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(54) Title: MULTI DRUG RESPONSE MARKERS FOR BREAST CANCER CELLS

(57) Abstract: The present invention provides methods for preparing a gene expression profile of a breast cancer cell, tumor, or cell line, where the gene expression profile may be evaluated for one or more gene expression signatures indicative of multidrug resistance. The signature may be indicative of resistance to one or more chemotherapeutic agents selected from a Taxol (e.g., Docetaxel or Paclitaxel), an antibiotic (e.g., Doxorubicin or Epirubicin), an antimetabolite (e.g., Fluorouracil and/or Gemcitabine), and an alkylating agent (e.g., Cyclophosphamide). Generally, the gene expression profile contains the level of expression for a plurality of genes listed in Figures 3, 4, and/or 5. Gene expression profiles for evaluating multidrug resistance for ER positive and ER negative breast cancers are also provided.



WO 2011/068832 A1

MULTI DRUG RESPONSE MARKERS FOR BREAST CANCER CELLS

PRIORITY

[001] This provisional application claims priority to U.S. Provisional Application No. 61/265,588 filed December 1, 2009, and U.S. Provisional Application No. 61/364,446 filed July 15, 2010, which are both hereby incorporated by reference in their entireties.

BACKGROUND

[002] A major obstacle in the effective treatment of breast cancer with chemotherapeutic agents is the phenomenon of multidrug resistance. Standards of care have involved various neoadjuvant approaches to chemotherapy and surgical resection, with the greatest success occurring when tumor tissue is surgically removed and patients are subsequently treated with chemotherapy. Generally, the success rate is less than 50% with primary breast cancer, and chemotherapeutic agents are less effective in treating recurrent disease due to drug resistance. In fact, resistant patients tend to be resistant to multiple drugs despite their different cytotoxic mechanisms.

[003] Understanding the molecular mechanisms of multidrug resistance has important biological significance and potential clinical, diagnostic, and prognostic utility, for example, by facilitating drug selection studies, identifying new therapeutic targets, in addition to individualizing patient therapy.

[004] Recent advances in genomic technology have provided an opportunity to identify genes associated with cancer drug resistance. Studies using tumor tissue from breast cancer patients have identified gene expression profiles potentially associated with clinical outcome (van de Vijver, He et al. 2002; Chang, Wooten et al. 2003; Gianni, Zambetti et al. 2005; Iwao-Koizumi, Matoba et al. 2005; Wang, Klijn et al. 2005; Hess, Anderson et al. 2006; Paik, Tang et al. 2006; Liedtke, Hatzis et al. 2009). However, in identifying gene expression profiles with clinical or biological significance, use of patient tumor tissue can be disadvantageous, due to the limited source of tissue, the long time necessary to assess clinical outcome, and the fact that each patient can be initially treated with only one panel of drugs. To overcome these problems, cell lines may be used as a proxy for patient tumor tissue using chemosensitivity and resistance assays

(CSRA) (Staunton, Slonim et al. 2001; Dan, Tsunoda et al. 2002; Mariadason, Arango et al. 2003; Kang, Kim et al. 2004); (Gyorffy, Surowiak et al. 2006). While gene expression profiles have been identified with some correlation to multi-drug response, most studies have used cell lines of heterogeneous origin, e.g., not exclusively breast cancer cell lines. Moreover, since breast cancer cell lines are very heterogeneous, including ER positive and ER negative cell lines, breast cancer cells may have several distinct response patterns to chemotherapeutic agents. That is, different cellular mechanisms may contribute to multidrug resistance.

[005] Multidrug response gene expression profiles are needed to assess chemosensitivity/resistance in breast cancer cells, including in ER+ and ER- breast cancer cells.

SUMMARY OF THE INVENTION

[006] The present invention provides methods for preparing a gene expression profile of a breast cancer cell, tumor, or cell line, where the gene expression profile contains the expression level for genes indicative of multidrug responsiveness (sensitivity or resistance). The profile may be evaluated for the presence of one or more gene expression signatures indicative of responsiveness to one or more drugs. The gene expression signature may be indicative of sensitivity or resistance to one or more chemotherapeutic agents selected from a taxol (e.g., docetaxel or paclitaxel), an antibiotic (e.g., doxorubicin or epirubicin), an antimetabolite (e.g., fluorouracil and/or gemcitabine), and an alkylating agent (e.g., cyclophosphamide). The gene expression signature may be indicative of a multidrug resistant breast cancer cell.

[007] Generally, the gene expression signatures described herein can be defined by the level of gene expression exhibited by drug-sensitive breast cancer cell lines (immortal cell lines), versus the level of gene expression exhibited by drug-resistant breast cancer cell lines (immortal cell lines). Drug-sensitive and drug-resistant cell lines are defined by their drug response in an in vitro chemosensitivity assay, as described more fully herein. A collection of publicly available breast cancer cell lines, and their relative sensitivity to a panel of chemotherapeutic agents is described herein (see Figure 2).

[008] In certain embodiments, the gene expression profile contains the level of expression for a plurality of genes listed in Figure 5, and as described in detail herein. In

certain embodiments, the profile contains the level of expression for DBI, TOP2A, and PMVK which are differentially expressed in both estrogen receptor (ER) positive and ER negative multidrug resistant breast cancer cell lines.

[009] In certain embodiments, the ER status of the tumor is determined or is known, which can aid evaluation of the gene expression profile for a gene expression signature indicative of drug response (e.g., multidrug resistance).

[010] For example, where the breast cancer, tumor, or cell line is ER positive, the gene expression profile is evaluated for the presence of a gene expression signature that is indicative of drug sensitivity or resistance for an Estrogen Receptor (ER) positive breast cancer cell. In such embodiments, the ER positive gene expression signatures may be defined by the level of gene expression exhibited by ER positive drug-sensitive breast cancer cell lines (immortal cell lines), versus the level of gene expression exhibited by ER positive drug-resistant breast cancer cell lines (immortal cell lines). For example, the ER positive gene expression profile may contain the level of expression for a plurality of genes listed in Figure 3, as described in detail herein.

[011] In other embodiments where the breast cancer, tumor, or cell line is ER negative, the gene expression profile is evaluated for the presence of a gene expression signature that is indicative of drug sensitivity or resistance for an ER negative breast cancer cell. In such embodiments, the gene expression signatures may be defined by the level of gene expression exhibited by ER negative drug-sensitive breast cancer cell lines (immortal cell lines), versus the level of gene expression exhibited by ER negative drug-resistant breast cancer cell lines (immortal). The ER negative gene expression profile may contain the level of expression for a plurality of genes listed in Figure 4, as described in detail herein.

[012] In other aspects, the invention provides methods for determining whether a breast tumor is sensitive or resistant to multiple drugs, such as a plurality of agents selected from taxol (e.g., docetaxel or paclitaxel), an antibiotic (e.g., doxorubicin or epirubicin), an antimetabolite (e.g., fluorouracil and/or gemcitabine), and an alkylating agent (e.g., cyclophosphamide). The method generally comprises determining the gene expression profiles described herein for the breast tumor or malignant cells thereof, and evaluating the profile for the presence or absence of a gene expression signature indicative of multidrug response (e.g. resistance). In some embodiments, the ER status

is also determined or is known, and gene expression signatures specific to ER-positive and ER-negative breast cancer cells are described herein.

[013] As exemplified herein, 27 well-studied breast cancer cell lines were used to identify genes that are related to multidrug resistance in ER- and ER+ breast cancer cell lines. An in vitro chemoresponse assay was used as a proxy of drug response to determine the sensitivity of these cell lines to seven chemotherapy agents commonly used to treat breast cancer patients. The drug response profile of the breast cancer cell lines demonstrated that the in vitro assay is a good proxy for drug response. Through pharmacogenomic analysis, the expression levels for 524 genes were identified as related to multidrug resistance for all breast cell lines (Figure 5). Many of these genes are related to ER status, which is consistent with the fact that ER status is related to drug response. Furthermore, 32 genes were identified that are related to multidrug response in ER negative breast cancer cell lines (Figure 4), and 188 genes were identified that are related to multidrug response in ER positive cell lines (Figure 3). Only 3 genes are in-common in both profiles (DBI, PMVK and TOP2A). Thus, the present application discloses that different genes are associated with multidrug response in ER-positive and ER-negative breast cancer cells.

DESCRIPTION OF THE FIGURES

[014] **Figure 1** is a heatmap of drug response for 27 breast cancer cell lines as determined by the CHEMOFX assay. Darker boxes represent sensitivity. The bar across the top indicates ER status of the cell line in the column below. Black corresponds to ER positive and grey corresponds to ER negative.

[015] **Figure 2** summarizes the chemosensitivity of 27 breast cancer cell lines to 7 different drugs, measured by CHEMOFX. Lower numbers indicate sensitivity.

[016] **Figure 3** lists 188 genes whose expression level is associated with multidrug resistance in ER-positive breast cancer cell lines (FIG 3A). Figure 3 includes measures of fold change between sensitive and resistant cell lines (FIG 3B).

[017] **Figure 4** lists 32 genes whose expression level is associated with multidrug resistance in ER-negative breast cancer cell lines (FIG 4A). Figure 4 includes measures of fold change between sensitive and resistant cell lines (FIG 4B).

[018] **Figure 5** lists 524 genes whose expression level is associated with multidrug resistance in all breast cancer cell lines (FIG 5A). Figure 5 includes measures of fold change between sensitive and resistant cell lines (FIG 5B).

DETAILED DESCRIPTION OF THE INVENTION

[019] The invention provides methods for preparing gene expression profiles for breast tumor specimens or cell lines, as well as methods for evaluating a breast cancer's sensitivity and/or resistance to one or more chemotherapeutic agents or combinations of agents. For example, the gene expression profile generated for a tumor specimen, or cultured cells derived therefrom, is evaluated for the presence of one or more indicative gene expression signatures. The gene expression signatures are indicative of response (sensitivity or resistance) to one or more chemotherapeutic agents as described herein. In this aspect, the invention may provide information to guide a physician in designing/administering an individualized chemotherapeutic regimen for a breast cancer patient.

[020] The patient generally is a breast cancer patient, and the tumor is generally a solid tumor of epithelial origin. The tumor specimen may be obtained from the patient by surgery, or may be obtained by biopsy, such as a fine needle biopsy or other procedure prior to the selection/initiation of neoadjuvant therapy. In certain embodiments, the breast cancer is preoperative or post-operative breast cancer. In certain embodiments, the patient has not undergone treatment to remove the breast tumor, and therefore is a candidate for neoadjuvant therapy.

[021] The breast cancer may be primary or recurrent, and may be of any type (as described above), stage (e.g., Stage I, II, III, or IV or an equivalent of other staging system), and/or histology. The patient may be of any age, sex, performance status, and/or extent and duration of remission.

[022] In certain embodiments, the patient is a candidate for treatment with one or more of taxol (e.g., docetaxel or paclitaxel), doxorubicin, epirubicin, an antimetabolite (e.g., fluorouracil and/or gemcitabine), and an alkylating agent (e.g., cyclophosphamide).

[023] The gene expression profile is determined for the tumor tissue or cell sample, such as a tumor sample removed from the patient by surgery or biopsy. The tumor sample may be "fresh," in that it was removed from the patient within about five days of processing, and remains suitable or amenable to culture. In some embodiments,

the tumor sample is not "fresh," in that the sample is not suitable or amenable to culture. Tumor samples are generally not fresh after from 3 to 7 days (e.g., about five days) of removal from the patient. The sample may be frozen after removal from the patient, and preserved for later RNA isolation. The sample for RNA isolation may be a formalin-fixed paraffin-embedded (FFPE) tissue. In certain embodiments, the tissue sample is not suitable for growing out malignant cells in a monolayer culture.

[024] In certain embodiments, the tissue specimen is a transcutaneous biopsy-sized specimen, and generally contains less than about 100 mg of tissue, or in certain embodiments, contains about 50 mg of tissue or less. The tumor specimen (or biopsy) may contain from about 20 mg to about 50 mgs of tissue, such as about 35 mg of tissue. The tissue may be obtained, for example, as one or more (e.g., 1, 2, 3, 4, or 5) core needle biopsies (e.g., using a 14-gauge needle or other suitable size).

[025] In certain embodiments, the malignant cells are enriched or expanded in culture by forming a monolayer culture from tumor sample explants. For example, cohesive multicellular particulates (explants) are prepared from a patient's tissue sample (e.g., a biopsy sample or surgical specimen) using mechanical fragmentation. This mechanical fragmentation of the explant may take place in a medium substantially free of enzymes that are capable of digesting the explant. Some enzymatic digestion may take place in certain embodiments, such as for ovarian or colorectal tumors.

[026] For example, where it is desirable to expand and/or enrich malignant cells in culture relative to non-malignant cells that reside in the tumor, the tissue sample is systematically minced using two sterile scalpels in a scissor-like motion, or mechanically equivalent manual or automated opposing incisor blades. This cross-cutting motion creates smooth cut edges on the resulting tissue multicellular particulates. The tumor particulates each measure from about 0.25 to about 1.5 mm³, for example, about 1 mm³. After the tissue sample has been minced, the particles are plated in culture flasks. The number of explants plated per flask may vary, for example, between one and 25, such as from 5 to 20 explants per flask. For example, about 9 explants may be plated per T-25 flask, and 20 particulates may be plated per T-75 flask. For purposes of illustration, the explants may be evenly distributed across the bottom surface of the flask, followed by initial inversion for about 10-15 minutes. The flask may then be placed in a non-inverted position in a 37°C CO₂ incubator for about 5-10 minutes. Flasks are checked regularly for growth and contamination. Over a period of days to a few weeks a cell monolayer will form.

[027] Further, it is believed that malignant cells grow out from the multicellular explant prior to stromal cells. Thus, by initially maintaining the tissue cells within the explants and removing the explants at a predetermined time (e.g., at about 10 to about 50 percent confluency, or at about 15 to about 25 percent confluency), growth of the tumor cells (as opposed to stromal cells) into a monolayer is facilitated. In certain embodiments, the tumor explants may be agitated to substantially loosen or release tumor cells from the tumor explants, and the released cells cultured to produce a cell culture monolayer. The use of this procedure to form a cell culture monolayer helps maximize the growth of representative malignant cells from the tissue sample. Monolayer growth rate and/or cellular morphology (e.g., epithelial character) may be monitored using, for example, a phase-contrast inverted microscope. In some embodiments, the cells may be sub-cultured. Generally, the cells of the monolayer should be actively growing at the time the cells are suspended for RNA extraction.

[028] The process for enriching or expanding malignant cells in culture is described in US Patents 5,728,541, 6,900,027, 6,887,680, 6,933,129, 6,416,967, 7,112,415, 7,314,731, 7,642,048, 7,501,260, and 7,642,048 (all of which are hereby incorporated by reference in their entireties). The process may further employ the variations described in US Published Patent Application No. 2007/0059821, which is hereby incorporated by reference in its entirety.

[029] The breast tumors may be classified into estrogen receptor positive (ER+) and negative (ER-) subtypes by any suitable method, including immunohistochemistry or other immunoassay with antibody against ER. Alternatively, ER status may be determined by ER+ or ER- gene expression signatures, as described, for example, in Gruvberger, S. et al., (2001) Estrogen receptor status in breast cancer is associated with remarkably distinct gene expression patterns. *Cancer Res.*, 61, 5979–5984; West, M. et al. (2001) Predicting the clinical status of human breast cancer by using gene expression profiles. *Proc. Natl Acad. Sci. USA*, 98, 11462–11467; and Kun Yu et al., Classifying the estrogen receptor status of breast cancers by expression profiles reveals a poor prognosis subpopulation exhibiting high expression of the ERBB2 receptor, *Human Molecular Genetics* 12(24):3245-3258 (2003).

[030] In preparing the gene expression profile, RNA is extracted from the tumor tissue or cultured cells by any known method. For example, RNA may be purified from cells using a variety of standard procedures as described, for example, in RNA Methodologies, A laboratory guide for isolation and characterization, 2nd edition, 1998, Robert E. Farrell, Jr., Ed., Academic Press. In addition, there are various products

commercially available for RNA isolation which may be used. Total RNA or polyA⁺ RNA may be used for preparing gene expression profiles in accordance with the invention.

[031] The gene expression profile is then generated for the samples using any of various techniques known in the art. Such methods generally include, without limitation, hybridization-based assays, such as microarray analysis and similar formats (e.g., Whole Genome DASL[™] Assay, Illumina, Inc.), polymerase-based assays, such as RT-PCR (e.g., Taqman[™]), flap-endonuclease-based assays (e.g., Invader[™]), as well as direct mRNA capture with branched DNA (QuantiGene[™]) or Hybrid Capture[™] (Digene). In certain embodiments, the gene expression profile is determined using a microarray format, such as the Affymetrix HGU133A, or relevant probes therefrom. The polynucleotide sequences of the genes listed in Figures 3-5 are publicly available, and are hereby incorporated by reference. Further, Affymetrix probe sequences for such genes, as employed with the HGU133A array, are also hereby incorporated by reference.

[032] The gene expression profile contains gene expression levels for a plurality of genes whose expression levels are predictive or indicative of the tumor's resistance to one or a combination of chemotherapeutic agents. The gene expression signatures can be defined by the level of gene expression exhibited by drug-sensitive breast cancer cell lines (immortal cell lines), versus the level of gene expression exhibited by drug-resistant (multi drug-resistant) breast cancer cell lines (immortal cell lines). Drug-sensitive and drug-resistant cell lines are defined by their drug response in an in vitro chemosensitivity assay (described herein). In certain embodiments, the gene expression signature is defined by the gene expression levels of the breast cancer cell lines of Figure 2, as grouped according to their chemosensitivity profile and/or ER status.

[033] As used herein, the term "gene," refers to a DNA sequence expressed in a sample as an RNA transcript, and may be a full-length gene (protein encoding or non-encoding) or an expressed portion thereof such as expressed sequence tag or "EST." Thus, the genes listed in Figures 3-5 are each independently a full-length gene sequence, whose expression product is present in samples, or is a portion of an expressed sequence detectable in samples, such as an EST sequence.

[034] The genes listed in Figures 3-5 may be differentially expressed in drug-sensitive cells versus drug-resistant cells (e.g., multidrug resistant samples). As used herein, "differentially expressed" means that the level or abundance of an RNA transcript (or abundance of an RNA population sharing a common target (or probe-hybridizing) sequence, such as a group of splice variant RNAs) is significantly higher or lower in a

sample (e.g., a drug-resistant sample) as compared to a reference level (e.g., a drug sensitive sample). For example, the level of the RNA or RNA population may be higher or lower than a reference level. The reference level may be the level of the same RNA or RNA population in a control sample or control population (e.g., a Mean or Median level for a drug-sensitive cell), or may represent a cut-off or threshold level for a sensitive or resistant designation.

[035] The gene expression profile generally contains the expression levels for at least about 3, 5, 7, 10, 25, 50, 100 or more (e.g., all or substantially all) genes listed in one or more of Figures 3-5. As discussed, the expression levels for these genes represent the gene expression state of the patient's malignant cells or tumor, and together this profile is evaluated for the presence of one or more gene signatures indicative of the tumor's sensitivity and/or resistance to chemotherapeutic agents. In some embodiments, the profile is prepared with the use of a custom array or bead set (or other gene expression detection format), so as to quantify the level of 500 genes or less, 250 genes or less, 150 genes or less, or 100 genes or less, including genes listed in Figures 3-5.

[036] Alternatively or in addition, the gene expression profile may contain the levels of expression for at least about 3 genes listed in Figure 3. In some embodiments, the patient's gene expression profile contains the levels of expression for at least about 5, 7, 10, 12, 15, 20, 25, 50, or all genes listed in Figure 3, such genes being differentially expressed in multidrug-resistant ER positive breast cancer cells versus drug sensitive ER positive breast cancer cells. In some embodiments, the gene expression profile may contain the levels of expression for all or substantially all genes listed in Figure 3. In some embodiments, the profile is prepared with the use of a custom array or bead set (or other gene expression detection format), so as to quantify the level of 500 genes or less, 250 genes or less, 150 genes or less, or 100 genes or less, including genes listed in Figure 3.

[037] Alternatively or in addition, the gene expression profile may contain the levels of expression for at least about 3 genes listed in Figure 4. In some embodiments, the patient's gene expression profile contains the levels of expression for at least about 5, 7, 10, 12, 15, 20, 25, or all genes listed in Figure 4, such genes being differentially expressed in multidrug-resistant ER negative breast cancer cells versus drug sensitive ER negative breast cancer cells. In some embodiments, the gene expression profile may contain the levels of expression for all or substantially all genes listed in Figure 4. In some embodiments, the profile is prepared with the use of a custom array or bead set (or

other gene expression detection format), so as to quantify the level of 500 genes or less, 250 genes or less, 150 genes or less, or 100 genes or less, including genes listed in Figure 4.

[038] In certain embodiments, the gene expression profile contains a measure of expression level for the plurality of genes (e.g., 5, 7, 10, 12, 15, 50, etc.) that are each, independently, expressed in multidrug-sensitive versus drug-resistant samples by a fold change magnitude (up or down) of at least about 1.2 (up) or about 0.8 (down). Fold change magnitude is defined as mean sensitive score / mean resistant score. In some embodiments, the plurality of genes are differentially expressed in drug sensitive versus drug resistant cells by a fold change magnitude (up) of at least 1.5, or at least about 1.7, or at least about 2, or at least about 2.5, or by a fold magnitude (down) of less than about 0.7, about 0.5, or about 0.4. Alternatively, the expression levels (mean sensitive and mean resistant) may differ by at least about 2-, 3-, 4-, or 5-, 10-fold, or more.

[039] The gene expression profile prepared according to this aspect of the invention is evaluated for the presence of one or more gene expression signatures indicative of drug responsiveness (e.g., a multidrug resistant signature). The gene expression signature(s) comprise or are derived from (mathematically) the gene expression levels indicative of a drug-sensitive and/or multidrug-resistant cells, so as to enable a classification of the tumor's profile as sensitive or resistant. Specifically, the gene expression signature comprises or is derived from indicative gene expression levels for a plurality of genes listed in one or more of Figures 3-5, such as at least 5, 7, 10, 12, 15, 20, 25, 40, 50, 75, 100, 200, 250, 300, 400, or 500 genes listed in one or more of Figures 3-5. The signature may comprise or be derived from the Mean or Median expression levels, or alternatively, may use other statistical criteria.

[040] The gene expression signature(s) may be in a format consistent with any nucleic acid detection format, such as those described herein, and will generally be comparable to the format used for profiling patient samples. For example, the gene expression signature and patient profiles may both be prepared by nucleic acid hybridization method, and with the same hybridization platform and controls so as to facilitate comparisons. The gene expression signatures may further embody any number of statistical measures to distinguish drug-sensitive and/or drug-resistant levels, including Mean or median expression levels and/or cut-off or threshold values. Such signatures may be prepared from the data sets disclosed herein or independent gene expression data sets.

[041] Once the gene expression profile for patient samples are prepared, the profile is evaluated for the presence of one or more of the gene signatures, by scoring or classifying the patient profile against each gene signature.

[042] Various classification schemes are known for classifying samples between two or more classes or groups, and these include, without limitation: Principal Components Analysis, Naïve Bayes, Support Vector Machines, Nearest Neighbors, Decision Trees, Logistic, Artificial Neural Networks, and Rule-based schemes. In addition, the predictions from multiple models can be combined to generate an overall prediction. For example, a “majority rules” prediction may be generated from the outputs of a Naïve Bayes model, a Support Vector Machine model, and a Nearest Neighbor model.

[043] Thus, a classification algorithm or “class predictor” may be constructed to classify samples. The process for preparing a suitable class predictor is reviewed in R. Simon, Diagnostic and prognostic prediction using gene expression profiles in high-dimensional microarray data, *British Journal of Cancer* (2003) 89, 1599-1604, which review is hereby incorporated by reference in its entirety.

[044] Generally, the gene expression profiles for patient specimens are scored or classified as drug-sensitive signatures or drug-resistant signatures, including with stratified or continuous intermediate classifications or scores reflective of drug resistance or sensitivity. As discussed, such signatures may be assembled from publicly available gene expression data, or prepared from independent data sets. The signatures may be stored in a database and correlated to patient tumor gene expression profiles in response to user inputs.

[045] After comparing the patient’s gene expression profile to the drug-sensitive and/or drug-resistant signature, the sample is classified as, or for example, given a probability of being, a drug-sensitive profile or a drug-resistant profile (e.g., a multidrug resistant profile). The classification may be determined computationally based upon known methods as described above. The result of the computation may be displayed on a computer screen or presented in a tangible form, for example, as a probability (e.g., from 0 to 100%) of the patient responding to a given treatment. The report will aid a physician in selecting a course of treatment for the cancer patient. For example, in certain embodiments of the invention, the patient’s gene expression profile will be determined to be a drug-sensitive profile on the basis of a probability, and the patient will be subsequently treated with that drug or combination. In other embodiments, the

patient's profile will be determined to be a drug-resistant profile, such as a multidrug resistant profile, thereby allowing the physician to exclude one or more candidate treatments for the patient, thereby sparing the patient the unnecessary toxicity.

[046] In various embodiments, the method according to this aspect of the invention distinguishes a drug-sensitive tumor from a multidrug-resistant tumor with at least about 60%, 75%, 80%, 85%, 90%, 95% or greater accuracy. In this respect, the method according to this aspect may lend additional or alternative predictive value over standard methods, such as for example, gene expression tests known in the art, or chemoresponse testing.

[047] The methods of the invention aid the prediction of an outcome of treatment, e.g., based on a probability. That is, the gene expression signatures are each predictive of an outcome upon treatment with a candidate agent or combination. The outcome may be quantified in a number of ways. For example, the outcome may be an objective response, a clinical response, or a pathological response to a candidate treatment. The outcome may be determined based upon the techniques for evaluating response to treatment of solid tumors as described in Therasse et al., New Guidelines to Evaluate the Response to Treatment in Solid Tumors, *J. of the National Cancer Institute* 92(3):205-207 (2000), which is hereby incorporated by reference in its entirety. For example, the outcome may be survival (including overall survival or the duration of survival), progression-free interval, or survival after recurrence. The timing or duration of such events may be determined from about the time of diagnosis or from about the time treatment (e.g., chemotherapy) is initiated. Alternatively, the outcome may be based upon a reduction in tumor size, tumor volume, or tumor metabolism, or based upon overall tumor burden, or based upon levels of serum markers especially where elevated in the disease state. The outcome in some embodiments may be characterized as a complete response, a partial response, stable disease, and progressive disease, as these terms are understood in the art.

[048] In certain embodiments, the presence or absence of a gene signature is indicative of a pathological complete response upon treatment with a particular candidate agent or combination (as already described). A pathological complete response, e.g., as determined by a pathologist following examination of tissue (e.g., breast or nodes in the case of breast cancer) removed at the time of surgery, generally refers to an absence of histological evidence of invasive tumor cells in the surgical specimen.

[049] The present invention may further comprise conducting chemoresponse testing with a panel of chemotherapeutic agents on cultured cells from a cancer patient, to thereby add additional predictive value. That is, the presence of one or more gene expression signatures in tumor cells, and the *in vitro* chemoresponse results for the tumor specimen, are used to predict an outcome of treatment (e.g., survival, pCR, etc.). For example, where the gene expression profile and chemoresponse test both indicate that a tumor is sensitive or resistant to a particular treatment, the predictive value of the method may be particularly high. Chemoresponse testing may be performed via the CHEMOFX test, as described herein and as known in the art.

EXAMPLES

Materials and Methods

[050] In this study, 27 breast cancer cell lines (as shown in Figure 1) were obtained from American Type Culture Collection, Manassas, VA, USA. Cells were cultured in RPMI 1640 (Mediatech, Herndon, VA, USA). FBS was purchased from HyClone (Logan, UT, USA). The following chemotherapeutic agents were used in the current study and prepared as recommended by the manufacturer in the growth media used for cell growth: paclitaxel, docetaxel, gemcitabine, cyclophosphamide, fluorouracil, doxorubicin, and epirubicin.

[051] The CHEMOFX assay was performed as described previously (Mi, Holmes et al. 2008). Briefly, cells were treated with chemotherapeutic agents (untreated cells were used as a control). For each chemotherapeutic agent, ten serially diluted drug concentrations were tested in triplicate. After an incubation period of 72 hours, the cells were fixed, stained, and counted. The number of cells remaining after drug treatment was used to determine survival fraction ($SF = \text{average cell count dose } x / \text{average cell count control}$). Dose-response curves were plotted to determine the chemosensitivity, which is based on area under the curve (AUC) [(Mi, Holmes et al. 2008)]. Lower drug response scores indicate greater sensitivity. Lower drug response scores indicate greater sensitivity. The cells with the one third lowest values of AUC were deemed “sensitive,” while the cells with the highest one third values of AUC were deemed to be “resistant.”

[052] Two dimensional hierarchical clustering was applied to the chemosensitivity data resulting from the CHEMOFX assay analyses. Cells that showed similar patterns of sensitivities to the drugs tested were grouped together. Likewise, drugs that showed similar response patterns among the cell lines tested were grouped together. For example, the two taxanes (paclitaxel and docetaxel) and the two anthracycline antitumor antibiotics (epirubicin and doxorubicin) were each clustered together.

[053] Raw gene expression data were downloaded from ArrayExpress, a public Affymetrix IDs were mapped to gene symbols. If a gene symbol was associated with multiple Affymetrix IDs, the one with the maximum IQR was chosen. Bioconductor software was used to apply non-specific gene filtering to these data sets. Briefly, the program filters the data as follows: suppose x denotes the expression value of gene i , then genes that do not satisfy the following two conditions are filtered out: 1) $IQR(x) < 0.5$; 2) $median(x) < \log_2(100)$.

[054] To analyze how gene expression is related to multidrug response in breast cell lines, ER positive breast cells or ER negative breast cells, meta-analysis on breast cell lines, ER positive breast cell lines, and ER negative breast cell lines was conducted separately.

[055] The algorithms used to perform the meta-analysis are as follows. Suppose there are a total of G genes and K studies ($K=7$ for this case). Let x_{gsk} denote the gene expression value of gene g , cell line s for drug k , $s, 1 \leq g \leq G, 1 \leq s \leq S, 1 \leq k \leq K$. Let y_{sk} denote the AUC value for the cell line s for drug k . The regression coefficient β_{1gk} for gene g for drug k was computed using a standard linear regression model $y_{sk} = \beta_{0gk} + \beta_{1gk} x_{gsk} + \epsilon_{sgk}$, where ϵ_{sgk} is the normal error. Let $t_{gk} = \beta_{1gk} / s_{gk}$, where s_{gk} is the standard deviation of β_{1gk} . s_{gk} is the standard deviation of β_{1gk} .

[056] For each drug, the p-value of each gene was calculated by the following steps:

- a. Compute the t_{gk} for gene g and drug k .
- b. Permute the cell line's labels for B times, and similarly calculate the permuted statistics, $t_{gk}^{(b)}$, where $1 \leq g \leq G, 1 \leq k \leq K, 1 \leq b \leq B$.

c. Estimate the p-value of t_{gk} as $p_{gk} = \frac{\sum_{b=1}^B \sum_{g'=1}^G I(|t_{g'k}^{(b)}| \geq |t_{gk}|)}{B \cdot G}$ and similarly

$$\text{calculate } p_{gk}^{(b)} = \frac{\sum_{b'=1}^B \sum_{g'=1}^G I(|t_{g'k}^{(b')}| \geq |t_{gk}^{(b)}|)}{B \cdot G}.$$

d. Estimate $\pi_0(k)$, the proportion of non-DE genes, as

$$\hat{\pi}_0(k) = \frac{\sum_{g=1}^G I(p_{gk} \in A)}{G \cdot l(A)} \quad [1]. \text{ We chose } A=[0.5, 1] \text{ and thus } l(A)=0.5.$$

e. Estimate the q-value of t_{gk} as $q_{gk} = \frac{\hat{\pi}_0(k) \cdot \sum_{b=1}^B \sum_{g'=1}^G I(|t_{g'k}^{(b)}| \geq |t_{gk}|)}{B \cdot \sum_{g'=1}^G I(|t_{g'k}| \geq |t_{gk}|)}$.

The following steps are meta-analysis procedures to identify multi-drug response genes:

a. The r th rand statistic is used for meta-analysis: $V_g = p_{g(5)}$. Define

$$V_g^{(b)} = p_{g(5)}^{(b)}.$$

b. Estimate the p-value of the genes in meta-analysis as

$$p(V_g) = \frac{\sum_{b=1}^B \sum_{g'=1}^G I(V_{g'}^{(b)} \leq V_g)}{B \cdot G}.$$

c. Estimate π_0 , the proportion of non-DE genes in the meta-analysis, as

$$\hat{\pi}_0 = \frac{\sum_{g=1}^G I(p(V_g) \in A)}{G \cdot l(A)}. \text{ We chose } A=[0.5, 1] \text{ and thus } l(A)=0.5.$$

d. Estimate the q-value in the meta-analysis as

$$q(V_g) = \frac{\hat{\pi}_0 \cdot \sum_{b=1}^B \sum_{g'=1}^G I(V_{g'}^{(b)} \leq V_g)}{B \cdot \sum_{g'=1}^G I(V_{g'} \leq V_g)}.$$
 DE genes detected by the meta-analysis

are denoted as $G_{meta} = \{g : q(V_g) \leq 0.01\}$. These DE genes are considered as multi-drug response genes in this study.

Finally, multi-drug response genes were defined as those genes that were associated with resistance to at least 5 different drugs. We then referred to the Molecular Signature Database to evaluate the reported biological function of these genes.

Fold change values between sensitive and resistant cell lines were calculated by sorting the cell lines based on their AUC values. The top 1/3 of the cell lines are defined as sensitive and the bottom 1/3 of the cell lines are defined as resistant. For the fold change the calculation is done as follows for each gene: mean raw expression value for the drug sensitive group/mean raw expression value for the drug resistant group.

Results

[057] ChemoFx analysis was performed on 27 well-characterized breast cancer cell lines to measure their response to the following 7 widely used chemotherapeutic agents: paclitaxel, docetaxel, gemcitabine, cyclophosphamide, fluorouracil, doxorubicin, and epirubicin (**Fig. 1**).

[058] As with primary tumors, these cell lines exhibited a heterogeneous response to the drugs (**Fig. 2**). Generally speaking, three clusters of cell lines were identified based on their responses to the different agents resulted. The first cluster consisted of 9 cell lines that were pan-resistant to the tested drugs. This cluster was enriched (7/8) in estrogen receptor (ER) positive cells. The second cluster included 8 cell lines that were pan-sensitive to the tested drugs. All of them were ER negative. The third cluster consisted of 11 cell lines that showed a heterogeneous response to the tested drugs and were both ER positive (4) and ER negative (7).

[059] We also performed hierarchical clustering on the 7 chemotherapeutic drugs based on the drug response patterns of the cells. We found that paclitaxel and docetaxel were clustered together as were doxorubicin and epirubicin.

[060] Through pharmacogenomic analysis, 524 genes were identified to be related to multidrug response for all breast cell lines. Many of these genes are related to ER status. In ER negative breast cancer cell lines, 32 genes were identified to be related to multidrug response, and 21 of them are in the list of 524 genes. In ER positive cell lines, 188 genes were related to multidrug response, and 70 of them exist in the list of 524 genes. Only 3 gene was related to multidrug response for both ER positive breast cell lines and ER negative breast cell lines (DBI, TOP2A, PMVK).

Discussion

[061] A pharmacogenomic analysis of 27 breast cancer cell lines identified 32 genes related to multidrug response in ER negative breast cells, and 188 genes related to multidrug response in ER positive cell lines.

[062] A functional analysis of these genes indicates that they are related to several diverse biological functions, supporting the current understanding that multidrug response is the result of multiple mechanisms.

[063] A key issue of using cell lines is how good the surrogate can approximate patient outcome. To date, various CSRA analysis have been used, including MTT and ATP. In this example, we applied CHEMOFX. Specifically, 7 classical drugs were tested in a collection of 27 breast cell lines. The drug response pattern of cell lines also suggests that CHEMOFX is a good proxy through several aspects. First, these cell lines show (exhibit) heterogeneous responses, similar to clinical observations. In addition, these cell lines show that ER status strongly correlates with drug responses for most chemotherapy drugs -- ER positive cell lines tend to be more resistant, while ER negative cell lines tend to be sensitive. This is consistent with previous publications. Furthermore, our drug clustering also supports the accuracy of CHEMOFX. The 7 drugs tested represent the major classes of anticancer drugs. Cyclophosphamide is an alkylating agent. Doxorubicin and Epirubicin are antibiotics. Paclitaxel and Docetaxel are taxanes, and "5-Fu" is an antimetabolite that acts as a thymidylate synthase inhibitor. Thus, Paclitaxel and Docetaxel were clustered together, and Epirubicin and Doxorubicin were clustered together.

[064] The analysis disclosed herein is useful for understanding multidrug resistance to cytotoxic chemotherapy drugs, and to individualize patient treatment.

[065] For instance, where a multidrug resistant signature is present, a physician might consider some less conventional chemotherapeutic treatments (e.g., not represented by the agents disclosed herein), or might consider more aggressive radiation or surgical intervention.

[066] Further, genes associated with multiple drug resistance have helped determine how some cancers can be resistant to drug treatment and have provided potential targets. Similarly, analysis of oncogenes has demonstrated that such genes have wild-type counterparts often involved in signal transduction for growth control

pathways. Many of these genes code for proteins that are regulated by tyrosine kinases, making phospho-tyrosine a popular target for drug development.

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CLAIMS:

1. A method for preparing a gene expression profile of a breast cancer cell, tumor, or cell line, the profile being indicative of drug response, comprising, extracting RNA from a breast tumor sample or cell culture derived therefrom, and determining the gene expression level of genes listed in one or more of Figures 3, 4, and/or 5.
2. The method of claim 1, wherein the breast tumor or cell line is ER positive, and the gene expression profile contains the level of expression for a plurality of genes listed in Figure 3.
3. The method of claim 1, wherein the breast tumor or cell line is ER negative, and the gene expression profile contains the level of expression for a plurality of genes listed in Figure 4.
4. The method of any one of claims 1 to 3, wherein the gene expression profile is indicative of response to at least two agents selected from a Taxol; an antibiotic; an antimetabolite; and an alkylating agent.
5. The method of claim 4, wherein the Taxol is docetaxel or paclitaxel.
6. The method of claim 4 or 5, wherein the antimetabolite is 5-fluorouracil or gemcitabine.
7. The method of any one of claims 4 to 7, wherein the alkylating agent is cyclophosphamide.
8. The method of any one of claims 4 to 8, wherein the antibiotic is doxorubicin or epirubicin.
9. The method of any one of claims 1 to 8, further comprising, determining the presence of one or more gene expression signatures indicative of multidrug response.
10. The method of any one of claims 1 to 9, further comprising conducting a Chemoresponse assay.
11. A method for preparing a gene expression profile of a breast tumor, comprising,

determining an estrogen receptor (ER) status for the tumor;

extracting RNA from the tumor sample or cell culture derived therefrom; and

determining a gene expression profile for the tumor, where the gene expression profile includes the level of expression for a plurality of genes listed in one or more of Figures 3, 4, and/or 5.

12. The method of claim 11, wherein the breast tumor or cell line is ER positive, and the gene expression profile contains the level of expression for a plurality of genes listed in Figure 3.

13. The method of claim 11, wherein the breast tumor or cell line is ER negative, and the gene expression profile contains the level of expression for a plurality of genes listed in Figure 4.

14. The method of any one of claims 11 to 13, wherein the gene expression profile is indicative of resistance to at least two agents selected from a Taxol; an antibiotic; an antimetabolite; and an alkylating agent.

15. The method of claim 14, wherein the Taxol is docetaxel or paclitaxel.

16. The method of claim 14 or 15, wherein the antimetabolite is 5-fluorouracil or gemcitabine.

17. The method of any one of claims 14 to 17, wherein the alkylating agent is cyclophosphamide.

18. The method of any one of claims 14 to 18, wherein the antibiotic is doxorubicin or epirubicin.

19. The method of any one of claims 11 to 18, further comprising, determining the presence of one or more gene expression signatures indicative of multidrug resistance.

20. The method of any one of claims 11 to 19, further comprising conducting a Chemoresponse assay.

Figure 1:

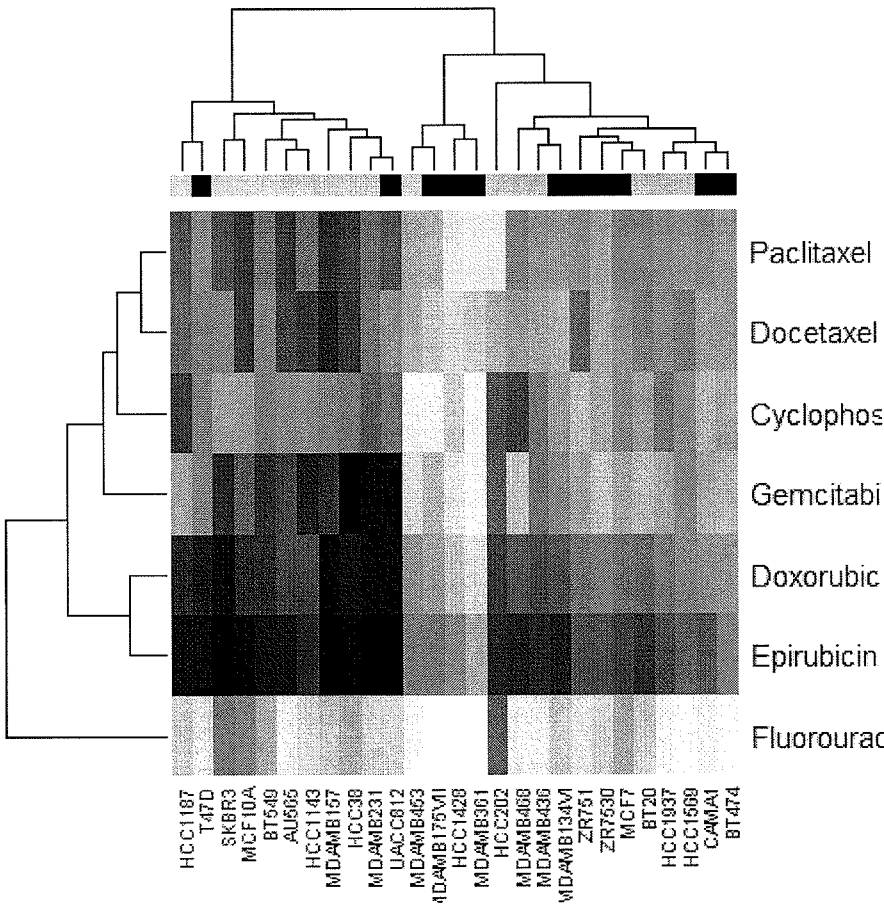


FIGURE 2

	Taxol		antitumor antibiotic		Antimetabolites		alkylating agents	
	Docetaxel	Paclitaxel	Doxorubicin	Epirubicin	Fluorouracil	Gemcitabine	Cyclophosphamide	ER
AU565	5.67	5.47	5.50	4.42	9.16	5.53	6.90	neg
BT20	6.70	7.06	6.38	5.47	8.86	8.47	7.73	neg
BT474	7.57	7.64	7.64	7.04	9.88	8.41	7.86	pos
BT549	6.56	6.33	5.00	4.31	7.79	5.25	6.41	neg
CAMA1	7.69	7.28	7.53	6.13	9.55	8.26	8.36	pos
HCC1143	5.41	6.24	5.57	5.07	8.73	4.81	7.02	neg
HCC1187	6.02	5.91	4.89	4.10	8.37	7.41	5.28	neg
HCC1428	8.60	9.00	8.38	7.01	10.69	8.91	8.33	pos
HCC1569	6.76	7.55	7.35	6.39	9.76	7.43	7.30	neg
HCC1937	7.17	7.37	6.96	6.07	9.57	8.13	6.70	neg
HCC202	7.81	9.21	5.48	5.07	6.06	6.07	5.95	neg
HCC38	5.38	5.49	4.36	3.59	7.85	3.09	6.44	neg
MCF10A	5.33	5.44	5.00	4.02	6.76	6.00	7.31	neg
MCF7	7.29	7.04	6.54	5.76	8.09	7.99	7.12	pos
MDAMB134VI	8.23	7.63	5.98	4.95	8.63	7.22	7.62	pos
MDAMB157	4.81	5.30	4.02	3.16	8.33	5.10	6.74	neg
MDAMB175VII	8.32	7.88	7.50	6.52	10.54	7.94	9.24	pos
MDAMB231	6.34	6.29	3.91	3.11	8.72	3.92	5.97	neg
MDAMB361	8.45	9.26	8.96	8.10	9.93	9.43	9.56	pos
MDAMB436	7.79	7.46	5.80	5.24	9.28	6.38	6.60	neg
MDAMB453	7.75	7.83	7.15	6.59	9.51	8.69	9.10	neg
MDAMB468	7.42	6.92	5.93	4.98	9.29	8.67	5.71	neg
SKBR3	6.65	5.78	4.06	3.26	6.35	5.24	7.39	neg
T47D	6.49	6.93	4.62	3.78	8.85	6.69	6.51	pos
UACC812	7.03	5.95	3.88	2.97	8.65	3.89	6.31	pos
ZR751	6.19	7.40	6.62	5.98	9.28	7.96	8.52	pos
ZR7530	7.87	7.93	6.88	5.93	8.86	8.61	7.93	pos

FIGURE 3A

ProbeID	gene	Gene.Title
205142_x_at	ABCD1	ATP-binding cassette, sub-family D (ALD), member 1
202003_s_at	ACAA2	acetyl-Coenzyme A acyltransferase 2
213198_at	ACVR1B	activin A receptor, type IB
217007_s_at	ADAM15	ADAM metalloproteinase domain 15
201272_at	AKR1B1	aldo-keto reductase family 1, member B1 (aldose reductase)
200011_s_at	ARF3	ADP-ribosylation factor 3
217852_s_at	ARL8B	ADP-ribosylation factor-like 8B
219918_s_at	ASPM	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)
201089_at	ATP6V1B2	ATPase, H ⁺ transporting, lysosomal 56/58kDa, V1 subunit B2
203188_at	B3GNT1	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1
201170_s_at	BHLHE40	basic helix-loop-helix family, member e40
212547_at	BRD3	bromodomain containing 3
200777_s_at	BZW1	basic leucine zipper and W2 domains 1
218213_s_at	C11ORF10	NA
213617_s_at	C18ORF10	NA
218008_at	C7ORF42	NA
203538_at	CAMLG	calcium modulating ligand
201850_at	CAPG	capping protein (actin filament), gelsolin-like
218384_at	CARHSP1	calcium regulated heat stable protein 1, 24kDa
207842_s_at	CASC3	cancer susceptibility candidate 3
209213_at	CBR1	carbonyl reductase 1
201091_s_at	CBX3	NA
218288_s_at	CCDC90B	coiled-coil domain containing 90B
214710_s_at	CCNB1	cyclin B1
208796_s_at	CCNG1	cyclin G1
211297_s_at	CDK7	cyclin-dependent kinase 7
209357_at	CITED2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2
201897_s_at	CKS1B	CDC28 protein kinase regulatory subunit 1B
203953_s_at	CLDN3	claudin 3
218250_s_at	CNOT7	CCR4-NOT transcription complex, subunit 7
202164_s_at	CNOT8	CCR4-NOT transcription complex, subunit 8
209796_s_at	CNPY2	canopy 2 homolog (zebrafish)
219397_at	COQ10B	coenzyme Q10 homolog B (S. cerevisiae)
212228_s_at	COQ9	coenzyme Q9 homolog (S. cerevisiae)
202575_at	CRABP2	cellular retinoic acid binding protein 2
212180_at	CRKL	v-crk sarcoma virus CT10 oncogene homolog (avian)-like
202950_at	CRYZ	crystallin, zeta (quinone reductase)
202521_at	CTCF	CCCTC-binding factor (zinc finger protein)
209389_x_at	DBI	diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein)
212919_at	DCP2	DCP2 decapping enzyme homolog (S. cerevisiae)
203261_at	DCTN6	dynactin 6
208152_s_at	DDX21	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21
220890_s_at	DDX47	DEAD (Asp-Glu-Ala-Asp) box polypeptide 47

ProbeID	gene	Gene.Title
202673_at	DPM1	dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit
218845_at	DUSP22	dual specificity phosphatase 22
203590_at	DYNC1LI2	dynein, cytoplasmic 1, light intermediate chain 2
201024_x_at	EIF5B	eukaryotic translation initiation factor 5B
212087_s_at	ERAL1	Era G-protein-like 1 (E. coli)
203550_s_at	FAM189B	NA
217896_s_at	FAM192A	NA
201889_at	FAM3C	family with sequence similarity 3, member C
202949_s_at	FHL2	four and a half LIM domains 2
218530_at	FHOD1	formin homology 2 domain containing 1
201637_s_at	FXR1	fragile X mental retardation, autosomal homolog 1
218084_x_at	FXYD5	FXYD domain containing ion transport regulator 5
212378_at	GART	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase
215380_s_at	GGCT	gamma-glutamyl cyclotransferase
208843_s_at	GORASP2	golgi reassembly stacking protein 2, 55kDa
212070_at	GPR56	G protein-coupled receptor 56
202831_at	GPX2	glutathione peroxidase 2 (gastrointestinal)
202680_at	GTF2E2	general transcription factor IIE, polypeptide 2, beta 34kDa
203314_at	GTPBP6	GTP binding protein 6 (putative)
218450_at	HEBP1	heme binding protein 1
200904_at	HLA-E	major histocompatibility complex, class I, E
207165_at	HMMR	hyaluronan-mediated motility receptor (RHAMM)
218120_s_at	HMOX2	heme oxygenase (decycling) 2
200598_s_at	HSP90B1	heat shock protein 90kDa beta (Grp94), member 1
205133_s_at	HSPE1	heat shock 10kDa protein 1 (chaperonin 10)
218611_at	IER5	immediate early response 5
204169_at	IMPDH1	IMP (inosine monophosphate) dehydrogenase 1
201892_s_at	IMPDH2	IMP (inosine monophosphate) dehydrogenase 2
202809_s_at	INTS3	integrator complex subunit 3
212766_s_at	ISG20L2	interferon stimulated exonuclease gene 20kDa-like 2
201474_s_at	ITGA3	integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor)
205176_s_at	ITGB3BP	integrin beta 3 binding protein (beta3-endonexin)
221004_s_at	ITM2C	integral membrane protein 2C
202220_at	KIAA0907	KIAA0907
201552_at	LAMP1	lysosomal-associated membrane protein 1
212193_s_at	LARP1	La ribonucleoprotein domain family, member 1
221790_s_at	LDLRAP1	low density lipoprotein receptor adaptor protein 1
218253_s_at	LGTN	ligatin
201847_at	LIPA	lipase A, lysosomal acid, cholesterol esterase
217993_s_at	MAT2B	methionine adenosyltransferase II, beta
212269_s_at	MCM3AP	minichromosome maintenance complex component 3 associated protein
200948_at	MLF2	myeloid leukemia factor 2
219220_x_at	MRPS22	mitochondrial ribosomal protein S22
212145_at	MRPS27	mitochondrial ribosomal protein S27

ProbeID	gene	Gene.Title
218112_at	MRPS34	mitochondrial ribosomal protein S34
212708_at	MSL1	male-specific lethal 1 homolog (Drosophila)
206461_x_at	MT1H	metallothionein 1H
211456_x_at	MT1P2	metallothionein 1 pseudogene 2
208581_x_at	MT1X	metallothionein 1X
212185_x_at	MT2A	metallothionein 2A
202258_s_at	N4BP2L2	NEDD4 binding protein 2-like 2
202268_s_at	NAE1	NEDD8 activating enzyme E1 subunit 1
212789_at	NCAPD3	non-SMC condensin II complex, subunit D3
218201_at	NDUFB2	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2, 8kDa
203606_at	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase)
208926_at	NEU1	sialidase 1 (lysosomal sialidase)
214427_at	NOP2	NOP2 nucleolar protein homolog (yeast)
214722_at	NOTCH2NL	Notch homolog 2 (Drosophila) N-terminal like
201468_s_at	NQO1	NAD(P)H dehydrogenase, quinone 1
218768_at	NUP107	nucleoporin 107kDa
213947_s_at	NUP210	nucleoporin 210kDa
202188_at	NUP93	nucleoporin 93kDa
202397_at	NUTF2	nuclear transport factor 2
202696_at	OXSRI	oxidative-stress responsive 1
202336_s_at	PAM	peptidylglycine alpha-amidating monooxygenase
219148_at	PBK	PDZ binding kinase
203660_s_at	PCNT	pericentrin
211023_at	PDHB	pyruvate dehydrogenase (lipoamide) beta
212412_at	PDLIM5	PDZ and LIM domain 5
202658_at	PEX11B	peroxisomal biogenesis factor 11 beta
203972_s_at	PEX3	peroxisomal biogenesis factor 3
200886_s_at	PGAM1	phosphoglycerate mutase 1 (brain)
212506_at	PICALM	phosphatidylinositol binding clathrin assembly protein
204484_at	PIK3C2B	phosphoinositide-3-kinase, class 2, beta polypeptide
204267_x_at	PKMYT1	protein kinase, membrane associated tyrosine/threonine 1
201050_at	PLD3	phospholipase D family, member 3
203515_s_at	PMVK	phosphomevalonate kinase
218866_s_at	POLR3K	polymerase (RNA) III (DNA directed) polypeptide K, 12.3 kDa
202313_at	PPP2R2A	protein phosphatase 2 (formerly 2A), regulatory subunit B, alpha isoform
203338_at	PPP2R5E	protein phosphatase 2, regulatory subunit B', epsilon isoform
201923_at	PRDX4	peroxiredoxin 4
205053_at	PRIM1	primase, DNA, polypeptide 1 (49kDa)
209678_s_at	PRKCI	protein kinase C, iota
202251_at	PRPF3	PRP3 pre-mRNA processing factor 3 homolog (S. cerevisiae)
209586_s_at	PRUNE	prune homolog (Drosophila)
212296_at	PSMD14	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14
200772_x_at	PTMA	prothymosin, alpha
202716_at	PTPN1	protein tyrosine phosphatase, non-receptor type 1
204214_s_at	RAB32	RAB32, member RAS oncogene family

ProbeID	gene	Gene.Title
219125_s_at	RAG1AP1	recombination activating gene 1 activating protein 1
201330_at	RARS	arginyl-tRNA synthetase
218194_at	REXO2	REX2, RNA exonuclease 2 homolog (S. cerevisiae)
202963_at	RFX5	regulatory factor X, 5 (influences HLA class II expression)
221647_s_at	RIC8A	resistance to inhibitors of cholinesterase 8 homolog A (C. elegans)
218262_at	RMND5B	required for meiotic nuclear division 5 homolog B (S. cerevisiae)
203403_s_at	RNF6	ring finger protein (C3H2C3 type) 6
208270_s_at	RNPEP	arginyl aminopeptidase (aminopeptidase B)
218394_at	ROGDI	rogdi homolog (Drosophila)
200715_x_at	RPL13A	ribosomal protein L13a
214041_x_at	RPL37A	ribosomal protein L37a
213350_at	RPS11	ribosomal protein S11
201890_at	RRM2	ribonucleotide reductase M2 polypeptide
209360_s_at	RUNX1	runt-related transcription factor 1
212416_at	SCAMP1	secretory carrier membrane protein 1
200961_at	SEPHS2	selenophosphate synthetase 2
221263_s_at	SF3B5	splicing factor 3b, subunit 5, 10kDa
214882_s_at	SFRS2	splicing factor, arginine/serine-rich 2
214853_s_at	SHC1	SHC (Src homology 2 domain containing) transforming protein 1
212833_at	SLC25A46	solute carrier family 25, member 46
211988_at	SMARCE1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1
202505_at	SNRPB2	small nuclear ribonucleoprotein polypeptide B"
215424_s_at	SNW1	SNW domain containing 1
202113_s_at	SNX2	sorting nexin 2
221498_at	SNX27	sorting nexin family member 27
201471_s_at	SQSTM1	sequestosome 1
208921_s_at	SRI	sorcin
200889_s_at	SSR1	signal sequence receptor, alpha
200652_at	SSR2	signal sequence receptor, beta (translocon-associated protein beta)
201331_s_at	STAT6	signal transducer and activator of transcription 6, interleukin-4 induced
208855_s_at	STK24	serine/threonine kinase 24 (STE20 homolog, yeast)
212894_at	SUPV3L1	suppressor of var1, 3-like 1 (S. cerevisiae)
221189_s_at	TARS2	threonyl-tRNA synthetase 2, mitochondrial (putative)
202371_at	TCEAL4	transcription elongation factor A (SII)-like 4
202396_at	TCERG1	transcription elongation regulator 1
212121_at	TCTN3	tectonic family member 3
201174_s_at	TERF2IP	telomeric repeat binding factor 2, interacting protein
218099_at	TEX2	testis expressed 2
218996_at	TFPT	TCF3 (E2A) fusion partner (in childhood Leukemia)
203167_at	TIMP2	TIMP metalloproteinase inhibitor 2
217766_s_at	TMEM50A	transmembrane protein 50A
221255_s_at	TMEM93	transmembrane protein 93
212281_s_at	TMEM97	transmembrane protein 97
202510_s_at	TNFAIP2	tumor necrosis factor, alpha-induced protein 2
207196_s_at	TNIP1	TNFAIP3 interacting protein 1

ProbeID	gene	Gene.Title
201512_s_at	TOMM70A	translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)
201291_s_at	TOP2A	topoisomerase (DNA) II alpha 170kDa
209109_s_at	TSPAN6	tetraspanin 6
205807_s_at	TUFT1	tuftelin 1
209142_s_at	UBE2G1	ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, yeast)
202779_s_at	UBE2S	NA
202038_at	UBE4A	ubiquitination factor E4A (UFD2 homolog, yeast)
214323_s_at	UPF3A	UPF3 regulator of nonsense transcripts homolog A (yeast)
202261_at	VPS72	vacuolar protein sorting 72 homolog (S. cerevisiae)
212051_at	WIPF2	WAS/WASL interacting protein family, member 2
202749_at	WRB	tryptophan rich basic protein

FIGURE 3B

gene	Docetaxel	Paclitaxel	Doxorubicin	Epirubicin	Fluorouracil	Gemcitabine	Cyclophosphamide
ABCD1	0.77	0.8	0.8	0.83	0.99	0.9	0.88
ACAA2	1.59	2.09	2.04	2.01	1.77	2	2.21
ACVR1B	0.82	0.81	0.75	0.75	0.87	0.73	0.69
ADAM15	1.01	1.08	1.16	1.14	1.12	1.21	1.12
AKR1B1	1.3	5.77	4.09	4.15	1.63	0.75	1.48
ARF3	0.84	0.86	0.97	0.95	0.99	0.89	0.99
ARL8B	1.39	1.59	1.35	1.29	1.39	1.76	1.22
ASPM	1.79	1.66	1.58	1.53	1.31	1.21	1.41
ATP6V1B2	1.15	1.17	1.39	1.3	1.01	1.21	1.42
B3GNT1	0.85	0.97	1.06	1.05	0.91	0.99	1.14
BHLHE40	0.96	1.32	1.41	1.4	1.02	1.2	2.08
BRD3	0.98	0.85	0.83	0.81	0.88	0.72	0.87
BZW1	0.76	0.77	0.75	0.79	0.85	0.67	0.64
C11ORF10	1.16	1.22	1.39	1.42	1.2	1.23	1.63
C18ORF10	1.03	1.02	1.56	1.44	1.64	1.42	1.81
C7ORF42	1.13	1.16	1.25	1.19	1.12	1.11	1.1
CAMLG	1.2	1.29	1.38	1.33	1.29	1.14	1.14
CAPG	2.34	3.12	2.19	2.23	1.51	2.1	3.42
CARHSP1	0.75	0.76	0.77	0.74	0.87	0.76	0.9
CASC3	1.92	3.13	2.53	2.4	1.47	2.79	2.15
CBR1	2.71	2.83	2.43	2.49	1.67	2.37	2.68
CBX3	1.53	1.39	1.18	1.07	0.97	1	1.04
CCDC90B	1.43	1.54	1.62	1.62	1.05	1.21	2.04
CCNB1	1.46	1.25	1.53	1.5	1.26	1.18	1.4
CCNG1	1.81	2.1	2.05	1.83	1.41	1.51	1.71
CDK7	1.37	1.32	1.43	1.29	1.22	1.22	1.06
CITED2	1.35	1.89	1.78	1.49	1.07	2.09	1.63
CKS1B	1.29	1.23	1.17	1.13	1.02	1.08	1.15
CLDN3	0.54	0.69	1.46	1.53	2.1	1.23	2.57
CNOT7	1.92	2.45	2.53	2.19	1.83	1.97	2.29
CNOT8	1.28	1.4	1.17	1.1	0.97	0.9	1.2
CNPY2	1.1	1.12	1.31	1.29	1.35	1.31	1.11
COQ10B	1.08	1.13	1.01	0.99	0.96	0.92	0.85
COQ9	0.84	0.9	0.81	0.81	0.76	0.76	0.86
CRABP2	0.67	0.98	1.13	1.09	0.97	0.87	1.88
CRKL	1.33	1.31	1.24	1.11	0.99	1.23	1.07
CRYZ	1.39	1.59	2.31	2.34	1.85	2.17	2.52
CTCF	0.82	0.72	0.77	0.72	0.76	0.62	0.66
DBI	0.66	0.59	0.58	0.57	0.67	0.72	0.66
DCP2	1	0.97	1.02	0.96	0.78	0.77	0.99

gene	Docetaxel	Paclitaxel	Doxorubicin	Epirubicin	Fluorouracil	Gemcitabine	Cyclophosphamide
DCTN6	1.25	1.24	1.33	1.27	1.13	1.2	1.12
DDX21	2.24	2.57	2.35	2.3	1.92	2.32	1.65
DDX47	1.18	1.3	1.15	1.16	0.94	0.98	1.26
DPM1	1.4	1.6	1.46	1.41	1.1	1.38	1.29
DUSP22	1.38	1.35	1.32	1.35	1.04	0.95	1.39
DYNC1LI2	1.1	1.06	0.98	0.98	0.95	0.87	0.95
EIF5B	1.14	1.15	1.09	1.13	0.99	1.12	1.02
ERAL1	0.95	1.13	1.34	1.38	1.32	1.39	1.37
FAM189B	1.4	1.59	1.49	1.48	1.29	1.66	1.53
FAM192A	0.91	0.97	0.86	0.88	0.8	0.84	0.91
FAM3C	1.56	1.64	1.27	1.23	1.04	1.85	1.06
FHL2	1.69	2.25	2.05	3.1	0.71	0.83	1.35
FHOD1	0.72	0.76	0.8	0.8	0.84	0.71	0.68
FXR1	1.93	1.72	1.58	1.45	1.22	1.41	1.42
FXYD5	3.7	3.39	3.01	3.14	1.51	1.87	2.6
GART	1.39	1.74	1.6	1.69	1.31	1.32	1.59
GGCT	0.73	0.64	0.63	0.58	0.66	0.63	0.59
GORASP2	0.71	0.74	0.69	0.71	0.69	0.68	0.65
GPR56	0.56	0.6	0.42	0.46	0.43	0.46	0.46
GPX2	0.48	0.49	0.38	0.39	0.46	0.52	0.43
GTF2E2	1.5	1.61	1.87	1.81	1.46	1.55	1.84
GTPBP6	0.82	0.82	0.84	0.87	0.99	0.9	0.76
HEBP1	0.64	0.69	0.64	0.65	0.77	0.61	0.76
HLA-E	2.08	2.18	1.83	1.82	1.04	1.18	2.39
HMMR	1.75	1.53	1.29	1.16	1.03	1.02	1.39
HMOX2	0.96	0.97	1.01	1	1.13	1.05	0.65
HSP90B1	1.45	1.35	1.56	1.45	1.24	1.46	1.34
HSPE1	0.95	0.98	0.85	0.91	0.86	0.84	0.85
IER5	1.71	1.76	1.46	1.41	0.8	0.92	1.94
IMPDH1	1.16	1.24	0.95	0.93	1.04	1.24	0.78
IMPDH2	1.2	1.27	1.35	1.22	1.19	1.3	1.17
INTS3	0.96	1.07	1.05	0.99	1.06	1.12	0.98
ISG20L2	1.2	1.37	1.17	1.22	0.97	1.26	1.07
ITGA3	1.24	1.4	1.56	1.63	1.65	1.22	1.16
ITGB3BP	0.95	1.18	1.31	1.4	1.09	1.07	1.78
ITM2C	1.37	1.04	0.92	0.92	0.87	1.35	1.18
KIAA0907	1.42	1.73	1.52	1.6	1.06	1.3	1.69
LAMP1	0.82	0.95	0.9	0.89	0.93	0.87	1.12
LARP1	1.77	1.79	1.58	1.59	1.43	1.6	1.31
LDLRAP1	0.81	0.82	0.79	0.79	0.88	0.81	0.74
LGTN	1.23	1.34	1.2	1.07	0.97	1.36	0.87
LIPA	1.36	1.45	1.66	1.83	1.44	1.3	1.35

gene	Docetaxel	Paclitaxel	Doxorubicin	Epirubicin	Fluorouracil	Gemcitabine	Cyclophosphamide
MAT2B	1.45	1.52	1.37	1.45	1.05	1.09	1.61
MCM3AP	1.15	1.32	1.45	1.44	0.99	1.08	1.13
MLF2	0.96	0.93	0.86	0.84	0.89	0.87	0.89
MRPS22	1.38	1.46	1.38	1.36	1.14	1.29	1.29
MRPS27	1.33	1.35	1.44	1.36	1.26	1.41	1.2
MRPS34	0.73	0.81	0.84	0.83	0.84	0.83	0.81
MSL1	2.64	4.9	4	3.51	2.54	5.51	2.29
MT1H	1.3	1.44	1.39	1.72	1.28	1.01	0.87
MT1P2	1.35	1.53	1.45	1.77	1.38	1.07	0.86
MT1X	1.41	1.63	1.58	2.08	1.43	1.05	0.91
MT2A	1.35	1.59	1.55	2	1.38	1.07	0.95
N4BP2L2	1.23	1.35	1.35	1.37	1.3	1.15	1.36
NAE1	1.08	1.1	0.99	1.01	0.87	0.78	0.76
NCAPD3	1.51	1.4	1.36	1.33	1.04	1.1	1.41
NDUFB2	0.86	0.88	0.87	0.87	1.04	1.08	0.84
NDUFS6	0.96	0.95	0.81	0.86	0.82	0.79	0.77
NEU1	1.02	1.16	1.38	1.46	1.36	1.22	1.44
NOP2	1.17	1.33	1.21	1.15	1.12	1.21	1.18
NOTCH2NL	2.21	2.33	2.04	2.02	1.83	1.53	1.8
NQO1	0.71	0.66	0.63	0.69	0.6	0.59	0.45
NUP107	1.41	1.61	1.55	1.51	1.22	1.52	1.51
NUP210	0.95	1.1	0.99	1.04	1.11	1.04	1.22
NUP93	1.02	1.11	1.02	1.08	0.95	0.94	1.08
NUTF2	0.84	0.74	0.78	0.75	0.69	0.69	0.77
OXSR1	1.75	2.23	1.88	1.81	1.5	1.82	1.49
PAM	4	2.28	1.76	1.71	1.12	3.56	3.32
PBK	1.93	1.79	2.39	2.16	1.93	2.3	1.89
PCNT	1.26	1.23	1.18	1.23	1.05	0.94	1.02
PDHB	1.22	1.35	1.64	1.67	1.19	1.39	1.57
PDLIM5	1.53	1.29	1.03	1.06	0.85	1.55	0.97
PEX11B	0.96	1.08	1.08	1.02	0.99	1.21	0.97
PEX3	1.29	1.5	1.29	1.28	1.09	1.33	1.35
PGAM1	1.01	0.99	1.32	1.25	1.18	1.3	1.27
PICALM	1.52	1.87	1.65	1.63	1.12	1.29	1.78
PIK3C2B	0.8	0.96	0.99	1.02	1.03	1.02	0.98
PKMYT1	0.82	0.78	0.79	0.83	0.92	0.82	0.78
PLD3	0.93	0.99	1.13	1.15	1.18	1.05	1.37
PMVK	0.73	0.8	0.91	0.94	0.86	0.94	0.98
POLR3K	0.76	0.83	0.83	0.86	0.9	0.86	0.77
PPP2R2A	1.4	1.42	1.61	1.63	1.42	1.57	1.53
PPP2R5E	1.09	1.07	1.05	1.04	0.98	0.99	0.91
PRDX4	1.05	1.09	1.24	1.25	1.04	1.31	1.27

gene	Docetaxel	Paclitaxel	Doxorubicin	Epirubicin	Fluorouracil	Gemcitabine	Cyclophosphamide
PRIM1	1.05	1.02	0.99	0.98	0.91	0.94	1.03
PRKCI	1.31	1.49	0.99	0.98	0.76	0.9	1.1
PRPF3	1.28	1.6	1.56	1.55	1.41	1.24	1.78
PRUNE	1.23	1.42	1.36	1.34	1.38	1.15	1.26
PSMD14	0.89	0.91	0.89	0.92	0.81	0.76	0.89
PTMA	0.84	0.81	0.78	0.74	0.83	0.86	0.81
PTPN1	1.19	0.91	0.92	0.93	0.88	1.32	0.96
RAB32	1.04	1.49	2.01	2.08	1.95	2.16	2.27
RAG1AP1	0.87	1.09	1.09	1.02	0.85	1.1	1.17
RARS	1.37	1.4	1.3	1.27	1	1.06	1.39
REXO2	2.23	1.78	1.7	1.81	1.09	1.2	1.84
RFX5	1.36	1.38	1.35	1.3	1.28	1.41	1.37
RIC8A	1.14	1.42	1.55	1.7	1.4	1.32	1.29
RMND5B	0.79	0.95	0.81	0.84	0.89	0.89	0.93
RNF6	1.23	1.26	1.1	1.05	0.92	0.88	0.8
RNPEP	0.83	0.83	0.81	0.81	0.89	0.77	0.67
ROGDI	0.61	0.55	0.65	0.66	0.98	0.7	0.61
RPL13A	1.5	1.49	1.48	1.4	1.44	1.41	1.13
RPL37A	0.74	0.75	0.83	0.86	0.92	1.02	0.78
RPS11	1.31	1.92	2.21	2.2	1.96	2.2	1.61
RRM2	0.97	1.14	1.01	1.03	0.84	0.91	0.76
RUNX1	1.21	1.35	0.92	0.95	0.91	1.54	1.01
SCAMP1	0.99	1.01	1.18	1.15	1.07	1.08	1.04
SEPHS2	0.7	0.65	0.63	0.6	0.69	0.66	0.58
SF3B5	1.41	1.41	1.33	1.38	1.19	1.52	1.58
SFRS2	0.92	0.9	0.89	0.9	0.85	0.89	0.89
SHC1	2.15	1.8	1.79	1.85	1.57	1.97	1.31
SLC25A46	1.7	1.76	1.9	1.9	1.43	1.6	1.61
SMARCE1	1.32	1.76	1.82	1.65	1.27	1.83	1.4
SNRNPB2	1.36	1.33	1.42	1.46	1.21	1.45	1.24
SNW1	1.3	1.28	1.29	1.2	1.21	1.14	1.06
SNX2	1.29	1.38	1.42	1.36	1.12	1.28	1.09
SNX27	1.07	1.49	1.48	1.5	1.26	1.47	1.39
SQSTM1	1.01	1.19	0.96	1	0.96	0.95	1.17
SRI	1.5	1.61	1.42	1.47	1.17	1.59	2.25
SSR1	1.38	1.3	1.3	1.24	1.04	1.02	1.31
SSR2	1.25	1.46	1.51	1.41	1.3	1.71	1.54
STAT6	1.16	1.06	0.98	0.99	1.17	0.96	0.82
STK24	1.04	1.12	0.89	0.93	0.82	0.85	1.07
SUPV3L1	1.05	1.21	1.27	1.24	1.09	1.12	1.39
TARS2	1.04	1.13	1.15	1.09	1.2	1.21	1.16
TCEAL4	0.92	1.08	1.28	1.24	1.32	1.09	1.17

gene	Docetaxel	Paclitaxel	Doxorubicin	Epirubicin	Fluorouracil	Gemcitabine	Cyclophosphamide
TCERG1	1.34	1.64	1.37	1.37	1.16	1.22	1.22
TCTN3	0.95	0.95	1.28	1.28	1.18	1.3	1.34
TERF2IP	0.86	0.75	0.86	0.85	0.8	0.68	0.78
TEX2	0.54	0.57	0.54	0.54	0.62	0.56	0.47
TFPT	0.81	0.85	0.88	0.85	0.91	0.83	0.67
TIMP2	2.27	2.67	2.41	2.48	2.1	2.58	1.52
TMEM50A	0.89	0.93	0.84	0.86	0.81	0.82	0.87
TMEM93	1.24	1.26	1.46	1.44	1.28	1.32	1.42
TMEM97	0.75	0.84	1.32	1.43	1.49	1.37	1.41
TNFAIP2	2.11	2.66	1.68	1.8	1.21	1.04	2.44
TNIP1	1.26	1.76	1.29	1.31	1.18	1.27	1.67
TOMM70A	1.33	1.42	1.25	1.15	1.04	1.23	0.97
TOP2A	1.86	2.34	2.69	2.21	2.12	2.35	1.64
TSPAN6	1.42	1.42	1.39	1.48	0.99	1.13	2.33
TUFT1	0.98	1.16	1.13	1.08	0.97	0.94	0.94
UBE2G1	1.51	1.67	1.55	1.58	1.31	1.35	1.53
UBE2S	1.41	1.42	1.42	1.42	1.29	1.2	1.27
UBE4A	1.89	1.72	1.66	1.54	1.12	1.31	1.68
UPF3A	1.29	1.4	1.18	1.15	0.9	0.71	1.26
VPS72	1.1	1.28	1.25	1.28	1.26	1.07	1.27
WIPF2	1.84	4.22	3.5	3.39	1.38	3.89	3.09
WRB	0.83	0.94	1.13	1.14	0.99	1.18	1.26

FIGURE 4

probeID	Gene	Gene.Title
204942_s_at	ALDH3B2	aldehyde dehydrogenase 3 family, member B2
218187_s_at	C8ORF33	NA
218500_at	C8ORF55	NA
200998_s_at	CKAP4	cytoskeleton-associated protein 4
201560_at	CLIC4	chloride intracellular channel 4
209389_x_at	DBI	diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein)
212561_at	DENND5A	DENN/MADD domain containing 5A
201842_s_at	EFEMP1	EGF-containing fibulin-like extracellular matrix protein 1
45297_at	EHD2	EH-domain containing 2
202021_x_at	EIF1	eukaryotic translation initiation factor 1
211628_x_at	FTHL5	NA
205164_at	GCAT	glycine C-acetyltransferase (2-amino-3-ketobutyrate coenzyme A ligase)
202593_s_at	GDE1	glycerophosphodiester phosphodiesterase 1
202718_at	IGFBP2	insulin-like growth factor binding protein 2, 36kDa
210239_at	IRX5	iroquois homeobox 5
213564_x_at	LDHB	lactate dehydrogenase B
201037_at	PFKP	phosphofructokinase, platelet
205273_s_at	PITRM1	pitrilysin metallopeptidase 1
202337_at	PMF1	polyamine-modulated factor 1
203515_s_at	PMVK	phosphomevalonate kinase
39729_at	PRDX2	peroxiredoxin 2
220964_s_at	RAB1B	RAB1B, member RAS oncogene family
200018_at	RPS13	ribosomal protein S13
202276_at	SHFM1	split hand/foot malformation (ectrodactyly) type 1
204928_s_at	SLC10A3	solute carrier family 10 (sodium/bile acid cotransporter family), member 3
209453_at	SLC9A1	solute carrier family 9 (sodium/hydrogen exchanger), member 1
217789_at	SNX6	sorting nexin 6
217995_at	SQRDL	sulfide quinone reductase-like (yeast)
203221_at	TLE1	transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)
201291_s_at	TOP2A	topoisomerase (DNA) II alpha 170kDa
212519_at	UBE2E1	ubiquitin-conjugating enzyme E2E 1 (UBC4/5 homolog, yeast)
221746_at	UBL4A	ubiquitin-like 4A

FIGURE 4B

gene	Docetaxel	Paclitaxel	Doxorubicin	Epirubicin	Fluorouracil	Gemcitabine	Cyclophosphamide
ALDH3B2	0.28	0.23	0.27	0.26	0.72	0.29	0.42
C8ORF33	0.75	0.78	0.69	0.67	0.65	0.53	1.15
C8ORF55	0.53	0.53	0.51	0.53	0.71	0.68	0.75
CKAP4	1.38	1.23	1.41	1.51	1.47	1.49	1.03
CLIC4	2.02	1.94	1.71	1.78	1.37	1.46	1.65
DBI	0.66	0.59	0.58	0.57	0.67	0.72	0.66
DENND5A	1.33	1.48	1.75	1.68	1.81	1.69	1.41
EFEMP1	3.55	5.39	2.69	2.61	2.26	3.86	2.17
EHD2	1.47	1.57	1.66	1.71	1.78	1.94	1.41
EIF1	1.5	1.4	1.34	1.15	1.21	1.35	1.05
FTHL5	0.69	0.7	0.78	0.87	0.88	0.7	1.14
GCAT	0.64	0.62	0.63	0.66	0.71	0.67	0.78
GDE1	0.59	0.54	0.6	0.57	0.68	0.48	0.63
IGFBP2	0.25	0.27	0.4	0.4	0.3	0.28	0.44
IRX5	0.4	0.31	0.33	0.31	0.5	0.23	0.44
LDHB	2.02	2.16	1.71	1.72	1.34	3.17	2.97
PFKP	2.04	1.84	2.22	1.9	2.1	2.13	1.56
PITRM1	1.56	1.49	1.61	1.77	1.53	1.42	1.34
PMF1	0.78	0.77	0.76	0.83	0.81	0.69	0.85
PMVK	0.73	0.8	0.91	0.94	0.86	0.94	0.98
PRDX2	0.55	0.58	0.72	0.71	0.85	0.61	0.98
RAB1B	0.65	0.62	0.66	0.67	0.62	0.64	0.77
RPS13	1.35	1.35	1.34	1.34	1.36	1.34	1.13
SHFM1	1.14	1.15	1.11	1.2	1.19	1.35	1.04
SLC10A3	0.67	0.69	0.75	0.76	0.71	0.71	0.86
SLC9A1	0.75	0.71	0.72	0.73	0.92	0.8	0.8
SNX6	1.5	1.65	1.44	1.42	1.37	1.39	1.16
SQRDL	0.52	0.61	0.58	0.62	0.49	0.5	0.83
TLE1	0.89	0.9	0.82	0.75	0.82	0.79	1.03
TOP2A	1.86	2.34	2.69	2.21	2.12	2.35	1.64
UBE2E1	1.83	2.05	1.8	1.85	1.58	1.75	1.66
UBL4A	0.52	0.62	0.68	0.69	0.74	0.67	0.88

FIGURE 5

probeID	gene	Gene.Title
202852_s_at	AAGAB	NA
202804_at	ABCC1	ATP-binding cassette, sub-family C (CFTR/MRP), member 1
212895_s_at	ABR	active BCR-related gene
202003_s_at	ACAA2	acetyl-Coenzyme A acyltransferase 2
208636_at	ACTN1	actinin, alpha 1
213198_at	ACVR1B	activin A receptor, type IB
202912_at	ADM	adrenomedullin
217729_s_at	AES	amino-terminal enhancer of split
215535_s_at	AGPAT1	1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase, alpha)
209173_at	AGR2	anterior gradient homolog 2 (Xenopus laevis)
200903_s_at	AHCY	S-adenosylhomocysteine hydrolase
216381_x_at	AKR7A3	aldo-keto reductase family 7, member A3 (aflatoxin aldehyde reductase)
218373_at	AKTIP	AKT interacting protein
204942_s_at	ALDH3B2	aldehyde dehydrogenase 3 family, member B2
203722_at	ALDH4A1	aldehyde dehydrogenase 4 family, member A1
201612_at	ALDH9A1	aldehyde dehydrogenase 9 family, member A1
200966_x_at	ALDOA	aldolase A, fructose-bisphosphate
212360_at	AMPD2	adenosine monophosphate deaminase 2 (isoform L)
221505_at	ANP32E	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E
206200_s_at	ANXA11	annexin A11
201613_s_at	AP1G2	adaptor-related protein complex 1, gamma 2 subunit
218261_at	AP1M2	adaptor-related protein complex 1, mu 2 subunit
214953_s_at	APP	amyloid beta (A4) precursor protein
201176_s_at	ARCN1	archain 1
201526_at	ARF5	ADP-ribosylation factor 5
202956_at	ARFGEF1	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited)
213039_at	ARHGEF18	rho/rac guanine nucleotide exchange factor (GEF) 18
209435_s_at	ARHGEF2	rho/rac guanine nucleotide exchange factor (GEF) 2
212614_at	ARID5B	AT rich interactive domain 5B (MRF1-like)
217852_s_at	ARL8B	ADP-ribosylation factor-like 8B
219918_s_at	ASPM	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)
208836_at	ATP1B3	ATPase, Na ⁺ /K ⁺ transporting, beta 3 polypeptide
207335_x_at	ATP5I	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit E
200818_at	ATP5O	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, O subunit
207809_s_at	ATP6AP1	ATPase, H ⁺ transporting, lysosomal accessory protein 1

probelD	gene	Gene.Title
201444_s_at	ATP6AP2	ATPase, H+ transporting, lysosomal accessory protein 2
200954_at	ATP6V0C	ATPase, H+ transporting, lysosomal 16kDa, V0 subunit c
212041_at	ATP6V0D1	ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d1
213587_s_at	ATP6V0E2	ATPase, H+ transporting V0 subunit e2
208737_at	ATP6V1G1	ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G1
209464_at	AURKB	aurora kinase B
221485_at	B4GALT5	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 5
202985_s_at	BAG5	BCL2-associated athanogene 5
203304_at	BAMBI	BMP and activin membrane-bound inhibitor homolog (Xenopus laevis)
210125_s_at	BANF1	barrier to autointegration factor 1
202391_at	BASP1	brain abundant, membrane attached signal protein 1
40093_at	BCAM	basal cell adhesion molecule (Lutheran blood group)
202315_s_at	BCR	breakpoint cluster region
202076_at	BIRC2	baculoviral IAP repeat-containing 2
202592_at	BLOC1S1	biogenesis of lysosomal organelles complex-1, subunit 1
202201_at	BLVRB	biliverdin reductase B (flavin reductase (NADPH))
203082_at	BMS1	BMS1 homolog, ribosome assembly protein (yeast)
218792_s_at	BSPRY	B-box and SPRY domain containing
205548_s_at	BTG3	BTG family, member 3
200777_s_at	BZW1	basic leucine zipper and W2 domains 1
203571_s_at	C10ORF116	NA
218213_s_at	C11ORF10	NA
218448_at	C20ORF11	NA
219288_at	C3ORF14	NA
218500_at	C8ORF55	NA
204480_s_at	C9ORF16	NA
203963_at	CA12	carbonic anhydrase XII
211985_s_at	CALM1	NA
200935_at	CALR	calreticulin
213812_s_at	CAMKK2	calcium/calmodulin-dependent protein kinase kinase 2, beta
212765_at	CAMSAP1L1	calmodulin regulated spectrin-associated protein 1-like 1
200625_s_at	CAP1	CAP, adenylate cyclase-associated protein 1 (yeast)
201850_at	CAPG	capping protein (actin filament), gelsolin-like
201950_x_at	CAPZB	capping protein (actin filament) muscle Z-line, beta
218384_at	CARHSP1	calcium regulated heat stable protein 1, 24kDa
212971_at	CARS	cysteinyl-tRNA synthetase
207842_s_at	CASC3	cancer susceptibility candidate 3
211208_s_at	CASK	calcium/calmodulin-dependent serine protein kinase (MAGUK family)
201432_at	CAT	catalase

probelD	gene	Gene.Title
209213_at	CBR1	carbonyl reductase 1
218288_s_at	CCDC90B	coiled-coil domain containing 90B
200873_s_at	CCT8	chaperonin containing TCP1, subunit 8 (theta)
208650_s_at	CD24	CD24 molecule
201005_at	CD9	CD9 molecule
201725_at	CDC123	cell division cycle 123 homolog (S. cerevisiae)
202870_s_at	CDC20	cell division cycle 20 homolog (S. cerevisiae)
201853_s_at	CDC25B	cell division cycle 25 homolog B (S. pombe)
201131_s_at	CDH1	cadherin 1, type 1, E-cadherin (epithelial)
209112_at	CDKN1B	cyclin-dependent kinase inhibitor 1B (p27, Kip1)
203973_s_at	CEBPD	CCAAT/enhancer binding protein (C/EBP), delta
221743_at	CELF1	NA
201933_at	CHMP1A	chromatin modifying protein 1A
209834_at	CHST3	carbohydrate (chondroitin 6) sulfotransferase 3
218597_s_at	CISD1	CDGSH iron sulfur domain 1
212832_s_at	CKAP5	cytoskeleton associated protein 5
204170_s_at	CKS2	CDC28 protein kinase regulatory subunit 2
201428_at	CLDN4	claudin 4
201560_at	CLIC4	chloride intracellular channel 4
200614_at	CLTC	clathrin, heavy chain (Hc)
218250_s_at	CNOT7	CCR4-NOT transcription complex, subunit 7
208912_s_at	CNP	2',3'-cyclic nucleotide 3' phosphodiesterase
208818_s_at	COMT	catechol-O-methyltransferase
217749_at	COPG	coatamer protein complex, subunit gamma
202078_at	COPS3	COP9 constitutive photomorphogenic homolog subunit 3 (Arabidopsis)
200086_s_at	COX4I1	cytochrome c oxidase subunit IV isoform 1
200925_at	COX6A1	cytochrome c oxidase subunit VIa polypeptide 1
201754_at	COX6C	cytochrome c oxidase subunit VIc
213059_at	CREB3L1	cAMP responsive element binding protein 3-like 1
208978_at	CRIP2	cysteine-rich protein 2
202950_at	CRYZ	crystallin, zeta (quinone reductase)
212072_s_at	CSNK2A1	casein kinase 2, alpha 1 polypeptide
202521_at	CTCF	CCCTC-binding factor (zinc finger protein)
200764_s_at	CTNNA1	catenin (cadherin-associated protein), alpha 1, 102kDa
201487_at	CTSC	cathepsin C
203531_at	CUL5	cullin 5
221488_s_at	CUTA	cutA divalent cation tolerance homolog (E. coli)
213315_x_at	CXORF40A	NA
212961_x_at	CXORF40B	NA
209163_at	CYB561	cytochrome b-561
201289_at	CYR61	cysteine-rich, angiogenic inducer, 61
221934_s_at	DALRD3	DALR anticodon binding domain containing 3

probelD	gene	Gene.Title
200794_x_at	DAZAP2	DAZ associated protein 2
209389_x_at	DBI	diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein)
204977_at	DDX10	DEAD (Asp-Glu-Ala-Asp) box polypeptide 10
208152_s_at	DDX21	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21
212561_at	DENND5A	DENN/MADD domain containing 5A
218333_at	DERL2	Der1-like domain family, member 2
203694_s_at	DHX16	DEAH (Asp-Glu-Ala-His) box polypeptide 16
209190_s_at	DIAPH1	diaphanous homolog 1 (Drosophila)
218325_s_at	DIDO1	death inducer-obliterator 1
204405_x_at	DIMT1L	DIM1 dimethyladenosine transferase 1-like (S. cerevisiae)
213546_at	DKFZP586I1420	hypothetical protein DKFZp586I1420
203764_at	DLGAP5	discs, large (Drosophila) homolog-associated protein 5
202416_at	DNAJC7	DnaJ (Hsp40) homolog, subfamily C, member 7
201937_s_at	DNPEP	aspartyl aminopeptidase
218567_x_at	DPP3	dipeptidyl-peptidase 3
217901_at	DSG2	desmoglein 2
200035_at	DULLARD	dullard homolog (Xenopus laevis)
204274_at	EBAG9	estrogen receptor binding site associated, antigen, 9
201323_at	EBNA1BP2	EBNA1 binding protein 2
219298_at	ECHDC3	enoyl Coenzyme A hydratase domain containing 3
203279_at	EDEM1	ER degradation enhancer, mannosidase alpha-like 1
209572_s_at	EED	embryonic ectoderm development
201842_s_at	EFEMP1	EGF-containing fibulin-like extracellular matrix protein 1
209343_at	EFHD1	EF-hand domain family, member D1
201983_s_at	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)
45297_at	EHD2	EH-domain containing 2
202021_x_at	EIF1	eukaryotic translation initiation factor 1
200023_s_at	EIF3F	eukaryotic translation initiation factor 3, subunit F
218028_at	ELOVL1	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1
204975_at	EMP2	epithelial membrane protein 2
217956_s_at	ENOPH1	enolase-phosphatase 1
201839_s_at	EPCAM	epithelial cell adhesion molecule
221665_s_at	EPS8L1	EPS8-like 1
202454_s_at	ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)
218135_at	ERGIC2	ERGIC and golgi 2
208959_s_at	ERP44	NA
219121_s_at	ESRP1	NA
219395_at	ESRP2	NA
201995_at	EXT1	exostoses (multiple) 1

probeID	gene	Gene.Title
202535_at	FADD	Fas (TNFRSF6)-associated via death domain
212400_at	FAM102A	family with sequence similarity 102, member A
213166_x_at	FAM128A	family with sequence similarity 128, member A
203550_s_at	FAM189B	NA
221591_s_at	FAM64A	family with sequence similarity 64, member A
219016_at	FASTKD5	FAST kinase domains 5
212987_at	FBXO9	F-box protein 9
201275_at	FDPS	farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltranstransferase, geranyltranstransferase)
203647_s_at	FDX1	ferredoxin 1
209210_s_at	FERMT2	fermitin family homolog 2 (Drosophila)
215000_s_at	FEZ2	fasciculation and elongation protein zeta 2 (zygin II)
202949_s_at	FHL2	four and a half LIM domains 2
200709_at	FKBP1A	FK506 binding protein 1A, 12kDa
200894_s_at	FKBP4	FK506 binding protein 4, 59kDa
211719_x_at	FN1	fibronectin 1
204667_at	FOXA1	forkhead box A1
201637_s_at	FXR1	fragile X mental retardation, autosomal homolog 1
202489_s_at	FXYD3	FXYD domain containing ion transport regulator 3
218084_x_at	FXYD5	FXYD domain containing ion transport regulator 5
201503_at	G3BP1	GTPase activating protein (SH3 domain) binding protein 1
202275_at	G6PD	glucose-6-phosphate dehydrogenase
219956_at	GALNT6	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 6 (GalNAc-T6)
211934_x_at	GANAB	glucosidase, alpha; neutral AB
AFFX-HUMGAPDH/M3 3197_5_at	GAPDH	glyceraldehyde-3-phosphate dehydrogenase
212378_at	GART	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase
205164_at	GCAT	glycine C-acetyltransferase (2-amino-3-ketobutyrate coenzyme A ligase)
204867_at	GCHFR	GTP cyclohydrolase I feedback regulator
202593_s_at	GDE1	glycerophosphodiester phosphodiesterase 1
219539_at	GEMIN6	gem (nuclear organelle) associated protein 6
202722_s_at	GFPT1	glutamine-fructose-6-phosphate transaminase 1
215380_s_at	GGCT	gamma-glutamyl cyclotransferase
221521_s_at	GIN52	GIN5 complex subunit 2 (Psf2 homolog)
214430_at	GLA	galactosidase, alpha
212294_at	GNG12	guanine nucleotide binding protein (G protein), gamma 12
202382_s_at	GNPDA1	glucosamine-6-phosphate deaminase 1
208843_s_at	GORASP2	golgi reassembly stacking protein 2, 55kDa

probelD	gene	Gene.Title
212070_at	GPR56	G protein-coupled receptor 56
202831_at	GPX2	glutathione peroxidase 2 (gastrointestinal)
219388_at	GRHL2	grainyhead-like 2 (Drosophila)
202680_at	GTF2E2	general transcription factor IIE, polypeptide 2, beta 34kDa
215091_s_at	GTF3A	general transcription factor IIIA
218238_at	GTPBP4	GTP binding protein 4
203314_at	GTPBP6	GTP binding protein 6 (putative)
200075_s_at	GUK1	guanylate kinase 1
208886_at	H1FO	H1 histone family, member O
204805_s_at	H1FX	H1 histone family, member X
202042_at	HARS	histidyl-tRNA synthetase
218450_at	HEBP1	heme binding protein 1
210428_s_at	HGS	hepatocyte growth factor-regulated tyrosine kinase substrate
215071_s_at	HIST1H2AC	histone cluster 1, H2ac
209806_at	HIST1H2BK	histone cluster 1, H2bk
218726_at	HJURP	Holliday junction recognition protein
200904_at	HLA-E	major histocompatibility complex, class I, E
208668_x_at	HMGN2	high-mobility group nucleosomal binding domain 2
209787_s_at	HMGN4	high mobility group nucleosomal binding domain 4
212115_at	HN1L	hematological and neurological expressed 1-like
207127_s_at	HNRNPH3	heterogeneous nuclear ribonucleoprotein H3 (2H9)
202282_at	HSD17B10	hydroxysteroid (17-beta) dehydrogenase 10
203089_s_at	HTRA2	HtrA serine peptidase 2
200825_s_at	HYOU1	hypoxia up-regulated 1
204744_s_at	IARS	isoleucyl-tRNA synthetase
210547_x_at	ICA1	islet cell autoantigen 1, 69kDa
207826_s_at	ID3	inhibitor of DNA binding 3, dominant negative helix-loop-helix protein
210418_s_at	IDH3B	isocitrate dehydrogenase 3 (NAD+) beta
201631_s_at	IER3	immediate early response 3
218611_at	IER5	immediate early response 5
201315_x_at	IFITM2	interferon induced transmembrane protein 2 (1-8D)
212203_x_at	IFITM3	interferon induced transmembrane protein 3 (1-8U)
220744_s_at	IFT122	intraflagellar transport 122 homolog (Chlamydomonas)
202718_at	IGFBP2	insulin-like growth factor binding protein 2, 36kDa
211959_at	IGFBP5	insulin-like growth factor binding protein 5
208931_s_at	ILF3	interleukin enhancer binding factor 3, 90kDa
203011_at	IMPA1	inositol(myo)-1(or 4)-monophosphatase 1
210239_at	IRX5	iroquois homeobox 5
209075_s_at	ISCU	iron-sulfur cluster scaffold homolog (E. coli)
218170_at	ISOC1	isochorismatase domain containing 1
210740_s_at	ITPK1	inositol 1,3,4-triphosphate 5/6 kinase

probeID	gene	Gene.Title
203752_s_at	JUND	jun D proto-oncogene
201015_s_at	JUP	junction plakoglobin
203712_at	KIAA0020	KIAA0020
212057_at	KIAA0182	KIAA0182
212441_at	KIAA0232	KIAA0232
202181_at	KIAA0247	KIAA0247
202220_at	KIAA0907	KIAA0907
222039_at	KIF18B	kinesin family member 18B
209408_at	KIF2C	kinesin family member 2C
207023_x_at	KRT10	keratin 10
200771_at	LAMC1	laminin, gamma 1 (formerly LAMB2)
212193_s_at	LARP1	La ribonucleoprotein domain family, member 1
201795_at	LBR	lamin B receptor
221790_s_at	LDLRAP1	low density lipoprotein receptor adaptor protein 1
201105_at	LGALS1	lectin, galactoside-binding, soluble, 1
201847_at	LIPA	lipase A, lysosomal acid, cholesterol esterase
221501_x_at	LOC339047	hypothetical protein LOC339047
214035_x_at	LOC399491	LOC399491 protein
212114_at	LOC552889	hypothetical protein LOC552889
47560_at	LPHN1	latrophilin 1
212276_at	LPIN1	lipin 1
212692_s_at	LRBA	LPS-responsive vesicle trafficking, beach and anchor containing
219491_at	LRFN4	leucine rich repeat and fibronectin type III domain containing 4
208190_s_at	LSR	lipolysis stimulated lipoprotein receptor
211686_s_at	MAK16	MAK16 homolog (S. cerevisiae)
202655_at	MANF	NA
217943_s_at	MAP7D1	MAP7 domain containing 1
210058_at	MAPK13	mitogen-activated protein kinase 13
217971_at	MAPKSP1	MAPK scaffold protein 1
204179_at	MB	myoglobin
201152_s_at	MBNL1	muscleblind-like (Drosophila)
212935_at	MCF2L	MCF.2 cell line derived transforming sequence-like
218163_at	MCTS1	malignant T cell amplified sequence 1
219051_x_at	METRNL	meteorin, glial cell differentiation regulator
209265_s_at	METTL3	methyltransferase like 3
207761_s_at	METTL7A	methyltransferase like 7A
201126_s_at	MGAT1	mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase
218138_at	MKKS	McKusick-Kaufman syndrome
218259_at	MKL2	MKL/myocardin-like 2
212508_at	MOAP1	modulator of apoptosis 1

probeID	gene	Gene.Title
212197_x_at	MPRIP	myosin phosphatase Rho interacting protein
219648_at	MREG	melanoregulin
218890_x_at	MRPL35	mitochondrial ribosomal protein L35
218558_s_at	MRPL39	mitochondrial ribosomal protein L39
219220_x_at	MRPS22	mitochondrial ribosomal protein S22
218398_at	MRPS30	mitochondrial ribosomal protein S30
218112_at	MRPS34	mitochondrial ribosomal protein S34
217942_at	MRPS35	mitochondrial ribosomal protein S35
212708_at	MSL1	male-specific lethal 1 homolog (Drosophila)
217772_s_at	MTCH2	mitochondrial carrier homolog 2 (C. elegans)
203207_s_at	MTFR1	mitochondrial fission regulator 1
202197_at	MTMR3	myotubularin related protein 3
212082_s_at	MYL6	NA
204173_at	MYL6B	myosin, light chain 6B, alkali, smooth muscle and non-muscle
218966_at	MYO5C	myosin VC
200049_at	MYST2	MYST histone acetyltransferase 2
201970_s_at	NASP	nuclear autoantigenic sperm protein (histone-binding)
212789_at	NCAPD3	non-SMC condensin II complex, subunit D3
218320_s_at	NDUFB11	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11, 17.3kDa
203478_at	NDUFC1	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1, 6kDa
202941_at	NDUFV2	NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa
220731_s_at	NECAP2	NECAP endocytosis associated 2
203045_at	NINJ1	ninjurin 1
204862_s_at	NME3	non-metastatic cells 3, protein expressed in
212739_s_at	NME4	non-metastatic cells 4, protein expressed in
201157_s_at	NMT1	N-myristoyltransferase 1
218244_at	NOL8	nucleolar protein 8
202443_x_at	NOTCH2	Notch homolog 2 (Drosophila)
214722_at	NOTCH2NL	Notch homolog 2 (Drosophila) N-terminal like
202679_at	NPC1	Niemann-Pick disease, type C1
200701_at	NPC2	Niemann-Pick disease, type C2
218086_at	NPDC1	neural proliferation, differentiation and control, 1
204538_x_at	NPIP	nuclear pore complex interacting protein
205129_at	NPM3	nucleophosmin/nucleoplasmin, 3
211671_s_at	NR3C1	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)
206303_s_at	NUDT4	NA
218768_at	NUP107	nucleoporin 107kDa
202397_at	NUTF2	nuclear transport factor 2
200790_at	ODC1	ornithine decarboxylase 1

probeID	gene	Gene.Title
201282_at	OGDH	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)
202074_s_at	OPTN	optineurin
209222_s_at	OSBPL2	oxysterol binding protein-like 2
211778_s_at	OVOL2	ovo-like 2 (Drosophila)
202696_at	OXSRI	oxidative-stress responsive 1
204088_at	P2RX4	purinergic receptor P2X, ligand-gated ion channel, 4
222125_s_at	P4HTM	prolyl 4-hydroxylase, transmembrane (endoplasmic reticulum)
200815_s_at	PAFAH1B1	platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa
203228_at	PAFAH1B3	platelet-activating factor acetylhydrolase, isoform Ib, gamma subunit 29kDa
202336_s_at	PAM	peptidylglycine alpha-amidating monooxygenase
218809_at	PANK2	pantothenate kinase 2
212148_at	PBX1	pre-B-cell leukemia homeobox 1
202847_at	PCK2	phosphoenolpyruvate carboxykinase 2 (mitochondrial)
203370_s_at	PDLIM7	PDZ and LIM domain 7 (enigma)
212053_at	PDXDC1	pyridoxal-dependent decarboxylase domain containing 1
210825_s_at	PEBP1	phosphatidylethanolamine binding protein 1
203972_s_at	PEX3	peroxisomal biogenesis factor 3
201037_at	PFKP	phosphofructokinase, platelet
201968_s_at	PGM1	phosphoglucomutase 1
202738_s_at	PHKB	phosphorylase kinase, beta
212506_at	PICALM	phosphatidylinositol binding clathrin assembly protein
202743_at	PIK3R3	phosphoinositide-3-kinase, regulatory subunit 3 (gamma)
214224_s_at	PIN4	protein (peptidylprolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin)
218942_at	PIP4K2C	phosphatidylinositol-5-phosphate 4-kinase, type II, gamma
205273_s_at	PITRM1	pitrilysin metalloproteinase 1
204267_x_at	PKMYT1	protein kinase, membrane associated tyrosine/threonine 1
210845_s_at	PLAUR	plasminogen activator, urokinase receptor
202185_at	PLOD3	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3
204441_s_at	POLA2	polymerase (DNA directed), alpha 2 (70kD subunit)
218866_s_at	POLR3K	polymerase (RNA) III (DNA directed) polypeptide K, 12.3 kDa
209433_s_at	PPAT	phosphoribosyl pyrophosphate amidotransferase
218010_x_at	PPDPF	NA
201214_s_at	PPP1R7	protein phosphatase 1, regulatory (inhibitor) subunit 7
208874_x_at	PPP2R4	protein phosphatase 2A activator, regulatory subunit 4
201594_s_at	PPP4R1	protein phosphatase 4, regulatory subunit 1
201494_at	PRCP	prolylcarboxypeptidase (angiotensinase C)
39729_at	PRDX2	peroxiredoxin 2
201300_s_at	PRNP	prion protein

probelD	gene	Gene.Title
209161_at	PRPF4	PRP4 pre-mRNA processing factor 4 homolog (yeast)
219127_at	PRR15L	NA
202525_at	PRSS8	protease, serine, 8
209040_s_at	PSMB8	proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional peptidase 7)
212219_at	PSME4	proteasome (prosome, macropain) activator subunit 4
218467_at	PSMG2	proteasome (prosome, macropain) assembly chaperone 2
208820_at	PTK2	PTK2 protein tyrosine kinase 2
200772_x_at	PTMA	prothymosin, alpha
202006_at	PTPN12	protein tyrosine phosphatase, non-receptor type 12
211600_at	PTPRO	protein tyrosine phosphatase, receptor type, O
203554_x_at	PTTG1	pituitary tumor-transforming 1
200677_at	PTTG1IP	pituitary tumor-transforming 1 interacting protein
209336_at	PWP2	PWP2 periodic tryptophan protein homolog (yeast)
212012_at	PXDN	peroxidasin homolog (Drosophila)
212265_at	QKI	quaking homolog, KH domain RNA binding (mouse)
200927_s_at	RAB14	RAB14, member RAS oncogene family
218931_at	RAB17	RAB17, member RAS oncogene family
220964_s_at	RAB1B	RAB1B, member RAS oncogene family
218186_at	RAB25	RAB25, member RAS oncogene family
204214_s_at	RAB32	RAB32, member RAS oncogene family
218699_at	RAB7L1	RAB7, member RAS oncogene family-like 1
209180_at	RABGGTB	Rab geranylgeranyltransferase, beta subunit
205037_at	RABL4	RAB, member of RAS oncogene family-like 4
201244_s_at	RAF1	v-raf-1 murine leukemia viral oncogene homolog 1
202845_s_at	RALBP1	ralA binding protein 1
209050_s_at	RALGDS	ral guanine nucleotide dissociation stimulator
203911_at	RAP1GAP	RAP1 GTPase activating protein
221830_at	RAP2A	RAP2A, member of RAS oncogene family, mRNA (cDNA clone MGC:41795 IMAGE:5278625)
201330_at	RARS	arginyl-tRNA synthetase
219286_s_at	RBM15	RNA binding motif protein 15
218035_s_at	RBM47	RNA binding motif protein 47
212397_at	RDX	radixin
208873_s_at	REEP5	receptor accessory protein 5
219041_s_at	REPIN1	replication initiator 1
218194_at	REXO2	REX2, RNA exonuclease 2 homolog (S. cerevisiae)
202963_at	RFX5	regulatory factor X, 5 (influences HLA class II expression)
218686_s_at	RHBDF1	rhomboid 5 homolog 1 (Drosophila)
212099_at	RHOB	ras homolog gene family, member B
209885_at	RHOD	ras homolog gene family, member D
212120_at	RHOQ	ras homolog gene family, member Q
221647_s_at	RIC8A	resistance to inhibitors of cholinesterase 8 homolog A (C.

probeID	gene	Gene.Title
		elegans)
221215_s_at	RIPK4	receptor-interacting serine-threonine kinase 4
217983_s_at	RNASET2	ribonuclease T2
212724_at	RND3	Rho family GTPase 3
202636_at	RNF103	ring finger protein 103
212155_at	RNF187	ring finger protein 187
218394_at	ROGDI	rogdi homolog (Drosophila)
200715_x_at	RPL13A	ribosomal protein L13a
222229_x_at	RPL26	NA
200018_at	RPS13	ribosomal protein S13
200091_s_at	RPS25	ribosomal protein S25
216342_x_at	RPS4X	ribosomal protein S4, X-linked
203777_s_at	RPS6KB2	ribosomal protein S6 kinase, 70kDa, polypeptide 2
201628_s_at	RRAGA	Ras-related GTP binding A
209567_at	RRS1	RRS1 ribosome biogenesis regulator homolog (S. cerevisiae)
218307_at	RSAD1	radical S-adenosyl methionine domain containing 1
201980_s_at	RSU1	Ras suppressor protein 1
203594_at	RTCD1	RNA terminal phosphate cyclase domain 1
218377_s_at	RWDD2B	RWD domain containing 2B
200872_at	S100A10	S100 calcium binding protein A10
215696_s_at	SEC16A	SEC16 homolog A (S. cerevisiae)
214433_s_at	SELENBP1	selenium binding protein 1
200961_at	SEPHS2	selenophosphate synthetase 2
201194_at	SEPW1	selenoprotein W, 1
217977_at	SEPX1	selenoprotein X, 1
209669_s_at	SERBP1	SERPINE1 mRNA binding protein 1
217756_x_at	SERF2	small EDRK-rich factor 2
219382_at	SERTAD3	SERTA domain containing 3
212465_at	SETD3	SET domain containing 3
218720_x_at	SEZ6L2	NA
221263_s_at	SF3B5	splicing factor 3b, subunit 5, 10kDa
204688_at	SGCE	sarcoglycan, epsilon
209091_s_at	SH3GLB1	SH3-domain GRB2-like endophilin B1
214853_s_at	SHC1	SHC (Src homology 2 domain containing) transforming protein 1
209339_at	SIAH2	seven in absentia homolog 2 (Drosophila)
204404_at	SLC12A2	solute carrier family 12 (sodium/potassium/chloride transporters), member 2
209610_s_at	SLC1A4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4
210010_s_at	SLC25A1	solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1
204342_at	SLC25A24	solute carrier family 25 (mitochondrial carrier; phosphate

probelD	gene	Gene.Title
		carrier), member 24
202825_at	SLC25A4	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4
212833_at	SLC25A46	solute carrier family 25, member 46
209326_at	SLC35A2	solute carrier family 35 (UDP-galactose transporter), member A2
202433_at	SLC35B1	solute carrier family 35, member B1
218826_at	SLC35F2	solute carrier family 35, member F2
212295_s_at	SLC7A1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1
209453_at	SLC9A1	solute carrier family 9 (sodium/hydrogen exchanger), member 1
201349_at	SLC9A3R1	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1
217828_at	SLTM	SAFB-like, transcription modulator
218391_at	SNF8	SNF8, ESCRT-II complex subunit, homolog (S. cerevisiae)
202505_at	SNRPB2	small nuclear ribonucleoprotein polypeptide B"
202567_at	SNRPD3	small nuclear ribonucleoprotein D3 polypeptide 18kDa
207438_s_at	SNUPN	snurportin 1
217789_at	SNX6	sorting nexin 6
205573_s_at	SNX7	sorting nexin 7
222154_s_at	SPATS2L	NA
220192_x_at	SPDEF	SAM pointed domain containing ets transcription factor
202826_at	SPINT1	serine peptidase inhibitor, Kunitz type 1
210715_s_at	SPINT2	serine peptidase inhibitor, Kunitz type, 2
204640_s_at	SPOP	speckle-type POZ protein
46256_at	SPSB3	splA/ryanodine receptor domain and SOCS box containing 3
208921_s_at	SRI	sorcin
200918_s_at	SRPR	signal recognition particle receptor (docking protein)
210378_s_at	SSNA1	Sjogren syndrome nuclear autoantigen 1
200652_at	SSR2	signal sequence receptor, beta (translocon-associated protein beta)
203217_s_at	ST3GAL5	ST3 beta-galactoside alpha-2,3-sialyltransferase 5
204542_at	ST6GALNAC2	ST6 (alpha-N-acetyl-neuraminy-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2
221610_s_at	STAP2	signal transducing adaptor family member 2
218424_s_at	STEAP3	STEAP family member 3
221727_at	SUB1	SUB1 homolog (S. cerevisiae)
44702_at	SYDE1	synapse defective 1, Rho GTPase, homolog 1 (C. elegans)
201079_at	SYNGR2	synaptogyrin 2
221580_s_at	TAF1D	TATA box binding protein (TBP)-associated factor, RNA polymerase I, D, 41kDa
210978_s_at	TAGLN2	transgelin 2

probelD	gene	Gene.Title
202307_s_at	TAP1	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)
208829_at	TAPBP	TAP binding protein (tapasin)
213400_s_at	TBL1X	transducin (beta)-like 1X-linked
200085_s_at	TCEB2	transcription elongation factor B (SIII), polypeptide 2 (18kDa, elongin B)
213311_s_at	TCF25	transcription factor 25 (basic helix-loop-helix)
219715_s_at	TDP1	tyrosyl-DNA phosphodiesterase 1
218104_at	TEX10	testis expressed 10
218099_at	TEX2	testis expressed 2
204623_at	TFF3	trefoil factor 3 (intestinal)
212910_at	THAP11	THAP domain containing 11
203167_at	TIMP2	TIMP metalloproteinase inhibitor 2
212770_at	TLE3	transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila)
200804_at	TMBIM6	transmembrane BAX inhibitor motif containing 6
212507_at	TMEM131	transmembrane protein 131
218531_at	TMEM134	transmembrane protein 134
202475_at	TMEM147	transmembrane protein 147
213285_at	TMEM30B	transmembrane protein 30B
212202_s_at	TMEM87A	transmembrane protein 87A
221255_s_at	TMEM93	transmembrane protein 93
202510_s_at	TNFAIP2	tumor necrosis factor, alpha-induced protein 2
207196_s_at	TNIP1	TNFAIP3 interacting protein 1
202704_at	TOB1	transducer of ERBB2, 1
204080_at	TOE1	target of EGR1, member 1 (nuclear)
201291_s_at	TOP2A	topoisomerase (DNA) II alpha 170kDa
210372_s_at	TPD52L1	tumor protein D52-like 1
210052_s_at	TPX2	TPX2, microtubule-associated, homolog (Xenopus laevis)
204985_s_at	TRAPPC6A	trafficking protein particle complex 6A
218145_at	TRIB3	tribbles homolog 3 (Drosophila)
202734_at	TRIP10	thyroid hormone receptor interactor 10
209129_at	TRIP6	thyroid hormone receptor interactor 6
208763_s_at	TSC22D3	TSC22 domain family, member 3
218245_at	TSKU	tsukushin
209114_at	TSPAN1	tetraspanin 1
217979_at	TSPAN13	tetraspanin 13
200973_s_at	TSPAN3	tetraspanin 3
209605_at	TST	thiosulfate sulfurtransferase (rhodanese)
209191_at	TUBB6	tubulin, beta 6
221253_s_at	TXNDC5	thioredoxin domain containing 5
201008_s_at	TXNIP	thioredoxin interacting protein
205546_s_at	TYK2	tyrosine kinase 2

probeID	gene	Gene.Title
202589_at	TYMS	thymidylate synthetase
208980_s_at	UBC	NA
212519_at	UBE2E1	ubiquitin-conjugating enzyme E2E 1 (UBC4/5 homolog, yeast)
210024_s_at	UBE2E3	ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast)
209142_s_at	UBE2G1	ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, yeast)
202038_at	UBE4A	ubiquitination factor E4A (UFD2 homolog, yeast)
209825_s_at	UCK2	uridine-cytidine kinase 2
209103_s_at	UFD1L	ubiquitin fusion degradation 1 like (yeast)
218757_s_at	UPF3B	UPF3 regulator of nonsense transcripts homolog B (yeast)
218190_s_at	UQCR10	NA
208970_s_at	UROD	uroporphyrinogen decarboxylase
218367_x_at	USP21	ubiquitin specific peptidase 21
212513_s_at	USP33	ubiquitin specific peptidase 33
218715_at	UTP6	UTP6, small subunit (SSU) processome component, homolog (yeast)
202546_at	VAMP8	vesicle-associated membrane protein 8 (endobrevin)
208780_x_at	VAPA	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa
200931_s_at	VCL	vinculin
217821_s_at	WBP11	WW domain binding protein 11
218512_at	WDR12	WD repeat domain 12
202908_at	WFS1	Wolfram syndrome 1 (wolframin)
200670_at	XBP1	X-box binding protein 1
219704_at	YBX2	Y box binding protein 2

FIGURE 5B

gene	Docetaxel	Paclitaxel	Doxorubicin	Epirubicin	Fluorouracil	Gemcitabine	Cyclophosphamide
AAGAB	0.73	0.69	0.74	0.74	0.75	0.64	0.66
ABCC1	1.25	1.52	1.45	1.41	1.46	1.35	1.52
ABR	1.31	1.2	1.4	1.39	1.32	1.49	1.26
ACAA2	1.59	2.09	2.04	2.01	1.77	2	2.21
ACTN1	1.56	1.64	1.52	1.56	1.31	1.28	1.34
ACVR1B	0.82	0.81	0.75	0.75	0.87	0.73	0.69
ADM	1.16	2.19	1.88	1.84	1.37	1.29	2.36
AES	0.72	0.71	0.68	0.66	0.79	0.78	0.64
AGPAT1	1.25	1.33	1.34	1.35	1.21	1.18	1.39
AGR2	0.5	0.34	0.5	0.59	0.4	0.51	0.62
AHCY	1.27	1.24	1.43	1.36	1.22	1.52	1.27
AKR7A3	0.67	0.66	0.69	0.62	0.8	0.69	0.58
AKTIP	0.78	0.9	0.59	0.62	0.49	0.57	0.74
ALDH3B2	0.28	0.23	0.27	0.26	0.72	0.29	0.42
ALDH4A1	0.37	0.35	0.42	0.39	0.63	0.42	0.58
ALDH9A1	0.83	0.79	0.74	0.75	0.64	0.71	0.76
ALDOA	0.66	0.73	0.73	0.71	0.77	0.8	0.8
AMPD2	1.36	1.62	1.33	1.36	1.19	1.07	1.01
ANP32E	2.09	2.63	2.38	2.57	1.62	2.08	3.05
ANXA11	1.37	1.7	1.29	1.44	1.12	1.52	1.3
AP1G2	0.92	0.83	0.65	0.62	0.73	0.7	0.67
AP1M2	0.71	0.76	0.69	0.68	0.6	0.62	1.09
APP	1.93	1.94	1.73	1.64	1.2	1.78	1.76
ARCN1	1.62	1.58	1.4	1.36	1.11	1.2	1.3
ARF5	0.73	0.82	0.72	0.73	0.91	0.82	0.71
ARFGEF1	0.79	0.61	0.62	0.58	0.62	0.62	0.51
ARHGEF18	1.51	1.55	1.24	1.23	0.98	1.16	1.27
ARHGEF2	1.28	1.36	1.31	1.31	1.15	1.4	1.5
ARID5B	0.62	0.57	0.59	0.59	0.58	0.73	1.07
ARL8B	1.39	1.59	1.35	1.29	1.39	1.76	1.22
ASPM	1.79	1.66	1.58	1.53	1.31	1.21	1.41
ATP1B3	1.57	1.66	1.42	1.45	1.15	1.42	1.72
ATP5I	0.83	0.79	0.84	0.82	1.01	0.83	0.65
ATP5O	1.18	1.3	1.23	1.22	1.05	1.24	1.2
ATP6AP1	0.46	0.52	0.63	0.63	0.85	0.73	0.86
ATP6AP2	0.68	0.73	0.81	0.78	0.75	0.82	0.9
ATP6V0C	0.69	0.7	0.77	0.77	0.85	0.76	0.87
ATP6V0D1	0.68	0.59	0.66	0.61	0.74	0.51	0.6
ATP6V0E2	0.33	0.36	0.49	0.51	0.89	0.62	0.7
ATP6V1G1	0.73	0.67	0.66	0.64	0.7	0.67	0.65
AURKB	1.56	1.49	1.74	1.68	1.61	1.46	1.66

gene	Docetaxel	Paclitaxel	Doxorubicin	Epirubicin	Fluorouracil	Gemcitabine	Cyclophosphamide
B4GALT5	1.84	1.96	1.43	1.5	1.33	1.74	1.44
BAG5	0.96	0.85	0.83	0.79	0.86	0.71	0.74
BAMBI	0.65	0.48	0.44	0.4	0.86	0.76	0.66
BANF1	0.87	0.82	0.86	0.85	0.77	0.71	1.03
BASP1	2.36	2.81	3.84	3.84	4.55	3.8	3.25
BCAM	0.6	0.64	0.64	0.71	0.83	0.72	0.54
BCR	0.77	0.75	0.71	0.7	0.73	0.76	0.76
BIRC2	2.7	2.35	2.05	1.93	1.25	1.59	2.14
BLOC1S1	0.65	0.66	0.79	0.85	0.99	0.78	0.83
BLVRB	0.53	0.42	0.39	0.46	0.54	0.41	0.45
BMS1	1.4	1.45	1.41	1.42	1.21	1.21	1.3
BSPRY	0.79	0.84	0.64	0.64	0.76	0.66	0.68
BTG3	2.54	2.5	1.79	1.74	1.27	2.54	3.15
BZW1	0.76	0.77	0.75	0.79	0.85	0.67	0.64
C10ORF116	0.26	0.28	0.24	0.3	0.42	0.41	0.27
C11ORF10	1.16	1.22	1.39	1.42	1.2	1.23	1.63
C20ORF11	0.71	0.62	0.66	0.62	0.72	0.66	0.65
C3ORF14	0.38	0.42	0.54	0.53	1.07	0.55	0.52
C8ORF55	0.53	0.53	0.51	0.53	0.71	0.68	0.75
C9ORF16	0.81	0.67	0.56	0.57	0.63	0.55	0.74
CA12	0.27	0.35	0.59	0.63	0.71	0.45	0.66
CALM1	0.64	0.61	0.61	0.6	0.68	0.72	0.48
CALR	1.69	1.48	1.72	1.7	1.43	1.79	2.04
CAMKK2	1.16	1.3	1.64	1.75	1.89	1.42	1.65
CAMSAP1L1	2.13	2.6	2.29	2.23	1.85	1.96	1.6
CAP1	1.13	1.27	1.37	1.47	1.14	1.19	1.38
CAPG	2.34	3.12	2.19	2.23	1.51	2.1	3.42
CAPZB	0.68	0.71	0.73	0.74	0.82	0.68	0.68
CARHSP1	0.75	0.76	0.77	0.74	0.87	0.76	0.9
CARS	1.18	1.39	1.58	1.66	1.36	1.12	1.34
CASC3	1.92	3.13	2.53	2.4	1.47	2.79	2.15
CASK	0.57	0.63	0.62	0.68	0.57	0.65	0.65
CAT	0.68	0.64	0.74	0.88	0.58	0.53	0.9
CBR1	2.71	2.83	2.43	2.49	1.67	2.37	2.68
CCDC90B	1.43	1.54	1.62	1.62	1.05	1.21	2.04
CCT8	1.33	1.41	1.61	1.49	1.19	1.44	1.48
CD24	0.79	0.84	0.53	0.48	0.6	0.64	0.71
CD9	0.47	0.57	0.35	0.42	0.43	0.5	0.47
CDC123	1.48	1.57	1.58	1.58	1.38	1.42	1.56
CDC20	1.83	1.72	1.76	1.77	1.34	1.23	1.97
CDC25B	2.01	2.13	1.74	1.77	1.76	1.71	1.63
CDH1	0.57	0.31	0.38	0.31	0.5	0.32	0.53

gene	Docetaxel	Paclitaxel	Doxorubicin	Epirubicin	Fluorouracil	Gemcitabine	Cyclophosphamide
CDKN1B	0.69	0.57	0.6	0.57	0.8	0.51	0.64
CEBPD	1.36	3.59	2.87	2.56	1.94	1.85	4.26
CELF1	1.33	1.4	1.46	1.45	1.22	1.18	1.4
CHMP1A	0.93	0.8	0.79	0.78	0.76	0.76	0.91
CHST3	1.42	1.46	1.35	1.33	1.27	1.36	1.45
CISD1	1.45	1.69	1.88	1.95	1.42	1.75	1.7
CKAP5	1.43	1.46	1.48	1.47	1.27	1.15	1.48
CKS2	1.24	1.53	1.55	1.5	1.29	1.3	1.7
CLDN4	0.68	0.63	0.61	0.66	0.72	0.76	0.74
CLIC4	2.02	1.94	1.71	1.78	1.37	1.46	1.65
CLTC	0.74	0.59	0.62	0.64	0.72	0.61	0.54
CNOT7	1.92	2.45	2.53	2.19	1.83	1.97	2.29
CNP	1.61	1.67	1.46	1.41	1.26	1.62	1.41
COMT	0.54	0.55	0.49	0.49	0.6	0.7	0.44
COPG	0.87	0.76	0.75	0.76	0.78	0.89	0.78
COPS3	1.63	1.51	1.66	1.63	1.39	1.45	1.55
COX4I1	0.8	0.75	0.76	0.72	0.71	0.66	0.88
COX6A1	0.65	0.63	0.77	0.79	0.99	0.8	0.94
COX6C	0.66	0.74	0.69	0.73	0.75	0.77	0.76
CREB3L1	0.63	0.61	0.73	0.79	0.77	0.87	0.75
CRIP2	0.82	0.57	0.71	0.64	0.92	0.76	0.7
CRYZ	1.39	1.59	2.31	2.34	1.85	2.17	2.52
CSNK2A1	1.28	1.26	1.21	1.26	1.15	1.28	1.34
CTCF	0.82	0.72	0.77	0.72	0.76	0.62	0.66
CTNNA1	0.8	0.86	0.74	0.77	0.79	0.88	0.66
CTSC	1.89	3.14	3.4	3.27	2.55	3.05	3.85
CUL5	1.91	2	1.85	1.76	1.21	1.34	1.65
CUTA	1.26	1.45	1.69	1.72	1.41	1.37	1.64
CXORF40A	0.43	0.46	0.71	0.71	0.98	0.61	0.99
CXORF40B	0.45	0.47	0.73	0.72	1.04	0.64	1.03
CYB561	0.55	0.51	0.5	0.49	0.68	0.6	0.56
CYR61	4.33	3.42	3.51	3.97	1.59	2.59	3.82
DALRD3	0.65	0.62	0.6	0.53	0.67	0.64	0.53
DAZAP2	1.03	0.86	0.85	0.8	0.9	0.84	0.67
DBI	0.66	0.59	0.58	0.57	0.67	0.72	0.66
DDX10	1.56	1.48	1.56	1.53	1.18	1.27	1.38
DDX21	2.24	2.57	2.35	2.3	1.92	2.32	1.65
DENND5A	1.33	1.48	1.75	1.68	1.81	1.69	1.41
DERL2	1.58	1.51	1.67	1.7	1.36	1.41	1.52
DHX16	1.16	1.28	1.25	1.27	1.09	1	1.19
DIAPH1	1.32	1.55	1.21	1.26	1.2	1.24	1.1
DIDO1	0.84	0.83	0.77	0.77	0.77	0.9	0.81

gene	Docetaxel	Paclitaxel	Doxorubicin	Epirubicin	Fluorouracil	Gemcitabine	Cyclophosphamide
DIMT1L	1.8	1.79	1.54	1.59	1.16	1.55	1.65
DKFZP58611420	0.8	0.72	0.65	0.61	0.69	0.66	0.54
DLGAP5	2	2.03	2.23	2.21	1.53	1.52	2.04
DNAJC7	1.47	1.69	1.51	1.42	1.3	1.53	1.27
DNPEP	0.89	0.91	0.81	0.76	0.87	0.82	0.75
DPP3	0.76	0.76	0.73	0.72	0.73	0.66	0.83
DSG2	2.72	2.93	2.75	2.53	2.27	2.82	2.49
DULLARD	1.22	1.28	1.43	1.47	1.41	1.44	1.39
EBAG9	0.64	0.63	0.59	0.78	0.69	0.61	0.51
EBNA1BP2	1.26	1.43	1.69	1.77	1.33	1.37	1.85
ECHDC3	1.32	1.46	1.57	1.54	1.42	1.59	1.37
EDEM1	1.05	1.36	1.26	1.33	1.18	1.39	1.31
EED	1.78	1.91	1.67	1.69	1.04	1.16	1.62
EFEMP1	3.55	5.39	2.69	2.61	2.26	3.86	2.17
EFHD1	0.53	0.56	0.54	0.54	0.57	0.5	0.7
EGFR	3.18	2.72	2.83	2.33	0.44	0.43	2.34
EHD2	1.47	1.57	1.66	1.71	1.78	1.94	1.41
EIF1	1.5	1.4	1.34	1.15	1.21	1.35	1.05
EIF3F	1.61	1.56	1.57	1.41	1.51	1.45	1.08
ELOVL1	1.05	1.17	1.29	1.36	1.33	1.3	1.25
EMP2	0.63	0.65	0.58	0.58	0.49	0.64	0.61
ENOPH1	0.8	0.81	0.76	0.77	0.73	0.76	0.71
EPCAM	0.65	0.57	0.4	0.38	0.56	0.48	0.52
EPS8L1	0.64	0.75	0.77	0.79	0.58	0.73	0.89
ERBB3	0.59	0.47	0.52	0.51	0.58	0.48	0.55
ERGIC2	0.85	0.74	0.78	0.76	0.73	0.75	0.66
ERP44	1.83	1.81	1.44	1.33	1.41	1.6	1.21
ESRP1	0.64	0.44	0.39	0.38	0.44	0.33	0.55
ESRP2	0.61	0.51	0.54	0.5	0.63	0.45	0.45
EXT1	1.68	2.1	1.89	2.06	1.52	1.59	2.05
FADD	0.61	0.63	0.75	0.72	1.03	0.8	0.67
FAM102A	0.6	0.51	0.53	0.54	0.75	0.56	0.64
FAM128A	0.73	0.71	0.79	0.77	0.98	0.81	0.84
FAM189B	1.4	1.59	1.49	1.48	1.29	1.66	1.53
FAM64A	1.47	1.37	1.43	1.4	1.34	1.26	1.26
FASTKD5	1.23	1.33	1.18	1.34	1.16	1.2	1.18
FBXO9	0.67	0.77	0.72	0.73	0.63	0.68	0.81
FDPS	1.16	1.46	1.43	1.65	1.3	1.42	1.57
FDX1	2.27	2.03	1.81	1.79	1.26	1.37	1.71
FERMT2	2.61	3.98	4.1	4.27	2.73	3.64	4.76
FEZ2	1.87	2.04	1.98	2.03	1.17	1.84	1.77
FHL2	1.69	2.25	2.05	3.1	0.71	0.83	1.35

gene	Docetaxel	Paclitaxel	Doxorubicin	Epirubicin	Fluorouracil	Gemcitabine	Cyclophosphamide
FKBP1A	1.99	1.85	1.64	1.68	1.42	1.73	1.71
FKBP4	0.53	0.43	0.56	0.56	0.7	0.47	0.52
FN1	2.01	3.41	5.34	5.55	4.95	5.82	5.45
FOXA1	0.37	0.26	0.33	0.34	0.61	0.3	0.36
FXR1	1.93	1.72	1.58	1.45	1.22	1.41	1.42
FXYD3	0.36	0.5	0.32	0.35	0.46	0.55	0.65
FXYD5	3.7	3.39	3.01	3.14	1.51	1.87	2.6
G3BP1	1.71	1.96	1.72	1.77	1.37	1.59	1.74
G6PD	0.43	0.53	0.45	0.45	0.7	0.5	0.37
GALNT6	0.32	0.68	0.66	0.71	0.6	0.68	0.5
GANAB	1.2	1.23	1.39	1.39	1.37	1.21	1.76
GAPDH	0.81	0.84	0.79	0.74	0.79	0.86	0.83
GART	1.39	1.74	1.6	1.69	1.31	1.32	1.59
GCAT	0.64	0.62	0.63	0.66	0.71	0.67	0.78
GCHFR	0.61	0.54	0.52	0.43	0.61	0.63	0.37
GDE1	0.59	0.54	0.6	0.57	0.68	0.48	0.63
GEMIN6	1.18	1.34	1.39	1.39	1.27	1.28	1.18
GFPT1	1.1	0.92	0.69	0.63	0.74	0.77	0.6
GGCT	0.73	0.64	0.63	0.58	0.66	0.63	0.59
GIN52	0.84	0.66	0.87	0.88	0.68	0.59	0.84
GLA	1.15	1.34	1.57	1.65	1.94	1.5	1.74
GNG12	1.81	2.04	2.31	2.55	1.75	1.78	2.02
GNPDA1	1.08	1.31	1.25	1.35	1.29	1.37	1.38
GORASP2	0.71	0.74	0.69	0.71	0.69	0.68	0.65
GPR56	0.56	0.6	0.42	0.46	0.43	0.46	0.46
GPX2	0.48	0.49	0.38	0.39	0.46	0.52	0.43
GRHL2	0.72	0.57	0.51	0.53	0.54	0.45	0.61
GTF2E2	1.5	1.61	1.87	1.81	1.46	1.55	1.84
GTF3A	0.68	0.79	0.78	0.8	0.77	0.72	0.77
GTPBP4	1.66	1.56	1.63	1.59	1.37	1.55	1.49
GTPBP6	0.82	0.82	0.84	0.87	0.99	0.9	0.76
GUK1	0.91	0.7	0.7	0.62	0.81	0.77	0.68
H1F0	0.71	0.6	0.52	0.5	0.49	0.7	0.66
H1FX	0.71	0.51	0.62	0.61	0.71	0.56	0.75
HARS	1.54	1.71	1.74	1.78	1.5	1.69	1.36
HEBP1	0.64	0.69	0.64	0.65	0.77	0.61	0.76
HGS	1.27	1.14	1.2	1.15	1.15	1.24	1.13
HIST1H2AC	0.42	0.68	0.55	0.54	0.54	0.46	1.5
HIST1H2BK	0.8	0.73	0.71	0.68	0.77	0.59	0.9
HJURP	1.36	1.43	1.47	1.44	1.29	1.22	1.25
HLA-E	2.08	2.18	1.83	1.82	1.04	1.18	2.39
HMGN2	0.78	0.76	0.87	0.85	0.91	0.75	0.95

gene	Docetaxel	Paclitaxel	Doxorubicin	Epirubicin	Fluorouracil	Gemcitabine	Cyclophosphamide
HMGN4	1.69	2.2	2.03	2.02	1.49	1.33	2.03
HN1L	0.8	0.75	0.79	0.78	0.75	0.74	0.71
HNRNPH3	1.58	1.69	1.78	1.72	1.35	1.23	1.53
HSD17B10	0.56	0.54	0.68	0.67	0.88	0.72	0.93
HTRA2	1.11	1.29	1.28	1.34	1.3	1.28	1.39
HYOU1	1.74	1.49	1.48	1.46	1.13	1.45	1.63
IARS	1.24	1.48	1.34	1.42	1.3	1.2	1.4
ICA1	0.8	0.67	0.77	0.69	0.81	0.64	0.76
ID3	1.19	1.45	1.78	1.82	2.27	1.63	2.05
IDH3B	1.24	1.49	1.36	1.4	1.19	1.31	1.55
IER3	1.34	1.89	1.87	2.11	1.22	1.21	2.24
IER5	1.71	1.76	1.46	1.41	0.8	0.92	1.94
IFITM2	2	2.32	1.41	1.44	1.02	1.52	2.05
IFITM3	2.57	2.7	1.65	1.67	1.07	1.82	3.49
IFT122	0.67	0.66	0.74	0.7	0.73	0.76	0.77
IGFBP2	0.25	0.27	0.4	0.4	0.3	0.28	0.44
IGFBP5	0.18	0.29	0.38	0.44	0.46	0.27	0.6
ILF3	1.95	2.02	2.02	2.02	1.44	1.41	2.08
IMPA1	2.33	2.58	2.85	2.66	2.01	2.66	2.52
IRX5	0.4	0.31	0.33	0.31	0.5	0.23	0.44
ISCU	0.91	0.82	0.79	0.86	0.74	0.73	0.71
ISOC1	0.46	0.53	0.46	0.42	0.7	0.43	0.37
ITPK1	0.74	0.65	0.61	0.64	0.82	0.72	0.53
JUND	0.73	0.71	0.75	0.73	0.86	0.62	0.76
JUP	0.78	0.76	0.65	0.64	0.73	0.75	0.68
KIAA0020	1.43	2.05	1.82	1.75	1.51	1.78	1.86
KIAA0182	0.83	0.47	0.64	0.56	0.55	0.39	0.66
KIAA0232	0.59	0.62	0.54	0.57	0.69	0.55	0.48
KIAA0247	0.6	0.59	0.51	0.52	0.64	0.65	0.53
KIAA0907	1.42	1.73	1.52	1.6	1.06	1.3	1.69
KIF18B	1.73	1.7	1.61	1.58	1.29	1.36	1.42
KIF2C	1.66	1.67	1.77	1.77	1.44	1.2	1.83
KRT10	1.66	1.66	1.15	1.1	0.91	1.09	1.3
LAMC1	1.61	1.72	1.98	1.88	1.87	1.92	2.35
LARP1	1.77	1.79	1.58	1.59	1.43	1.6	1.31
LBR	1.79	1.88	1.82	1.82	1.43	1.48	1.79
LDLRAP1	0.81	0.82	0.79	0.79	0.88	0.81	0.74
LGALS1	1.4	2.01	1.69	1.77	1.5	2.03	1.62
LIPA	1.36	1.45	1.66	1.83	1.44	1.3	1.35
LOC339047	0.88	0.81	0.84	0.83	0.9	0.75	0.96
LOC399491	0.92	0.86	0.85	0.84	0.88	0.79	0.95
LOC552889	0.77	0.7	0.83	0.83	0.91	0.66	0.85

gene	Docetaxel	Paclitaxel	Doxorubicin	Epirubicin	Fluorouracil	Gemcitabine	Cyclophosphamide
LPHN1	0.66	0.63	0.64	0.64	0.73	0.76	0.81
LPIN1	1.37	1.29	1.32	1.33	1.19	1.49	1.35
LRBA	0.69	0.62	0.57	0.52	0.61	0.57	0.49
LRFN4	1.31	1.42	1.54	1.55	1.68	1.4	1.64
LSR	0.67	0.69	0.52	0.53	0.65	0.56	0.97
MAK16	1.84	2.1	2.2	2.05	1.59	1.85	1.91
MANF	1.21	1.19	1.42	1.41	1.2	1.65	1.59
MAP7D1	1.46	1.45	1.5	1.53	1.43	1.43	1.58
MAPK13	0.5	0.44	0.52	0.49	0.44	0.37	0.65
MAPKSP1	0.7	0.74	0.7	0.72	0.73	0.76	0.65
MB	0.85	0.82	0.66	0.56	0.7	0.89	0.57
MBNL1	2.56	2.27	1.74	1.7	1.23	1.73	1.75
MCF2L	0.86	0.71	0.72	0.72	0.81	0.68	0.84
MCTS1	1.23	1.45	1.46	1.45	1.23	1.16	1.23
METRNL	0.54	0.72	0.73	0.74	0.76	0.94	0.76
METTL3	1.03	1.22	1.3	1.29	1.24	1.38	1.29
METTL7A	0.66	0.47	0.55	0.54	0.55	0.47	0.47
MGAT1	1.23	1.44	1.35	1.39	1.24	1.28	1.29
MKKS	1.34	1.52	1.33	1.4	1.19	1.44	1.2
MKL2	0.64	0.57	0.65	0.62	0.75	0.54	0.61
MOAP1	0.63	0.56	0.63	0.63	0.89	0.54	0.51
MPRIIP	1.47	1.43	1.5	1.54	1.38	1.4	1.36
MREG	0.45	0.56	0.55	0.59	0.76	0.63	0.48
MRPL35	1.3	1.59	1.47	1.42	1.21	1.44	1.61
MRPL39	1.43	1.65	1.76	1.63	1.25	1.6	1.75
MRPS22	1.38	1.46	1.38	1.36	1.14	1.29	1.29
MRPS30	1.51	1.64	1.42	1.38	1.22	1.23	1.41
MRPS34	0.73	0.81	0.84	0.83	0.84	0.83	0.81
MRPS35	0.87	0.75	0.74	0.69	0.69	0.68	0.67
MSL1	2.64	4.9	4	3.51	2.54	5.51	2.29
MTCH2	1.34	1.33	1.32	1.3	1.01	1.16	1.36
MTFR1	0.94	0.78	0.84	0.78	0.85	0.86	0.75
MTMR3	0.9	0.82	0.74	0.71	0.77	0.82	0.76
MYL6	0.72	0.72	0.78	0.8	0.86	0.77	0.77
MYL6B	1.01	1.11	1.42	1.41	1.55	1.37	1.41
MYO5C	0.65	0.71	0.56	0.59	0.58	0.54	0.52
MYST2	0.7	0.57	0.67	0.7	0.85	0.61	0.78
NASP	1.6	1.63	1.78	1.82	1.56	1.36	1.98
NCAPD3	1.51	1.4	1.36	1.33	1.04	1.1	1.41
NDUFB11	0.64	0.59	0.69	0.69	0.73	0.73	0.71
NDUFC1	0.61	0.71	0.65	0.66	0.72	0.74	0.72
NDUFV2	1.45	1.37	1.32	1.2	1.02	1.09	1.18

gene	Docetaxel	Paclitaxel	Doxorubicin	Epirubicin	Fluorouracil	Gemcitabine	Cyclophosphamide
NECAP2	1.19	1.3	1.3	1.29	1.24	1.19	1.27
NINJ1	0.72	0.78	0.74	0.78	0.9	0.7	0.68
NME3	0.6	0.61	0.64	0.6	0.75	0.76	0.71
NME4	0.57	0.48	0.77	0.72	1.01	0.81	0.86
NMT1	1.5	1.59	1.46	1.4	1.12	1.34	1.23
NOL8	1.29	1.86	1.53	1.49	1.4	1.37	1.73
NOTCH2	1.28	1.85	1.59	1.52	1.25	1.29	1.42
NOTCH2NL	2.21	2.33	2.04	2.02	1.83	1.53	1.8
NPC1	1.49	2.51	2.1	1.93	1.9	2.38	2.51
NPC2	1.42	1.58	1.79	1.72	1.73	1.85	1.38
NPDC1	0.54	0.46	0.54	0.53	0.68	0.51	0.53
NPIP	0.91	0.84	0.84	0.82	0.91	0.77	0.99
NPM3	1.35	1.58	1.61	1.62	1.43	1.64	1.45
NR3C1	2.34	2.89	2.58	2.44	2.28	1.99	2.42
NUDT4	0.55	0.54	0.58	0.63	0.61	0.58	0.56
NUP107	1.41	1.61	1.55	1.51	1.22	1.52	1.51
NUTF2	0.84	0.74	0.78	0.75	0.69	0.69	0.77
ODC1	1.8	2.17	1.99	2.05	1.49	2.03	2.29
OGDH	1.31	1.31	1.32	1.38	1.39	1.32	1.37
OPTN	2.43	2.53	2.55	2.5	2.02	2.04	3.37
OSBPL2	0.72	0.68	0.67	0.64	0.73	0.69	0.66
OVOL2	0.82	0.74	0.56	0.55	0.7	0.74	0.6
OXSRI	1.75	2.23	1.88	1.81	1.5	1.82	1.49
P2RX4	0.65	0.63	0.72	0.73	0.77	0.68	0.84
P4HTM	0.68	0.68	0.7	0.67	0.96	0.78	0.63
PAFAH1B1	1.41	1.58	1.59	1.5	1.42	1.17	1.35
PAFAH1B3	0.65	0.6	0.71	0.69	0.83	0.63	0.74
PAM	4	2.28	1.76	1.71	1.12	3.56	3.32
PANK2	1.72	1.76	1.45	1.53	1.15	1.22	1.58
PBX1	0.72	0.71	0.52	0.5	0.55	0.73	0.4
PCK2	0.52	0.49	0.65	0.66	1.04	0.62	1.1
PDLIM7	1.5	1.63	1.75	1.76	1.62	1.54	1.39
PDXDC1	0.78	0.63	0.63	0.63	0.71	0.61	0.62
PEBP1	0.7	0.63	0.72	0.73	0.82	0.73	0.81
PEX3	1.29	1.5	1.29	1.28	1.09	1.33	1.35
PFKP	2.04	1.84	2.22	1.9	2.1	2.13	1.56
PGM1	2.07	2.26	2.11	1.8	1.37	1.67	2.29
PHKB	0.82	0.76	0.6	0.61	0.58	0.58	0.47
PICALM	1.52	1.87	1.65	1.63	1.12	1.29	1.78
PIK3R3	0.48	0.52	0.51	0.56	0.6	0.42	0.63
PIN4	1.32	1.47	1.41	1.4	1.31	1.52	1.33
PIP4K2C	0.87	0.82	0.76	0.76	0.83	0.75	0.77

gene	Docetaxel	Paclitaxel	Doxorubicin	Epirubicin	Fluorouracil	Gemcitabine	Cyclophosphamide
PITRM1	1.56	1.49	1.61	1.77	1.53	1.42	1.34
PKMYT1	0.82	0.78	0.79	0.83	0.92	0.82	0.78
PLAUR	1.81	2.15	1.89	1.86	1.18	1.72	2.1
PLOD3	1.28	1.16	1.25	1.27	1.39	1.97	1.53
POLA2	0.74	0.75	0.72	0.75	0.79	0.7	0.81
POLR3K	0.76	0.83	0.83	0.86	0.9	0.86	0.77
PPAT	1.34	1.71	1.54	1.67	1.43	1.63	1.38
PPDPF	0.5	0.48	0.55	0.54	0.72	0.59	0.58
PPP1R7	0.72	0.75	0.82	0.8	0.86	0.75	0.86
PPP2R4	0.79	0.71	0.77	0.77	0.9	0.78	0.78
PPP4R1	1.94	1.8	1.78	1.74	1.22	1.21	1.64
PRCP	1.69	1.54	1.7	1.67	1.29	2.01	1.8
PRDX2	0.55	0.58	0.72	0.71	0.85	0.61	0.98
PRNP	7.99	4.5	2.14	2.13	1.48	2.27	3.45
PRPF4	1.29	1.4	1.3	1.32	1.19	1.17	1.41
PRR15L	0.82	0.64	0.38	0.32	0.42	0.71	0.39
PRSS8	0.7	0.82	0.76	0.73	0.79	0.91	0.9
PSMB8	2.71	2.8	2.22	2.29	1.14	0.91	4.15
PSME4	1.43	1.53	1.48	1.45	1.35	1.37	1.43
PSMG2	1.76	1.57	1.37	1.23	0.94	0.95	1.39
PTK2	0.61	0.64	0.64	0.69	0.6	0.67	0.77
PTMA	0.84	0.81	0.78	0.74	0.83	0.86	0.81
PTPN12	1.49	1.83	1.61	1.61	1.33	1.52	1.63
PTPRO	0.74	0.58	0.66	0.66	0.81	0.66	0.83
PTTG1	1.4	1.4	1.4	1.4	1.07	1.12	1.64
PTTG1IP	1.38	1.32	1.33	1.36	1.31	1.85	1.31
PWP2	1.41	1.27	1.24	1.23	1.06	1.39	1.4
PXDN	2.28	2.34	2.71	3	2.36	2.29	2
QKI	2.05	2.72	2.33	2.39	1.65	2.39	2.55
RAB14	1.06	0.9	0.83	0.76	0.74	0.79	0.77
RAB17	0.81	0.85	0.76	0.76	0.8	0.76	0.62
RAB1B	0.65	0.62	0.66	0.67	0.62	0.64	0.77
RAB25	0.7	0.75	0.56	0.56	0.5	0.65	0.63
RAB32	1.04	1.49	2.01	2.08	1.95	2.16	2.27
RAB7L1	1.33	1.7	1.7	1.63	1.45	1.85	1.41
RABGGTB	2.04	2.24	2.2	2.12	1.73	1.82	1.67
RABL4	0.48	0.46	0.53	0.54	0.69	0.55	0.58
RAF1	1.46	1.52	1.41	1.44	1.33	1.27	1.49
RALBP1	2.32	2.06	1.58	1.52	1.17	1.24	1.69
RALGDS	0.91	0.83	0.89	0.87	1.07	0.71	0.97
RAP1GAP	0.64	0.73	0.6	0.68	0.79	0.73	0.5
RAP2A	1.52	1.67	1.61	1.54	1.42	1.35	1.41

gene	Docetaxel	Paclitaxel	Doxorubicin	Epirubicin	Fluorouracil	Gemcitabine	Cyclophosphamide
RARS	1.37	1.4	1.3	1.27	1	1.06	1.39
RBM15	1.58	1.49	1.5	1.36	1.14	1.22	1.44
RBM47	0.47	0.46	0.32	0.32	0.41	0.4	0.32
RDX	3.6	3.79	4.07	3.88	3.11	2.66	3
REEP5	0.57	0.49	0.53	0.53	0.48	0.5	0.39
REPIN1	0.85	0.8	0.72	0.68	0.82	0.77	0.71
REXO2	2.23	1.78	1.7	1.81	1.09	1.2	1.84
RFX5	1.36	1.38	1.35	1.3	1.28	1.41	1.37
RHBDF1	0.71	0.69	0.69	0.71	0.76	0.7	0.78
RHOB	0.26	0.33	0.34	0.31	0.61	0.41	0.31
RHOD	0.77	0.71	0.82	0.83	0.77	0.55	0.83
RHOQ	1.5	1.73	1.86	1.97	1.88	2.29	1.73
RIC8A	1.14	1.42	1.55	1.7	1.4	1.32	1.29
RIPK4	2.57	2.43	1.56	1.61	1.23	1.34	1.45
RNASET2	0.57	0.87	0.82	0.79	0.71	1.17	0.93
RND3	1.58	1.83	1.4	1.46	1.01	1.3	2.41
RNF103	0.59	0.59	0.62	0.6	0.86	0.64	0.58
RNF187	0.74	0.71	0.75	0.74	0.86	0.78	0.79
ROGDI	0.61	0.55	0.65	0.66	0.98	0.7	0.61
RPL13A	1.5	1.49	1.48	1.4	1.44	1.41	1.13
RPL26	1.27	1.35	1.35	1.28	1.23	1.34	1.27
RPS13	1.35	1.35	1.34	1.34	1.36	1.34	1.13
RPS25	1.46	1.33	1.31	1.26	1.12	1.18	1.29
RPS4X	1.16	1.24	1.24	1.14	1.29	1.45	1.09
RPS6KB2	0.73	0.63	0.79	0.75	0.97	0.8	0.83
RRAGA	1	1.15	1.49	1.51	1.67	1.34	1.55
RRS1	0.91	0.79	0.94	0.95	0.97	0.92	0.83
RSAD1	0.73	0.66	0.79	0.83	0.93	0.82	0.81
RSU1	1.57	1.65	1.52	1.66	1.54	1.75	1.45
RTCD1	1.61	2.41	2.03	1.9	1.25	1.6	1.84
RWDD2B	1.16	1.2	1.17	1.17	1.02	1.12	1.31
S100A10	1.74	1.99	1.68	1.75	1.32	1.47	1.32
SEC16A	0.65	0.57	0.54	0.54	0.56	0.53	0.49
SELENBP1	0.76	0.83	0.53	0.5	0.97	0.94	0.49
SEPHS2	0.7	0.65	0.63	0.6	0.69	0.66	0.58
SEPW1	0.62	0.66	0.64	0.77	0.73	0.71	0.68
SEPX1	0.7	0.76	0.73	0.75	0.81	0.76	0.75
SERBP1	1.38	1.64	1.66	1.72	1.35	1.28	1.77
SERF2	0.61	0.61	0.61	0.63	0.67	0.69	0.61
SERTAD3	0.88	0.81	0.85	0.8	0.85	0.82	0.77
SETD3	0.85	0.79	0.73	0.73	0.82	0.75	0.63
SEZ6L2	0.79	0.79	0.64	0.6	0.74	0.86	0.75

gene	Docetaxel	Paclitaxel	Doxorubicin	Epirubicin	Fluorouracil	Gemcitabine	Cyclophosphamide
SF3B5	1.41	1.41	1.33	1.38	1.19	1.52	1.58
SGCE	1.56	1.91	2.13	2.26	1.85	2.69	1.96
SH3GLB1	1.31	1.52	1.55	1.54	1.23	1.36	1.74
SHC1	2.15	1.8	1.79	1.85	1.57	1.97	1.31
SIAH2	0.78	0.59	0.68	0.67	0.79	0.57	0.7
SLC12A2	0.37	0.38	0.36	0.39	0.36	0.31	0.67
SLC1A4	0.45	0.27	0.36	0.31	0.59	0.31	0.38
SLC25A1	0.8	0.77	0.72	0.69	0.71	0.86	0.65
SLC25A24	1.65	2.01	1.77	1.64	1.26	1.27	1.44
SLC25A4	0.68	0.61	0.64	0.65	0.65	0.62	0.73
SLC25A46	1.7	1.76	1.9	1.9	1.43	1.6	1.61
SLC35A2	0.79	0.69	0.75	0.75	0.63	0.79	0.7
SLC35B1	0.6	0.51	0.67	0.67	0.91	0.67	0.89
SLC35F2	1.94	1.92	1.68	1.64	1.02	1.18	1.65
SLC7A1	1.18	1.71	1.59	1.63	1.47	1.26	1.5
SLC9A1	0.75	0.71	0.72	0.73	0.92	0.8	0.8
SLC9A3R1	0.33	0.32	0.37	0.35	0.48	0.34	0.45
SLTM	0.87	0.85	0.72	0.69	0.68	0.7	0.61
SNF8	0.64	0.57	0.65	0.72	0.77	0.64	0.71
SNRPB2	1.36	1.33	1.42	1.46	1.21	1.45	1.24
SNRPD3	0.81	0.74	0.78	0.77	0.78	0.77	0.84
SNUPN	1.29	1.18	1.29	1.18	1.19	1.26	1.04
SNX6	1.5	1.65	1.44	1.42	1.37	1.39	1.16
SNX7	2.21	2.47	2.1	1.99	1.22	1.64	2.45
SPATS2L	2.33	2.23	1.8	1.82	1.26	1.14	1.76
SPDEF	0.4	0.33	0.33	0.32	0.51	0.38	0.34
SPINT1	0.85	0.77	0.63	0.63	0.7	0.79	0.59
SPINT2	0.51	0.54	0.47	0.49	0.67	0.53	0.63
SPOP	0.76	0.57	0.68	0.69	0.83	0.63	0.78
SPSB3	0.85	0.75	0.73	0.7	0.78	0.74	0.72
SRI	1.5	1.61	1.42	1.47	1.17	1.59	2.25
SRPR	1.89	1.55	1.45	1.4	0.98	1.17	1.59
SSNA1	0.71	0.73	0.78	0.78	0.84	0.74	0.76
SSR2	1.25	1.46	1.51	1.41	1.3	1.71	1.54
ST3GAL5	0.61	0.55	0.59	0.6	0.88	0.62	0.64
ST6GALNAC2	0.34	0.26	0.31	0.3	0.42	0.31	0.33
STAP2	0.89	0.71	0.67	0.62	0.69	0.56	0.67
STEAP3	1.29	1.61	1.41	1.33	1.14	1.49	1.59
SUB1	0.88	0.72	0.75	0.75	0.79	0.81	0.66
SYDE1	0.98	1.63	1.83	1.76	1.57	1.88	2.33
SYNGR2	0.68	0.61	0.67	0.61	0.66	0.68	0.69
TAF1D	2.54	2.73	2.32	2.12	1.76	1.94	2.06

gene	Docetaxel	Paclitaxel	Doxorubicin	Epirubicin	Fluorouracil	Gemcitabine	Cyclophosphamide
TAGLN2	1.71	1.61	1.29	1.25	1.17	1.3	1.27
TAP1	2.57	2.46	2.65	2.59	1.63	1.11	3.42
TAPBP	1.82	1.96	1.69	1.74	1.51	1.23	1.94
TBL1X	0.59	0.57	0.69	0.71	0.85	0.7	0.69
TCEB2	0.61	0.64	0.7	0.75	0.8	0.74	0.72
TCF25	0.88	0.78	0.89	0.83	0.91	0.76	0.89
TDP1	1.25	1.27	1.23	1.25	1.28	1.26	1.04
TEX10	1.63	1.7	1.54	1.52	1.4	1.38	1.18
TEX2	0.54	0.57	0.54	0.54	0.62	0.56	0.47
TFF3	0.07	0.44	0.44	0.48	0.07	0.74	0.43
THAP11	0.86	0.76	0.81	0.76	0.75	0.73	0.74
TIMP2	2.27	2.67	2.41	2.48	2.1	2.58	1.52
TLE3	0.8	0.66	0.7	0.69	0.77	0.61	0.8
TMBIM6	0.71	0.64	0.7	0.72	0.73	0.69	0.61
TMEM131	0.75	0.74	0.76	0.74	0.78	0.84	0.71
TMEM134	0.66	0.42	0.57	0.49	0.86	0.57	0.58
TMEM147	0.97	1.22	1.21	1.31	1.27	1.21	1.19
TMEM30B	0.55	0.66	0.58	0.59	0.55	0.57	0.55
TMEM87A	0.94	0.83	0.68	0.63	0.67	0.82	0.61
TMEM93	1.24	1.26	1.46	1.44	1.28	1.32	1.42
TNFAIP2	2.11	2.66	1.68	1.8	1.21	1.04	2.44
TNIP1	1.26	1.76	1.29	1.31	1.18	1.27	1.67
TOB1	0.45	0.31	0.42	0.43	0.54	0.36	0.46
TOE1	1.15	1.21	1.27	1.3	1.27	1.21	1.25
TOP2A	1.86	2.34	2.69	2.21	2.12	2.35	1.64
TPD52L1	0.58	0.63	0.47	0.5	0.57	0.42	0.55
TPX2	1.84	1.55	1.45	1.38	1.35	1.37	1.5
TRAPPC6A	0.8	0.78	0.63	0.63	0.67	0.77	0.66
TRIB3	0.64	0.72	0.57	0.6	0.53	0.63	0.68
TRIP10	1.59	1.54	1.36	1.31	1.02	1.05	1.41
TRIP6	1.03	1.22	1.24	1.12	1.33	1.47	1.31
TSC22D3	0.5	0.69	0.71	0.7	0.67	0.73	0.75
TSKU	0.63	0.6	0.62	0.66	0.73	0.67	0.61
TSPAN1	0.42	0.4	0.44	0.54	0.7	0.48	0.64
TSPAN13	0.52	0.46	0.47	0.49	0.55	0.47	0.53
TSPAN3	1.45	1.32	1.39	1.49	1.23	2.01	1.85
TST	0.76	0.72	0.61	0.63	0.57	0.7	0.76
TUBB6	3.31	3.92	3.88	3.99	3.03	3.19	4.1
TXNDC5	1.55	1.52	1.51	1.57	1.3	1.49	1.3
TXNIP	0.74	0.55	0.42	0.33	0.66	0.79	0.58
TYK2	1.32	1.33	1.29	1.31	1.08	1.02	1.42
TYMS	1.65	1.66	1.52	1.47	1.17	1.36	1.62

gene	Docetaxel	Paclitaxel	Doxorubicin	Epirubicin	Fluorouracil	Gemcitabine	Cyclophosphamide
UBC	0.8	0.75	0.81	0.83	0.9	0.79	0.88
UBE2E1	1.83	2.05	1.8	1.85	1.58	1.75	1.66
UBE2E3	2.74	3.19	2.62	2.58	1.78	1.86	2.1
UBE2G1	1.51	1.67	1.55	1.58	1.31	1.35	1.53
UBE4A	1.89	1.72	1.66	1.54	1.12	1.31	1.68
UCK2	1.39	1.52	1.34	1.34	1.12	1.2	1.32
UFD1L	0.82	0.77	0.7	0.7	0.77	0.82	0.71
UPF3B	2	2.43	2.28	2.27	1.25	0.83	2
UQCR10	0.76	0.72	0.74	0.72	0.83	0.85	0.75
UROD	1.19	1.47	1.88	2.05	1.52	1.59	2.11
USP21	0.91	0.77	0.81	0.82	0.86	0.76	0.93
USP33	1.65	1.83	1.91	2.09	1.28	1.21	1.89
UTP6	1.46	1.31	1.32	1.26	1.05	1.23	1.38
VAMP8	0.63	0.7	0.64	0.64	0.58	0.69	0.58
VAPA	1.61	1.54	1.45	1.32	1.02	1.06	1.22
VCL	1.53	1.93	2.07	2.13	1.65	2	2.08
WBP11	0.79	0.7	0.75	0.7	0.94	0.7	0.9
WDR12	1.31	1.43	1.47	1.46	1.32	1.22	1.38
WFS1	0.56	0.67	0.7	0.77	0.78	0.71	0.69
XBP1	0.44	0.31	0.41	0.39	0.51	0.41	0.33
YBX2	0.8	0.72	0.68	0.65	0.88	0.89	0.78

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 10/58499

A. CLASSIFICATION OF SUBJECT MATTER

IPC(8) - C12Q 1/68, C40B 40/06 (2011.01)

USPC - 435/6, 506/6

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

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

SPC -- 435/6, 506/6

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
 PubWEST -- PGPB,USPT,USOC,EPAB,JPAB; Dialog Classic Files -- 654, 652, 35, 65, 155; USPTO Web Page; Google Scholar; Search terms -- gene expression profile, mRNA sample, breast cancer tissue, TOP2A, IGFBP2, CCNB1, drug response, taxol, docetaxel, antimetabolite, fluorouracil, estrogen receptor status

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	US 2003/0225528 A1 (BAKER et al.) 04 December 2003 (04.12.2003) para [0003], [0009], [0037], [0049], [0060], [0063], [0064], [0066], [0093], [0095], [0164], [0165], [0190], [0193], [0373], [0555], [0586]	1-5, 11-15
X	US 2007/0105133 A1 (CLARKE et al.) 10 May 2007 (10.05.2007) para [0004], [0017], [0018], [0173], [0226], [0368], [0473]	1-5, 11-15

☐ Further documents are listed in the continuation of Box C.


* 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 another 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

15 January 2011 (15.01.2011)

Date of mailing of the international search report

08 FEB 2011

Name and mailing address of the ISA/US

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INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 10/58499

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.:
because they relate to subject matter not required to be searched by this Authority, namely:

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.: 6-10 and 16-20
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 additional fees, this Authority did not invite payment of additional fees.
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.