NUSAP1, DTL, PLK1	7.46E-08	8.72E-04
54	CDKN3, SKA1, NUSAP1, DTL, CDK1	3.34E-08	2.38E-04
55	CDKN3, SKA1, NUSAP1, PLK1, CDK1	9.86E-08	2.14E-03
56	CDKN3, SKA1, DTL, PLK1, CDK1	6.67E-08	1.63E-03

Sub-Panel #	Genes in Sub-Panel	uni pval	multi pval
57	CDKN3, BUB1B, KIF20A, RRM2, ASPM	2.07E-08	3.97E-04
58	CDKN3, BUB1B, KIF20A, RRM2, NUSAP1	1.77E-08	4.25E-04
59	CDKN3, BUB1B, KIF20A, RRM2, DTL	2.63E-08	4.48E-04
60	CDKN3, BUB1B, KIF20A, RRM2, PLK1	1.51E-08	2.17E-03
61	CDKN3, BUB1B, KIF20A, RRM2, CDK1	4.07E-08	1.22E-03
62	CDKN3, BUB1B, KIF20A, ASPM, NUSAP1	4.51E-08	5.64E-04
63	CDKN3, BUB1B, KIF20A, ASPM, DTL	8.92E-08	7.01E-04
64	CDKN3, BUB1B, KIF20A, ASPM, PLK1	2.49E-08	2.07E-03
65	CDKN3, BUB1B, KIF20A, ASPM, CDK1	1.09E-07	1.61E-03
66	CDKN3, BUB1B, KIF20A, NUSAP1, DTL	5.37E-08	6.18E-04
67	CDKN3, BUB1B, KIF20A, NUSAP1, PLK1	2.00E-08	2.38E-03
68	CDKN3, BUB1B, KIF20A, NUSAP1, CDK1	8.00E-08	1.65E-03
69	CDKN3, BUB1B, KIF20A, DTL, PLK1	5.40E-08	2.82E-03
70	CDKN3, BUB1B, KIF20A, DTL, CDK1	5.43E-08	1.44E-03
71	CDKN3, BUB1B, KIF20A, PLK1, CDK1	6.86E-08	7.02E-03
72	CDKN3, BUB1B, RRM2, ASPM, NUSAP1	2.93E-08	2.97E-04
73	CDKN3, BUB1B, RRM2, ASPM, DTL	5.17E-08	3.75E-04
74	CDKN3, BUB1B, RRM2, ASPM, PLK1	2.15E-08	1.32E-03
75	CDKN3, BUB1B, RRM2, ASPM, CDK1	6.18E-08	8.69E-04
76	CDKN3, BUB1B, RRM2, NUSAP1, DTL	3.29E-08	2.73E-04
77	CDKN3, BUB1B, RRM2, NUSAP1, PLK1	2.07E-08	1.51E-03
78	CDKN3, BUB1B, RRM2, NUSAP1, CDK1	4.79E-08	7.44E-04
79	CDKN3, BUB1B, RRM2, DTL, PLK1	4.92E-08	1.77E-03
80	CDKN3, BUB1B,	2.89E-08	6.51E-04

Sub-Panel #	Genes in Sub-Panel	uni pval	multi pval
	RRM2, DTL, CDK1		
81	CDKN3, BUB1B, RRM2, PLK1, CDK1	5.51E-08	4.25E-03
82	CDKN3, BUB1B, ASPM, NUSAP1, DTL	8.10E-08	3.69E-04
83	CDKN3, BUB1B, ASPM, NUSAP1, PLK1	2.68E-08	1.26E-03
84	CDKN3, BUB1B, ASPM, NUSAP1, CDK1	9.33E-08	8.50E-04
85	CDKN3, BUB1B, ASPM, DTL, PLK1	7.96E-08	1.67E-03
86	CDKN3, BUB1B, ASPM, DTL, CDK1	7.12E-08	8.11E-04
87	CDKN3, BUB1B, ASPM, PLK1, CDK1	7.44E-08	3.62E-03
88	CDKN3, BUB1B, NUSAP1, DTL, PLK1	5.29E-08	1.56E-03
89	CDKN3, BUB1B, NUSAP1, DTL, CDK1	4.50E-08	6.65E-04
90	CDKN3, BUB1B, NUSAP1, PLK1, CDK1	5.69E-08	3.78E-03
91	CDKN3, BUB1B, DTL, PLK1, CDK1	5.09E-08	3.37E-03
92	CDKN3, KIF20A, RRM2, ASPM, NUSAP1	3.48E-08	4.66E-04
93	CDKN3, KIF20A, RRM2, ASPM, DTL	5.21E-08	5.28E-04
94	CDKN3, KIF20A, RRM2, ASPM, PLK1	2.79E-08	2.18E-03
95	CDKN3, KIF20A, RRM2, ASPM, CDK1	8.29E-08	1.45E-03
96	CDKN3, KIF20A, RRM2, NUSAP1, DTL	4.25E-08	5.17E-04
97	CDKN3, KIF20A, RRM2, NUSAP1, PLK1	3.12E-08	2.75E-03
98	CDKN3, KIF20A, RRM2, NUSAP1, CDK1	8.31E-08	1.64E-03
99	CDKN3, KIF20A, RRM2, DTL, PLK1	6.36E-08	3.04E-03
100	CDKN3, KIF20A, RRM2, DTL, CDK1	5.00E-08	1.45E-03
101	CDKN3, KIF20A, RRM2, PLK1, CDK1	1.04E-07	8.46E-03
102	CDKN3, KIF20A, ASPM, NUSAP1, DTL	1.02E-07	6.98E-04
103	CDKN3, KIF20A, ASPM, NUSAP1, PLK1	3.59E-08	2.31E-03
104	CDKN3, KIF20A, ASPM, NUSAP1, CDK1	1.56E-07	1.87E-03
105	CDKN3, KIF20A,	9.36E-08	2.88E-03

Sub-Panel #	Genes in Sub-Panel	uni pval	multi pval
	ASPM, DTL, PLK1		
106	CDKN3, KIF20A, ASPM, DTL, CDK1	1.18E-07	1.78E-03
107	CDKN3, KIF20A, ASPM, PLK1, CDK1	1.25E-07	7.29E-03
108	CDKN3, KIF20A, NUSAP1, DTL, PLK1	7.06E-08	3.01E-03
109	CDKN3, KIF20A, NUSAP1, DTL, CDK1	9.74E-08	1.95E-03
110	CDKN3, KIF20A, NUSAP1, PLK1, CDK1	1.13E-07	8.44E-03
111	CDKN3, KIF20A, DTL, PLK1, CDK1	1.01E-07	7.80E-03
112	CDKN3, RRM2, ASPM, NUSAP1, DTL	6.86E-08	3.36E-04
113	CDKN3, RRM2, ASPM, NUSAP1, PLK1	3.92E-08	1.51E-03
114	CDKN3, RRM2, ASPM, NUSAP1, CDK1	1.04E-07	9.23E-04
115	CDKN3, RRM2, ASPM, DTL, PLK1	9.00E-08	1.88E-03
116	CDKN3, RRM2, ASPM, DTL, CDK1	7.16E-08	9.01E-04
117	CDKN3, RRM2, ASPM, PLK1, CDK1	1.09E-07	4.59E-03
118	CDKN3, RRM2, NUSAP1, DTL, PLK1	8.70E-08	1.99E-03
119	CDKN3, RRM2, NUSAP1, DTL, CDK1	6.85E-08	8.66E-04
120	CDKN3, RRM2, NUSAP1, PLK1, CDK1	1.21E-07	5.33E-03
121	CDKN3, RRM2, DTL, PLK1, CDK1	1.01E-07	4.94E-03
122	CDKN3, ASPM, NUSAP1, DTL, PLK1	9.54E-08	1.61E-03
123	CDKN3, ASPM, NUSAP1, DTL, CDK1	1.06E-07	8.78E-04
124	CDKN3, ASPM, NUSAP1, PLK1, CDK1	1.10E-07	3.97E-03
125	CDKN3, ASPM, DTL, PLK1, CDK1	1.07E-07	3.82E-03
126	CDKN3, NUSAP1, DTL, PLK1, CDK1	9.66E-08	4.27E-03
127	SKA1, BUB1B, KIF20A, RRM2, ASPM	4.89E-08	4.34E-04
128	SKA1, BUB1B, KIF20A, RRM2, NUSAP1	4.38E-08	4.81E-04
129	SKA1, BUB1B, KIF20A, RRM2, DTL	3.86E-08	3.36E-04
130	SKA1, BUB1B, KIF20A,	3.27E-08	1.77E-03

Sub-Panel #	Genes in Sub-Panel	uni pval	multi pval
	RRM2, PLK1		
131	SKA1, BUB1B, KIF20A, RRM2, CDK1	6.17E-08	8.30E-04
132	SKA1, BUB1B, KIF20A, ASPM, NUSAP1	9.68E-08	5.81E-04
133	SKA1, BUB1B, KIF20A, ASPM, DTL	1.15E-07	4.90E-04
134	SKA1, BUB1B, KIF20A, ASPM, PLK1	5.76E-08	1.84E-03
135	SKA1, BUB1B, KIF20A, ASPM, CDK1	1.45E-07	1.03E-03
136	SKA1, BUB1B, KIF20A, NUSAP1, DTL	7.03E-08	4.28E-04
137	SKA1, BUB1B, KIF20A, NUSAP1, PLK1	4.76E-08	2.06E-03
138	SKA1, BUB1B, KIF20A, NUSAP1, CDK1	1.08E-07	1.05E-03
139	SKA1, BUB1B, KIF20A, DTL, PLK1	9.64E-08	2.09E-03
140	SKA1, BUB1B, KIF20A, DTL, CDK1	4.86E-08	6.41E-04
141	SKA1, BUB1B, KIF20A, PLK1, CDK1	1.19E-07	4.46E-03
142	SKA1, BUB1B, RRM2, ASPM, NUSAP1	7.83E-08	3.52E-04
143	SKA1, BUB1B, RRM2, ASPM, DTL	7.87E-08	2.82E-04
144	SKA1, BUB1B, RRM2, ASPM, PLK1	5.31E-08	1.17E-03
145	SKA1, BUB1B, RRM2, ASPM, CDK1	1.01E-07	6.17E-04
146	SKA1, BUB1B, RRM2, NUSAP1, DTL	5.51E-08	2.21E-04
147	SKA1, BUB1B, RRM2, NUSAP1, PLK1	5.26E-08	1.33E-03
148	SKA1, BUB1B, RRM2, NUSAP1, CDK1	8.51E-08	5.66E-04
149	SKA1, BUB1B, RRM2, DTL, PLK1	9.16E-08	1.29E-03
150	SKA1, BUB1B, RRM2, DTL, CDK1	3.31E-08	3.27E-04
151	SKA1, BUB1B, RRM2, PLK1, CDK1	1.03E-07	2.72E-03
152	SKA1, BUB1B, ASPM, NUSAP1, DTL	1.26E-07	2.98E-04
153	SKA1, BUB1B, ASPM, NUSAP1, PLK1	7.99E-08	1.32E-03
154	SKA1, BUB1B, ASPM, NUSAP1, CDK1	1.53E-07	6.45E-04
155	SKA1, BUB1B, ASPM,	1.75E-07	1.47E-03

Sub-Panel #	Genes in Sub-Panel	uni pval	multi pval
	DTL, PLK1		
156	SKA1, BUB1B, ASPM, DTL, CDK1	7.62E-08	4.17E-04
157	SKA1, BUB1B, ASPM, PLK1, CDK1	1.64E-07	2.78E-03
158	SKA1, BUB1B, NUSAP1, DTL, PLK1	1.22E-07	1.35E-03
159	SKA1, BUB1B, NUSAP1, DTL, CDK1	5.14E-08	3.55E-04
160	SKA1, BUB1B, NUSAP1, PLK1, CDK1	1.30E-07	2.83E-03
161	SKA1, BUB1B, DTL, PLK1, CDK1	1.03E-07	2.24E-03
162	SKA1, KIF20A, RRM2, ASPM, NUSAP1	8.55E-08	5.06E-04
163	SKA1, KIF20A, RRM2, ASPM, DTL	7.75E-08	3.80E-04
164	SKA1, KIF20A, RRM2, ASPM, PLK1	6.11E-08	1.78E-03
165	SKA1, KIF20A, RRM2, ASPM, CDK1	1.23E-07	9.39E-04
166	SKA1, KIF20A, RRM2, NUSAP1, DTL	6.37E-08	3.72E-04
167	SKA1, KIF20A, RRM2, NUSAP1, PLK1	6.77E-08	2.18E-03
168	SKA1, KIF20A, RRM2, NUSAP1, CDK1	1.24E-07	1.06E-03
169	SKA1, KIF20A, RRM2, DTL, PLK1	1.05E-07	2.03E-03
170	SKA1, KIF20A, RRM2, DTL, CDK1	5.04E-08	6.54E-04
171	SKA1, KIF20A, RRM2, PLK1, CDK1	1.60E-07	4.82E-03
172	SKA1, KIF20A, ASPM, NUSAP1, DTL	1.35E-07	4.66E-04
173	SKA1, KIF20A, ASPM, NUSAP1, PLK1	8.61E-08	2.00E-03
174	SKA1, KIF20A, ASPM, NUSAP1, CDK1	2.07E-07	1.14E-03
175	SKA1, KIF20A, ASPM, DTL, PLK1	1.70E-07	2.13E-03
176	SKA1, KIF20A, ASPM, DTL, CDK1	1.05E-07	7.69E-04
177	SKA1, KIF20A, ASPM, PLK1, CDK1	2.13E-07	4.60E-03
178	SKA1, KIF20A, NUSAP1, DTL, PLK1	1.28E-07	2.13E-03
179	SKA1, KIF20A, NUSAP1, DTL, CDK1	8.56E-08	8.19E-04
180	SKA1, KIF20A,	1.92E-07	5.09E-03

Sub-Panel #	Genes in Sub-Panel	uni pval	multi pval
	NUSAP1, PLK1, CDK1		
181	SKA1, KIF20A, DTL, PLK1, CDK1	1.52E-07	4.24E-03
182	SKA1, RRM2, ASPM, NUSAP1, DTL	1.16E-07	2.62E-04
183	SKA1, RRM2, ASPM, NUSAP1, PLK1	1.01E-07	1.35E-03
184	SKA1, RRM2, ASPM, NUSAP1, CDK1	1.79E-07	6.68E-04
185	SKA1, RRM2, ASPM, DTL, PLK1	1.72E-07	1.39E-03
186	SKA1, RRM2, ASPM, DTL, CDK1	8.13E-08	4.37E-04
187	SKA1, RRM2, ASPM, PLK1, CDK1	2.02E-07	2.95E-03
188	SKA1, RRM2, NUSAP1, DTL, PLK1	1.65E-07	1.42E-03
189	SKA1, RRM2, NUSAP1, DTL, CDK1	8.10E-08	4.39E-04
190	SKA1, RRM2, NUSAP1, PLK1, CDK1	2.21E-07	3.32E-03
191	SKA1, RRM2, DTL, PLK1, CDK1	1.62E-07	2.70E-03
192	SKA1, ASPM, NUSAP1, DTL, PLK1	2.22E-07	1.40E-03
193	SKA1, ASPM, NUSAP1, DTL, CDK1	1.19E-07	4.49E-04
194	SKA1, ASPM, NUSAP1, PLK1, CDK1	2.46E-07	2.96E-03
195	SKA1, ASPM, DTL, PLK1, CDK1	2.10E-07	2.54E-03
196	SKA1, NUSAP1, DTL, PLK1, CDK1	1.90E-07	2.74E-03
197	BUB1B, KIF20A, RRM2, ASPM, NUSAP1	6.29E-08	7.50E-04
198	BUB1B, KIF20A, RRM2, ASPM, DTL	1.02E-07	8.13E-04
199	BUB1B, KIF20A, RRM2, ASPM, PLK1	4.73E-08	3.09E-03
200	BUB1B, KIF20A, RRM2, ASPM, CDK1	1.29E-07	1.90E-03
201	BUB1B, KIF20A, RRM2, NUSAP1, DTL	7.27E-08	7.59E-04
202	BUB1B, KIF20A, RRM2, NUSAP1, PLK1	4.55E-08	3.73E-03
203	BUB1B, KIF20A, RRM2, NUSAP1, CDK1	1.11E-07	2.02E-03
204	BUB1B, KIF20A, RRM2, DTL, PLK1	1.00E-07	3.94E-03
205	BUB1B, KIF20A,	7.94E-08	1.85E-03

Sub-Panel #	Genes in Sub-Panel	uni pval	multi pval
	RRM2, DTL, CDK1		
206	BUB1B, KIF20A, RRM2, PLK1, CDK1	1.31E-07	9.62E-03
207	BUB1B, KIF20A, ASPM, NUSAP1, DTL	1.97E-07	1.04E-03
208	BUB1B, KIF20A, ASPM, NUSAP1, PLK1	6.26E-08	3.26E-03
209	BUB1B, KIF20A, ASPM, NUSAP1, CDK1	2.41E-07	2.39E-03
210	BUB1B, KIF20A, ASPM, DTL, PLK1	1.71E-07	3.84E-03
211	BUB1B, KIF20A, ASPM, DTL, CDK1	2.12E-07	2.33E-03
212	BUB1B, KIF20A, ASPM, PLK1, CDK1	1.86E-07	8.58E-03
213	BUB1B, KIF20A, NUSAP1, DTL, PLK1	1.16E-07	3.90E-03
214	BUB1B, KIF20A, NUSAP1, DTL, CDK1	1.55E-07	2.42E-03
215	BUB1B, KIF20A, NUSAP1, PLK1, CDK1	1.48E-07	9.52E-03
216	BUB1B, KIF20A, DTL, PLK1, CDK1	1.56E-07	9.03E-03
217	BUB1B, RRM2, ASPM, NUSAP1, DTL	1.22E-07	5.29E-04
218	BUB1B, RRM2, ASPM, NUSAP1, PLK1	6.11E-08	2.16E-03
219	BUB1B, RRM2, ASPM, NUSAP1, CDK1	1.46E-07	1.23E-03
220	BUB1B, RRM2, ASPM, DTL, PLK1	1.48E-07	2.53E-03
221	BUB1B, RRM2, ASPM, DTL, CDK1	1.19E-07	1.23E-03
222	BUB1B, RRM2, ASPM, PLK1, CDK1	1.46E-07	5.46E-03
223	BUB1B, RRM2, NUSAP1, DTL, PLK1	1.22E-07	2.55E-03
224	BUB1B, RRM2, NUSAP1, DTL, CDK1	9.41E-08	1.09E-03
225	BUB1B, RRM2, NUSAP1, PLK1, CDK1	1.37E-07	6.00E-03
226	BUB1B, RRM2, DTL, PLK1, CDK1	1.33E-07	5.69E-03
227	BUB1B, ASPM, NUSAP1, DTL, PLK1	1.64E-07	2.20E-03
228	BUB1B, ASPM, NUSAP1, DTL, CDK1	1.77E-07	1.18E-03
229	BUB1B, ASPM, NUSAP1, PLK1, CDK1	1.55E-07	4.75E-03
230	BUB1B, ASPM, DTL,	1.74E-07	4.66E-03

Sub-Panel #	Genes in Sub-Panel	uni pval	multi pval
	PLK1, CDK1		
231	BUB1B, NUSAP1, DTL, PLK1, CDK1	1.35E-07	4.95E-03
232	KIF20A, RRM2, ASPM, NUSAP1, DTL	1.34E-07	8.68E-04
233	KIF20A, RRM2, ASPM, NUSAP1, PLK1	7.99E-08	3.69E-03
234	KIF20A, RRM2, ASPM, NUSAP1, CDK1	2.10E-07	2.33E-03
235	KIF20A, RRM2, ASPM, DTL, PLK1	1.69E-07	4.06E-03
236	KIF20A, RRM2, ASPM, DTL, CDK1	1.64E-07	2.29E-03
237	KIF20A, RRM2, ASPM, PLK1, CDK1	2.31E-07	1.01E-02
238	KIF20A, RRM2, NUSAP1, DTL, PLK1	1.58E-07	4.52E-03
239	KIF20A, RRM2, NUSAP1, DTL, CDK1	1.68E-07	2.66E-03
240	KIF20A, RRM2, NUSAP1, PLK1, CDK1	2.52E-07	1.21E-02
241	KIF20A, RRM2, DTL, PLK1, CDK1	2.42E-07	1.17E-02

Sub-Panel #	Genes in Sub-Panel	uni pval	multi pval
242	KIF20A, ASPM, NUSAP1, DTL, PLK1	1.93E-07	3.91E-03
243	KIF20A, ASPM, NUSAP1, DTL, CDK1	3.09E-07	2.89E-03
244	KIF20A, ASPM, NUSAP1, PLK1, CDK1	2.56E-07	9.70E-03
245	KIF20A, ASPM, DTL, PLK1, CDK1	2.83E-07	9.69E-03
246	KIF20A, NUSAP1, DTL, PLK1, CDK1	2.59E-07	1.14E-02
247	RRM2, ASPM, NUSAP1, DTL, PLK1	2.11E-07	2.65E-03
248	RRM2, ASPM, NUSAP1, DTL, CDK1	2.08E-07	1.43E-03
249	RRM2, ASPM, NUSAP1, PLK1, CDK1	2.52E-07	6.34E-03
250	RRM2, ASPM, DTL, PLK1, CDK1	2.61E-07	6.39E-03
251	RRM2, NUSAP1, DTL, PLK1, CDK1	3.02E-07	7.61E-03
252	ASPM, NUSAP1, DTL, PLK1, CDK1	2.63E-07	5.44E-03

Table 34: Predictive power (both univariate and multivariate) for all 6-gene sub-panels chosen from the top 10 genes (ranked by p-value) of Panel O.

Sub-Panel #	Genes in Sub-Panel	uni pval	multi pval
1	CDKN3, SKA1, BUB1B, KIF20A, RRM2, ASPM	2.60E-08	2.69E-04
2	CDKN3, SKA1, BUB1B, KIF20A, RRM2, NUSAP1	2.28E-08	2.83E-04
3	CDKN3, SKA1, BUB1B, KIF20A, RRM2, DTL	2.58E-08	2.39E-04
4	CDKN3, SKA1, BUB1B, KIF20A, RRM2, PLK1	1.76E-08	9.63E-04
5	CDKN3, SKA1, BUB1B, KIF20A, RRM2, CDK1	3.87E-08	5.21E-04
6	CDKN3, SKA1, BUB1B, KIF20A, ASPM, NUSAP1	4.69E-08	3.50E-04
7	CDKN3, SKA1, BUB1B, KIF20A, ASPM, DTL	6.64E-08	3.41E-04
8	CDKN3, SKA1, BUB1B, KIF20A, ASPM, PLK1	2.97E-08	1.04E-03
9	CDKN3, SKA1, BUB1B, KIF20A, ASPM, CDK1	8.29E-08	6.56E-04

Sub-Panel #	Genes in Sub-Panel	uni pval	multi pval
10	CDKN3, SKA1, BUB1B, KIF20A, NUSAP1, DTL	4.29E-08	2.97E-04
11	CDKN3, SKA1, BUB1B, KIF20A, NUSAP1, PLK1	2.45E-08	1.11E-03
12	CDKN3, SKA1, BUB1B, KIF20A, NUSAP1, CDK1	6.26E-08	6.41E-04
13	CDKN3, SKA1, BUB1B, KIF20A, DTL, PLK1	5.47E-08	1.27E-03
14	CDKN3, SKA1, BUB1B, KIF20A, DTL, CDK1	2.95E-08	4.00E-04
15	CDKN3, SKA1, BUB1B, KIF20A, PLK1, CDK1	6.79E-08	2.53E-03
16	CDKN3, SKA1, BUB1B, RRM2, ASPM, NUSAP1	3.72E-08	2.18E-04
17	CDKN3, SKA1, BUB1B, RRM2, ASPM, DTL	4.62E-08	2.06E-04
18	CDKN3, SKA1, BUB1B, RRM2, ASPM, PLK1	2.63E-08	6.70E-04

Sub-Panel #	Genes in Sub-Panel	uni pval	multi pval
19	CDKN3, SKA1, BUB1B, RRM2, ASPM, CDK1	5.84E-08	4.07E-04
20	CDKN3, SKA1, BUB1B, RRM2, NUSAP1, DTL	3.27E-08	1.61E-04
21	CDKN3, SKA1, BUB1B, RRM2, NUSAP1, PLK1	2.48E-08	7.17E-04
22	CDKN3, SKA1, BUB1B, RRM2, NUSAP1, CDK1	4.76E-08	3.61E-04
23	CDKN3, SKA1, BUB1B, RRM2, DTL, PLK1	4.90E-08	7.97E-04
24	CDKN3, SKA1, BUB1B, RRM2, DTL, CDK1	2.01E-08	2.15E-04
25	CDKN3, SKA1, BUB1B, RRM2, PLK1, CDK1	5.67E-08	1.56E-03
26	CDKN3, SKA1, BUB1B, ASPM, NUSAP1, DTL	6.87E-08	2.18E-04
27	CDKN3, SKA1, BUB1B, ASPM, NUSAP1, PLK1	3.77E-08	7.50E-04
28	CDKN3, SKA1, BUB1B, ASPM, NUSAP1, CDK1	8.30E-08	4.25E-04
29	CDKN3, SKA1, BUB1B, ASPM, DTL, PLK1	8.91E-08	9.32E-04
30	CDKN3, SKA1, BUB1B, ASPM, DTL, CDK1	4.22E-08	2.77E-04
31	CDKN3, SKA1, BUB1B, ASPM, PLK1, CDK1	8.88E-08	1.67E-03
32	CDKN3, SKA1, BUB1B, NUSAP1, DTL, PLK1	6.33E-08	8.41E-04
33	CDKN3, SKA1, BUB1B, NUSAP1, DTL, CDK1	2.89E-08	2.30E-04
34	CDKN3, SKA1, BUB1B, NUSAP1, PLK1, CDK1	6.97E-08	1.63E-03
35	CDKN3, SKA1, BUB1B, DTL, PLK1, CDK1	5.16E-08	1.27E-03
36	CDKN3, SKA1, KIF20A, RRM2, ASPM, NUSAP1	4.24E-08	3.01E-04
37	CDKN3, SKA1, KIF20A, RRM2, ASPM, DTL	4.85E-08	2.68E-04
38	CDKN3, SKA1, KIF20A, RRM2, ASPM, PLK1	3.19E-08	9.86E-04
39	CDKN3, SKA1, KIF20A, RRM2, ASPM, CDK1	7.25E-08	5.85E-04
40	CDKN3, SKA1, KIF20A, RRM2, NUSAP1, DTL	3.88E-08	2.52E-04
41	CDKN3, SKA1, KIF20A, RRM2, NUSAP1, PLK1	3.28E-08	1.13E-03
42	CDKN3, SKA1, KIF20A, RRM2, NUSAP1, CDK1	6.79E-08	6.17E-04
43	CDKN3, SKA1, KIF20A, RRM2, DTL, PLK1	5.90E-08	1.20E-03

Sub-Panel #	Genes in Sub-Panel	uni pval	multi pval
44	CDKN3, SKA1, KIF20A, RRM2, DTL, CDK1	2.98E-08	3.87E-04
45	CDKN3, SKA1, KIF20A, RRM2, PLK1, CDK1	8.66E-08	2.62E-03
46	CDKN3, SKA1, KIF20A, ASPM, NUSAP1, DTL	7.80E-08	3.23E-04
47	CDKN3, SKA1, KIF20A, ASPM, NUSAP1, PLK1	4.34E-08	1.11E-03
48	CDKN3, SKA1, KIF20A, ASPM, NUSAP1, CDK1	1.13E-07	6.97E-04
49	CDKN3, SKA1, KIF20A, ASPM, DTL, PLK1	9.41E-08	1.32E-03
50	CDKN3, SKA1, KIF20A, ASPM, DTL, CDK1	5.90E-08	4.70E-04
51	CDKN3, SKA1, KIF20A, ASPM, PLK1, CDK1	1.18E-07	2.63E-03
52	CDKN3, SKA1, KIF20A, NUSAP1, DTL, PLK1	7.14E-08	1.27E-03
53	CDKN3, SKA1, KIF20A, NUSAP1, DTL, CDK1	4.67E-08	4.71E-04
54	CDKN3, SKA1, KIF20A, NUSAP1, PLK1, CDK1	1.02E-07	2.77E-03
55	CDKN3, SKA1, KIF20A, DTL, PLK1, CDK1	7.67E-08	2.24E-03
56	CDKN3, SKA1, RRM2, ASPM, NUSAP1, DTL	6.38E-08	1.88E-04
57	CDKN3, SKA1, RRM2, ASPM, NUSAP1, PLK1	4.61E-08	7.40E-04
58	CDKN3, SKA1, RRM2, ASPM, NUSAP1, CDK1	9.29E-08	4.18E-04
59	CDKN3, SKA1, RRM2, ASPM, DTL, PLK1	8.90E-08	8.62E-04
60	CDKN3, SKA1, RRM2, ASPM, DTL, CDK1	4.43E-08	2.75E-04
61	CDKN3, SKA1, RRM2, ASPM, PLK1, CDK1	1.06E-07	1.70E-03
62	CDKN3, SKA1, RRM2, NUSAP1, DTL, PLK1	7.98E-08	8.38E-04
63	CDKN3, SKA1, RRM2, NUSAP1, DTL, CDK1	4.01E-08	2.57E-04
64	CDKN3, SKA1, RRM2, NUSAP1, PLK1, CDK1	1.05E-07	1.79E-03
65	CDKN3, SKA1, RRM2, DTL, PLK1, CDK1	7.42E-08	1.43E-03
66	CDKN3, SKA1, ASPM, NUSAP1, DTL, PLK1	1.12E-07	8.82E-04
67	CDKN3, SKA1, ASPM, NUSAP1, DTL, CDK1	6.06E-08	2.82E-04
68	CDKN3, SKA1, ASPM, NUSAP1, PLK1, CDK1	1.26E-07	1.72E-03

Sub-Panel #	Genes in Sub-Panel	uni pval	multi pval
69	CDKN3, SKA1, ASPM, DTL, PLK1, CDK1	1.00E-07	1.43E-03
70	CDKN3, SKA1, NUSAP1, DTL, PLK1, CDK1	8.59E-08	1.45E-03
71	CDKN3, BUB1B, KIF20A, RRM2, ASPM, NUSAP1	2.84E-08	4.25E-04
72	CDKN3, BUB1B, KIF20A, RRM2, ASPM, DTL	5.19E-08	5.13E-04
73	CDKN3, BUB1B, KIF20A, RRM2, ASPM, PLK1	2.33E-08	1.71E-03
74	CDKN3, BUB1B, KIF20A, RRM2, ASPM, CDK1	6.61E-08	1.09E-03
75	CDKN3, BUB1B, KIF20A, RRM2, NUSAP1, DTL	3.80E-08	4.71E-04
76	CDKN3, BUB1B, KIF20A, RRM2, NUSAP1, PLK1	2.18E-08	1.95E-03
77	CDKN3, BUB1B, KIF20A, RRM2, NUSAP1, CDK1	5.58E-08	1.12E-03
78	CDKN3, BUB1B, KIF20A, RRM2, DTL, PLK1	5.18E-08	2.29E-03
79	CDKN3, BUB1B, KIF20A, RRM2, DTL, CDK1	3.89E-08	9.89E-04
80	CDKN3, BUB1B, KIF20A, RRM2, PLK1, CDK1	6.84E-08	5.20E-03
81	CDKN3, BUB1B, KIF20A, ASPM, NUSAP1, DTL	9.23E-08	6.46E-04
82	CDKN3, BUB1B, KIF20A, ASPM, NUSAP1, PLK1	3.01E-08	1.81E-03
83	CDKN3, BUB1B, KIF20A, ASPM, NUSAP1, CDK1	1.14E-07	1.35E-03
84	CDKN3, BUB1B, KIF20A, ASPM, DTL, PLK1	8.44E-08	2.32E-03
85	CDKN3, BUB1B, KIF20A, ASPM, DTL, CDK1	9.32E-08	1.26E-03
86	CDKN3, BUB1B, KIF20A, ASPM, PLK1,	9.61E-08	4.85E-03

Sub-Panel #	Genes in Sub-Panel	uni pval	multi pval
	CDK1		
87	CDKN3, BUB1B, KIF20A, NUSAP1, DTL, PLK1	5.97E-08	2.30E-03
88	CDKN3, BUB1B, KIF20A, NUSAP1, DTL, CDK1	6.90E-08	1.26E-03
89	CDKN3, BUB1B, KIF20A, NUSAP1, PLK1, CDK1	7.68E-08	5.17E-03
90	CDKN3, BUB1B, KIF20A, DTL, PLK1, CDK1	7.19E-08	4.73E-03
91	CDKN3, BUB1B, RRM2, ASPM, NUSAP1, DTL	5.93E-08	3.49E-04
92	CDKN3, BUB1B, RRM2, ASPM, NUSAP1, PLK1	2.82E-08	1.21E-03
93	CDKN3, BUB1B, RRM2, ASPM, NUSAP1, CDK1	7.15E-08	7.33E-04
94	CDKN3, BUB1B, RRM2, ASPM, DTL, PLK1	7.22E-08	1.56E-03
95	CDKN3, BUB1B, RRM2, ASPM, DTL, CDK1	5.54E-08	7.01E-04
96	CDKN3, BUB1B, RRM2, ASPM, PLK1, CDK1	7.56E-08	3.16E-03
97	CDKN3, BUB1B, RRM2, NUSAP1, DTL, PLK1	5.85E-08	1.52E-03
98	CDKN3, BUB1B, RRM2, NUSAP1, DTL, CDK1	4.25E-08	6.03E-04
99	CDKN3, BUB1B, RRM2, NUSAP1, PLK1, CDK1	6.77E-08	3.31E-03
100	CDKN3, BUB1B, RRM2, DTL, PLK1, CDK1	6.01E-08	3.03E-03
101	CDKN3, BUB1B, ASPM, NUSAP1, DTL, PLK1	7.94E-08	1.40E-03
102	CDKN3, BUB1B, ASPM, NUSAP1, DTL, CDK1	7.68E-08	6.76E-04
103	CDKN3, BUB1B, ASPM, NUSAP1, PLK1, CDK1	7.99E-08	2.80E-03
104	CDKN3, BUB1B, ASPM, DTL, PLK1, CDK1	7.89E-08	2.64E-03
105	CDKN3, BUB1B, NUSAP1, DTL, PLK1, CDK1	6.09E-08	2.68E-03
106	CDKN3, KIF20A, RRM2, ASPM, NUSAP1, DTL	6.68E-08	5.30E-04
107	CDKN3, KIF20A, RRM2, ASPM, NUSAP1, PLK1	3.76E-08	1.96E-03
108	CDKN3, KIF20A, RRM2, ASPM, NUSAP1, CDK1	9.99E-08	1.26E-03

Sub-Panel #	Genes in Sub-Panel	uni pval	multi pval
109	CDKN3, KIF20A, RRM2, ASPM, DTL, PLK1	8.62E-08	2.38E-03
110	CDKN3, KIF20A, RRM2, ASPM, DTL, CDK1	7.53E-08	1.20E-03
111	CDKN3, KIF20A, RRM2, ASPM, PLK1, CDK1	1.17E-07	5.46E-03
112	CDKN3, KIF20A, RRM2, NUSAP1, DTL, PLK1	7.70E-08	2.52E-03
113	CDKN3, KIF20A, RRM2, NUSAP1, DTL, CDK1	7.10E-08	1.30E-03
114	CDKN3, KIF20A, RRM2, NUSAP1, PLK1, CDK1	1.18E-07	6.18E-03
115	CDKN3, KIF20A, RRM2, DTL, PLK1, CDK1	1.04E-07	5.79E-03
116	CDKN3, KIF20A, ASPM, NUSAP1, DTL, PLK1	9.78E-08	2.33E-03
117	CDKN3, KIF20A, ASPM, NUSAP1, DTL, CDK1	1.29E-07	1.47E-03
118	CDKN3, KIF20A, ASPM, NUSAP1, PLK1, CDK1	1.29E-07	5.31E-03
119	CDKN3, KIF20A, ASPM, DTL, PLK1, CDK1	1.27E-07	5.09E-03
120	CDKN3, KIF20A, NUSAP1, DTL, PLK1, CDK1	1.11E-07	5.65E-03
121	CDKN3, RRM2, ASPM, NUSAP1, DTL, PLK1	9.89E-08	1.59E-03
122	CDKN3, RRM2, ASPM, NUSAP1, DTL, CDK1	8.63E-08	7.62E-04
123	CDKN3, RRM2, ASPM, NUSAP1, PLK1, CDK1	1.20E-07	3.51E-03
124	CDKN3, RRM2, ASPM, DTL, PLK1, CDK1	1.13E-07	3.39E-03
125	CDKN3, RRM2, NUSAP1, DTL, PLK1, CDK1	1.16E-07	3.76E-03
126	CDKN3, ASPM, NUSAP1, DTL, PLK1, CDK1	1.13E-07	2.93E-03
127	SKA1, BUB1B, KIF20A, RRM2, ASPM, NUSAP1	6.50E-08	4.76E-04
128	SKA1, BUB1B, KIF20A, RRM2, ASPM, DTL	7.76E-08	4.13E-04
129	SKA1, BUB1B, KIF20A, RRM2, ASPM, PLK1	4.75E-08	1.46E-03
130	SKA1, BUB1B, KIF20A, RRM2, ASPM, CDK1	9.88E-08	7.90E-04
131	SKA1, BUB1B, KIF20A, RRM2, NUSAP1, DTL	5.74E-08	3.79E-04
132	SKA1, BUB1B, KIF20A, RRM2, NUSAP1, PLK1	4.47E-08	1.64E-03

Sub-Panel #	Genes in Sub-Panel	uni pval	multi pval
133	SKA1, BUB1B, KIF20A, RRM2, NUSAP1, CDK1	8.44E-08	8.05E-04
134	SKA1, BUB1B, KIF20A, RRM2, DTL, PLK1	8.32E-08	1.68E-03
135	SKA1, BUB1B, KIF20A, RRM2, DTL, CDK1	4.18E-08	5.29E-04
136	SKA1, BUB1B, KIF20A, RRM2, PLK1, CDK1	1.05E-07	3.26E-03
137	SKA1, BUB1B, KIF20A, ASPM, NUSAP1, DTL	1.26E-07	4.90E-04
138	SKA1, BUB1B, KIF20A, ASPM, NUSAP1, PLK1	6.63E-08	1.63E-03
139	SKA1, BUB1B, KIF20A, ASPM, NUSAP1, CDK1	1.56E-07	9.26E-04
140	SKA1, BUB1B, KIF20A, ASPM, DTL, PLK1	1.46E-07	1.85E-03
141	SKA1, BUB1B, KIF20A, ASPM, DTL, CDK1	9.14E-08	6.51E-04
142	SKA1, BUB1B, KIF20A, ASPM, PLK1, CDK1	1.59E-07	3.32E-03
143	SKA1, BUB1B, KIF20A, NUSAP1, DTL, PLK1	1.04E-07	1.76E-03
144	SKA1, BUB1B, KIF20A, NUSAP1, DTL, CDK1	6.71E-08	6.34E-04
145	SKA1, BUB1B, KIF20A, NUSAP1, PLK1, CDK1	1.28E-07	3.42E-03
146	SKA1, BUB1B, KIF20A, DTL, PLK1, CDK1	1.07E-07	2.86E-03
147	SKA1, BUB1B, RRM2, ASPM, NUSAP1, DTL	9.74E-08	3.00E-04
148	SKA1, BUB1B, RRM2, ASPM, NUSAP1, PLK1	6.58E-08	1.12E-03
149	SKA1, BUB1B, RRM2, ASPM, NUSAP1, CDK1	1.21E-07	5.81E-04
150	SKA1, BUB1B, RRM2, ASPM, DTL, PLK1	1.30E-07	1.24E-03
151	SKA1, BUB1B, RRM2, ASPM, DTL, CDK1	6.47E-08	3.99E-04
152	SKA1, BUB1B, RRM2, ASPM, PLK1, CDK1	1.34E-07	2.19E-03
153	SKA1, BUB1B, RRM2, NUSAP1, DTL, PLK1	1.06E-07	1.18E-03
154	SKA1, BUB1B, RRM2, NUSAP1, DTL, CDK1	5.24E-08	3.57E-04
155	SKA1, BUB1B, RRM2, NUSAP1, PLK1, CDK1	1.21E-07	2.24E-03
156	SKA1, BUB1B, RRM2, DTL, PLK1, CDK1	9.44E-08	1.84E-03
157	SKA1, BUB1B, ASPM, NUSAP1, DTL, PLK1	1.68E-07	1.27E-03

Sub-Panel #	Genes in Sub-Panel	uni pval	multi pval
158	SKA1, BUB1B, ASPM, NUSAP1, DTL, CDK1	9.01E-08	4.05E-04
159	SKA1, BUB1B, ASPM, NUSAP1, PLK1, CDK1	1.65E-07	2.22E-03
160	SKA1, BUB1B, ASPM, DTL, PLK1, CDK1	1.45E-07	1.89E-03
161	SKA1, BUB1B, NUSAP1, DTL, PLK1, CDK1	1.14E-07	1.87E-03
162	SKA1, KIF20A, RRM2, ASPM, NUSAP1, DTL	1.02E-07	4.15E-04
163	SKA1, KIF20A, RRM2, ASPM, NUSAP1, PLK1	7.80E-08	1.65E-03
164	SKA1, KIF20A, RRM2, ASPM, NUSAP1, CDK1	1.50E-07	8.81E-04
165	SKA1, KIF20A, RRM2, ASPM, DTL, PLK1	1.41E-07	1.75E-03
166	SKA1, KIF20A, RRM2, ASPM, DTL, CDK1	8.15E-08	6.22E-04
167	SKA1, KIF20A, RRM2, ASPM, PLK1, CDK1	1.80E-07	3.42E-03
168	SKA1, KIF20A, RRM2, NUSAP1, DTL, PLK1	1.25E-07	1.78E-03
169	SKA1, KIF20A, RRM2, NUSAP1, DTL, CDK1	7.59E-08	6.64E-04
170	SKA1, KIF20A, RRM2, NUSAP1, PLK1, CDK1	1.78E-07	3.72E-03
171	SKA1, KIF20A, RRM2, DTL, PLK1, CDK1	1.41E-07	3.18E-03
172	SKA1, KIF20A, ASPM, NUSAP1, DTL, PLK1	1.74E-07	1.80E-03
173	SKA1, KIF20A, ASPM, NUSAP1, DTL, CDK1	1.26E-07	7.23E-04
174	SKA1, KIF20A, ASPM, NUSAP1, PLK1, CDK1	2.14E-07	3.49E-03
175	SKA1, KIF20A, ASPM, DTL, PLK1, CDK1	1.89E-07	3.07E-03
176	SKA1, KIF20A, NUSAP1, DTL, PLK1, CDK1	1.64E-07	3.26E-03
177	SKA1, RRM2, ASPM, NUSAP1, DTL, PLK1	1.85E-07	1.25E-03
178	SKA1, RRM2, ASPM, NUSAP1, DTL, CDK1	1.07E-07	4.38E-04
179	SKA1, RRM2, ASPM, NUSAP1, PLK1, CDK1	2.13E-07	2.39E-03
180	SKA1, RRM2, ASPM, DTL, PLK1, CDK1	1.78E-07	2.07E-03
181	SKA1, RRM2, NUSAP1, DTL, PLK1, CDK1	1.81E-07	2.23E-03
182	SKA1, ASPM, NUSAP1, DTL, PLK1, CDK1	2.10E-07	2.05E-03

Sub-Panel #	Genes in Sub-Panel	uni pval	multi pval
183	BUB1B, KIF20A, RRM2, ASPM, NUSAP1, DTL	1.07E-07	7.41E-04
184	BUB1B, KIF20A, RRM2, ASPM, NUSAP1, PLK1	5.42E-08	2.58E-03
185	BUB1B, KIF20A, RRM2, ASPM, NUSAP1, CDK1	1.36E-07	1.57E-03
186	BUB1B, KIF20A, RRM2, ASPM, DTL, PLK1	1.28E-07	3.00E-03
187	BUB1B, KIF20A, RRM2, ASPM, DTL, CDK1	1.15E-07	1.52E-03
188	BUB1B, KIF20A, RRM2, ASPM, PLK1, CDK1	1.50E-07	6.25E-03
189	BUB1B, KIF20A, RRM2, NUSAP1, DTL, PLK1	1.04E-07	3.07E-03
190	BUB1B, KIF20A, RRM2, NUSAP1, DTL, CDK1	9.73E-08	1.57E-03
191	BUB1B, KIF20A, RRM2, NUSAP1, PLK1, CDK1	1.36E-07	6.83E-03
192	BUB1B, KIF20A, RRM2, DTL, PLK1, CDK1	1.34E-07	6.52E-03
193	BUB1B, KIF20A, ASPM, NUSAP1, DTL, PLK1	1.49E-07	2.92E-03
194	BUB1B, KIF20A, ASPM, NUSAP1, DTL, CDK1	1.97E-07	1.83E-03
195	BUB1B, KIF20A, ASPM, NUSAP1, PLK1, CDK1	1.69E-07	6.04E-03
196	BUB1B, KIF20A, ASPM, DTL, PLK1, CDK1	1.85E-07	5.89E-03
197	BUB1B, KIF20A, NUSAP1, DTL, PLK1, CDK1	1.47E-07	6.32E-03
198	BUB1B, RRM2, ASPM, NUSAP1, DTL, PLK1	1.38E-07	2.00E-03
199	BUB1B, RRM2, ASPM, NUSAP1, DTL, CDK1	1.23E-07	9.77E-04
200	BUB1B, RRM2, ASPM, NUSAP1, PLK1, CDK1	1.44E-07	4.01E-03
201	BUB1B, RRM2, ASPM, DTL, PLK1, CDK1	1.51E-07	3.93E-03
202	BUB1B, RRM2, NUSAP1, DTL, PLK1, CDK1	1.37E-07	4.18E-03
203	BUB1B, ASPM, NUSAP1, DTL, PLK1, CDK1	1.56E-07	3.42E-03
204	KIF20A, RRM2, ASPM, NUSAP1, DTL, PLK1	1.66E-07	3.15E-03
205	KIF20A, RRM2, ASPM, NUSAP1, DTL, CDK1	1.77E-07	1.84E-03
206	KIF20A, RRM2, ASPM, NUSAP1, PLK1, CDK1	2.23E-07	7.07E-03

Sub-Panel #	Genes in Sub-Panel	uni pval	multi pval	Sub-Panel #	Genes in Sub-Panel	uni pval	multi pval
207	KIF20A, RRM2, ASPM, DTL, PLK1, CDK1	2.30E-07	7.02E-03	209	KIF20A, ASPM, NUSAP1, DTL, PLK1, CDK1	2.49E-07	6.68E-03
208	KIF20A, RRM2, NUSAP1, DTL, PLK1, CDK1	2.35E-07	8.05E-03	210	RRM2, ASPM, NUSAP1, DTL, PLK1, CDK1	2.42E-07	4.57E-03

[00169] All publications and patent applications mentioned in the specification are indicative of the level of those skilled in the art to which this invention pertains. All publications and patent applications are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference. The mere mentioning of the publications and patent applications does not necessarily constitute an admission that they are prior art to the instant application.

[00170] Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be obvious that certain changes and modifications may be practiced within the scope of the appended claims.

CLAIMS

What is claimed is:

1. An *in vitro* method of determining the prognosis of a patient having breast cancer or the likelihood of cancer recurrence in said patient, comprising:
 - obtaining a sample from said patient;
 - determining the expression levels of a panel of genes in said sample, wherein said panel comprises at least 4 genes chosen from Table 25 and optionally includes *ABCC5* or *PGR* or both;
 - providing a test value by (1) weighting the determined expression of each of a plurality of test genes selected from said panel of genes with a predefined coefficient, and (2) combining the weighted expression to provide said test value, wherein genes chosen from Table 25 are weighted to contribute at least 25% of the test value and wherein said plurality of test genes optionally includes *ABCC5* or *PGR* or both; and
 - classifying said patient as having a poor or a good prognosis or a an increased or not increased likelihood of cancer recurrence based at least in part on said test value.
2. The method of Claim 1, wherein said plurality of test genes comprises a sub-panel chosen from any of Tables 30 to 34.
3. The method of Claim 1, wherein at least 50%, at least 75%, at least 85% or at least 95% of said plurality of test genes are genes chosen from Table 25.
4. The method of Claim 1, wherein said at least 4 genes are chosen from the top 20, 15, 10, 8, or 6 genes in Table 25.
5. The method of any one of Claims 1 to 4, wherein said determining step comprises:
 - measuring the amount of mRNA in said tumor sample transcribed from each of between 6 and 200 cell-cycle genes; and
 - measuring the amount of mRNA of one or more housekeeping genes in said tumor sample.

6. The method of any one of Claims 1 to 5, wherein the expression of at least 6 genes chosen from Table 25 are determined and weighted.

7. The method of any one of Claims 1 to 6, further comprising comparing said test value to a reference value, wherein the patient is classified as having a poor prognosis if said test value is greater than said reference value.

8. A method of determining the prognosis of a patient having breast cancer or the likelihood of cancer recurrence in said patient, comprising:

obtaining a sample from said patient;
determining the expression levels of a panel of genes in said sample including *ABCC5* or *PGR* or both, and at least 4 cell-cycle genes;
providing a test value by (1) weighting the determined expression of each of a plurality of test genes selected from said panel of genes with a predefined coefficient, and (2) combining the weighted expression to provide said test value, wherein said plurality of test genes includes *ABCC5* or *PGR* or both, and at least 75%, at least 85% or at least 95% of said plurality of test genes are cell-cycle genes; and
determining the prognosis using said test value.

9. The method of Claim 8, wherein the combined weight given to said at least 4 CCGs is at least 40% of the total weight given to the expression of all of said plurality of test genes.

10. The method of Claim 8 or 9, wherein said determining step comprises:
measuring the amount of mRNA in said tumor sample transcribed from each of between 6 and 200 cell-cycle genes; and
measuring the amount of mRNA of one or more housekeeping genes in said tumor sample.

11. The method of Claim 8 or 9 or 10, wherein the expression of at least 8 cell-cycle genes are determined and weighted.

12. The method of any one of Claims 8 to 11, further comprising comparing said test value to a reference value, wherein a correlation to a poor prognosis is made if said test value is greater than said reference value.

13. The method of any one of Claims 8 to 12, wherein the expression levels of from 6 to about 200 cell-cycle genes are measured.

14. A method of treating cancer in a patient having breast cancer, comprising:
determining in a sample from said patient the expression of a panel of genes in said sample including *ABCC5* or *PGR* or both, and at least 4 cell-cycle genes;
providing a test value by (1) weighting the determined expression of each of a plurality of test genes selected from said panel of genes with a predefined coefficient, and (2) combining the weighted expression to provide said test value, wherein said plurality of test genes includes *ABCC5* or *PGR* or both, and at least 60% or 75% of said plurality of test genes are cell-cycle genes, wherein an increased level of expression of said plurality of test genes indicates a poor prognosis and/or an increased likelihood of response to a treatment regimen comprising chemotherapy; and
administering to said patient an anti-cancer drug, or recommending or prescribing or initiating a treatment regimen comprising chemotherapy based at least in part on whether a poor prognosis and/or an increased likelihood of response to a treatment regimen comprising chemotherapy is indicated.

15. A diagnostic kit for prognosing cancer in a patient having breast cancer, comprising, in a compartmentalized container:

a plurality of PCR primer pairs for PCR amplification of at least 8 test genes including *ABCC5* or *PGR* or both, and less than 30% or less than 40% of all of said at least 8 test genes are non-cell-cycle genes; and

one or more PCR primer pairs for PCR amplification of at least one housekeeping gene.

16. A diagnostic kit for prognosing cancer in a patient having breast cancer and/or for determining the likelihood of response to a treatment regimen comprising chemotherapy, comprising, in a compartmentalized container:

a plurality of probes for hybridizing to at least 8 test genes under stringent hybridization conditions, wherein less than 10%, 30% or less than 40% of all of said at least 8 test genes are non-cell-cycle genes;

one or more probes for hybridizing to *ABCC5* or *PGR* or both; and

one or more probes for hybridizing to at least one housekeeping gene.

17. A kit consisting essentially of, in a compartmentalized container:

a first plurality of PCR reaction mixtures for PCR amplification of between 5 or 10 and 300 test genes, wherein at least 50%, at least 60% or at least 80% of said 5 or 10 to 300 test genes are cell-cycle genes, and wherein each reaction mixture comprises a PCR primer pair for PCR amplifying one of said test genes;

a second plurality of PCR reaction mixtures for PCR amplification of *ABCC5* or *PGR* or both;

a third plurality of PCR reaction mixtures for PCR amplification of at least one housekeeping gene.

18. The kit of any one of Claims 15 to 17, wherein cell-cycle genes constitute no less than 10% of the total number of said test genes.

19. The kit of any one of Claims 15 to 17, wherein cell-cycle genes constitute no less than 20% of the total number of said test genes.

20. Use of

(1) a plurality of PCR primer pairs suitable for PCR amplification of at least 4 cell-cycle genes;

(2) PCR primer pairs suitable for PCR amplification of *ABCC5* or *PGR* or both; and

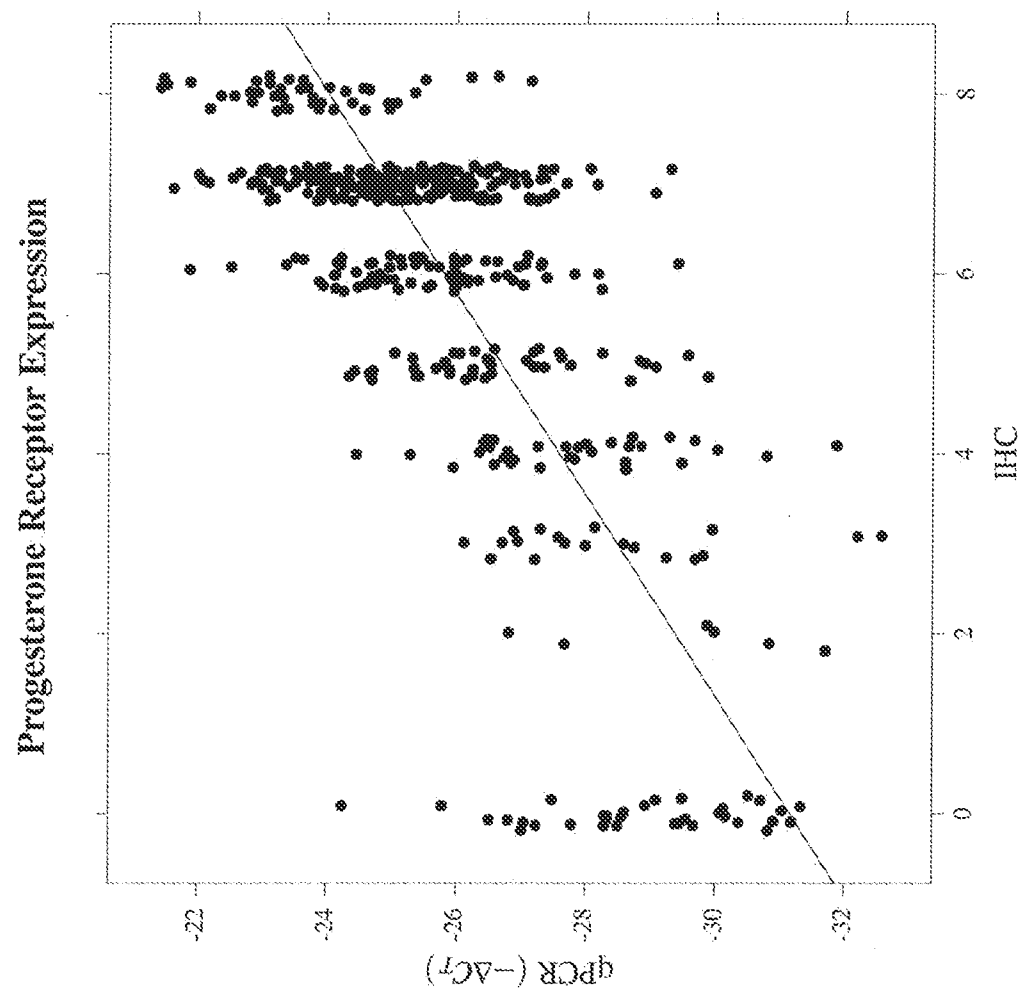
(3) one or more PCR primer pairs suitable for PCR amplification of at least one housekeeping gene,

for the manufacture of a diagnostic product for determining the expression of said test genes in a sample from a patient having breast cancer, to predict the prognosis of cancer in said patient.

21. A system for prognosing cancer in a patient having breast cancer, comprising:
a sample analyzer for determining the expression levels of a panel of genes in a sample including *ABCC5* or *PGR* or both, and at least 4 cell-cycle genes, wherein the sample analyzer contains the sample which is from said patient, or cDNA molecules from mRNA expressed from the panel of genes; and
a first computer program for (a) receiving gene expression data on at least 4 test genes selected from the panel of genes, (b) weighting the determined expression of each of the test genes, and (c) combining the weighted expression to provide a test value, wherein at least 50%, at least at least 75% of at least 4 test genes are cell-cycle genes; and
a second computer program for comparing the test value to one or more reference values each associated with a predetermined prognosis.

22. A system for prognosing cancer in a patient having breast cancer, comprising:
(1) a sample analyzer for determining the expression levels of a panel of genes including *ABCC5* or *PGR* or both, and at least 4 cell-cycle genes in a sample from said patient, wherein the sample analyzer contains the tumor sample, RNA expressed from the panel of genes, or DNA synthesized from such RNA; and
(2) a first computer subsystem programmed for (a) receiving gene expression data on at least 4 test genes selected from the panel of genes, (b) weighting the determined expression of each of the test genes, and (c) combining the weighted expression to provide a test value, wherein the combined weight given to said at least 4 cell-cycle genes is at least 40% of the total weight given to the expression of all of said plurality of test genes; and
(3) a second computer subsystem programmed for comparing the test value to one or more reference values each associated with a predetermined prognosis.

23. The system of Claim 21 or Claim 22, further comprising a display module displaying the comparison between the test value to the one or more reference values, or displaying a result of the comparing step.



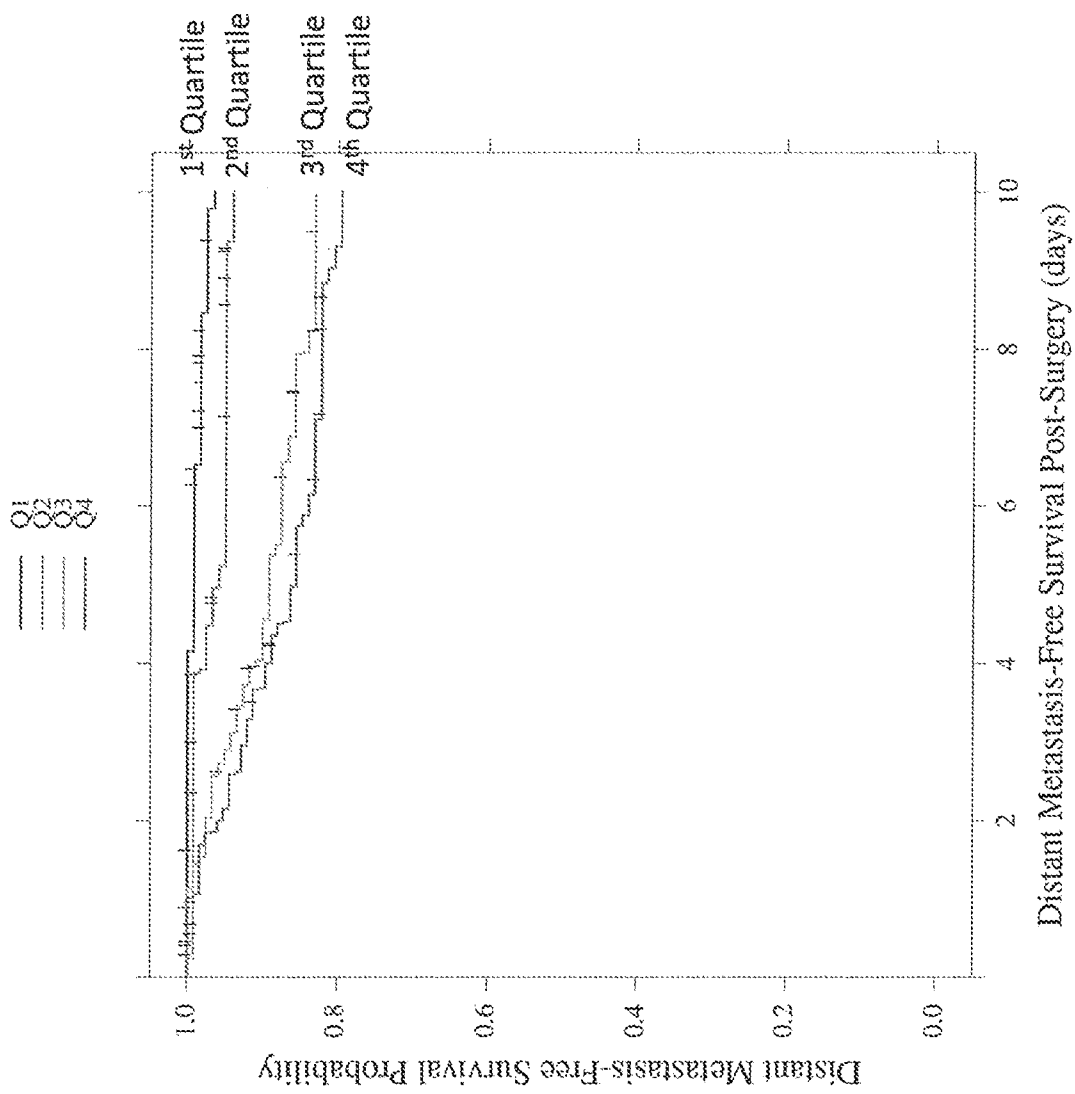


FIGURE 2

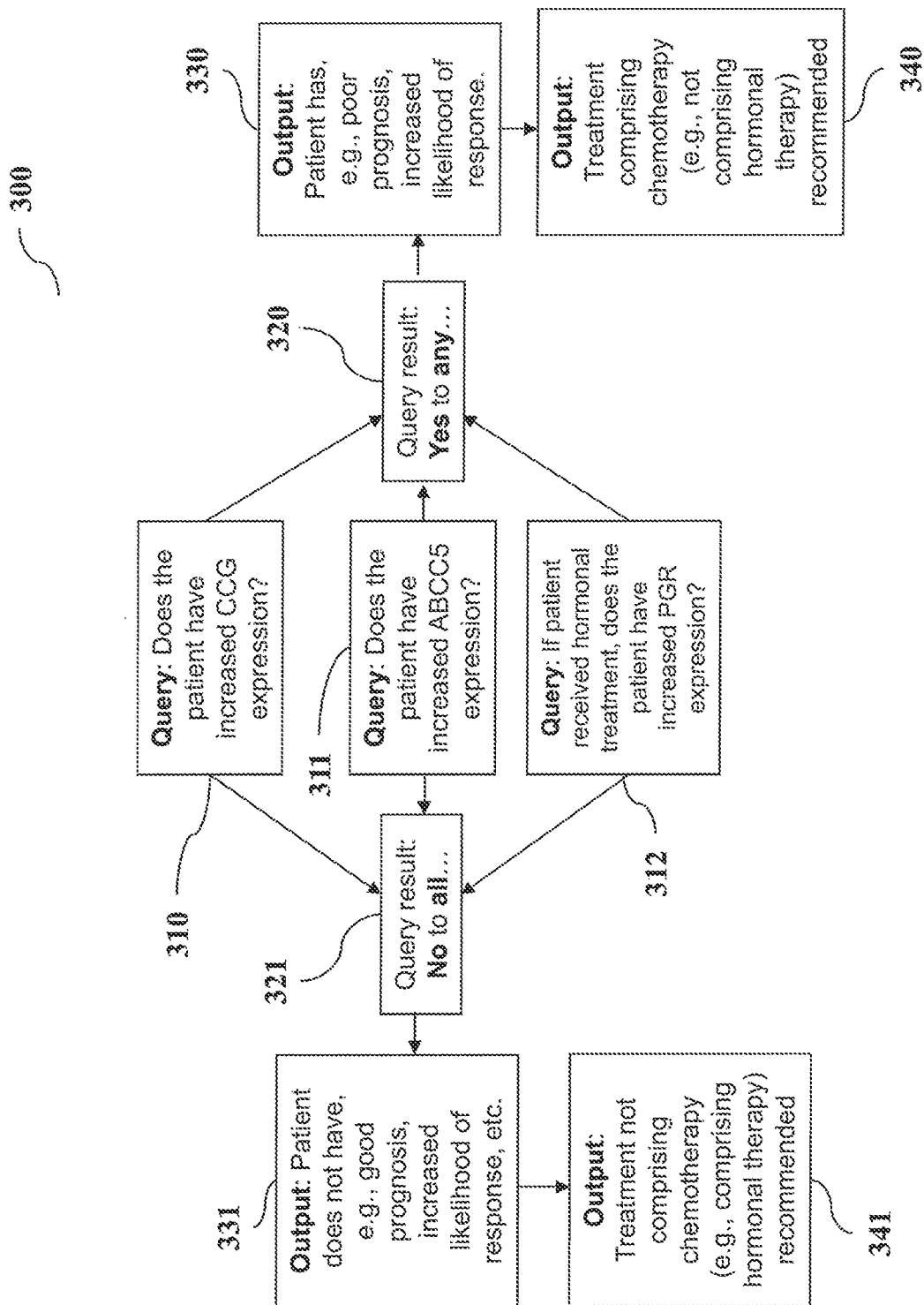


FIGURE 3

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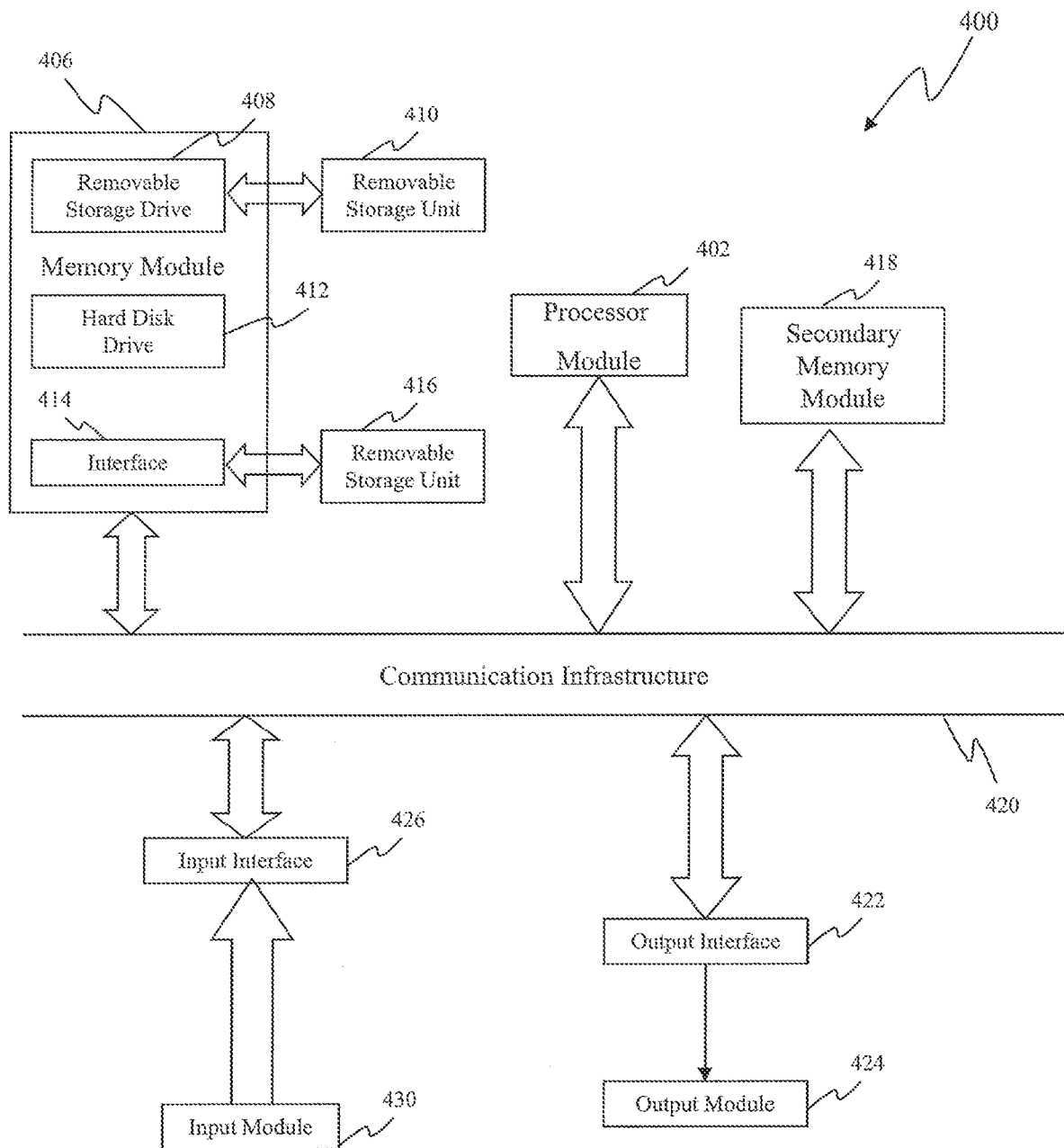


Figure 4

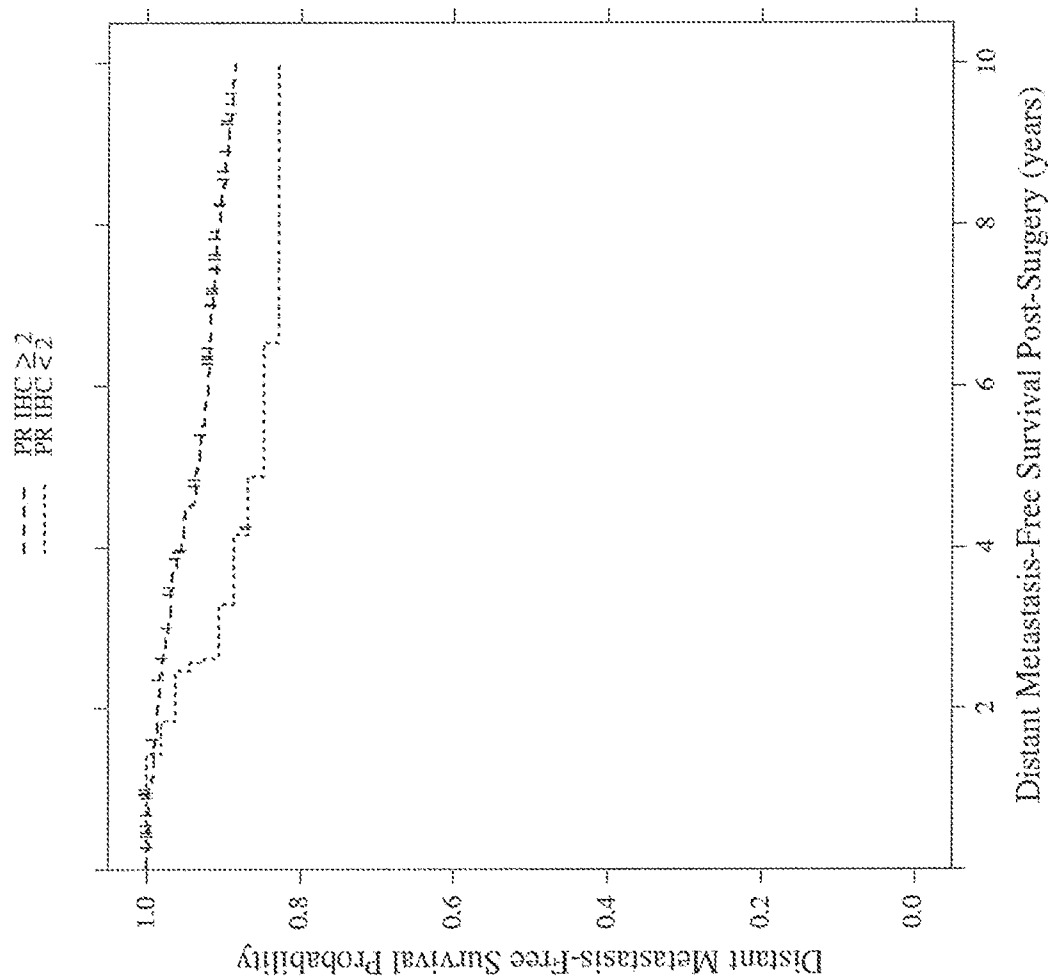


FIGURE 5

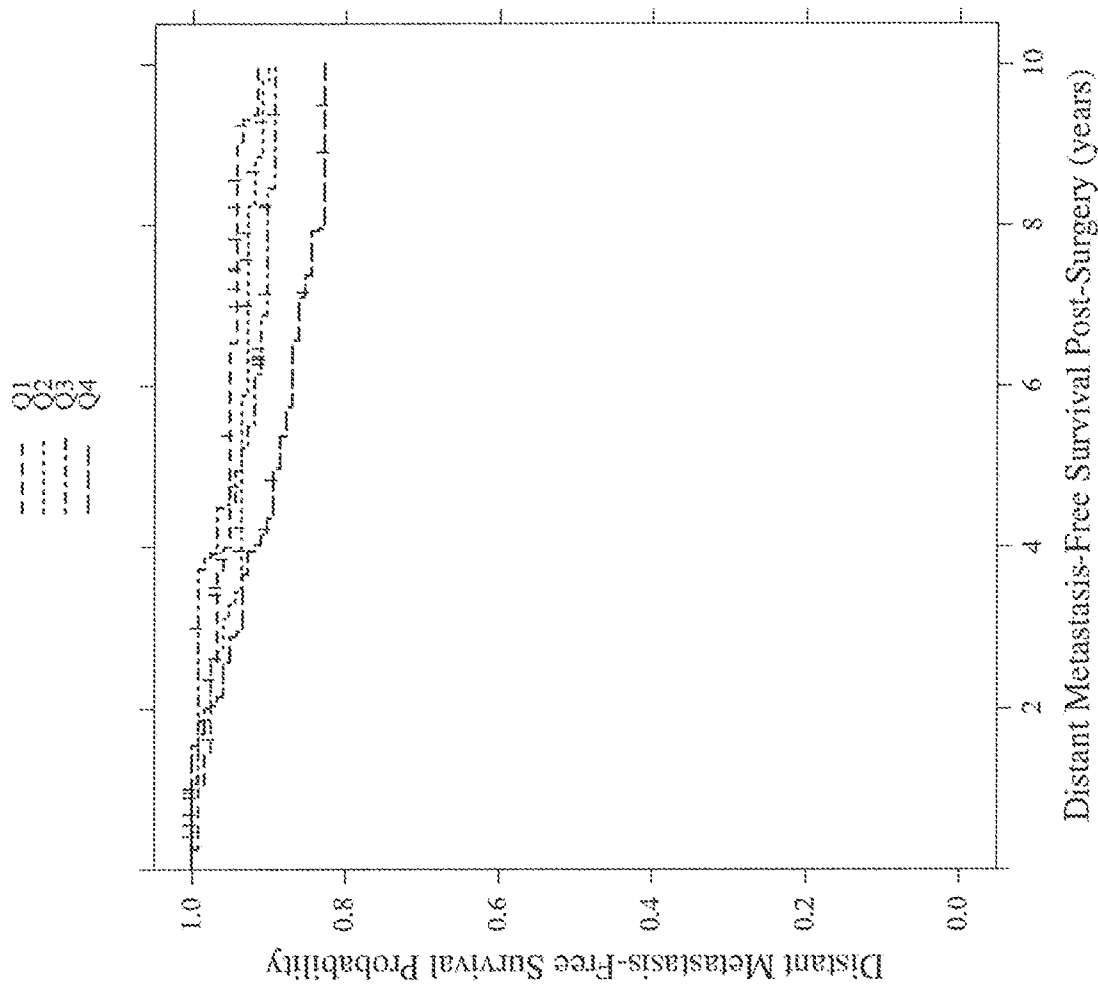


FIGURE 6

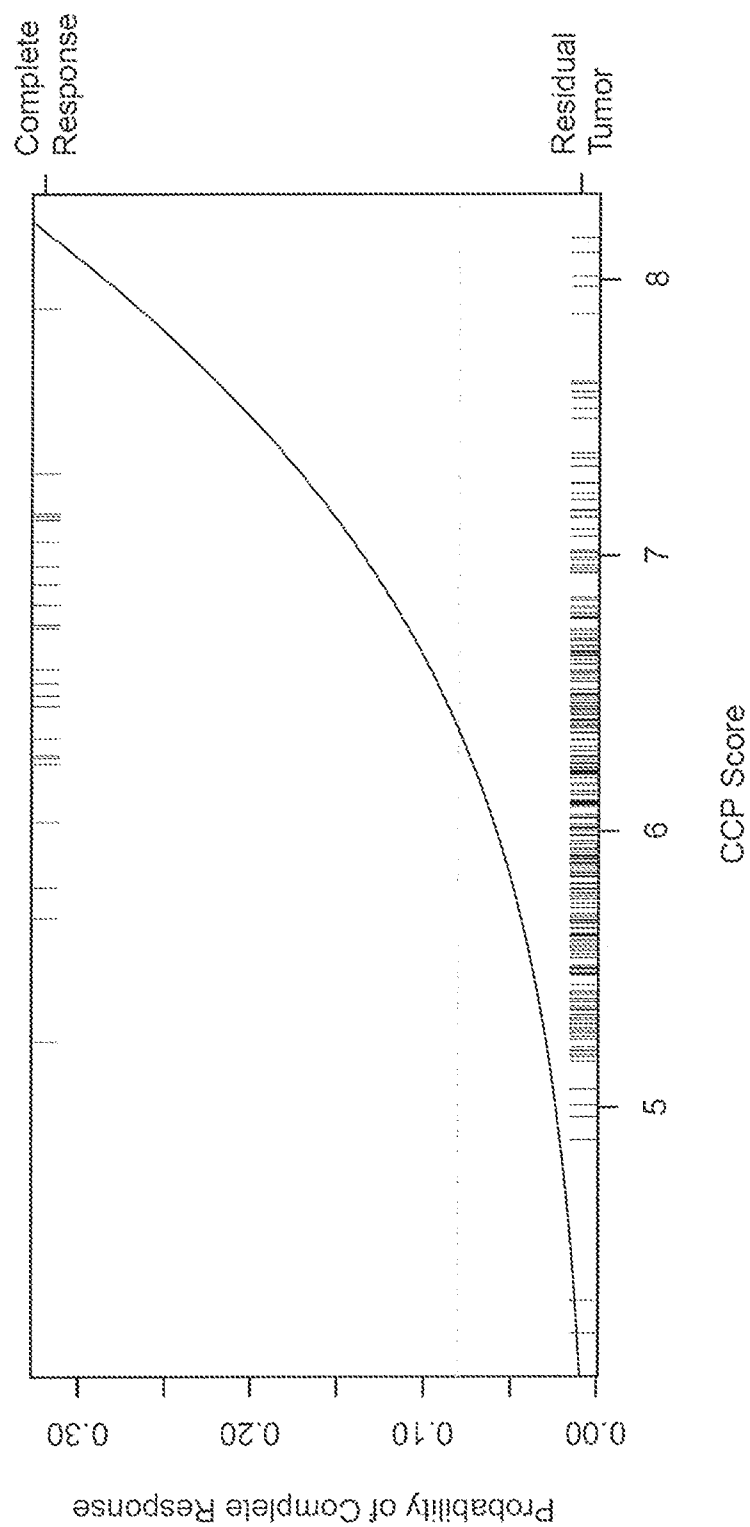


FIGURE 7

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2013/021839**A. CLASSIFICATION OF SUBJECT MATTER****G01N 33/574(2006.01)i, G01N 33/68(2006.01)i, C12Q 1/68(2006.01)i, C12N 15/11(2006.01)i**

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHEDMinimum documentation searched (classification system followed by classification symbols)
G01N 33/574Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
Korean utility models and applications for utility models
Japanese utility models and applications for utility modelsElectronic data base consulted during the international search (name of data base and, where practicable, search terms used)
eKOMPASS(KIPO internal) & Keywords: breast cancer prognosis, ABCC5, PGR**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	TOILLON et al., `Estrogens decrease $\gamma$ -ray-induced senescence and maintain cell cycle progression in breast cancer cells independently of p53` International Journal of Radiation Oncology, Biology, Physics, Vol.67, No.4, pp.1187-1200 (15 March 2007) See abstract and table 1.	1-5
A		15-23
X	WO 2008-077165 A1 (AUSTRIAN RES CENTERS GMBH ARC et al.) 3 July 2008 See abstract and claims 1-15.	15-20
A		1-5, 21-23
X	US 2011-0178374 A1 (BAKER et al.) 21 July 2011 See abstract and claims 1, 31.	21-23
A		1-5, 15-20
A	US 2011-0129833 A1 (BAKER et al.) 2 June 2011 See abstract and claims 1, 25.	1-5, 15-23



Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search

27 May 2013 (27.05.2013)

Date of mailing of the international search report

29 May 2013 (29.05.2013)

Name and mailing address of the ISA/KR

Korean Intellectual Property Office
189 Cheongsu-ro, Seo-gu, Daejeon Metropolitan City,
302-701, Republic of Korea

Facsimile No. 82-42-472-7140

Authorized officer

KIM, Seung Beom

Telephone No. 82-42-481-3371



INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2013/021839

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.: 8-14
because they relate to subject matter not required to be searched by this Authority, namely:
Claims 8-14 pertain to methods for treatment of the human body by therapy, as well as diagnostic methods, and thus relate to a subject matter which this ISA is not required, under Article 17(2)(a)(i) of the PCT and Rule 39.1(iv) of the Regulations under the PCT, to search.
2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☒ Claims Nos.: 6-7, 11-13
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.
- ☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.
- ☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No.

PCT/US2013/021839

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
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