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(54) Title: METHODS FOR IDENTIFICATION OF TUMOR PHENOTYPE AND TREATMENT

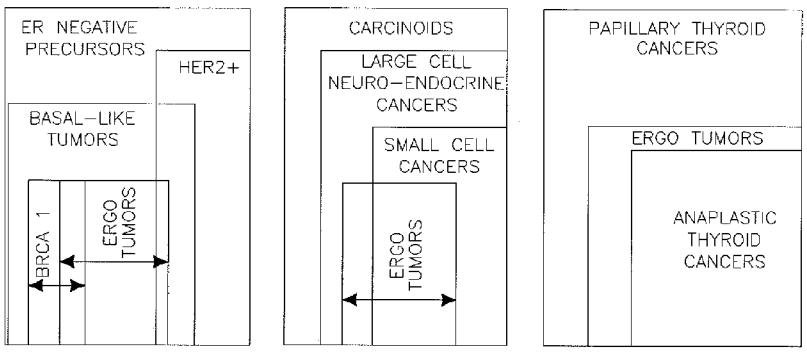

FIG.7

(57) Abstract: The disclosure relates to methods for identifying a tumor as an E2F-responsive gene over-expressing (ERGO) tumor, methods of determining the likelihood that an ERGO tumor patient will survive to a future date, methods of treating an ERGO tumor in a patient, and methods of selecting patients diagnosed as ERGO tumor prostate cancer patients for aggressive clinical treatment. The methods of the disclosure are applicable to ERGO tumors present in different human organs and tissues such as breast, lung, thyroid, ovary, and prostate.

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METHODS FOR IDENTIFICATION OF TUMOR PHENOTYPE AND TREATMENT

Related Application

This patent application claims the benefit of US Provisional Application No. 61/199,295 filed 14 November 2008.

Field of the Disclosure

The disclosure relates to methods for identifying a tumor as an E2F-responsive gene over-expressing (ERGO) tumor, methods of determining the likelihood that an ERGO tumor patient will survive to a future date, methods of treating an ERGO tumor in a patient, and methods of selecting patients diagnosed as ERGO tumor prostate cancer patients for aggressive clinical treatment. The methods of the disclosure are applicable to ERGO tumors present in different human organs and tissues such as breast, lung, thyroid, ovary, and prostate.

Background of the Disclosure

A major challenge in cancer treatment is to target specific therapies to distinct tumor types in order to maximize efficacy and minimize toxicity. Meeting this challenge requires that physicians and others involved in the treatment of cancer patients be able to identify distinct tumor types, determine the likelihood of patient survival given the patient's distinct tumor type, and be able to select appropriate treatments.

In the oncology field it is currently standard practice to identify tumor types using the microscopic histopathologic appearance of fixed and stained tumor samples, and to utilize the tumor-node-metastasis (TNM) system to determine the clinical extent of tumor spread. The TNM system uses the size of the tumor, the presence or absence of tumors in regional lymph nodes, and the presence or absence of distant metastases to assign a stage to the tumor. The tumor type and the stage assigned to a tumor are used as a basis for the selection of appropriate therapy and for prognostic purposes. However, this approach has serious limitations. This is because tumors with similar histopathologic appearance can exhibit significant variability in terms of clinical course and response to therapy. For example, some tumors spread early to distant sites and are rapidly progressive while others are not, and some tumors respond readily to hormonal therapy or chemotherapy while others are resistant.

Basal-like breast cancer tumors are one example of a tumor type that grows rapidly and which typically are not treated effectively with conventional adjuvant therapies such as

hormonal therapy or chemotherapy. Clinically, basal-like breast cancers behave aggressively, and while they may respond to chemotherapy initially, these responses are generally of brief duration, and survival times for most patients with these tumors are relatively short. Histologically, most basal-like breast cancers are poorly differentiated ductal carcinomas. Breast cancer tumors are normally classified as basal-like in the clinical setting based on whether the tumors have a so-called "triple-negative" phenotype characterized by a lack of over-expression of human epidermal growth factor receptor 2 (HER2), the estrogen receptor (ER), and the progesterone receptor (PR) and if the tumor over-expresses basal-like cytokeratins or other basal-like markers. Unfortunately, therapeutic options for patients with basal-like breast cancers are limited, because patients with such tumors are not candidates for hormonal therapy or targeted therapy against HER2 and there currently is no clear understanding of the underlying pathobiology of basal-like breast cancers. Importantly, basal-like tumors and distinct subsets of such tumors may also arise in other tissues and organs such as lung, thyroid, ovarian, and prostate tissues, but this has been poorly studied.

Furthermore, many tumors have aberrations in the expression or biological activity of proteins encoded by tumor suppressor genes. Aberrations in the biological activity of proteins encoded by tumor suppressor genes due to mutations in these genes or decreased gene transcription at the level of mRNA or protein expression can lead to unrestrained cell division. The Rb protein is an example of a protein encoded by a tumor suppressor gene. Normally, the Rb tumor suppressor protein binds to the E2F transcription factor and regulates E2F mediated gene transcription to negatively modulate and control cell proliferation. Importantly, the role of Rb and E2F in basal-like tumors in breast tissues and other tissues such as lung, thyroid, ovarian, and prostate tissues is also poorly understood.

Thus, there is a need for methods to identify tumors that over-express E2F responsive genes, methods for determining the likelihood that a patient diagnosed with a particular distinct tumor type will survive to a future date, methods for identifying and treating distinct tumor types, and methods for identifying target proteins expressed by a distinct tumor type in different tissues such as breast, lung, thyroid, ovarian prostate and other tissues.

Summary of the Disclosure

One aspect of the disclosure is a method of identifying a tumor as an ERGO tumor comprising the steps of providing a tumor sample; providing a reference; measuring an indicator of gene transcript levels in the tumor sample to produce an indicator value for each of

the following gene transcripts having the nucleic acid sequences shown in SEQ ID NO:s 12-14, 20-21, 35, 37, 39, 43-44, 46-47, 49-51, 54, 56, 58-72, 75, 79-84, 86, 88, 91, 93-95, 102-105, 107-110, 112, 116, 118-120, 122-123, 125-126, 128-129, 131, 145-146, 148-149, 151, 154, 156-157, 160, 163-166, 169, 171, 173-174, 176-177, 180, 184, 186, 188, 193, 196, 198, 200-201, 203, 205, 209, 217, 246-247, 249, 254, 259, 267, 269, 274-275, 292-295, 298, 307, 311, 316, 321-323, 331, 333, and 335-340; measuring the reference to produce a reference value; and comparing the indicator value to the reference value to determine which of the gene transcripts is over-expressed; whereby the tumor is identified as an ERGO tumor if at least 21 of these gene transcripts are over-expressed.

Another aspect of the disclosure is a method of determining the odds that an individual ERGO tumor patient will survive to a future date comprising the steps of providing a tumor sample from an individual patient; providing a reference; measuring an indicator of gene transcript levels in the tumor sample to produce an indicator value for each of the following gene transcripts having the nucleic acid sequences shown in SEQ ID NO:s 12-14, 20-21, 35, 37, 39, 43-44, 46-47, 49-51, 54, 56, 58-72, 75, 79-84, 86, 88, 91, 93-95, 102-105, 107-110, 112, 116, 118-120, 122-123, 125-126, 128-129, 131, 145-146, 148-149, 151, 154, 156-157, 160, 163-166, 169, 171, 173-174, 176-177, 180, 184, 186, 188, 193, 196, 198, 200-201, 203, 205, 209, 217, 246-247, 249, 254, 259, 267, 269, 274-275, 292-295, 298, 307, 311, 316, 321-323, 331, 333, and 335-340; measuring the reference to produce a reference value; and comparing the indicator value to the reference value to determine which of the gene transcripts is over-expressed, whereby the tumor is identified as an ERGO tumor and the individual patient is diagnosed as an ERGO tumor patient if at least 21 of these gene transcripts are over-expressed; plotting the fraction of surviving patients in a population of patients diagnosed as ERGO tumor patients as a function of the time since diagnosis of the ERGO tumor to generate a survival plot; and selecting a future date after the individual patient is diagnosed as an ERGO tumor patient and determining the fraction of surviving patients in the population from the survival plot; whereby the fraction of surviving patients on the survival plot at the future date predicts the odds that an individual tumor patient will survive to the future date.

Another aspect of the disclosure is a method of treating an ERGO tumor in a patient comprising the steps of providing a tumor sample from a patient; providing a reference; measuring an indicator of gene transcript levels in the tumor sample to produce an indicator value for each of the following gene transcripts having the nucleic acid sequences shown in SEQ ID NO:s 12-14, 20-21, 35, 37, 39, 43-44, 46-47, 49-51, 54, 56, 58-72, 75, 79-84, 86, 88,

91, 93-95, 102-105, 107-110, 112, 116, 118-120, 122-123, 125-126, 128-129, 131, 145-146, 148-149, 151, 154, 156-157, 160, 163-166, 169, 171, 173-174, 176-177, 180, 184, 186, 188, 193, 196, 198, 200-201, 203, 205, 209, 217, 246-247, 249, 254, 259, 267, 269, 274-275, 292-295, 298, 307, 311, 316, 321-323, 331, 333, and 335-340; measuring the reference to produce a reference value; comparing the indicator value to the reference value to determine which of the gene transcripts is over-expressed, whereby the tumor is identified as an ERGO tumor if at least 21 of these gene transcripts are over-expressed; selecting a drug capable of killing or inhibiting division of an ERGO tumor cell expressing at least one protein encoded by at least one gene transcript selected from the group consisting of the following gene transcripts having the nucleic acid sequences shown in SEQ ID NO:s 12-14, 20-21, 35, 37, 39, 43-44, 46-47, 49-51, 54, 56, 58-72, 75, 79-84, 86, 88, 91, 93-95, 102-105, 107-110, 112, 116, 118-120, 122-123, 125-126, 128-129, 131, 145-146, 148-149, 151, 154, 156-157, 160, 163-166, 169, 171, 173-174, 176-177, 180, 184, 186, 188, 193, 196, 198, 200-201, 203, 205, 209, 217, 246-247, 249, 254, 259, 267, 269, 274-275, 292-295, 298, 307, 311, 316, 321-323, 331, 333, and 335-340; and administering a pharmaceutically acceptable amount of the drug to the patient; whereby the ERGO tumor in the patient is treated.

Another aspect of the disclosure is a method of identifying an individual tumor in a population of tumors as an ERGO tumor comprising the steps of providing a population of tumor samples; providing a reference; measuring gene transcript levels in the tumor samples to produce a transcript value for each of the following gene transcripts having the nucleic acid sequences shown in SEQ ID NO:s 10-340; comparing the transcript value to the reference value for each tumor to identify the gene transcripts over-expressed by each tumor; ranking the tumors in the population with a rank ordering algorithm to order the tumors according to the number of the gene transcripts over-expressed by each tumor; and removing individual tumors from the population that over-express the smallest number of each gene transcript per cell and that have the lowest levels of over-expression of each gene transcript per cell until at least 20% of the individual tumors remaining in the population over-express at least 20% of the gene transcripts; whereby an individual tumor remaining in the population of tumors is identified as an ERGO tumor.

Another aspect of the disclosure is a method of identifying an individual tumor in a population of tumors as an ERGO tumor comprising the steps of providing a population of tumor samples; providing a reference; measuring gene transcript levels in the tumor samples to produce a transcript value for each of the following gene transcripts having the nucleic acid

sequence shown in SEQ ID NO:s 10-340; comparing the transcript value to the reference value for each tumor to identify the gene transcripts over-expressed by each tumor; and applying a principle component analysis algorithm in which the analyzed gene set is restricted to each gene transcript having the nucleic acid sequence shown in SEQ ID NO:s 10-340 to identify a tumor cluster over-expressing these E2F-responsive genes; whereby an individual tumor in the population of tumors in the cluster is identified as an ERGO tumor.

Another aspect of the disclosure is a method of selecting treatment for a prostate cancer patient comprising the steps of providing a tumor sample from a prostate cancer patient; providing a reference; measuring an indicator of gene transcript levels in the tumor sample to produce an indicator value for each of the following gene transcripts having the nucleic acid sequences shown in SEQ ID NO:s 12-14, 20-21, 35, 37, 39, 43-44, 46-47, 49-51, 54, 56, 58-72, 75, 79-84, 86, 88, 91, 93-95, 102-105, 107-110, 112, 116, 118-120, 122-123, 125-126, 128-129, 131, 145-146, 148-149, 151, 154, 156-157, 160, 163-166, 169, 171, 173-174, 176-177, 180, 184, 186, 188, 193, 196, 198, 200-201, 203, 205, 209, 217, 246-247, 249, 254, 259, 267, 269, 274-275, 292-295, 298, 307, 311, 316, 321-323, 331, 333, and 335-340; measuring the reference to produce a reference value; and comparing the indicator value to the reference value to determine which of the gene transcripts is over-expressed, whereby the tumor is identified as an ERGO tumor and the prostate cancer patient is diagnosed as an ERGO tumor prostate cancer patient if at least 21 of these gene transcripts are over-expressed; and choosing at least one treatment selected from the group consisting of removal of at least one tumor and adjuvant therapy, if the patient is diagnosed as an ERGO tumor prostate cancer patient; whereby a treatment is selected for the prostate cancer patient.

Brief Description of the Figures

Fig. 1 shows microarray data of a selected gene expression profile for the ERGO, non-ERGO HER2-over-expressing, ER/PR over-expressing non-ERGO, and triple-non-positive non-ERGO tumor subsets identified in the Van't Veer human breast cancer microarray set (s1).

Fig. 2A shows a tumor cluster consisting of 38 samples identified by PCA of all tumors in the Van't Veer human breast cancer microarray set (s1).

Fig. 2B shows non-ERGO tumors clustered separately from the ERGO tumors identified by refined PCA analysis of basal-like tumors identified in the Van't Veer human breast cancer microarray set (s1).

Fig. 2C shows the transitional basal-like HER2 over-expressing tumors identified by refined PCA of all tumors in the purged Dai human breast cancer microarray set (s2).

Fig. 2D shows clusters comprising 30 ERGO and 36 non-ERGO tumor subsets identified by refined PCA of basal-like tumors in the purged Dai human breast cancer microarray set (s2).

Fig. 2E shows a cluster of tumors that contained carcinoids, large cell neuroendocrine tumors, and small cell lung cancers identified by PCA of all tumors in the Jones human lung cancer microarray set.

Fig. 2F shows carcinoids, large cell neuroendocrine tumors, and small cell lung cancer clusters identified by refined PCA of the neuroendocrine tumors in the Jones human lung cancer microarray set.

Fig. 2G shows anaplastic thyroid cancer clusters identified by PCA of all tumors in the Salvatore human thyroid cancer microarray set.

Fig. 3A shows a continuous strand of genes strung along the axis of the first principal component, rather than discrete gene clusters, identified by refined PCA gene clustering with the basal-like tumors from the Van't Veer microarray set as input.

Fig. 3B is a graph comparing the genes identified by refined PCA clustering of the basal-like tumors from the Van't Veer human breast cancer microarray set in Fig. 3A with the most frequently over-expressed E2F-responsive genes in the ERGO tumors identified by the weighted rank ordering of all tumors from the Van't Veer microarray set.

Fig. 3C shows a comparison of the frequency of over-expressed E2F-responsive genes per basal-like tumor sample identified by PCA gene clustering in Fig. 3A with the most frequently over-expressed E2F-responsive genes in ERGO tumors.

Fig. 4 shows microarray data for HER2 positive tumors identified by PCA of the purged Dai human breast cancer microarray set (s2) and per ERGO tumor sample identified by refined PCA of the basal-like tumors in this microarray set.

Fig. 5 shows a schematic diagram of genes that are targets of the dRM/dREAM/LINC complex and the downstream consequences of aberrations of the components of this complex (shown at far left).

Fig. 6 shows the number of over-expressed FOXM1-associated DNA replication genes and mitotic genes per ERGO tumor as a function of the relative level of FOXM1 over-expression per ERGO tumor.

Fig. 7 is a schematic diagram of the phylogenetic origin of ERGO tumors at different organ sites. The schematic is based on results obtained with the weighted rank ordering methods and PCA based methods described in the Examples below.

Fig. 8 shows the selected gene expression profile for the ERGO, non-ERGO HER2-over-expressing, ER/PR over-expressing non-ERGO, and triple-non-positive non-ERGO tumor subsets of Fig. 1 in greater detail.

Fig. 9 shows the clinical survival data for PCA basal-like breast cancers and non-basal-like tumors identified by PCA analysis. "Survival" on the Y-axis indicates the fraction of all patients diagnosed with PCA basal-like breast cancers that survive at a given time.

Fig. 10 shows the most frequently over-expressed E2F-responsive genes in ERGO tumors identified by weighted rank ordering of tumors in the Van't Veer set (s1) and purged Dai microarray set (s2).

Fig. 11 shows microarray data for HER2 positive basal-like tumors identified by PCA of the purged Dai human breast cancer microarray set (s2).

Fig. 12 shows a comparison of the most highly over-expressed E2F-responsive genes in ERGO tumors identified by PCA of the Van't Veer human breast cancer microarray set (s1) and ERGO tumors identified by refined PCA of the purged Dai human breast cancer microarray set (s2).

Fig. 13 shows a comparison of the most highly over-expressed E2F-responsive genes of ERGO tumors identified by refined PCA in the Van't Veer human breast cancer microarray set (s1), and ERGO tumors identified by refined PCA in the purged Dai human breast cancer microarray set (s2) with small cell lung cancer tumors identified by PCA in the Jones human lung cancer microarray set.

Fig. 14 shows microarray data for ERGO tumors identified by refined PCA, as well as large cell neuroendocrine tumors and carcinoid tumors identified by PCA of the Jones human lung cancer microarray set.

Fig. 15 shows a comparison of the most highly over-expressed E2F-responsive genes of ERGO tumors identified by refined PCA in the Van't Veer human breast cancer microarray set (s1) and ERGO tumors identified by refined PCA in the purged Dai human breast cancer microarray set (s2) with small cell lung cancer tumors identified by PCA in the Salvatore human thyroid cancer microarray set.

Fig. 16 shows microarray data for ERGO tumors identified by refined PCA, as well as large cell papillary cancer tumors identified by PCA of the Salvatore human thyroid cancer microarray set.

Fig. 17 shows the over-expressed genes in ERGO tumors identified by refined PCA analysis in the Van't Veer human breast cancer microarray set (s1), the purged Dai human breast cancer microarray set (s2), the Jones human lung cancer microarray set, and the Salvatore human thyroid cancer microarray set. Genes are further identified as belonging to a group comprising two prominent subclasses of E2F-responsive genes, a group that affects the G1/S cell cycle phase transition, and group that affects the G2M portion of the cell cycle.

Fig. 18 shows microarray data from basal-like and non-basal like tumors identified by PCA for the top 25 most highly over-expressed published basal-like marker genes and the top 50 most highly over-expressed basal-like marker genes.

Fig. 19 shows the clinical survival data for ERGO tumors, non-ERGO basal-like tumors, and HER2 over-expressing tumors (Panel A) subsets as well as the non-ERGO "triple non-positive" tumors subsets identified by PCA analysis. "Survival" on the Y-axis indicates the fraction of all patients diagnosed with PCA basal-like breast cancers that survive at a given time.

Fig. 20 shows microarray data from prostate cancer patients and the identification of ERGO genes and ERGO tumors in cancers from such patients.

Fig. 21 shows details of the positive feedback loops and regulatory aspects of the cascade of changes associated with dysregulation of the members of the Syn/MULVB/DRM/DREAM/LINC multiprotein repressor/activator complex.

Fig. 22 shows a tumor cluster identified by PCA of primary prostate cancer tumor without metastases in the Chandran microarray set human prostate cancer microarray set.

Fig. 23 shows microarray data from normal fallopian tube epithelium and high grade serous fallopian tube and ovarian carcinomas in both patients carrying BRCA1 gene mutations and patients that do not carry such mutations and the identification of ERGO genes and ERGO tumors in cancers from such patients as indicated.

Fig. 24 shows microarray data from the Van't Veer microarray set, showing the non-E2F responsive genes that are statistically significantly differentially under-expressed in basal-like breast cancers relative to non-basal-like breast cancers.

Fig. 25 shows microarray data from the Van't Veer microarray set, showing the non-E2F responsive genes that are statistically significantly differentially under-expressed in basal-like breast cancers relative to non-basal-like breast cancers.

Fig. 26 shows microarray data from bladder cancer patients and the identification of ERGO genes and ERGO tumors in cancers from such patients.

Fig. 27 shows microarray data from hepatoma patients and the identification of ERGO genes and ERGO tumors in such patients.

Detailed Description of the Disclosure

The term "agonist" as used herein means a molecule that partially or completely activates, by any mechanism, a biological activity or effect of another molecule or complex of molecules. As used herein, an "agonist" is a molecule that is capable of, directly or indirectly, substantially activating, stimulating, or increasing the biological activity or effects of another molecule or complex of molecules. Such agonists may be, for example, small organic molecules, peptides, antibodies, antibody fragments, or polynucleotides. Increasing the expression of a molecule or complex of molecules can be used to agonize the biological activities or effects of the molecule or complex of molecules. For example, an over-expressed molecule or a complex of molecules can be considered to be an "agonist."

The term "antagonist" as used herein means a molecule that partially or completely inhibits, by any mechanism, a biological activity or effect of another molecule or complex of molecules. As used herein, an "antagonist" is a molecule that is capable of, directly or indirectly, substantially counteracting, reducing or inhibiting the biological activity or effects of another molecule or complex of molecules. Such antagonists may be, for example, small organic molecules, peptides, antibodies, antibody fragments, or polynucleotides.

The term "aurora kinase" as used herein means a peptide chain which is at least 90% identical to the mature form of the *Homo sapiens* Aurora A kinase amino acid sequence shown in SEQ ID NO: 1 (described by Accession Number NP_003591), the mature form of the *Homo sapiens* Aurora B kinase amino acid sequence shown in SEQ ID NO: 2 (described by Accession Number NP_004208); or the *Homo sapiens* Aurora C kinase amino acid sequence shown in SEQ ID NO: 3 (described by Accession Number NP_001015878) as determined using the default settings of the CLUSTALW algorithm.

As used herein the term "date" as used herein means a specified time. For example, a date may be a specific time or day in the future.

The term "drug" as used herein means a substance which produces physiological effects in an organism, or effects on cells, that result in the cure, mitigation, treatment, or prevention of a pathological condition.

The term "E2F" as used herein means a peptide chain which is at least 90% identical to the mature form of the *Homo sapiens* E2F-1 amino acid sequence shown in SEQ ID NO: 6 (described by Accession Number NP_005216), the mature form of the *Homo sapiens* E2F-2 amino acid sequence shown in SEQ ID NO: 7 (described by Accession Number NP_004082); or the *Homo sapiens* E2F-3a amino acid sequence shown in SEQ ID NO: 8 (described by Accession Number NP_005215) as determined using the default settings of the CLUSTALW algorithm.

The term "FOXM1" as used herein means a peptide chain which is at least 90% identical to the mature form of the *Homo sapiens* FOXM1 amino acid sequence shown in SEQ ID NO: 5 (described by Accession Number NP_068772) as determined using the default settings of the CLUSTALW algorithm.

The term "indicator of gene transcript levels" as used herein means a measurable endpoint that correlates to the level of a gene transcript. Such indicators may be nucleic acids corresponding to mRNA gene transcripts (*e.g.* cDNAs) or peptide chains, such as proteins and other polypeptides, that correlate to a gene transcript from which they are translated. Indicators that correlate to a given gene transcript may also comprise other nucleic acids such as splice variants, nucleic acids encoding different peptide chain isoforms, or other nucleic acid sequence variants capable of hybridizing to any portion of a gene transcript including both non-coding sequences such as 5' and 3' untranslated regions or coding sequences.

The term "LINC protein complex" as used herein means a complex of proteins comprising a peptide chain which is at least 90% identical to the mature form of the *Homo sapiens* LIN-9 amino acid sequence shown in SEQ ID NO: 9 (described by Accession Number NP_775106) as determined using the default settings of the CLUSTALW algorithm and which has the biological activity of repressing gene transcription. The LINC multiprotein complex is also known to contain human LIN-37, RbAP48, which is a human homolog of LIN-53, B-MYB, and DKFZp686L1814, a human homolog of *C. elegans* LIN-54, and LIN-52. Tesmin is another human homolog of LIN-54 and Rb, p107, p130, and E2F isoforms also associate with the core complex in different phases of the cell cycle. *See Schmit et al.*, 6 Cell Cycle 1903 (2007).

The term "normalizing" as used herein means means placing a measured value in a first data set, and a measured value in a second data set, on a common scale to facilitate the comparison of the measured values in the first data set and the measured values in the second data set. Typically, normalization of measured values in different data sets (*e.g.* tumor sample data set and reference data) is performed by identifying a parameter common to both the first data set and second data sets, measuring the value of common parameter in both the first data set and second data set, dividing measured values in the first data set by the value of the common parameter in the first data set and dividing measured values in the second data set by the value of the common parameter in the second data set to place the data in the first data set and second data set on a common scale so they can be easily compared. For example, in the methods of the disclosure an indicator value can be measured for a first gene transcript (*e.g.* SEQ ID NO: 12) in a tumor sample, an indicator value can be measured for the first gene transcript (*e.g.* SEQ ID NO: 12) in a reference such as a normal tissue sample, an indicator value can be measured for a second gene transcript (*e.g.* a housekeeping gene such as SEQ ID NO: 162) in the tumor sample to produce a housekeeping value, an indicator value can be measured for the second gene transcript (*e.g.* a housekeeping gene such as SEQ ID NO: 162) in the normal tissue sample to produce a housekeeping value, the indicator value of the first gene transcript in the tumor sample can be divided by the housekeeping value for the tumor sample, the indicator value of the first gene transcript in the normal tissue sample can be divided by the housekeeping value for the normal tissue sample and the resulting normalized values, which are now on a common scale, can be compared. Importantly, as those of ordinary skill in the art will readily recognize a variety of approaches may be taken to normalize data such as, for example, normalizing to an aggregate of common parameter values (*e.g.* for multiple housekeeping genes). Normalization may also be performed across an entire data set (*e.g.* all indicator values for every gene transcript on an array) or for only a portion a data set (*e.g.* an individual indicator value for a single gene transcript on an array).

The term "nucleic acid" as used herein means a molecule comprising at least two nucleic acid residues linked to form a chain. Such nucleic acid residues may be those found in DNA or RNA. Small nucleic acids of less than 50 residues may be referred to as "oligonucleotides."

The term "over-expressed" as used herein means that a measured indicator of gene transcript levels is greater than a reference value. Over-expression occurs when an indicator

value is, for example, at least 1.5 times greater than a reference value or at least 1.8 times greater than a reference value.

The term "peptide chain" as used herein means a molecule comprising at least two amino acid residues linked by a peptide bond to form a chain. Large peptide chains of more than 50 amino acids may be referred to as "polypeptides" or "proteins." Small peptide chains of less than 50 amino acids may be referred to as "peptides."

The term "principal component analysis algorithm" as used herein mean an algorithm that performs a mathematical procedure that transforms a number of potentially correlated variables into a smaller number of uncorrelated variables called principal components. Principle component analysis (PCA) is mathematically defined as an orthogonal linear transformation that transforms data to a new coordinate system such that the greatest variance by any projection of the data comes to lie on the first coordinate which is called the first principal component, the second greatest variance on the second coordinate, and so on. PCA is theoretically the optimum transform for a given data in least square terms. Depending on the field of application, PCA is also named the discrete Karhunen-Loève transform (KLT), the Hotelling transform or proper orthogonal decomposition (POD). PCA and methods steps utilizing can be performed on a computer.

The term "rank ordering algorithm" as used herein mean an algorithm that performs a mathematical procedure that orders data based on use selected data. Data can be rank ordered in any coordinate system such as a graph or table using user defined criteria. In one application of such an algorithm varying degrees of stringency and criteria may be used such as the following:

a) Each tumor in a tumor subset to be ordered must over-express at least X percent of 325 E2F responsive genes having the nucleic acid sequence shown in SEQ ID NO:s 10-334; and

b) Each of the 325 E2F responsive genes having the nucleic acid sequence shown in SEQ ID NO:s 10-334 in the tumor subset must be over-expressed in at least X percent of the tumors in the tumor subset;

where X might be 14%, 17%, 20%, 25%, or 33% and the value of X reflects increasing degrees of stringency. Rank ordering algorithms and method steps using rank orderin algorithms can be performed on a computer.

The term "reference" as used herein means a standard of comparison. A reference may be normal cells or tissues. Alternatively, a reference may be the average of the signal intensity

values from all sample-probed gene spots on a microarray set. A reference may also be a signal corresponding to one or more gene transcripts, such as a housekeeping genes like GAPDH or others, which are assumed not to vary significantly in living cells.

The term "survival plot" as used herein means a plot in a coordinate system such as a graph or table in which an indicator of the number of surviving patients in a population is described as a function of the time after the patients in the population were diagnosed as having a particular condition.

The term "survivin" as used herein means a peptide chain which is at least 90% identical to the mature form of the *Homo sapiens* survivin amino acid sequence shown in SEQ ID NO: 4 (described by Accession Number NP_001012270) as determined using the default settings of the CLUSTALW algorithm.

The term "therapeutically effective amount" as used herein means those doses of a drug that, in a given individual patient, produce a response that results in the killing of an ERGO tumor cell or that inhibits the division of an ERGO tumor cell. Therapeutically effective amounts, or doses, appropriate for an individual patient can be readily determined using routine clinical techniques well known by those of skill in the art (*e.g.* dose response plots).

The term "tissue" as used herein means an aggregate of cells that form a structure in an organ or other part of an animal.

The term "tumor sample" as used herein means a portion of a tumor from a patient. Tumor samples can comprise individual cells isolated from a tumor, cell lines isolated from a tumor, or larger portions of a tumor comprising multiple different cells in the tumor. A tumor sample can also comprise a portion of molecules from a tumor such as a collection of peptide chain molecules expressed by a tumor or a collection of nucleic acids such as reverse transcribed mRNAs (*i.e.* cDNAs) from a tumor.

One aspect of the disclosure is a method of identifying a tumor as an ERGO tumor comprising the steps of providing a tumor sample; providing a reference; measuring an indicator of gene transcript levels in the tumor sample to produce an indicator value for each of the following gene transcripts having the nucleic acid sequences shown in SEQ ID NO:s 12-14, 20-21, 35, 37, 39, 43-44, 46-47, 49-51, 54, 56, 58-72, 75, 79-84, 86, 88, 91, 93-95, 102-105, 107-110, 112, 116, 118-120, 122-123, 125-126, 128-129, 131, 145-146, 148-149, 151, 154, 156-157, 160, 163-166, 169, 171, 173-174, 176-177, 180, 184, 186, 188, 193, 196, 198, 200-201, 203, 205, 209, 217, 246-247, 249, 254, 259, 267, 269, 274-275, 292-295, 298, 307, 311, 316, 321-323, 331, 333, and 335-340; measuring the reference to produce a reference value;

and comparing the indicator value to the reference value to determine which of the gene transcripts is over-expressed; whereby the tumor is identified as an ERGO tumor if at least 21 of these gene transcripts are over-expressed.

Importantly, the methods of the disclosure and the steps of the disclosed methods can be performed on a specifically programmed computer including, for example, a personal computer or programmable logic controller. In particular, the comparison steps of the methods or the application of PCA or rank ordering algorithms can be performed using such a computer. The methods of the disclosure and steps of the disclosed methods may also be tied to a nucleic acid array analyzer, capable of detecting signals correlated to the amount of a particular probe nucleic acid on an nucleic acid array which has hybridized to a nucleic acid present in a sample such as a tumor sample. The GeneChip® Array Station manufactured by Affymetrix, Inc. (Santa Clara, CA) is one example of such a nucleic acid array analyzer. Typically, such nucleic acid array analyzers comprise a nucleic acid array, a fluid handler, an oven or other means such as a heat block for maintaining a specific temperature (*e.g.* a specific hybridization temperature), a hybridization signal detection means (*e.g.* photomultiplier, scintillation counter, phosphor imager *etc.*), and a data collection means such as a computer or other means for collecting data (*e.g.* conventional photographic film or digital photographic film). Optionally, such nucleic acid array analyzers can comprise one or more automated nucleic acid array autoloaders for providing nucleic acid arrays to be analyzed. The output representing the physical transformation associated with a nucleic acid hybridization or other result produced by the methods of the disclosure can also be displayed on an output display such as a video monitor or printer. The methods of the disclosure and the steps of these methods can also produce a physical transformation because nucleic acid hybridization can be a result of performing the steps of the methods. Last, any combination of the above machines and apparatuses or physical transformations may be used in performing the methods of the disclosure or a method step of the disclosure.

In the methods of the disclosure a tumor is identified as an ERGO tumor if at least 21 of gene transcripts of SEQ ID NO:s 12-14, 20-21, 35, 37, 39, 43-44, 46-47, 49-51, 54, 56, 58-72, 75, 79-84, 86, 88, 91, 93-95, 102-105, 107-110, 112, 116, 118-120, 122-123, 125-126, 128-129, 131, 145-146, 148-149, 151, 154, 156-157, 160, 163-166, 169, 171, 173-174, 176-177, 180, 184, 186, 188, 193, 196, 198, 200-201, 203, 205, 209, 217, 246-247, 249, 254, 259, 267, 269, 274-275, 292-295, 298, 307, 311, 316, 321-323, 331, 333, and 335-340; are expressed. Alternatively, a tumor is may be as an ERGO tumor if from 20% to 100% of these gene

transcripts are overexpressed. Importantly, the recitation of this range is intended to support the recitation of any value in the range (*e.g.* 20%, 100% or all values between 20% and 100%).

In a method of the disclosure it is preferred that cDNA microarrays be used for the measurement of indicators of gene transcript levels and reference values. Importantly, gene transcript levels, as measured in microarray experiments, are generally regarded by those of ordinary skill in the art as a proxy for gene (protein) expression levels. Consequently, the measurement of gene transcripts is referred to in the art and in some instances herein as the measurement of gene expression, over-expression, or under-expression depending on the type of analysis being performed.

DNA microarrays consist of multiple of different DNAs, such as oligonucleotide DNA nucleic acid chains or cDNAs, spotted onto known locations on a solid support, such as a glass microscope slide. The cDNAs are typically obtained by PCR amplification of plasmid library inserts using primers complementary to the vector backbone portion of the plasmid or to the gene itself for genes where sequence is known. PCR products suitable for production of microarrays are typically between 0.5 and 2.5 kb in length. Full length cDNAs, expressed sequence tags (ESTs), or randomly chosen cDNAs from any library of interest can be chosen. ESTs are partially sequenced cDNAs as described. In general, the cDNAs are of sufficient length to hybridize to cDNAs obtained from mRNAs representing splice variants or nucleic acids encoding different peptide chain isoforms derived from a single gene or the polymorphs of a single gene under the hybridization conditions of a microarray experiment. The DNAs immobilized on an array may also be nucleic acid chains comprising less than 100 nucleic acid residues (*e.g.* oligonucleotides). Nucleic acids immobilized on an array may also comprise alternative backbone chemistries such as phosphothiorate bond based chemistries, and alternative nucleoside residues such as modified residues capable of pairing with multiple nucleoside base residues. Those skilled in the art will recognize a variety of chemical modifications that can be made to the basic nucleic acid structure to create non-naturally occurring molecules with improved properties which are still capable of hybridizing to other nucleic acid molecules. In general, such modifications are those that improve the stability of such molecules, the hybridization properties of such molecules, or the ability of such molecules to couple to a substrate such as an immobilized substrate.

In a typical microarray experiment, a microarray is hybridized with differentially labeled RNA or DNA populations derived from two different samples. Most commonly RNA is isolated from cells or tissues of interest and is reverse transcribed to yield cDNA. Such RNA

may be either total RNA or polyadenylated RNA. Labeling is usually performed during reverse transcription by incorporating a labeled nucleotide in the reaction mixture, but RNAs can also be labeled. Although various different labels can be used, most commonly the nucleotide is conjugated with fluorophores such as the fluorescent dyes Cy3 or Cy5 (*e.g.*, Cy5-dUTP and Cy3-dUTP). cDNA or RNA derived from one sample representing, for example, a particular cell type, tissue type or growth condition is labeled with one fluorophore while cDNA or RNA derived from a second sample representing, for example, a different cell type, tissue type, or growth condition is labeled with the second fluorophore. Similar amounts of labeled material from the two samples are hybridized to the microarray. In the case of a microarray experiment in which the samples are labeled with Cy5 which fluoresces red light and Cy3 which fluoresces green light, the primary data obtained by scanning the microarray using a detector capable of quantitatively detecting fluorescence intensity are ratios of red/green fluorescence intensity. These ratios represent the relative concentrations of labeled cDNA or RNA molecules that hybridized to the DNA on the microarray and thus reflect the relative expression levels of the mRNA corresponding to each cDNA or gene represented on the microarray.

Alternatively, different labeled probe samples can be hybridized to an array at different times by hybridizing a first sample, collecting fluorescence intensity data for the first sample, stripping the array, collecting background fluorescence intensity data, hybridizing the second sample, and then collecting fluorescence intensity data. This type of approach can be used to probe an array with a tumor sample and then a reference such as a sample from normal tissue to measure an indicator of gene transcript levels in a tumor sample or to measure a reference to produce a reference value. Those of ordinary skill in the art will recognize other strategies for measuring an indicator of gene transcript levels in a tumor sample and measuring a reference to produce a reference value. Additionally, those of ordinary skill in the art will recognize hybridization based analyses can be performed in other non-array based formats, and that when array based formats are used the array need not be on the micro-scale and can instead be provided in other formats.

Hybridizations to arrays can be performed under a variety of stringent conditions by varying temperature or salt, detergent, and crowding agent concentrations. Additionally, microarray hybridization reagents are commercially available such as, for example, the Agilent Gene Expression Hybridization Kit (part number 5188-5242; Agilent Technologies Inc. Santa Clara, CA) or Agilent Oligo aCGH Hybridization Kit (part number 5188-5220; Agilent Technologies Inc. Santa Clara, CA). The term "stringent hybridization conditions" as used

herein means those conditions which promote the hybridization of a given nucleic acid sequence to its sequence complement, without that sequence hybridizing significantly with sequences having a lesser degree of complementarity (*e.g.* having one or more mismatches or less than 85% or less than 90% sequence identity as measured by CLUSTALW alignment using the default settings of the CLUSTALW algorithm). More generally, "stringent hybridization conditions" means conditions which allow hybridization of a given sequence with its intended targets, without significant hybridization of the sequence with other, nucleic acid sequences having different nucleic acid sequences that may be present.

Tumor samples for use in the methods of the disclosure can be prepared by collecting a fresh portion of the tumor by core needle biopsy or surgery. Tumor samples to be used for microarray or other nucleic acid hybridization based analyses can then be placed in cold RNALATER™ (Applied Biosystems/Ambion Inc., Austin, TX) on ice for 30 minutes followed by freezing at -80°C until RNA extraction. RNA can be extracted from tumor samples using the RNEASY™ system (Qiagen Inc., Valencia, CA) and contaminating DNAs can be removed with TURBO™ DNAse (Applied Biosystems/Ambion Inc., Austin, TX). Each tumor sample RNA preparation can then be assayed for purity by PCR/reverse transcription-PCR differential amplification analysis to confirm satisfactory removal of contaminating DNAs from the preparation. Each tumor sample RNA preparation can also be assessed for RNA quality using capillary electrophoresis RNA 6000 Ladder LABCHIP™ kits and an Agilent 2100 Bioanalyzer system (Agilent Technologies Inc. Santa Clara, CA) to produce electropherograms for assessment of RNA quality. RNA quality can be evaluated by examining electropherograms to confirm the 18 S and 28 S rRNA subunit peaks are present and in the appropriate 1:2 ratio. Assessment of 18 S and 28 S rRNA by this and other techniques is accepted in the art as an indicator of the relative intactness or quality of other isolated RNAs in a sample such as mRNAs and as an indicator of RNAse degradation of such isolated RNAs.

The Agilent 2100 Bioanalyzer system can also assess RNA quality using software that produces a RNA integrity number (RIN) for estimating the integrity of total RNA samples. This software automatically assigns an integrity number to RNA sample. Such that sample integrity is no longer determined by the ratio of the ribosomal bands, but instead by the entire electrophoretic trace in an electropherogram prepared using the RNA sample. This includes the presence or absence of degradation products. RIN based analyses facilitates interpretation of an electropherogram comparison of samples and helps ensure the reproducibility of experiments or

analysis. Importantly, the assigned RIN is independent of sample concentration, instrument and analyst.

Only tumor sample RNA preparations satisfying the differential amplification assay and electropherogram assay or other RNA integrity analyses are used to generate probes for the microarray analysis or other hybridization based analyses. Tumor sample RNA preparations can be labeled for use as probes as described above, or by using a commercially available labeling kits according to the manufacturer's instructions. The Invitrogen SUPERSCRIPT™ Indirect cDNA Labeling System (Invitrogen Inc., Carlsbad, CA) is one example of such a commercially available kit. Those of ordinary skill in the art will readily recognize others. Alternatively, RNA preparations can be converted to DNA preparations by reverse transcription and RNAse treatment, labeled and used as probes as discussed above in more detail.

In the methods of the disclosure indicators of gene transcript levels and reference values can be determined using techniques such as multi-dimensional gel electrophoresis, chromatography based techniques for measuring expressed peptide chains encoded by a gene, and other techniques such as fluorescence activated cell sorting or protein array analyses. In chromatography based techniques the presence of a given protein in a sample can be determined by techniques such as mass spectroscopy or antibody based detection techniques (e.g. ELISA), which are well known in the art.

A protein microarray, sometimes referred to as a protein binding microarray, comprises a substrate such as glass on which different molecules of protein have been affixed at specific locations in an ordered manner to form an array. The most common protein microarray is the antibody microarray, where antibodies specific to different individual expressed peptide chains are spotted onto the substrate and are used as capture molecules to detect the level of the different individual expressed peptide chains (*e.g.*, specific proteins) cell lysate solutions. This is typically done by blocking the array to minimize non-specific signals, incubating a lysate sample with the array, washing the array, blocking again, and probing the array. Additional wash and blocking steps may be necessary depending on the strategy selected for probing the array and the method used to detect peptide chains bound to the probed array. Expressed peptide chains binding to antibody arrays may be detected directly or via a secondary antibodies in a sandwich type immuno-assay (*e.g.*, ELISA). Expressed peptide chains present in a lysate can be directly labeled with an appropriate chromophore or fluorophore using well known techniques. Where pairs of antibodies specific to the same expressed peptide chain are available, sandwich immunoassays provide high specificity and sensitivity. Additionally, label-

free methods for detecting expressed peptide chains binding to an antibody array are available and include mass spectrometry, surface plasmon resonance and atomic force microscopy. Multichannel fluorescence activated cell sorting can also be used in conjunction with a selected panel of peptide chain specific antibodies to identify cells expressing a given set of peptide chains. Those of ordinary skill in the art will recognize other techniques, as well as variations on the techniques described above, for measuring an indicator of gene transcript levels and reference values which are suitable for use in the methods of the invention.

In one embodiment of the methods of the disclosure, the tumor sample is from lung tissue.

In another embodiment of the methods of the disclosure, the tumor sample is from thyroid tissue.

In another embodiment of the methods of the disclosure, the tumor sample is from ovarian tissue.

In another embodiment of the methods of the disclosure, the tumor sample is from prostate tissue.

In another embodiment of the methods of the disclosure, the indicator value is at least 1.8 times greater than the reference value for each of the gene transcripts.

Another aspect of the disclosure is a method of determining the odds that an individual ERGO tumor patient will survive to a future date comprising the steps of providing a tumor sample from an individual patient; providing a reference; measuring an indicator of gene transcript levels in the tumor sample to produce an indicator value for each of the following gene transcripts having the nucleic acid sequences shown in SEQ ID NO:s 12-14, 20-21, 35, 37, 39, 43-44, 46-47, 49-51, 54, 56, 58-72, 75, 79-84, 86, 88, 91, 93-95, 102-105, 107-110, 112, 116, 118-120, 122-123, 125-126, 128-129, 131, 145-146, 148-149, 151, 154, 156-157, 160, 163-166, 169, 171, 173-174, 176-177, 180, 184, 186, 188, 193, 196, 198, 200-201, 203, 205, 209, 217, 246-247, 249, 254, 259, 267, 269, 274-275, 292-295, 298, 307, 311, 316, 321-323, 331, 333, and 335-340; measuring the reference to produce a reference value; and comparing the indicator value to the reference value to determine which of the gene transcripts is over-expressed, whereby the tumor is identified as an ERGO tumor and the individual patient is diagnosed as an ERGO tumor patient if at least 21 of these gene transcripts are over-expressed; plotting the fraction of surviving patients in a population of patients diagnosed as ERGO tumor patients as a function of the time since diagnosis of the ERGO tumor to generate a survival plot; and selecting a future date after the individual patient is diagnosed as an ERGO tumor patient

and determining the fraction of surviving patients in the population from the survival plot; whereby the fraction of surviving patients on the survival plot at the future date predicts the odds that an individual tumor patient will survive to the future date.

In one embodiment of the methods of the disclosure the tumor sample is from lung tissue and the population of patients is diagnosed as ERGO lung tumor patients.

In another embodiment of the methods of the disclosure the tumor sample is from thyroid tissue and the population of patients is diagnosed as ERGO thyroid tumor patients.

In another embodiment of the methods of the disclosure the tumor sample is from ovarian tissue and the population of patients is diagnosed as ERGO ovarian tumor patients.

In another embodiment of the methods of the disclosure, the tumor sample is from prostate tissue and the population of patients is diagnosed as ERGO prostate tumor patients.

Another aspect of the disclosure is a method of treating an ERGO tumor in a patient comprising the steps of providing a tumor sample from a patient; providing a reference; measuring an indicator of gene transcript levels in the tumor sample to produce an indicator value for each of the following gene transcripts having the nucleic acid sequences shown in SEQ ID NO:s 12-14, 20-21, 35, 37, 39, 43-44, 46-47, 49-51, 54, 56, 58-72, 75, 79-84, 86, 88, 91, 93-95, 102-105, 107-110, 112, 116, 118-120, 122-123, 125-126, 128-129, 131, 145-146, 148-149, 151, 154, 156-157, 160, 163-166, 169, 171, 173-174, 176-177, 180, 184, 186, 188, 193, 196, 198, 200-201, 203, 205, 209, 217, 246-247, 249, 254, 259, 267, 269, 274-275, 292-295, 298, 307, 311, 316, 321-323, 331, 333, and 335-340; measuring the reference to produce a reference value; and comparing the indicator value to the reference value to determine which of the gene transcripts is over-expressed, whereby the tumor is identified as an ERGO tumor if at least 21 of these gene transcripts are over-expressed; selecting a drug capable of killing or inhibiting division of an ERGO tumor cell expressing at least one protein encoded by at least one gene transcript selected from the group consisting of the following gene transcripts having the nucleic acid sequences shown in SEQ ID NO:s 12-14, 20-21, 35, 37, 39, 43-44, 46-47, 49-51, 54, 56, 58-72, 75, 79-84, 86, 88, 91, 93-95, 102-105, 107-110, 112, 116, 118-120, 122-123, 125-126, 128-129, 131, 145-146, 148-149, 151, 154, 156-157, 160, 163-166, 169, 171, 173-174, 176-177, 180, 184, 186, 188, 193, 196, 198, 200-201, 203, 205, 209, 217, 246-247, 249, 254, 259, 267, 269, 274-275, 292-295, 298, 307, 311, 316, 321-323, 331, 333, and 335-340; and administering a pharmaceutically acceptable amount of the drug to the patient; whereby the ERGO tumor in the patient is treated.

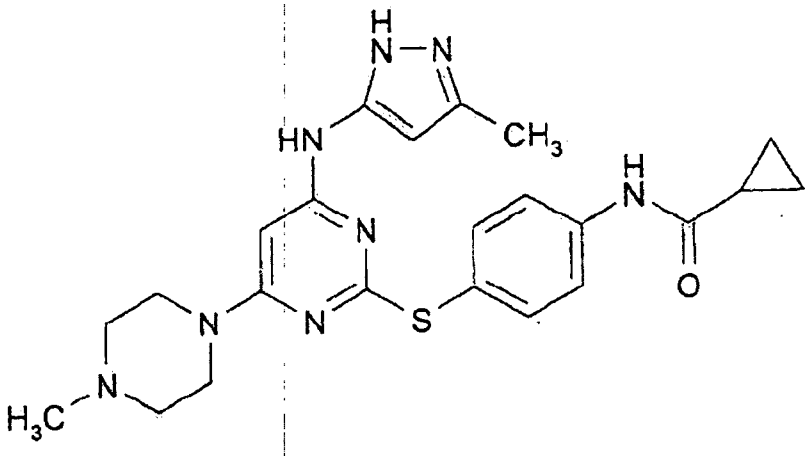
Drugs useful in the methods of the disclosure may be, for example, small organic molecules, peptides, antibodies, antibody fragments or polynucleotides. Such drugs may kill ERGO tumors or inhibit the division of an ERGO tumor cell. Division of an ERGO tumor cell is inhibited when the division of an ERGO tumor cell treated with a drug is decreased relative to an ERGO tumor cell which has not been treated with the compound.

In the methods of the disclosure, drugs may be administered by a variety of routes including, for example, orally, intravenously, intramuscularly, intra-arterially, subcutaneously, intraventricularly, transdermally, rectally, intravaginally, intraperitoneally, topically, or bucally, as a spray, aerosol, power, liquid or ointment. In general, the most appropriate route of administration will depend upon a variety of factors including the nature of the compound (*e.g.* its stability in the environment of the gastrointestinal tract), the condition of the patient (*e.g.* whether the patient is able to tolerate oral administration) *etc.* At present, the intravenous route is most commonly used to deliver therapeutic antibodies and nucleic acids. However, the disclosure encompasses the delivery of the pharmaceutical composition by any appropriate route. Those of ordinary skill in the art will recognize additional routes and techniques for the administration of drugs to a patient.

In the methods of the disclosure, drugs can be provided in a pharmaceutical composition. Such pharmaceutical compositions may comprise a number of different dosage forms such as solids or liquids or combinations of these. Such drugs can also be provided in pharmaceutically effective amounts sufficient to kill ERGO tumors or inhibit the division of an ERGO tumor cell. Pharmaceutically effective amounts of drugs can be readily identified using dose-response curves and other techniques well known the art.

In one embodiment of the methods of the disclosure the drug is an aurora kinase antagonist. A number of aurora kinase inhibitors have been in clinical phase I trial and results were reported in abstract form in 2008 for the SNS-314 aurora kinase inhibitor compound, Abstract #1462; the aurora kinase inhibitor compounds ZM 447439 (American Society of Clinical Oncology 2008 Meeting Abstract #2203), PF-03814735 (American Society of Clinical Oncology 2008 Meeting Abstract # 2517), PHA-739358 (American Society of Clinical Oncology 2008 Meeting Abstract # 3507), AS703569 (American Society of Clinical Oncology 2008 Meeting Abstract #14130), and MLN8054 (American Society of Clinical Oncology 2008 Meeting Abstract #3577). These drugs produced disease stabilization in some 20-40% of patients with tolerable toxicities and are suitable for use in the methods of the disclosure.

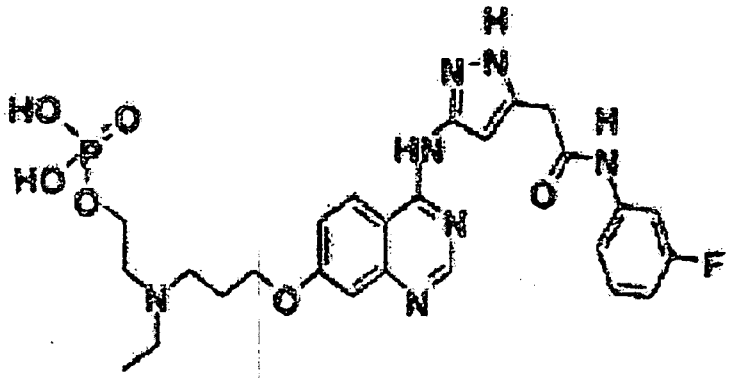
In another embodiment of the methods of the disclosure the aurora kinase antagonist is at least one molecule selected from the group consisting of VX-680, MLN8237, MLN8054, AZD1152, hesperadin, and ZM-447439. VX-680 has the structure shown below and includes the pharmaceutically acceptable derivatives of this compound.



VX-680

VX-680 is an aurora kinase inhibitor manufactured by Merck and Company Inc. (Whitehouse Station, NJ) which has been shown to block cell proliferation, disrupt bipolar spindle formation, and lead to accumulation of cells with 4N or greater numbers of chromosomal DNA copies and eventual cell death (reviewed in Agnese, V et al., Annals of Oncology 18: vi47–vi52, 2007). *In vivo*, VX-680 blocks cell-cycle progression and induces apoptosis in a wide range of human tumor types (Pan et al, Oral Oncol. 2008 Jul;44(7):639-45). VX-680 causes substantial inhibition of tumor growth in xenograft models, leading to regression of leukemia, colon and pancreatic tumors at well-tolerated doses (Harrington E, et al., Nat. Med. 2004 Mar;10(3):262-7). The results of a phase I clinical trial with VX-680 were reported at the ASCO 2008 Annual Meeting, in abstract #3009. In the trial three of 16 patients achieved stable disease at dose levels that were well below those which cause dose-limiting toxicity.

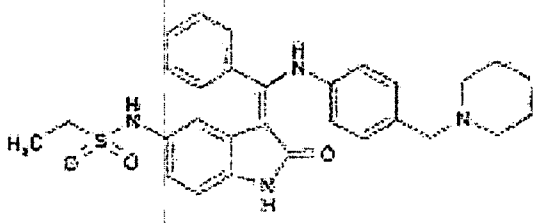
The compound AZD-1152 has the structure shown below and includes the pharmaceutically acceptable derivatives of this compound.



AZD1152

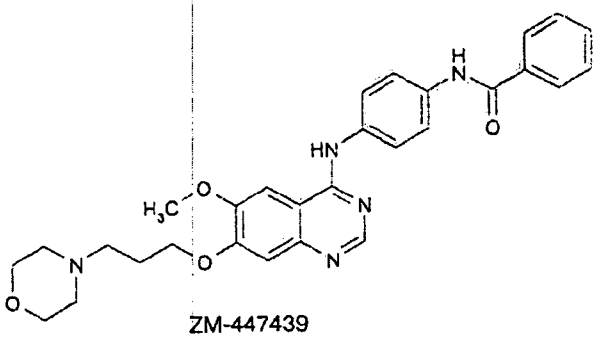
AD1152 is an aurora kinase inhibitor manufactured by AstraZeneca PLC (London, GB) that has been in phase I clinical trials. In the trial 5 of 12 patients had significant disease stabilization, with neutropenia as the only significant toxicity (Abstract #3008, American Society of Clinical Oncology (ASCO) 2008 Annual meeting).

The compound hesperadin has the structure shown below and includes pharmaceutically acceptable derivatives of this compound.



Hesperadin

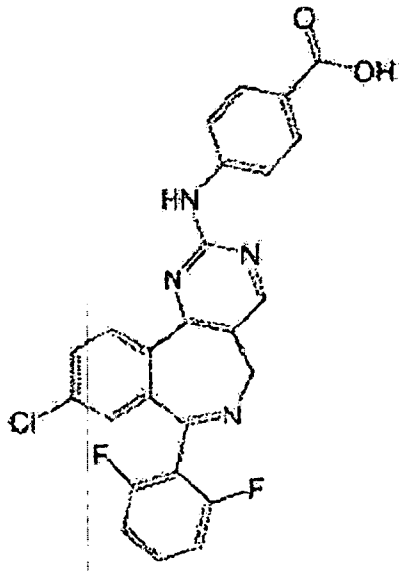
The compound ZM-447439 has the structure shown below and includes pharmaceutically acceptable derivatives of this compound.



ZM-447439

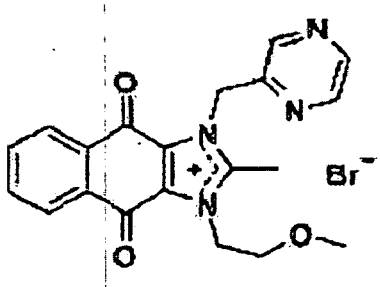
MLN8237 is an aurora A kinase inhibitor manufactured by Millenium Pharmaceuticals, Inc. (Cambridge, MA). The results of *in vivo* studies with MLN8237 were reported at the American Association for Cancer Research (AACR) 2008 Annual Meeting, in abstract #3237. The treatment of cultured human tumor cells with MLN8237 resulted in mitotic spindle abnormalities, mitotic accumulation, inhibition of cell proliferation and apoptosis. MLN8237 is orally bioavailable and has a favorable pharmacokinetic profile. A single oral administration of MLN8237 to nude mice bearing subcutaneous human tumor xenografts resulted in a time dependent accumulation of mitotic cells, consistent with the pharmacological effect being mediated through aurora A inhibition. Repeated oral administration of MLN8237 at well tolerated doses to nude mice bearing subcutaneous human tumor xenografts resulted in dramatic tumor growth inhibition in all tumor models evaluated. In these models MLN8237 induced mitotic accumulation and apoptosis. MLN8237 did not appreciably inhibit aurora B at efficacious concentrations, as indicated by measuring phosphorylated histone H3 Ser10 staining. MLN8237 is currently in Phase I clinical trials in patients with advanced malignancies.

MLN8054 is a selective small-molecule Aurora A kinase inhibitor that has entered Phase I clinical trials for advanced solid tumors. MLN8054 inhibits recombinant Aurora A kinase activity *in vitro* and is selective for Aurora A over the family member Aurora B in cultured cells. MLN8054 treatment results in G_2/M accumulation and spindle defects and inhibits proliferation in multiple cultured human tumor cells lines. Growth of human tumor xenografts in nude mice was dramatically inhibited after oral administration of MLN8054 at well tolerated doses. Moreover, the tumor growth inhibition was sustained after discontinuing MLN8054 treatment. In human tumor xenografts, MLN8054 induced mitotic accumulation and apoptosis, phenotypes consistent with inhibition of Aurora A. MLN8054 is a selective inhibitor of Aurora A kinase that robustly inhibits growth of human tumor xenografts and can be used in the treatment of cancers. The compound MLN8054 has the structure shown below and includes pharmaceutically acceptable derivatives of this compound. *See Manfredz et al.*, 104 Proc. Nat. Acad. *See* USA 4106 (2007).



In another embodiment of the methods of the disclosure the drug is a survivin antagonist.

In another embodiment of the methods of the disclosure the survivin antagonist is YM155. The compound YM155 has the structure shown below and includes pharmaceutically acceptable derivatives of this compound. YM155 is targeted therapy against survivin an E2F-responsive genes that is over-expressed in ERGO tumors. YM155 has also been in phase I clinical trials, and has shown clinical activity in solid tumors (American Society of Oncologist 2008 Meeting Abstracts # 3536, 5135, and 8538) with tolerable toxicity.



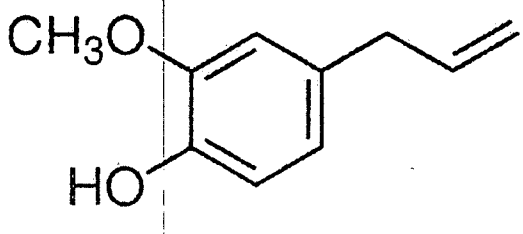
In another embodiment of the methods of the disclosure the drug is a FOXM1 antagonist. FOXM1 itself is a transcription factor that controls at least a dozen other E2F-responsive genes that are over-expressed ERGO tumors, including Aurora B kinase, survivin, and PLK1. A small peptide named $(D\text{-}Arg)_9$-p19ARF 26-44 has been developed that blocks

FOXM1, and is active both *in vitro* and *in vivo*, producing growth inhibition, reduction in levels of survivin, aurora B kinase, and PLK1 as well as inducing apoptosis (Gusarova, et al., J Clin Invest, 117: 99-111, 2007). Other small molecule inhibitors of FOXM1 have been found to be active *in vitro* and to down-regulate downstream targets of FOXM1 (American Association of Cancer Researchers 2008 Meeting Abstract #2663). These small molecule FOXM1 inhibitors can inducing apoptosis in breast cancer cell lines including the MDA-MB-231 basal-like breast cancer derived cell line (American Association of Cancer Researchers 2008 Meeting Abstract # 3280).

In another embodiment of the methods of the disclosure the FOXM1 antagonist is the $(D\text{-}Arg)_9$-p19ARF 26-44 peptide. The compound $(D\text{-}Arg)_9$-p19ARF 26-44 has the structure of rrrrrrrrrKFVRSRRPRTAS-CALAFVN containing nine D-Arg residues at the amino terminus and pharmaceutically acceptable derivatives of this compound.

In another embodiment of the methods of the disclosure the drug is an E2F antagonist.

In another embodiment of the methods of the disclosure the E2F antagonist is eugenol. Eugenol has the structure below and includes pharmaceutically acceptable derivatives of this compound.



Eugenol is the active agent in clove oil and has been reported to target E2F1 and kill melanoma cells *in vitro* (Ghosh, R., et al., J Biol Chem. 2005 Feb 18;280(7):5812-9).

In another embodiment of the methods of the disclosure, the drug is a LINC protein complex agonist. Such an agonist can be over-expressed LINC protein complexes.

Another aspect of the disclosure is a method of identifying an individual tumor in a population of tumors as an ERGO tumor comprising the steps of providing a population of tumor samples; providing a reference; measuring gene transcript levels in the tumor samples to produce a transcript value for each of the following gene transcripts having the nucleic acid sequences shown in SEQ ID NO:s 10-340; comparing the transcript value to the reference value for each tumor to identify the gene transcripts over-expressed by each tumor; ranking the tumors in the population with a rank ordering algorithm to order the tumors according to the number of the gene transcripts over-expressed by each tumor; and removing individual tumors

from the population that over-express the smallest number of each gene transcript per cell and that have the lowest levels of over-expression of each gene transcript per cell until at least 20% of the individual tumors remaining in the population over-express at least 20% of the gene transcripts; whereby an individual tumor remaining in the population of tumors is identified as an ERGO tumor.

Another aspect of the disclosure is a method of identifying an individual tumor in a population of tumors as an ERGO tumor comprising the steps of providing a population of tumor samples; providing a reference; measuring gene transcript levels in the tumor samples to produce a transcript value for each of the following gene transcripts having the nucleic acid sequence shown in SEQ ID NO:s 10-340; comparing the transcript value to the reference value for each tumor to identify the gene transcripts over-expressed by each tumor; and applying a principle component analysis algorithm in which the analyzed gene set is restricted to each gene transcript having the nucleic acid sequence shown in SEQ ID NO:s 10-340 to identify a tumor cluster over-expressing these E2F-responsive genes; whereby an individual tumor in the population of tumors in the cluster is identified as an ERGO tumor.

Another aspect of the disclosure is a method of selecting treatment for a prostate cancer patient comprising the steps of providing a tumor sample from a prostate cancer patient; providing a reference; measuring an indicator of gene transcript levels in the tumor sample to produce an indicator value for each of the following gene transcripts having the nucleic acid sequences shown in SEQ ID NO:s 12-14, 20-21, 35, 37, 39, 43-44, 46-47, 49-51, 54, 56, 58-72, 75, 79-84, 86, 88, 91, 93-95, 102-105, 107-110, 112, 116, 118-120, 122-123, 125-126, 128-129, 131, 145-146, 148-149, 151, 154, 156-157, 160, 163-166, 169, 171, 173-174, 176-177, 180, 184, 186, 188, 193, 196, 198, 200-201, 203, 205, 209, 217, 246-247, 249, 254, 259, 267, 269, 274-275, 292-295, 298, 307, 311, 316, 321-323, 331, 333, and 335-340; measuring the reference to produce a reference value; and comparing the indicator value to the reference value to determine which of the gene transcripts is over-expressed, whereby the tumor is identified as an ERGO tumor and the prostate cancer patient is diagnosed as an ERGO tumor prostate cancer patient if at least 21 of these gene transcripts are over-expressed; and choosing at least one treatment selected from the group consisting of removal of at least one tumor and adjuvant therapy, if the patient is diagnosed as an ERGO tumor prostate cancer patient; whereby a treatment is selected for the prostate cancer patient.

An important clinical problem for patients diagnosed with prostate cancer is that only about 15% of all such patients will ever die of their disease, but it is difficult to know whether

an individual patient is in this unfortunate population of 15% of all patients. Furthermore, many prostate tumors, including those in older patients, grow slowly and without metastasis. Consequently, patients diagnosed with prostate cancer and physicians have to select either of two approaches after a prostate cancer diagnosis. The first approach is known as the "watchful waiting" approach in which tumor growth and related indicators are monitored over time. In this approach no treatment is necessary until a change in disease severity or symptoms occurs. The second approach is to undergo a primary treatment such as conventional and other surgeries, cryosurgery, or radiation therapy to remove or kill the prostate cancer tumor and any metastasis. Additionally, as part of this approach adjuvant therapies such as chemotherapy or hormonal therapy may be necessary to help ensure effective treatment to prevent or postpone the prostate cancer from coming back after the primary treatment. Unfortunately, a number of side effects are potentially associated with the primary treatment and the adjuvant therapies of this second approach including impotence, urinary incontinence, nausea, fatigue, diarrhea, and infertility. Consequently, there is a need for methods of selecting treatment for patients diagnosed with prostate cancer to help insure a given treatment approach is appropriate for an individual patient and the patient's type of prostate tumor.

Importantly, the Applicant has discovered that about 20% of primary prostate cancers from individual patients are ERGO tumors irrespective of the Gleason score conventionally used to functionally classify prostate cancers assigned to these cancers. Furthermore, greater than 80% of all metastases associated with prostate cancer tumors are ERGO tumors. Consequently, the identification of prostate cancer ERGO tumors in patients diagnosed with prostate cancer provides a means for identifying those prostate cancer tumors that are most likely to metastasize or grow profusely and to select appropriate patient treatment.

In one aspect of the method of the disclosure the removal of at least one tumor is performed using at least one therapy selected from the group consisting of using focused energy, cryoablation, and radiation therapy. Examples of focused energy include light such as high intensity laser beams of appropriate wavelengths, and other forms of electromagnetic radiation such as microwaves, as well as X-rays or other types of ionizing radiation. In the methods of the disclosure, tumors are considered to be removed by these or other techniques such as cryoablation (freezing) and radiation therapy if the tumor or cells forming some portion of the tumor are killed, burned, or otherwise destroyed (*e.g.* by electromagnetic radiation).

In another aspect of the method of the disclosure the adjuvant therapy is at least one therapy selected from the group consisting of chemotherapy, hormone therapy, and

immunotherapy. Chemotherapy treatment with drugs such as small molecules that kill cancer cells. Examples of drugs useful in chemo-therapy include, for example, anthracyclines such as doxorubicin, epirubicin and liposomal doxorubicin; taxanes such as docetaxel, paclitaxel, and protein-bound paclitaxel; cyclophosphamide; capecitabine; 5-fluorouracil (5 FU); vinorelbine; emcitabine; mitoxantrone; estramustine; etoposide (VP-16); vinblastine; and carboplatin. These drugs, and others disclosed herein, may be used in the manufacture of medicaments for the treatment of ERGO tumors identified according to the disclosed methods. Hormone therapy is also called androgen deprivation therapy (ADT) or androgen suppression therapy. The goal of hormone therapy in prostate cancer patients is to reduce levels of the male hormones, called androgens, in the body. The main androgens are testosterone and dihydrotestosterone (DHT). Androgens, produced mainly in the testicles, stimulate prostate cancer cells to grow. Lowering androgen levels often makes prostate cancers shrink or grow more slowly. Drugs useful in such hormone therapy include, for example, luteinizing hormone-releasing hormone (LHRH) analogs including leuprolide, goserelin, and triptorelin; luteinizing hormone-releasing hormone (LHRH) antagonists such as abarelix; anti-androgens such as flutamide, bicalutamide, nilutamide; and ketoconazole. Hormone therapy may also require orchiectomy (surgical castration) to control androgen production. Immunotherapy treatments include treatments that stimulate a patient's own immune system to kill prostate tumors cells. The sipuleucel-T (PROVENGE™) treatment system (Dendreon Corp., Seattle, WA) is one example of an immunotherapy. In this system immune system white blood cells are removed from a prostate cancer patient, antigen presenting cells (APCs) are then isolated from these white blood cells by apheresis, and the patient's isolated APCs are co-cultured with a recombinant fusion protein antigen comprising prostatic acid phosphatase (PAP). The activated, antigen-loaded APCs at this point are designated as "sipuleucel–T" and injected into the prostate cancer patient. Once administered to the patient these APCs present the recombinant PAP antigen to T-cells and help stimulate the patient's own immune system to produce a killer T-cell response against his prostate cancer tumor cells. Those of ordinary skill in the art will recognize other chemotherapies, hormone therapies, and immunotherapies.

In another embodiment the methods of the disclosure further comprise measuring an indicator of gene transcript levels in at least one selected from the group consisting of the tumor sample and the reference to produce a housekeeping value for at least one gene transcript selected from the group consisting of the nucleic acid sequences shown in SEQ ID NO:s 162, 341-365 and 366; and normalizing at least one selected from the group consisting of the

indicator value and the reference value to the housekeeping value. This embodiment is particularly useful in relation to methods for the identification of ERGO tumors in prostate tissue and methods for the selection of treatment for a prostate cancer patient.

Another embodiment of the disclosure is the use of an aurora kinase antagonist in the manufacture of a medicament for the treatment of an ERGO tumor identified according to the methods of the disclosure.

Another embodiment of the disclosure is the use of VX-680 in the manufacture of a medicament for the treatment of an ERGO tumor identified according to the methods of the disclosure.

Another embodiment of the disclosure is the use of MLN8237 in the manufacture of a medicament for the treatment of an ERGO tumor identified according to the methods of the disclosure.

Another embodiment of the disclosure is the use of MLN8054 in the manufacture of a medicament for the treatment of an ERGO tumor identified according to the methods of the disclosure.

Another embodiment of the disclosure is the use of AZD1152 in the manufacture of a medicament for the treatment of an ERGO tumor identified according to the methods of the disclosure.

Another embodiment of the disclosure is the use of hesperadin in the manufacture of a medicament for the treatment of an ERGO tumor identified according to the methods of the disclosure.

Another embodiment of the disclosure is the use of ZM-447439 in the manufacture of a medicament for the treatment of an ERGO tumor identified according to the methods of the disclosure.

Another embodiment of the disclosure is the use of a survivin antagonist in the manufacture of a medicament for the treatment of an ERGO tumor identified according to the methods of the disclosure.

Another embodiment of the disclosure is the use of YM155 in the manufacture of a medicament for the treatment of an ERGO tumor identified according to the methods of the disclosure.

Another embodiment of the disclosure is the use of a FOXM1 antagonist in the manufacture of a medicament for the treatment of an ERGO tumor identified according to the methods of the disclosure.

Another embodiment of the disclosure is the use of the $(D\text{-}Arg)_9$-p19ARF 26-44 peptide in the manufacture of a medicament for the treatment of an ERGO tumor identified according to the methods of the disclosure.

Another embodiment of the disclosure is the use of an E2F antagonist in the manufacture of a medicament for the treatment of an ERGO tumor identified according to the methods of the disclosure.

Another embodiment of the disclosure is the use of eugenol in the manufacture of a medicament for the treatment of an ERGO tumor identified according to the methods of the disclosure.

Another embodiment of the disclosure is the use of a LINC protein complex agonist in the manufacture of a medicament for the treatment of an ERGO tumor identified according to the methods of the disclosure.

Another embodiment of the disclosure is an apparatus comprising a specifically programmed computer in communication with a nucleic acid array analyzer and an output display, wherein the specifically programmed computer is adapted to compare indicator values to reference values and to determine which gene transcripts are over-expressed in a tumor sample; a nucleic acid array comprising at least 21 of the nucleic acid sequences shown in SEQ ID NO:s 12-14, 20-21, 35, 37, 39, 43-44, 46-47, 49-51, 54, 56, 58-72, 75, 79-84, 86, 88, 91, 93-95, 102-105, 107-110, 112, 116, 118-120, 122-123, 125-126, 128-129, 131, 145-146, 148-149, 151, 154, 156-157, 160, 163-166, 169, 171, 173-174, 176-177, 180, 184, 186, 188, 193, 196, 198, 200-201, 203, 205, 209, 217, 246-247, 249, 254, 259, 267, 269, 274-275, 292-295, 298, 307, 311, 316, 321-323, 331, 333, and 335-340 adapted for hybridization to nucleic acids in a tumor sample; a memory containing an indicator value for each of the following gene transcripts having the nucleic acid sequences shown in SEQ ID NO:s 12-14, 20-21, 35, 37, 39, 43-44, 46-47, 49-51, 54, 56, 58-72, 75, 79-84, 86, 88, 91, 93-95, 102-105, 107-110, 112, 116, 118-120, 122-123, 125-126, 128-129, 131, 145-146, 148-149, 151, 154, 156-157, 160, 163-166, 169, 171, 173-174, 176-177, 180, 184, 186, 188, 193, 196, 198, 200-201, 203, 205, 209, 217, 246-247, 249, 254, 259, 267, 269, 274-275, 292-295, 298, 307, 311, 316, 321-323, 331, 333, and 335-340 produced by hybridization of the nucleic acid array to the nucleic acids in the tumor sample, and containing reference values for the gene transcripts; and an output display which shows the tumor sample is an ERGO tumor when the specifically programmed computer determines at least 21 of the gene transcripts are over-expressed in a tumor sample.

In another embodiment of the methods of the disclosure, the tumor sample is from liver tissue.

In another embodiment of the methods of the disclosure, the tumor sample is from bladder tissue.

In another embodiment of the methods of the disclosure, the tumor sample is from liver tissue and the population of patients is diagnosed as ERGO hepatoma tumor patients.

In another embodiment of the methods of the disclosure, the tumor sample is from bladder tissue and the population of patients is diagnosed as ERGO bladder tumor patients.

In another embodiment of the methods of the disclosure, the ERGO tumor is from a tissue selected from the group consisting of lung tissue, thyroid tissue, ovarian tissue, prostate tissue, liver tissue and bladder tissue.

In another embodiment of the methods of the disclosure, the tumor sample is from a tissue selected from the group consisting of lung tissue, thyroid tissue, ovarian tissue, prostate tissue, liver tissue and bladder tissue.

It is understood that modifications which do not substantially affect the activity of the various embodiments of this disclosure are also included within the definition of the disclosure provided herein. Accordingly, the following examples are intended to illustrate but not limit the present disclosure.

Examples

Example 1

Identification of Human Breast Cancer E2F Responsive Gene Over-Expressing (ERGO) Tumors

Breast Cancer Microarray Sets

A gene expression microarray set from 117 different patient breast cancer samples described by Van't Veer *et al.* was analyzed. This microarray set was selected for analysis because it included 18 tumors obtained from patients with known BRCA1 mutations. The breast cancer microarray set described by Dai *et al.* was used to confirm the analytical results obtained using the Van't Veer microarray set. The gene expression microarray sets of Van't Veer and Dai both contained 57 samples that were identical and were excluded from the analyses of the Dai microarray set (also referred to herein as the "purged Dai microarray set") in the present study.

Weighted Rank Ordering Methods and Criteria for Identification of ERGO Tumors

First, a reference signal intensity value was obtained by averaging the signal intensity values from all sample probed gene spots on the Van't Veer microarray set to be analyzed. The reference signal intensity value was obtained by averaging the signal intensity values from all sample probed gene spots on the Van't Veer microarray set to be analyzed.

Then "over-expressed," "under-expressed," and non-over-expressed genes were identified. Gene "over-expression" was determined to occur when the signal intensity corresponding to a given gene transcript in the microarray set was 1.8 fold greater than the reference signal intensity value discussed above. Gene "under-expression" was determined to occur when the signal intensity corresponding to a given gene transcript in the microarray was 1.8 fold less than a reference signal intensity value. Gene "non-over-expression" was determined to occur when a gene was neither "over-expressed" nor "under-expressed."

Next, weighted rank ordering methods were performed using EXCEL™ software (Microsoft Corp., Redmond, WA) to rank the over-expressed genes by their frequency of expression among the tumors. In these rank ordering analyses the most highly over-expressed genes were placed closest to the origin and the contribution of each tumor to the ranking was weighted by its proximity to the origin of the tumor axis.

These weighted rank ordering methods were then used to rank the tumors by the number of the 325 specific E2F-responsive genes, shown in Table 1 (shown below), over-expressed per tumor ("1" or other value indicates gene functions).

Table 1

gene-name	microaray name	trans-crip-tion, regu-lation	DNA repli-cation	DNA repair	check-point	mi-tosis	apop-tosis	other
BCL2L11*	BCL2L11							
FOXO1A*	FOXO1A							
CCNE2*	CCNE2		1					
CDKN2C*	CDKN2C		1		1			
CCNE1*	CCNE1		1					
MYC*	MYC							
FGFR3*	FGFR3							1
MAP3K5*	MAP3K5						1	
BMP2*	BMP2	1						2
MYB*	MYB	1						
LHX2**	LHX2							
GCH1*	GCH1							1

gene-name	microaray name	trans-crip-tion, regu-lation	DNA repli-cation	DNA repair	check-point	mi-tosis	apop-tosis	other
MAPK9*	MAPK9							1
MAPK8*	MAPK8							1
MAPK3*	MAPK3				1			1
MAPK1*	MAPK1				1		1	1
MAPK4*	MAPK4							1
MAP2K1*	MAP2K1							1
MAP2K2*	MAP2K2							1
FOXO3A*	FOXO3A	1			1		1	
GADD45B*	GADD45B						1	
MCL1*	MCL1						1	
BCL2**	BCL2						1	
CCND3*	CCND3				1			
CHES1**	CHES1	1			1	1		
MKI67**	MKI67							1
CDKN1C**	CDKN1C				1			
KIFC1**	KNSL2							
PRG4**	PRG4							1
PMS2**	PMS2							
PLK2**	SNK					1		
HRK*	HRK						1	
CASP8**	CASP8							
TYMS*	TYMS		1	1				
TK1*	TK1		1					
DUT**	DUT		1					
RRM1*	RRM1		1					
RRM2*	RRM2		1					
CDK2*	CDK2		1			1		
MCM3*	MCM3		1					
MCM7*	MCM7	1	1					
PCNA*	PCNA		1	1				
RFC3*	RFC3		1					
PRIM1**	PRIM1		1					
TOP2A*	TOP2A		1	1		1		
LIG1**	LIG1		1	1				
FEN1**	FEN1		1					
RAD51**	RAD51			1				
CDC20**	CDC20					1		
CDC2*	CDC2				1	1	1	
CCNA2*	CCNA2	1				1		
CCNB1*	CCNB1					1		
CCNB2**	CCNB2					1		
SMC2**	SMC2L1					1		
STMN1*	STMN1					1		1

gene-name	microarray name	trans-crip-tion, regu-lation	DNA repli-cation	DNA repair	check-point	mi-tosis	apop-tosis	other
NDC80**	HEC					1		
BUB1**	BUB1					1		
KPNA2*	KPNA2							
HMGB2**	HMG2	1	1	1				
EZH2*	EZH2	1						
AURKB*	STK12					1		
PTTG1**	PTTG1	1		1		1		
SLBP*	SLBP		1					
RB1*	RB1	1			1	1		
ANXA8*	ANXA8							1
DCK**	DCK							1
CDC25A*	CDC25A				1	1		
EPS8**	EPS8							1
FST*	FST	1						3
TMPO*	TMPO	1						
RAD51AP1**	PIR51			1				
ASF1B**	FLJ10604							3
CDCA4*	FLJ20764							
RFC4**	RFC4		1	1				
BLM**	BLM		1	1				
VRK1**	VRK1							1
BARD1**	BARD1		1	1				
BTG3**	BTG3							1
CHAF1A**	CHAF1A	1	1	1				3
NPAT*	NPAT							3
HUNK*	HUNK							1
DEK**	DEK	1						1
EED**	EED							3
MCM4**	MCM4	1	1					
MELK**	KIAA0175							1
TCF19**	TCF19	1						
FANCL**	FLJ10335			1				
PBX3**	PBX3	1						1
EGR1*	EGR1	1						
CDCA7L**	DKFZp762L0311	1						
SKP2*	SKP2							1
CTGF*	CTGF							2
CITED2**	CITED2							
SERPINE1*	SERPINE1							2
CCND1*	CCND1				1			
UHRF1*	ICBP90			1				
MCM5*	MCM5	1	1					
HMGB3**	HMG4	1						

gene-name	microaray name	trans-crip-tion, regu-lation	DNA repli-cation	DNA repair	check-point	mi-tosis	apop-tosis	other
MCM6*	MCM6	1	1					
CDC45L**	CDC45L		1		1			
CDC6*	CDC6		1		1	1		
ORC6L*	ORC6L		1			1		
CKS2**	CKS2					1		
GMNN*	GEM		1		1			
PRIM2**	PRIM2A		1					
CENPK**	FKSG14					1		
NUP155**	NUP155							1
FIGNL1**	FIGNL1							1
MAD2L1*	MAD2L1				1	1		
CCNF**	CCNF					1		
DNMT1*	DNMT1	1						
RPA1**	RPA1		1	1				
PRC1**	PRC1					1		
RBL1**	RBL1	1						
BRCA1*	BRCA1	1	1	1	1			
H2AFZ**	H2AFZ							3
DTYMK**	DTYMK							1
PLK1**	PLK					1		
POLA2*	POLA2		1					
PBK**	SPK					1		
CASP7*	CASP7						1	
MCM2*	MCM2	1	1					
RPA3**	RPA3		1	1				
GJA7**	GJA7							1
USP1**	USP1			1				
DNA2L**	DNA2L		1					
CITED1**	CITED1	1						
NASP**	NASP		1					1
RFC5**	RFC5		1	1				
SMARCA5**	SMARCA5	1						1
SHCBP1**	FLJ22009							1
SSX2IP**	KIAA0923							
MFAP1**	MFAP1							1
ROD1**	ROD1							1
BMPR1A*	BMPR1A							2
E2F3**	E2F3	1						
UNG*	UNG			1				
ENO3**	ENO3							1
MSH2**	MSH2			1			1	
PLK4**	STK18							1
ACTA2**	ACTA2							1

gene-name	microaray name	trans-cription, regu-lation	DNA repli-cation	DNA repair	check-point	mi-tosis	apop-tosis	other
TIMELESS**	TIMELESS	1						
BOK*	BOK						1	
KBTBD10**	SARCOSIN							1
BUB1B**	BUB1B				1	1		
NUP107**	NUP107							1
KIF2C**	KNSL6					1		
LMNB1*	LMNB1							1
RPA2**	RPA2		1					
CHEK2**	CDS1							1
COL11A1**	COL11A1							2
TGFB3**	TGFB3							2
CALR**	CALR	1					1	1
TTK*	TTK				1	1		
E2F2*	E2F2	1						
CKS1B**	CKS1							1
RFC2**	RFC2		1					
UMPS**	UMPS							1
DBF4*	ASK		1					
CHEK1**	CHEK1			1	1	1		
BUB3**	BUB3					1		
CENPE**	CENPE					1		
CSTF1**	CSTF1							1
RAD54L*	RAD54L			1				
POLD1**	POLD1			1				
MLH1**	MLH1			1				
CENPA**	CENPA					1		
SMC4**	SMC4L1					1		
HMGB1**	HMG1	1		1			1	
HIST1H3D**	H3FB							4
H2AFX**	H2AFX			1				1
CBX5**	CBX5							3
HIST1H2AC**	H2AFL							4
KIF22**	KNSL4					1		
NEK2*	NEK2					1		
KIF4A**	KIF4A					1		
HMMR**	HMMR							1
MTHFD1**	MTHFD1							1
GINS1*	KIAA0186		1					
SFPQ**	SFPQ	1		1				
HSP90B1*	TRA1	1		1				
MAP3K7**	MAP3K7							2
PLSCR1**	PLSCR1							1
ANLN**	ANLN					1		

gene-name	microaray name	trans-cription, regu-lation	DNA repli-cation	DNA repair	check-point	mi-tosis	apop-tosis	other
SFRS2**	SFRS2	1						
ID3**	ID3	1						
TEAD4*	TEAD4	1						
SRPR**	SRPR							1
UBE2T**	HSPC150							1
INCENP**	INCENP					1		
CDC25B**	CDC25B					1		
AURKA*	STK15					1		
DHFR*	DHFR							1
CDKN3**	CDKN3		1					
CDC7**	CDC7L1		1					
RACGAP1**	ID-GAP					1		
CSRP2**	CSRP2							1
MAF**	MAF	1						
CBX3**	CBX3	1						3
CHAF1B*	CHAF1B	1	1		1			3
ADAMTS1**	ADAMTS1							1
TCOF1**	TCOF1							1
LSM5**	LSM5							1
HNRPC**	HNRPC							1
APAF1*	APAF1						1	
ASH2L*	ASH2L	1						
BCL3*	BCL3	1						1
CASP3*	CASP3						1	
CAV1*	CAV1							1
CD58*	CD58							1
DMRT1*	DMRT1	1						
DYRK1A*	DYRK1A							1
LIMA1*	EPLIN							1
FGFR2*	FGFR2							1
HEY1*	HEY1	1						
INHBA*	INHBA	1					1	2
TBC1D2B*	KIAA1055							1
OSMR*	OSMR							1
FURIN*	PACE							1
PRKAR2B*	PRKAR2B							1
PTPNS1*	PTPNS1							1
RANBP9*	RANBP9							1
SOX9*	SOX9							1
SPHK1*	SPHK1							1
TACC1*	TACC1							1
TGFA*	TGFA							1
TGFB2*	TGFB2							2

gene-name	microaray name	trans-cription, regu-lation	DNA repli-cation	DNA repair	check-point	mi-tosis	apop-tosis	other
YY1*	YY1	1						
SNAPC1**	SNAPC1	1						
CCNG2**	CCNG2				1	1		
HOXA7**	HOXA7	1						
HOXA9**	HOXA9	1						1
PITX1**	PITX1	1						1
SMARCA2**	SMARCA2	1						
BACH1**	BACH1	1						
CBFB**	CBFB	1						
BIRC5*	BIRC5				1	1	1	
CDC25C**	CDC25C					1		
ORC3L**	ORC3L		1					
TOPBP1**	TOPBP1			1				
MRE11A**	MRE11A			1		1		
ATM*	ATM			1	1	1		
XRCC4**	XRCC4			1				
RECQL**	RECQL			1				
CENPF**	CENPF					1		
CENPH**	PMF1					1		
NOLC1**	NOLC1					1		
MPHOSPH1**	MPHOSPH1					1		
BMI1*	BMI1							3
HIST1H2AE**	H2AFA							3
HIST1H2AD**	H2AFG							4
HIST1H2BN**	H2BFD							4
HIST1H2BE**	H2BFH							4
HIST1H2BO**	H2BFN							4
HIST1H2BJ**	H2BFR							4
HIST1H3B**	H3FL							4
HIST2H4**	H4F2							4
HIST1H2BF**	H2BFG							4
HIST1H3E**	H3FD							4
KIF20A**	RAB6KIFL					1		3
FGFR1OP**	FOP							1
DHPS**	DHPS							1
PEX19**	PXF							1
PPM1D*	PPM1D					1		
E2F1*	E2F1	1					1	
PARP1**	ADPRT	1						
ORC2L**	ORC2L	1	1					
VEGFA**	VEGF						1	1
APOE**	APOE							3
PRPS1**	PRPS1							1

gene-name	microaray name	trans-crip-tion, regu-lation	DNA repli-cation	DNA repair	check-point	mi-tosis	apop-tosis	other
TGFB1I1*	TGFB1I1	1						
CXCR7*	RDC1							1
PDGFRA**	PDGFRA							1
SLPI*	SLPI							1
FAS**	TNFRSF6						1	
CPT1A*	CPT1A							1
PDCD4*	PDCD4	1					1	
TANK**	TANK							1
APBB2*	APBB2	1					1	1
GADD45A**	GADD45A			1			1	1
ACOX1**	ACOX1							1
CSDA*	CSDA	1				1		
UBE2C**	UBCH10					1		
TPX2**	C20orf1					1		
NUSAP1**	BM037					1		
SULT2A1*	SULT2A1							1
INMT*	INMT							1
ARHGAP4*	ARHGAP4							1
RAD52*	RAD52			1				
TNFSF9*	TNFSF9						1	
BAD*	BAD						1	
BAK1*	BAK1						1	
BID*	BID						1	
CFLAR*	CFLAR						1	
MAP3K14*	MAP3K14							1
PAWR*	PAWR	1					1	
FGF2•	FGF2						1	1
MMP16*	MMP16							1
TP53BP2*	TP53BP2						1	1
VEGFB*	VEGFB							1
IFNA2*	IFNA2						1	
SRGAP2*	KIAA0456							1
DIP*	KIAA0767						1	
SERPINF2*	SERPINF2							1
CCNU*	UNG2							1
TP73*	TP73	1		1	1		1	
POLE2*	POLE2		1					
RAD51C**	RAD51C			1				
PMS2L1**	PMS2L1			1				
DDB2*	DDB2			1				
NFKB2**	NFKB2	1						1
KIF11**	KNSL1					1		
FOXM1*	FOXM1	1						

gene-name	microarray name	trans-crip-tion, regu-lation	DNA repli-cation	DNA repair	check-point	mi-tosis	apop-tosis	other
PLAU*	PLAU							2
BBC3*	BBC3						1	
PMAIP1*	PMAIP1						1	
GAB2*	GAB2						1	1
SIVA1*	SIVA						1	
PPP1R13B*	PPP1R13B						1	
AXIN2*	AXIN2							1
DIABLO*	SMAC						1	
AR*	AR	1						1
NRP1*	NRP1							1
ECT2*	ECT2							1
ISYNA1*	ISYNA1							1

Tumors with the highest number of over-expressed genes per tumor were placed closest to the origin. The contribution of each gene to the ranking was positively weighted by its proximity to the origin of the gene axis.

Individual tumors with the lowest number of over-expressed genes per tumor, and individual genes with the lowest over-expression frequency among the tumors were then iteratively stripped out of the dataset, with recalculation of rankings, until predetermined stopping conditions were met. The stopping conditions were that at least 20% of the tumors remaining in the dataset over-express at least 20% of the remaining E2F-responsive genes. Tumors that remained in the data set after satisfaction of the stopping conditions were identified as ERGO tumors.

Identification of the ERGO Tumor Subset of Human Breast Cancers by Weighted Rank Ordering

The Van't Veer breast cancer microarray set was weighted rank ordered by the number of over-expressed E2F-responsive genes per tumor and by the number of tumors over-expressing E2F-responsive genes using the stopping criteria described above. These analyses resulted in identification of a group containing only 31 of the 117 tumors in the set analyzed and the identification of a set of 74 different E2F-responsive genes that met the stopping condition criteria that at least 20% of the tumors remaining in the set over-express at least 20% of the remaining E2F-responsive genes. These 31 tumors were identified as ERGO tumors because they remained in the data set after the criteria of the stopping conditions described above were satisfied.

The set of 74 different E2F-responsive genes identified are listed in Table 2 shown below.

Table 2

gene/protein name	P value, ERGO vs.non-ERGO	number of over-expressing tumors among total of 31 tumors
STK12	5.00E-16	23
KNSL6	5.00E-16	21
CENPA	5.00E-16	19
RAD54L	3.25E-12	18
FOXM1	3.25E-12	17
RAB6KIFL	0.00E+00	19
ANLN	5.21E-13	19
CDC20	0.00E+00	21
BTG3	1.10E-08	17
BUB1	1.11E-16	16
TYMS	3.25E-12	19
CCNB2	0.00E+00	16
STMN1	1.06E-13	17
C20orf1	0.00E+00	16
CDC2	3.25E-12	16
TTK	1.41E-12	16
BLM	3.31E-12	14
HRK	1.49E-06	15
PLSCR1	5.89E-07	15
EZH2	1.68E-12	16
HEC	3.26E-12	12
BIRC5	2.98E-13	13
CCNA2	3.04E-09	15
CDC25A	1.11E-16	14
MCM5	4.69E-11	15
MCM7	3.04E-11	15
PTTG1	2.10E-13	14
DEK	5.94E-06	15
KNSL2	1.22E-15	13
CDC45L	0.00E+00	15
UBCH10	1.44E-15	14
KIAA0175	3.68E-12	12
TEAD4	2.83E-07	13
CCNE1	2.59E-07	12
PRC1	3.25E-12	12
CHAF1B	2.03E-06	12
TK1	6.93E-08	12
SMC4L1	3.15E-08	13

gene/protein name	P value, ERGO vs.non-ERGO	number of over-expressing tumors among total of 31 tumors
RFC4	8.28E-11	10
MCM6	1.32E-11	12
CSRP2	3.07E-04	14
TGFA	2.10E-05	14
ORC6L	3.27E-12	11
PRIM2A	1.30E-09	10
KNSL1	6.25E-09	10
USP1	3.14E-06	13
MCM2	7.86E-09	11
MAD2L1	3.69E-12	14
TP53BP2	3.84E-07	9
CKS1	1.44E-09	9
NUP155	4.73E-09	8
NEK2	4.03E-13	10
STK15	2.34E-11	9
NASP	2.83E-08	10
DNA2L	2.22E-08	10
LMNB1	4.43E-09	13
NOLC1	1.03E-05	8
CKS2	3.29E-08	8
CSDA	3.35E-05	8
SOX9	6.86E-04	11
MYC	3.29E-05	9
KPNA2	4.49E-11	8
CCNE2	5.50E-08	11
FLJ22009	2.14E-09	8
KIF4A	8.99E-12	7
CCNB1	6.79E-12	9
RRM2	2.33E-11	8
CDC7L1	4.32E-08	6
CDC25B	2.86E-08	10
HMG4	6.95E-10	8
MAP3K14	8.30E-03	8
HMMR	5.27E-07	7
VEGF	3.75E-05	8
ANXA8	3.51E-05	9

This group of 74 different E2F-responsive genes was enriched for genes that are involved in the G_1/ S cell cycle transition stage and DNA replication (*e.g.* TYMS, TTK, ORC6L, MCM2, CCNE2MCM5, MCM6, MCM7, RFC4) and that are involved in the G_2/M cell cycle transition and mitosis (*e.g.* AURKB, KNSL6, CENPA, KIF20A, BUB1, CCNB2, STMN1, TPX2,

BIRC5, KNSL2). Differences between the frequencies of gene over-expression in ERGO and non-ERGO tumors were highly statistically significant for all genes in the ERGO subset and the P-values ranged from $1x10^{-5}$ to $< 1x10^{-16}$. However, these statistical comparisons are purely confirmatory in nature since the ERGO tumor subset was established by rank ordering.

In order to compare the ERGO tumors identified with other non-ERGO breast cancer tumor subsets, the non-ERGO tumors were subdivided into:

a) non-ERGO tumors over-expressing the HER2 receptor;

b) non-ERGO tumors over-expressing the estrogen receptor (ER) and/or the progesterone receptor (PR), and

c) non-ERGO tumors that do not over-express HER2, ER and/or PR.

Importantly, this last set of non-ERGO tumors which did not over-express HER2, ER and/or PR represents a residual "triple non-positive" tumor subset of non-HER2 over-expressing, non-ER over-expressing and/or non-PR over-expressing tumors. This tumor subset was designated the non-ERGO "triple non-positive" tumor subset. A selected gene expression profile for each of these subsets is shown in Fig. 1 and with more detail at Fig. 8.

The ERGO tumor subset is truly "triple-negative" or "triple non-positive," in that essentially all tumors in this set under-express the HER2 receptor, estrogen receptor (ER) and progesterone receptor (PR). This is significant because tumors over-expressing the HER2 receptor can be treated with trastuzumab, while tumors over-expressing the ER or PR receptors can be targeted with hormone therapy based treatment regimens using drugs that prevent estrogen and progesterone from stimulating these receptors. In contrast, "triple non-positive" tumors are unlikely to be responsive to treatments targeting over-expressed HER2, ER, or PR receptors.

Among the 31 ERGO tumors identified, 25 out of 31 (81%) of these tumors over-expressed cyclin E1, cyclin E2, and/or p16. However, over-expression of cyclin E1, cyclin E2, and/or p16 was observed in just 6 out of 46 (13%) of the non-ERGO "triple non-positive" tumors identified, 1 out of 26 (4%) of non-ERGO ER/PR over-expressing tumors, and 2 out of 14 (14%) of the non-ERGO HER2 over-expressing tumors. Importantly, this elevated expression of the cyclin E1, cyclin E2, and/or p16 genes in the ERGO tumor group indicates that E2F expression and E2F mediated regulation of the expression of these proteins is impaired in ERGO tumors, but not in most other tumors.

This is confirmed by the observation that among the 31 ERGO tumors identified 14 out of 31 (45%) of these tumors over-expressed E2F1, E2F2, and/or E2F3. In contrast, over-

expression of E2F1, E2F2, and/or E2F3 was observed in just 7 out 46 (15%) non-ERGO "triple non-positive" tumors identified, 8 out of 26 (31%) of the ER/PR over-expressing non-ERGO tumors identified (ER is known to induce E2F), and in none of the 14 HER2 over-expressing non-ERGO tumors identified. These findings are consistent with the conclusion that aberrant expression (*e.g.* under-expression) of E2Fs (such as E2F1) is occurring in the ERGO breast cancer tumors identified.

Additionally, 16 out of the 31 (52%) ERGO tumors identified over-expressed at least two basal-like tumor cytokeratin markers selected from the group consisting of the cytokeratin 5, cytokeratin 6A, cytokeratin 6B, cytokeratin 14, and cytokeratin 17 basal-like tumor markers. In contrast, over-expression of at least two of these basal-like tumor cytokeratin markers was observed in just 5 out of 46 (11%) non-ERGO "triple non-positive" tumors identified, 2 out of 26 (8%) of the ER/PR over-expressing non-ERGO tumors identified, and in none of the HER2 over-expressing non-ERGO tumors identified.

Importantly, over-expression of these cytokeratin markers is an important criterion for the identification of basal-like tumors. Consequently, the observation here that over-expression of at least two basal like cytokeratins occurred in both the ERGO tumors identified and non-ERGO "triple non-positive" tumor subset identified indicates that the basal-like tumors may represent a genus of tumors with a phenotype that includes both the "triple non-positive" ERGO tumor subset identified and the non-ERGO "triple non-positive" tumor subset identified.

The Van't Veer microarray set analyzed also included tumor samples from 18 patients with known hereditary BRCA1 mutations. Such BRCA1 mutations are believed to pre-dispose patients carrying such mutant genes to cancer. This is because the BRCA1 protein product is involved in DNA damage repair, ubiquitination, transcriptional regulation and other cellular functions. The BRCA1 protein and expression of the gene encoding BRCA1 is important because BRCA1 helps maintain genomic integrity by promoting high fidelity DNA repair when genomic DNA mutations occur. Mutations in the BRCA1 gene or defects in the expression of the gene encoding BRCA1 are believed to result in the accumulation of genomic DNA mutations that can lead to uncontrolled cell division and cancer.

Importantly, 11 of the 18 tumors (61%) from patients with BRCA1 mutations were ERGO tumors, and 8 of these 11 tumors (73%) over-expressed at least two basal-like tumor cytokeratin markers selected from the group consisting of cytokeratin 5, cytokeratin 6A, cytokeratin 6B, cytokeratin 14, and cytokeratin 17 basal-like tumor markers. The 7 other tumors (out of 18) from patients with BRCA1 mutations were non-ERGO "triple non-positive"

tumors, and only 2 of these 7 tumors (29%) over-expressed at least two of the basal-like tumor cytokeratin markers. These findings further confirm that the basal-like tumor genus includes both the ERGO tumor subset and the non-ERGO "triple non-positive" tumor subset. Additionally, these data also indicate that over-expression of basal-like cytokeratins alone is inadequate as a marker for identifying all members of the basal-like tumor genus. This is significant, because it indicates that the ability to identify ERGO tumors by using the gene expression profile of a tumor to determine if it is an ERGO tumor will permit the identification of appropriate tumor treatment regimens and survival predictions for an individual patient.

Last, ID4 which is a basal-like tumor marker was over-expressed in 10 out of 16 of the ERGO tumors (63%) identified, and 4 out of 4 of the non-ERGO "triple non-positive" tumors which over-expressed at least two of the basal-like tumor cytokeratins markers described above. However, ID4 was also over-expressed in 2 ERGO tumors and 3 non-ERGO BRCA1 tumors that did not over-express at least two basal-like cytokeratins. CDH3 which is another basal-like tumor marker was over-expressed in 14 out of 16 (88%) of the ERGO tumors over-expressing at least two basal-like cytokeratins, and in 3 out of 4 (75%) of the non-ERGO "triple non-positive" tumors identified that over-expressed at least two basal like cytokeratins. However, CDH3 was also over-expressed in 4 ERGO tumors and 4 non-ERGO tumors, including 3 non-ERGO tumors from patients with BRCA1 mutations that did not over-express at least two basal-like cytokeratins. Furthermore, ID4 and CDH3 over-expression was also observed in 3 non-ERGO tumors over-expressing the HER2 receptor. Together, these observations indicated that the basal-like tumor genus is not limited solely to ERGO tumors and non-ERGO "triple non-positive" tumors.

Principal component analysis and the basal-like subset.

Principal component analysis (PCA) was then performed on the Van't Veer microarray set using TM4 software version 4.1.01 (www.TM4.org; Dana-Farber Cancer Institute, Boston, MA, USA). This alternative methodology was used to confirm and validate the analytical results obtained with the weighted rank ordering method. PCA was performed using the default settings of the TM4 software unless otherwise indicated.

Principal component analysis of the Van't Veer microarray set revealed a tumor cluster consisting of 38 tumors (Fig. 2A) which all under-expressed the ER based on the criteria described above for "under-expression." 35 of these 38 tumors (92%) were "triple negative. Twenty (20) of these 38 tumors (53%) over-expressed at least two of the basal-like cytokeratins described above. Moreover, only 2 of the 79 tumors (3%) not included in this cluster over-

expressed at least two of these basal-like cytokeratins. Importantly, 91% of all tumors that over-expressed at least two basal-like cytokeratins were found in this cluster of 38 tumors.

Thirty-three (33) of the 38 tumors (87%) in the cluster over-expressed the basal-tumor markers ID4 and/or CDH3, but only 8 of the 79 (10%) tumors that were not in the cluster over-expressed these basal-tumor markers. Among 25 published markers for basal-like tumors (see Table 3 below) that are over-expressed in basal-like tumors, all members of the PCA cluster over-expressed at least 2 of these markers, and 35 out of 38 of the tumors in this cluster over-expressed at least 3 such markers (92%). Thus all members of this tumor cluster identified by PCA can be identified as basal-like tumors based on the over-expression of these markers.

Table 3

gene name	type	ref
CDH3	dx/prog	Ames,2005; Matos, 2005
KRT17	dx/prog	van de Rijn,2002
CRYAB	dx/prog	Moyano, 2006,2008
SNL/fascin	dx	Rodríguez-Pinilla, 2006
ID4	dx	turner, 2007
KRT5	dx/prog	van de Rijn,2002
VIM	dx/prog	Rodríguez-Pinilla, 2007
ACTG2	dx	livasy, 2006
CCNE1	dx/prog	Foulkes, 2004
EZH2	dx/prog	Collett,2006
LAMB3	dx	Rodríguez-Pinilla 2007
KRT6B	dx/prog	van de Rijn,2002
KRT14	dx/prog	Fulford, 2007
MSN	dx/prog	Charafe-Jauffret 2007
ANXA8	dx/prog	Stein, 2005
CCNE2	dx/prog	Foulkes, 2004
CD44	dx	Charafe-Jauffret, 2006
ITGB4	dx/prog	Lu, 2008
S100A9	dx/prog	Goncalves, 2008
MCAM/cd146	dx/prog	Garcia, 2007
KIT	dx	Nielsen, 2004
KRT6A	dx/prog	van de Rijn,2002
P63	dx	Matos, 2005
EGFR	dx	Nielsen, 2004
TGFBR2	prog	uck, 2004

This basal-like tumor cluster identified by PCA contained 27 of the 31 (87%) ERGO tumors identified by the rank ordering method and also included all 11 ERGO tumors from patients with BRCA1 mutations. Of the four ERGO tumors that were excluded from the basal-

like tumor cluster identified by PCA, three were borderline by the ranking method, and would have not been identified as ERGO tumors if the stopping criteria for the ranking method been more stringent (*e.g.*, requiring that ERGO tumors over-express at least 25% of over-expressed E2F-responsive genes instead of 20%). The basal-like tumor cluster identified by PCA also contained 6 out of 7 of the non-ERGO tumors identified from patients with BRCA1 mutations. Together, these results identify ERGO tumors as members of the basal-like breast cancer tumor subset identified by PCA, and confirms that both the ERGO tumors and non-ERGO tumors from patients with BRCA1 mutations identified by the rank ordering method are members of the basal-like tumor subset identified by the PCA method.

Refined Principal Component Analysis and the Identification of the ERGO Tumor Subset within the Basal-Like Tumor Subset Identified by PCA.

The basal-like tumor cluster identified by PCA as described above was further analyzed. This was done by using further refined PCA in which the analyzed gene set was restricted to the E2F-responsive genes listed in Table 1 shown above. In these analyses only those tumors in the basal-like tumor cluster identified by PCA as described above were used as input data. The result of this refined PCA analysis was that the non-ERGO tumors clustered separately from the ERGO tumors (Fig. 2B), although 2 of 27 ERGO tumors identified by the ranking method did not separate cleanly from the non-ERGO tumors.

This refined PCA gene clustering analysis revealed a continuous strand of genes strung along the axis of the first principal component, rather than discrete gene clusters (Fig. 3A). The group of genes shown in black in the upper left in Fig. 3A are the E2F-responsive genes over-expressed most frequently among the basal-like tumor cluster identified by PCA as described above. A list of the most frequently over-expressed genes in the basal-like tumors identified by PCA was then compared to a list of most frequently over-expressed E2F-responsive genes in the ERGO tumors identified by the weighted rank ordering method. As shown in Fig. 3B these two lists are essentially identical for genes that are over-expressed in greater than 35% of the basal-like tumors identified by PCA or the ERGO tumors identified by the weighted rank-ordering method. Very few of the genes that were over-expressed in less than 25% of the basal-like tumors identified by PCA were also over-expressed by the ERGO tumors identified by the rank ordering method. Importantly, it was the ERGO tumors identified by the refined PCA analysis of the basal-like tumor cluster identified by PCA that over-expressed the highest number of E2F-responsive genes per individual tumor (Fig. 3C).

Patterns of Over-Expression and Under-expression of Non-E2F-Responsive Genes in the Basal-Like Tumors Identified by PCA and the ERGO Tumors Identified by Refined PCA.

Over 850 non-E2F-responsive genes were over-expressed in at least 20% of PCA basal-like tumors identified by PCA, such that the differences in frequency of over-expression between the basal-like tumors identified by PCA and the non-basal-like tumors identified by PCA was statistically significant at the $P < 0.05$ level. See Fig. 25 and Table 4 below.

Table 4

PCA Basal-Like Cancers

gene name	mean(1) > mean(2)
KIAA0514	0
BCL11A	1.11E-16
LDHB	1.11E-16
TONDU	2.22E-16
SH2D2A	2.22E-16
NCK1	5.55E-16
CLCN4	6.66E-16
C2orf2	6.66E-16
FOXC1	1.22E-15
CDH3	1.44E-15
MSN	1.67E-15
LAMP3	2.78E-15
PDI2	2.89E-15
IMPA2	3.55E-15
PFKP	6.99E-15
LOC51323	7.22E-15
DKFZP564M2423	8.10E-15
CTSL2	1.30E-14
ODC1	2.28E-14
NSEP1	4.60E-14
LOC56963	5.01E-14
TNFAIP3	6.56E-14
CEBPG	7.44E-14
UGT8	2.06E-13
RBMS1	2.24E-13
ST5	2.75E-13
H1F1	4.00E-13
BA395L14.2	4.70E-13
KIAA1209	5.83E-13
ASNS	7.26E-13
FLJ10540	9.04E-13
DKFZP586C1619	9.71E-13
SCYD1	1.09E-12

gene name	mean(1) > mean(2)
FLJ23399	1.12E-12
FLJ11413	1.13E-12
FLJ22833	1.18E-12
DKFZp762A227	1.21E-12
SH3BP1	1.50E-12
KIAA0042	1.71E-12
AF070552	2.66E-12
KCNK5	3.25E-12
LMO4	3.25E-12
KIAA1350	3.25E-12
SIAT8A	3.25E-12
PSA	3.25E-12
CTPS	3.25E-12
DSC2	3.25E-12
KIAA1140	3.25E-12
GABRP	3.25E-12
PHGDH	3.25E-12
DKFZp762E1312	3.25E-12
PIM1	3.25E-12
SIL	3.25E-12
TM4SF1	3.25E-12
ATDC	3.26E-12
DKFZp564A026	3.27E-12
NFIL3	3.27E-12
PROML1	3.29E-12
AF052117	3.29E-12
PRO1659	3.29E-12
DIAPH3	3.30E-12
SCYA18	3.32E-12
ICB-1	3.33E-12
IL6	3.34E-12
GBP1	3.35E-12
SERPINB5	3.44E-12
KCNN4	3.49E-12
MID1	3.49E-12
KIP2	3.54E-12
MYBL2	3.55E-12
FLJ20005	3.63E-12
KIAA0074	3.64E-12
HMGIY	3.68E-12
NDRG1	3.75E-12
KIAA1553	3.79E-12
EXO1	4.20E-12
SNL	4.23E-12
HSU54999	4.36E-12

gene name	mean(1) > mean(2)
GZMB	4.53E-12
PRO2249	4.65E-12
MCCC1	5.09E-12
KIAA1285	5.21E-12
SMOC1	5.43E-12
KIAA0481	5.45E-12
TMEFF1	5.46E-12
NSAP1	5.53E-12
VIM	5.58E-12
FLJ20354	6.05E-12
RUNX3	6.14E-12
CHIC2	6.45E-12
FLJ13154	6.84E-12
FLJ10468	7.28E-12
UQCRH	7.88E-12
PRKCN	8.01E-12
ME1	8.11E-12
MARCO	8.25E-12
PRKX	8.73E-12
FLJ20186	8.79E-12
FZD9	9.40E-12
GMPS	9.44E-12
DKFZP762N2316	9.90E-12
KIAA0159	1.07E-11
LOC51700	1.07E-11
NMB	1.13E-11
LOC64148	1.42E-11
HSPC159	1.42E-11
GAPDS	1.43E-11
TRIM2	1.49E-11
LAD1	1.54E-11
ARL7	1.55E-11
HSRNASEB	1.55E-11
NMT2	1.60E-11
AL110202	1.61E-11
FLJ10156	1.66E-11
KRT16	1.73E-11
SOAT1	1.75E-11
SCYA13	1.80E-11
KIAA0746	1.85E-11
FLJ21079	2.01E-11
ITM2C	2.51E-11
DKFZP434G032	2.82E-11
DKFZP586G1517	2.82E-11
FLJ12649	3.04E-11

gene name	mean(1) > mean(2)
MRAS	3.17E-11
NFE2L3	3.79E-11
FLJ20425	4.24E-11
AF131753	4.39E-11
PTX3	4.77E-11
KIAA1448	4.81E-11
HSU93243	5.16E-11
VRK2	5.23E-11
DUSP9	5.30E-11
FLJ23293	5.74E-11
LRP8	6.19E-11
TFDP1	6.74E-11
SCHIP1	6.88E-11
FLJ10549	7.01E-11
EGFL6	7.63E-11
PCDH8	7.84E-11
GAPD	7.92E-11
FLJ23414	8.75E-11
KIAA1069	8.88E-11
CHI3L1	8.96E-11
SCYA2	9.14E-11
MGC4090	9.16E-11
MPB1	9.21E-11
CSPG6	9.66E-11
NOGOR	1.04E-10
FLJ11252	1.08E-10
KIAA0077	1.10E-10
TTYH1	1.18E-10
DUSP2	1.20E-10
HHGP	1.26E-10
SRPK1	1.30E-10
CA9	1.41E-10
FLJ11029	1.42E-10
ZNF267	1.45E-10
KIAA0095	1.48E-10
LPIN1	1.58E-10
PGM1	1.62E-10
KIAA1357	1.65E-10
KLK6	1.72E-10
CHST2	1.75E-10
IFRD1	1.75E-10
CIN85	1.93E-10
AL050151	1.97E-10
JRKL	2.09E-10
ADM	2.10E-10

gene name	mean(1) > mean(2)
RIPK2	2.12E-10
DJ742C19.2	2.47E-10
KIAA0008	2.60E-10
ENO1	2.68E-10
LOC56938	2.72E-10
AMD1	2.87E-10
SNN	3.00E-10
UMPK	3.11E-10
PLD1	3.19E-10
FABP7	3.21E-10
POLR2F	3.49E-10
SOX11	3.57E-10
AK001295	4.06E-10
SOX10	4.17E-10
FLJ22341	4.24E-10
SOD2	4.40E-10
PLCG2	4.61E-10
FLJ10549	4.68E-10
MMP12	4.70E-10
CALB2	4.77E-10
DAPK1	4.80E-10
EBI2	5.53E-10
RAB6B	5.84E-10
MIA	5.92E-10
PTTG2	6.06E-10
MYO10	6.25E-10
LIPG	6.43E-10
S100A6	6.56E-10
ADAMTS7	6.64E-10
MMP7	7.37E-10
GDF5	7.90E-10
RARRES1	8.20E-10
ILF2	8.56E-10
EIF2C2	8.85E-10
S100A10	8.88E-10
FLJ10829	1.02E-09
KLF5	1.05E-09
PLA2G4A	1.08E-09
LOC55971	1.09E-09
TCN2	1.12E-09
BENE	1.19E-09
KIAA1424	1.23E-09
HOMER-3	1.44E-09
ADORA2B	1.59E-09
FABP5	1.69E-09

gene name	mean(1) > mean(2)
CLSP	2.00E-09
LCK	2.20E-09
ADFP	2.21E-09
STRIN	2.32E-09
INDO	2.33E-09
CDK2AP1	2.51E-09
ASS	2.51E-09
SBBI26	2.52E-09
LOC51765	2.60E-09
FLJ10901	2.60E-09
BCL2A1	2.83E-09
GSTP1	2.94E-09
BPI	3.21E-09
CYP39A1	3.41E-09
D123	3.46E-09
ETV6	3.51E-09
DKFZP564D0462	3.67E-09
SLC2A1	3.72E-09
HK3	3.81E-09
D21S2056E	4.02E-09
LOC51053	4.07E-09
PRO2013	4.08E-09
DC11	4.22E-09
KRT17	4.34E-09
EDN1	5.04E-09
UCHL3	5.29E-09
KIAA1089	5.35E-09
DSG3	5.40E-09
RNASEH1	5.44E-09
CP	5.55E-09
RELB	5.66E-09
MALT1	5.90E-09
ETS1	5.93E-09
KIAA0275	6.02E-09
DYSF	6.07E-09
PRG1	6.08E-09
KIAA1035	6.11E-09
AMY2B	6.11E-09
LBP-9	6.44E-09
LCP1	6.53E-09
PKP1	6.67E-09
TGM1	6.80E-09
RAP2A	7.18E-09
ZIC1	7.30E-09
RASAL1	7.50E-09

gene name	mean(1) > mean(2)
PDXK	7.51E-09
FLJ21324	7.80E-09
TIA1	7.84E-09
PIST	8.06E-09
ABP/ZF	8.18E-09
P5	8.47E-09
DEFB1	8.66E-09
DSCR1	8.90E-09
AMY1A	9.14E-09
LILRB2	9.91E-09
ICAM1	9.93E-09
HRB	1.00E-08
CXADR	1.01E-08
MT1L	1.02E-08
BCL11B	1.04E-08
FLJ10517	1.04E-08
BM039	1.06E-08
NMI	1.08E-08
FAT	1.13E-08
NUMBL	1.17E-08
LOC55862	1.18E-08
SLC6A14	1.20E-08
CCR1	1.23E-08
GPM6B	1.25E-08
E48	1.25E-08
IGHG3	1.31E-08
MGC3180	1.36E-08
C1GALT1	1.43E-08
DKFZP586F2423	1.44E-08
ART3	1.47E-08
B4-2	1.49E-08
DKFZP586E1621	1.51E-08
HDGF	1.52E-08
SLC2A5	1.53E-08
MMP1	1.56E-08
KPNA2	1.57E-08
COL9A3	1.62E-08
TRIP13	1.71E-08
GGH	1.72E-08
FLJ10706	1.79E-08
TEL2	1.87E-08
PLA2G7	1.98E-08
AKAP2	1.98E-08
MAPRE2	1.99E-08
TAP1	2.02E-08

gene name	mean(1) > mean(2)
KRT5	2.12E-08
ARP3BETA	2.32E-08
KRT6B	2.35E-08
DSCR2	2.55E-08
AK000660	2.70E-08
CSTB	2.71E-08
FLJ23518	2.82E-08
GNB4	2.86E-08
KIAA0197	2.95E-08
IL15RA	2.95E-08
DMD	2.98E-08
CXCR4	3.13E-08
DONSON	3.51E-08
S100A1	3.54E-08
SLC16A1	3.78E-08
WARS	3.87E-08
LTB	3.89E-08
TPI1	3.92E-08
EPHA2	3.93E-08
DD96	4.11E-08
KIAA0173	4.11E-08
UBD	4.13E-08
EBBP	4.26E-08
SCYA5	4.30E-08
CRYAB	4.35E-08
SEMA4D	4.49E-08
BRUNOL4	4.53E-08
ALY	4.62E-08
DDXL	4.69E-08
STAC	4.89E-08
LILRB3	4.93E-08
AMY2A	4.96E-08
AK001380	5.07E-08
CYBB	5.23E-08
FXYD5	5.33E-08
GRO1	5.34E-08
FLJ10407	5.49E-08
CCNC	5.56E-08
FLJ10709	5.94E-08
PHRET1	6.01E-08
PDL2	6.10E-08
ARHGEF4	6.17E-08
KIAA0353	6.24E-08
DHCR7	6.38E-08
AL137342	6.47E-08

gene name	mean(1) > mean(2)
PTGS2	6.59E-08
BIN1	6.62E-08
SCYB11	6.86E-08
KIAA0552	6.92E-08
CD163	6.97E-08
GPRC5B	7.04E-08
FLJ20287	7.09E-08
FBL	7.11E-08
AD024	7.13E-08
PTPN14	7.16E-08
SFRP1	7.25E-08
FOXD1	7.28E-08
PSMB9	7.54E-08
FLJ21069	7.75E-08
UBA2	7.76E-08
ANKRD3	7.77E-08
DSC3	7.95E-08
AK001942	8.06E-08
FLJ10262	8.10E-08
KIAA1609	8.21E-08
MX2	8.47E-08
FBXO5	9.27E-08
DKFZP564J0863	9.33E-08
DKFZp434F2322	9.33E-08
TEGT	9.60E-08
FIGN	1.04E-07
RDX	1.05E-07
FLJ10359	1.05E-07
SGK	1.06E-07
PPP1CB	1.07E-07
PRAME	1.13E-07
CKS1	1.13E-07
TMSNB	1.13E-07
KIAA0062	1.17E-07
BCE-1	1.19E-07
CKAP2	1.27E-07
KLK7	1.30E-07
ATF4	1.35E-07
SCYB10	1.38E-07
EPHB1	1.39E-07
AK001630	1.45E-07
KNSL5	1.46E-07
DAPP1	1.53E-07
PDE4B	1.55E-07
TC21	1.56E-07

gene name	mean(1) > mean(2)
SPIB	1.63E-07
PFDN2	1.69E-07
GATA6	1.77E-07
CD3Z	1.82E-07
ST14	1.86E-07
KIAA0179	1.94E-07
KIAA1392	1.96E-07
PIR	2.06E-07
KRTHB1	2.18E-07
MPZL1	2.19E-07
KIAA0668	2.20E-07
TRAF1	2.41E-07
LYZ	2.56E-07
APS	2.60E-07
TRB@	2.64E-07
TCF20	2.66E-07
AK000208	2.72E-07
NF2	2.74E-07
NK4	2.93E-07
TUBB4	2.95E-07
DNMT2	3.21E-07
PCOLCE2	3.35E-07
C6orf34	3.54E-07
CRABP1	3.66E-07
OTRPC4	3.76E-07
CD83	3.84E-07
FLJ10316	3.91E-07
SOD3	4.05E-07
FLJ12505	4.17E-07
CCR7	4.26E-07
HLA-F	4.38E-07
ribosomal protein L39	4.39E-07
PTPLA	4.45E-07
EPHB3	4.53E-07
IL1B	4.70E-07
FUT4	4.83E-07
PTPRCAP	5.06E-07
KIAA0007	5.07E-07
TNF	5.16E-07
MTAP44	5.20E-07
AK000954	5.28E-07
NOL1	5.32E-07
TCF7	5.42E-07
CDH19	5.77E-07
CDKN2A	5.97E-07

gene name	mean(1) > mean(2)
LOC51316	6.00E-07
AK001394	6.11E-07
CTSS	6.24E-07
FLJ20371	6.44E-07
ADORA2BP	6.60E-07
H1F5	6.88E-07
TNFRSF1B	6.92E-07
NDUFA9	7.03E-07
TNFRSF11A	7.31E-07
AIM2	7.41E-07
NMU	7.42E-07
SFN	7.43E-07
UGP2	7.44E-07
DKFZP761H171	7.86E-07
MTR1	8.03E-07
WDR5	8.09E-07
G2	8.14E-07
DKFZP564L0862	8.46E-07
TRIP7	8.48E-07
P450RAI-2	8.50E-07
PRO2000	8.56E-07
YES1	8.62E-07
KLK5	8.66E-07
KIAA0449	8.81E-07
KIAA0680	8.94E-07
LOC51203	9.62E-07
MRPL37	9.98E-07
CAPN6	1.01E-06
PGAR	1.03E-06
HRASLS	1.04E-06
DXS9928E	1.05E-06
FLJ10697	1.06E-06
FLJ20330	1.06E-06
TNFSF13B	1.08E-06
LBP-32	1.08E-06
SACS	1.10E-06
CEBPB	1.13E-06
KIAA0870	1.17E-06
KIAA0237	1.24E-06
SCYA4	1.39E-06
FLJ10895	1.41E-06
CD3G	1.47E-06
CORO1A	1.48E-06
CD72	1.49E-06
FZD7	1.52E-06

gene name	mean(1) > mean(2)
FLJ10665	1.62E-06
RPC32	1.66E-06
CD3D	1.66E-06
TERA	1.66E-06
AK000770	1.67E-06
LY64	1.72E-06
FOXG1B	1.74E-06
TBPL1	1.77E-06
SIRP-b2	1.80E-06
RGS2	1.92E-06
POMC	1.95E-06
MIG	1.96E-06
ROR1	1.99E-06
SCRG1	1.99E-06
MYCL1	2.04E-06
KIAA0020	2.04E-06
LOC51668	2.06E-06
FLJ20485	2.11E-06
PCDHB9	2.14E-06
LOC51630	2.15E-06
MRPL15	2.16E-06
ZNF313	2.18E-06
IL8	2.21E-06
NFIB	2.22E-06
FLJ20435	2.25E-06
CYBA	2.27E-06
SCYA7	2.28E-06
FLJ20105	2.28E-06
POU2AF1	2.33E-06
KRT15	2.43E-06
SSR1	2.53E-06
FLNA	2.55E-06
HLA-B	2.74E-06
IL12RB2	2.78E-06
FLJ10470	2.80E-06
CPA4	2.90E-06
NCF2	2.94E-06
IL10RA	3.00E-06
CHI3L2	3.03E-06
KRT7	3.04E-06
FLJ11296	3.07E-06
PSMB2	3.10E-06
KIAA1214	3.13E-06
NDRG2	3.13E-06
DDX21	3.29E-06

gene name	mean(1) > mean(2)
KIAA1678	3.54E-06
FADS2	3.57E-06
LRP6	3.75E-06
CNGA1	3.84E-06
KRT14	3.84E-06
RNASE1	3.86E-06
S100A2	3.93E-06
FLJ20500	3.95E-06
IRAK1	4.39E-06
CD2	4.55E-06
AK000106	4.69E-06
Immunoglobulin	4.78E-06
FLJ20116	5.16E-06
SOX8	5.17E-06
IGKV3D-15	5.18E-06
ID4	5.26E-06
FLJ20038	5.28E-06
CD19	5.32E-06
NPR3	5.42E-06
KIAA0637	5.61E-06
GPR37	6.23E-06
LCP2	6.39E-06
AF103458	6.41E-06
FOLR1	6.55E-06
BIRC3	6.56E-06
GNA15	6.60E-06
GPR9	6.61E-06
DKK1	6.73E-06
PCANAP8	6.79E-06
PTGFR	7.36E-06
AK000776	7.40E-06
ISG20	7.73E-06
FLJ10292	7.84E-06
KLK8	7.96E-06
PRRG1	8.07E-06
TNFAIP2	8.38E-06
CHORDC1	8.59E-06
VCAM1	9.46E-06
CD5	9.48E-06
DKFZp434B1222	9.86E-06
ZWINT	1.01E-05
DKFZP586N2124	1.03E-05
IL2RB	1.07E-05
GNG4	1.14E-05
AL080059	1.19E-05

gene name	mean(1) > mean(2)
P2RX5	1.22E-05
ZNFN1A1	1.24E-05
SLC15A1	1.29E-05
KLK10	1.30E-05
AF063725	1.33E-05
AL133101	1.36E-05
PIM2	1.36E-05
IGHM	1.41E-05
CYP27A1	1.47E-05
ALG6	1.54E-05
M12.219	1.59E-05
FLJ10637	1.62E-05
AGM1	1.62E-05
AARS	1.67E-05
SELL	1.78E-05
ECGF1	1.90E-05
MSLN	1.99E-05
EPS15R	2.06E-05
TYMSTR	2.14E-05
MT1G	2.15E-05
AK000933	2.16E-05
IFRG28	2.23E-05
MFGE8	2.26E-05
CLDN1	2.30E-05
CD53	2.38E-05
HLA-E	2.38E-05
TSPAN-2	2.39E-05
W61000_RC	2.61E-05
PLS3	2.96E-05
NET1	3.04E-05
SAR1	3.10E-05
TNFSF6	3.10E-05
U96394	3.34E-05
DSP	3.48E-05
GCNT1	3.53E-05
MS4A4A	3.54E-05
FLJ20360	3.60E-05
PCTK3	3.90E-05
RAB27A	3.91E-05
FLJ21129	4.00E-05
IGLL1	4.01E-05
PTPRK	4.11E-05
FLJ22408	4.18E-05
IMP-2	4.19E-05
HEM1	4.24E-05

gene name	mean(1) > mean(2)
CD69	4.26E-05
SPS	4.48E-05
PLEK	4.48E-05
AL353948	4.52E-05
MAL	4.72E-05
variable region	4.83E-05
AF097495	5.06E-05
OS4	5.40E-05
KIAA0036	5.70E-05
PTPRC	5.86E-05
HUMMHCW1A	5.92E-05
FLJ20260	5.93E-05
ANXA3	6.00E-05
AL137346	6.02E-05
CD24	6.68E-05
SECTM1	7.57E-05
FLJ22028	7.65E-05
AF058075	8.00E-05
GPI	8.14E-05
FMO2	8.95E-05
AK002088	8.95E-05
PLCB4	9.26E-05
TCF8	9.29E-05
RASGRP2	9.29E-05
S100A9	9.32E-05
RPP40	9.49E-05
BM-005	9.62E-05
SELE	0.00010074
AL137736	0.00010102
GALNT3	0.00010121
AL133611	0.00010218
TNFRSF12	0.00010285
WSX-1	0.00010743
ARHE	0.00010941
ITGB4	0.00011071
LAMB3	0.00011149
X79782	0.00011171
SCYA19	0.00011704
SLC5A6	0.00011832
PAPSS1	0.00012229
CLC	0.00012443
CHRM3	0.00012635
EPHB2	0.00012862
AIM1	0.00013146
KIAA0667	0.00013373

gene name	mean(1) > mean(2)
HN1	0.00013498
GS3686	0.00013717
MACROH2A2	0.00013758
LCN2	0.00014652
FLJ10110	0.00015325
PLCB3NP	0.00015669
PTGDS	0.0001567
MS4A2	0.00015756
FLJ22477	0.00015882
HLA-DRB6	0.00016152
FLJ13204	0.00017364
FLJ10408	0.00018014
AKR1B1	0.00018344
CSR1	0.00019574
KIAA0786	0.00020194
cig5	0.00020328
GYPC	0.00020494
MX1	0.0002066
PPARGC1	0.00020788
TU3A	0.00020804
ALDH1A3	0.00021256
KIAA0167	0.0002174
CSPG4	0.00021782
MYBL1	0.00022132
ETV5	0.00022218
NFIX	0.00022432
MGC3040	0.00023986
FLJ21212	0.00024208
DKFZP564D206	0.00025636
KIAA1229	0.00025668
LOC57823	0.00025934
STAF50	0.00026248
USP18	0.00026452
AF035318	0.00026674
RIG-I	0.00026756
APEG1	0.00027352
LOC51678	0.00027438
KIAA0965	0.00027974
ACTG2	0.00029244
EIF4EBP1	0.00029248
DSG2	0.0002974
GW112	0.00030546
RGN	0.00031526
CASP1	0.00031578
MCAM	0.00031884

gene name	mean(1) > mean(2)
SIX3	0.00032956
LY6E	0.0003374
TGM5	0.00033884
FLJ14054	0.00034114
H1F3	0.00034446
DNCI1	0.00034532
KIAA1566	0.00036884
IFI30	0.00038314
RNASEHI	0.00039798
ZRF1	0.00040436
LOC51056	0.00041266
ITGA9	0.00043048
KIAA0172	0.0004343
AF131837	0.00044782
ITGA6	0.00044988
FLJ11106	0.0004756
ARGBP2	0.0004899
CD48	0.00050636
SAA1	0.0005154
OPRK1	0.0005226
GP1BA	0.0005325
CD36L1	0.00053766
KIAA1453	0.00056168
CBS	0.00056362
KIAA0403	0.0005869
FLJ12691	0.00059502
VLDLR	0.00059822
KIAA0554	0.00061354
TIMP2	0.0006222
AL049266	0.00062746
CYP1B1	0.00063132
OAS2	0.0006379
BRDG1	0.00067598
PFN2	0.00068956
AL137332	0.00077032
EVI2B	0.00078094
FLJ10970	0.00081688
TCF3	0.00082408
MT1E	0.00086288
GPR64	0.0009027
RGS10	0.00091806
STAT4	0.00094354
KIAA0092	0.00097058
PDK3	0.00097262
HMGCS1	0.0010899

gene name	mean(1) > mean(2)
FLJ20048	0.00117324
KDELR3	0.0012341
HNF3A	0.00124078
BIN2	0.00128052
MDFI	0.0012817
PTB	0.00135722
PODXL	0.00141214
AK001536	0.00142296
FLJ20401	0.00146878
HSU15552	0.00147042
LILRB4	0.00147626
AL110125	0.00148956
HSPC156	0.00150478
ANXA1	0.00160068
TRD@	0.00185688
FGL2	0.00186104
TNFRSF10B	0.00187774
IGL@	0.00197044
KLRB1	0.0020324
CEP4	0.0023878
CD38	0.002417
SLC22A3	0.0024792
CRHSP-24	0.0024844
KIAA0820	0.00252
KIAA0027	0.00253
PLXNA2	0.0025982
ZNF215	0.0026394
WIF-1	0.0028488
AF1Q	0.0029846
SLN	0.0030636
EDN2	0.0030818
CRLF1	0.0031166
AF055007	0.003125
CYR61	0.0032168
FLJ23384	0.0032198
PIK3C2A	0.0034572
PYGB	0.0037392
ZNF179	0.0038464
AKR1C1	0.0039554
ITGB8	0.004776
ISG15	0.004782
PFC	0.004949
DKFZp761P1010	0.0051658
SERPINB2	0.0054208
SLC16A8	0.005542

gene name	mean(1) > mean(2)
FLJ20510	0.0055696
PAX6	0.0058166
LOX	0.0059874
HPRP3P	0.0060524
FLJ21841	0.0070238
TRAG3	0.007268
KIT	0.0073464
PTPRR	0.0076296
PSIP1	0.007736
BITE	0.0080652
SPRY2	0.0085948
KIAA0469	0.0090724
LOC56932	0.0091562
VNN1	0.0092706
DPYSL2	0.0094624
AF103591	0.0095962
DKFZp434P086	0.009694
AKR1C2	0.0097626
KIAA1118	0.009955
SCYA21	0.0100306
AK001932	0.0101928
DKFZP434I216	0.0106252
MAGEA1	0.010632
A2M	0.0115294
IDH2	0.0126046
FLJ22215	0.0129192
ORM1	0.0131094
FLJ22002	0.0133204
FLJ20733	0.0139614
FLJ10811	0.0144508
IDI1	0.0146528
NR4A1	0.0150532
LOC51237	0.0157056
IRF4	0.0159874
LIF	0.0162782
MAPK8IP3	0.0165006
HML2	0.0165248
TNRC3	0.0184704
NDST3	0.021434
TCL1A	0.021436
PNUTL1	0.026414
EMP1	0.027848
RASGRP1	0.028092
FLJ10143	0.028706
AL137343	0.030014

gene name	mean(1) > mean(2)
KIAA1473	0.030696
HSPB2	0.03185
MMP3	0.032616
SHC3	0.03665
STX4A	0.038144
ELF5	0.040156
DFFB	0.042634
HLA-G	0.04326
AK000125	0.043288
PP13	0.044702
FLJ10781	0.04918
PDE9A	0.049704

For the top 100 over-expressed genes, P values ranged from $1x10^{-11}$ to $<1x10^{-16}$ (See first 100 genes listed in Table 4). The basal-like tumors identified by PCA also under-expressed over 1000 non-E2F-responsive genes in at least 20% of PCA basal-like tumor, such that the differences in frequency of under-expression between the basal-like tumors identified by PCA and the non-basal-like tumors identified by PCA was statistically significant at the $P < 0.05$ level. See Fig. 24. This further establishes that the basal-like tumors identified by PCA are members of a separate and distinct subset of human breast cancers. Additionally, these patterns of gene over-expression and under-expression were shared by both the ERGO tumors identified by refined PCA and non-ERGO tumors identified by refined PCA. Altogether, the analyses here indicate that ERGO tumors developed in, and evolved from, basal-like tumor precursors.

Reproducibility of Findings Across Microarray Sets.

The Dai microarray set was purged of patient tumors that overlapped with those included the Van't Veer microarray set (*i.e.* indentical tumor samples from identical patients), and was used to evaluate the reproducibility of the analytical results in the Van't Veer microarray set. The Figures and Tables herein may refer to the Van't Veer microarray set as "s1" and the purged Dai microarray set as "s2." Application of the weighted rank ordering method identified 33 tumors out of 236 total tumors (14%) in the purged Dai microarray set that over-expressed at least 20% of the top over-expressed E2F-responsive genes, and 82 E2F-responsive genes that were over-expressed in at least 20% of the ERGO tumors identified by the weighted rank ordering method in the purged Dai microarray set. Importantly, the lower 26% frequency of ERGO tumors identified in the purged Dai microarray set relative to the Van't Veer microarray set may be more representative of the overall frequency of ERGO

umors in the general population, since the purged Dai microarray set was not enriched with umors from patients having known BRCA1 mutations.

As described above, 74 E2F-responsive genes were over-expressed in the ERGO tumors dentified by the weighted rank ordering method using the Van't Veer microarray set. mportantly, 70 of these same E2F-responsive genes were also over-expressed in the ERGO umors identified in the purged Dai microarray set by the weighted rank ordering method. Sixty-one (61) of these 70 genes (87%) were over-expressed in the ERGO tumors identified by he weighted rank ordering method in both the purged Dai and Van't Veer microarray sets. The frequencies of over-expression of these individual E2F-responsive genes in the ERGO tumors dentified by weighted rank ordering methods and the level of statistical significance were comparable in the purged Dai microarray set (s2) and the Van't Veer microarray set (s1) and were preserved in the most highly over-expressed genes (Fig. 10).

PCA identified a cluster of 66 tumors in the purged Dai microarray set (s2) that exhibited the basal-like phenotype (Fig. 2C). These 66 tumors were then further analyzed. This was done by using refined PCA in which the analyzed gene set was restricted to the E2F-responsive genes listed in Table 1 shown above. In these analyses only those tumors in the basal-like tumor cluster identified by PCA were used as input data. Two clusters comprising 30 ERGO and 36 non-ERGO tumor subsets were identified by refined PCA analysis of these 66 umors (Fig. 2D). In the purged Dai microarray set, HER2 positive tumors were among the basal-like tumors identified by refined PCA which clearly exhibited a basal-like phenotype (Fig. 4). These data can be viewed in greater detail in Supplementary Fig. 4. There was also a group of HER2 over-expressing basal-like tumors identified by refined PCA in the purged Dai set that exhibited a "transitional" phenotype intermediate to that of the basal-like tumors and that that of non-basal-like HER2 over-expressing tumors identified by PCA. In Fig. 2C the transitional HER2-over-expressing basal-like tumors identified are marked with crosses and are found within the basal-like cluster. The presence of HER2 over-expressing basal-like tumors and the transitional subgroup were not apparent from the analyses of the Van't Veer microarray set (s1).

In general, the gene expression profiles of ERGO tumors and the other breast cancer subtypes identified and analyzed in the purged Dai microarray set (s2) was quite similar to those observed after analysis of the Van't Veer microarray set (s1) (*see* Fig. 1 and Tables 6, 7 and 8). In both datasets, the ERGO tumors identified were almost entirely "triple-non-positive" for HER2, ER, and PR over-expression, and virtually all of the basal-like tumors identified

under-expressed ER and PR. The under-expression of Rb, the over-expression of cyclin E1 and E2, the over-expression of $p16^{Ink4a}$, the over-expression of E2F1, and the under-expression of cyclin D1 were prominent in ERGO tumors. However, this was less pronounced in non-ERGO basal-like tumors, and rare in the other tumor subtypes. Together, these observations further indicated that aberrations in E2F1 mediated control of transcription and the cell cycle is a feature of ERGO tumors. Last, the over-expression of multiple basal cytokeratins and of other published basal-like tumor markers was restricted largely to ERGO tumors and non-HER2-over-expressing, non-ERGO basal-like tumors. Over-expression of the MYC proto-oncogene was more readily apparent as an ERGO tumor feature by inspection of the results from analysis of the purged Dai microarray set than by inspection of the results from the analysis of the Van't Veer microarray set.

One hundred and one (101) E2F-responsive genes were over-expressed in at least 25% of the ERGO tumors identified by refined PCA analysis of the purged Dai microarray set. In contrast, 86 E2F-responsive genes were over-expressed in at least 25% of the ERGO tumors identified by refined PCA analysis of the Van't Veer microarray set (Fig. 12). The 101 E2F-responsive genes identified by refined PCA analysis of the purged Dai microarray set and the 86 E2F-responsive genes identified by refined PCA analysis of the purged Van't Veer microarray set were then compared. This comparison showed that 74 of the 86 genes (86%) over-expressed in ERGO tumors identified by refined PCA in the purged Dai microarray set were also over-expressed in the ERGO tumors identified by refined PCA in the Van't Veer microarray set. Importantly, the relative frequencies of over-expression of individual genes among tumor were generally preserved in the two datasets especially among the most frequently over-expressed genes. In both the purged Dai microarray set and the Van't Veer microarray set the group of multiple E2F-responsive genes that were most frequently over-expressed in the ERGO tumor identified in these data sets by refined PCA were over-expressed only sporadically in PCA non-ERGO basal-like tumors identified in these microarray sets by refined PCA (Fig. 4).

In the Van't Veer microarray set both ERGO tumors identified by refined PCA and non-ERGO basal-like tumors identified by refined PCA differentially over-expressed and under-expressed hundreds of non-E2F-responsive genes. The top 50 most frequently over-expressed, and most frequently under-expressed, of these genes each are shown in Fig. 4. Surprisingly, these genes were reproducibly observed across both the purged Dai microarray set and the Van't Veer microarray sets. This observation was particularly apparent among the most

frequently over-expressed genes. For example, among the top 200 genes most frequently over-expressed genes in the basal-like tumor subset identified by PCA of the Van't Veer microarray set some 70% of these genes were also over-expressed in the purged Dai microarray set.

Patients with basal-like tumors as identified by PCA have an adverse clinical prognosis.

Detailed clinical survival data are available for 91 patients who provided tumor samples included in the Van't Veer microarray set. Clinical survival data are also available for the patients who provided tumor samples included in the Dai microarray set. The survival of patients with PCA basal-like breast cancer tumors, as identified by PCA, was shorter than for breast cancer patients identified by PCA as having other types of tumors ($P < 0.002$). Seventy five percent of patients with non-basal-like tumors as identified by PCA survived five years, whereas only fifty percent of patients with basal-like tumors as identified by PCA survived five years (Fig. 9). Patient survival data were plotted by the Kaplan-Meyer method and survival curves were compared using the Haentzel-Mantel statistic.

Detailed clinical survival data are also available for the 311 patients who provided tumor samples included in the Dai microarray set. Fig. 19 shows the clinical survival data for ERGO tumors, non-ERGO basal-like tumors, and the HER2 over-expressing tumors (Fig. 19A) subsets as well as the non-ERGO "triple non-positive" and all the remaining tumor subsets (Fig. 19B) identified by PCA analysis of the Dai microarray set. Patient survival data were plotted by the Kaplan-Meyer method and survival curves were compared using the Haentzel-Mantel statistic. Comparision of Figs 19A and 19B shows that patients with ERGO tumors, non-ERGO basal-like tumors, and the HER2 over-expressing tumors had a statistically significantly worse prognosis and odds of survival than all the remaining tumor subsets identified in the Dai microarray set by PCA analysis. These findings illustrate the point that different patient subsets with the same prognosis must be distinguished phenotypically for therapeutic purposes, even though the odds of survival are similar. This is because only HER2 over-expressing tumors can be treated with anti-HER2 therapeutics (*e.g.* trastuzumab) and only ERGO tumors can be considered for targeted therapy against ERGO tumor-associated genes. Stated differently, this data shows that individual HER2 over-expressing tumors and ERGO tumors must be classified and assigned to their appropriate treatment class followed by selection of an appropriate therapy for each individual patient having tumors in these clusters despite the similar survival prognosis for patients with tumors of either distinct type.

Example 2

Identification of E2F Responsive Gene Over-Expressing (ERGO) Tumors in Lung and Thyroid Organ Sites

Lung Cancer Microarray Set.

The lung cancer microarray set published by Jones *et al.* was used to investigate E2F-responsive gene expression in human lung cancers and human lung cancer derived cell lines. Gene expression data from tumor sample probed gene spots this microarray set was normalized to data from normal human lung tissue sample probed gene spots that were included in the microarray set. Preliminary analysis by rank ordering methods confirmed that results obtained from microarray samples identified as human small cell lung cancer clinical samples and from samples identified as human derived small cell lung cancer cell lines were sufficiently similar to justify including data from both sample types in the analyses here.

Thyroid cancer Microarray Set.

The gene expression microarray set published by Salvatore *et al.* was used to study E2F-responsive gene expression in human thyroid cancer. Microarray data from human thyroid cancer tumors were normalized to normal human thyroid tissue samples that were included in the microarray set. Gene expression data from tumor sample probed gene spots this microarray set was normalized to data from normal human thyroid tissue sample probed gene spots that were included in the microarray set.

Weighted Rank Ordering Methods and Criteria for Identification of ERGO Tumors in Lung and Thyroid Organ Sites.

First, a reference signal intensity value was obtained by determining the signal intensity values for the gene transcripts from normal lung or thyroid tissues samples as appropriate for a given array set to be analyzed. Then "over-expressed," "under-expressed," and non-over-expressed genes were identified. Gene "over-expression" was determined to occur when the signal intensity corresponding to a given gene transcript in the microarray set was 1.8 fold greater than the reference signal intensity value for the gene in normal lung or thyroid tissue as appropriate. Gene "under-expression" was determined to occur when the signal intensity corresponding to a given gene transcript in the microarray was 1.8 fold less than the reference signal intensity value for the gene in normal lung or thyroid tissue as appropriate. Gene "non-over-expression" was determined to occur when a gene was neither "over-expressed" nor "under-expressed."

Weighted rank ordering methods were performed using EXCEL™ software (Microsoft Corp., Redmond, WA) to rank the over-expressed genes by their frequency of expression

among tumors. In these rank ordering analyses the most highly over-expressed genes were placed closest to the origin and the contribution of each tumor to the ranking was weighted by its proximity to the origin of the tumor axis.

These weighted rank ordering methods were then used to rank the tumors by the number of the 325 specific E2F-responsive genes, shown above in Table 1, over-expressed per tumor. Tumors with the highest number of over-expressed genes per tumor were placed closest to the origin. The contribution of each gene to the ranking was positively weighted by its proximity to the origin of the gene axis.

Individual tumors with the lowest number of over-expressed genes per tumor, and individual genes with the lowest over-expression frequency among the tumors were then iteratively stripped out of the dataset, with recalculation of rankings, until predetermined stopping conditions were met. The stopping conditions were that at least 20% of the tumors remaining in the dataset over-express at least 20% of the remaining E2F-responsive genes. Tumors that remained in the data set after satisfaction of the stopping conditions were identified as ERGO tumors.

Identification of ERGO Tumors in Lung.

Microarray based studies of human lung cancer have been able to resolve adenocarcinomas, carcinoids, large cell cancers, and normal lung tissue, but have been unable to distinguish large cell neuroendocrine tumors from small cell lung cancers. The analyses here were undertaken because many small cell lung cancers are known to have Rb gene abnormalities. This is significant because normally the Rb tumor suppressor protein binds to E2F and regulates E2F mediated gene transcription. Thus, the analyses here sought to determine if some of these small cell lung cancers could be ERGO tumors and whether these ERGO tumors could be distinguished from non-ERGO neuroendocrine precursors by PCA based methods.

PCA analysis of the Jones lung cancer microarray set identified a cluster of tumors that contained carcinoids, large cell neuroendocrine tumors, and small cell lung cancers (Fig. 2E).

This lung cancer tumor cluster identified by PCA was then further analyzed. This was done by using further refined PCA in which the analyzed gene set was restricted to the E2F-responsive genes listed in Table 1 shown above. In these refined PCA analyses only those tumors in the lung cancer tumor cluster initially identified by PCA were used as input data.

The result of this refined PCA analysis was that three clusters corresponding to carcinoids, large cell neuroendocrine tumors, and small cell lung cancers were identified (Fig.

2F). The cluster consisting largely of small cell lung cancers over-expressed a number of E2F-responsive genes identical to those found in ERGO breast cancers such that over 50% of the E2F-responsive genes expressed in the ERGO breast cancer tumors identified by refined PCA and the E2F-responsive genes expressed in the small cell lung cancer cluster identified by refined PCA were identical (Fig. 13). This indicates that this sub-group of small cell lung cancers are ERGO tumors. The E2F-responsive genes that are over-expressed in ERGO lung cancers are over-expressed infrequently in most large cell neuroendocrine tumors and carcinoid tumors.

Small cell lung cancer ERGO tumors appear to have E2F regulatory defects (Fig. 14 and Table 8). Twenty-nine percent of small cell lung cancer ERGO tumors under-express Rb, and 36% over-express cyclin E1 or cyclin E2. This observation and the under-expression of cyclin D1 in 57% of small cell lung cancer ERGO tumors further indicates E2F dysregulation in ERGO tumors. There is no $p16^{ink4a}$ over-expression in small cell lung cancer ERGO tumors. However, p18 and p19, which like $p16^{ink4a}$ are cdk4 and cdk6 inhibitors that block phosphorylation of Rb by cyclin D1, are over-expressed in abundance and over-expression of p18 is found in 86% of the small cell lung cancer ERGO tumors 86% while over-expression of p19 is found in 71% of these small cell lung cancer ERGO tumors. p18 and p19 are believed to function analogously to $p16^{ink4a}$ and therefore their over-expression can be a marker for E2F dysregulation.

Additionally, the over-expression patterns of non-E2F–responsive genes in these small cell lung cancer ERGO tumors are shared with large cell neuroendocrine tumors, but not carcinoid tumors, indicating that these small cell lung cancers are derived from large-cell neuroendocrine tumors. In addition, there are non-E2F-responsive genes that are over-expressed in small cell tumors and large cell neuroendocrine tumors that are also over-expressed in carinoid tumors, indicating that both small cell tumors and large cell neuroendocrine tumors share a common heritage with carcinoids (Fig. 14).

Importantly, the E2F-responsive genes that are over-expressed in small cell lung cancer ERGO tumors identified by refined PCA and in breast cancer ERGO tumors identified by refined PCA strongly overlap, but the non-E2F responsive genes that are over-expressed in their respective precursor cells are mostly different, with several notable exceptions. Like breast cancer ERGO tumors, large cell neuroendocrine tumors over-express basal cytokeratins and other basal-like markers.

Microarray based studies have shown the phenotype of anaplastic thyroid cancers differs from that of papillary thyroid cancers and normal thyroid tissue with regard to the over-expression of genes involved in cell cycle control and chromosome segregation. The analyses here were undertaken because the transcriptional promoters of many of these cell cycle control and chromosome segregation genes are known to contain E2F binding sites.

Identification of ERGO Tumors in Thyroid.

The human thyroid cancer microarray set of Salvatore was also analyzed by PCA. Anaplastic thyroid cancers clustered separately by PCA (Fig. 2G), but this anaplastic thyroid cancer cluster also included two papillary thyroid cancers with transitional phenotypic patterns. There were 73 E2F-responsive genes that were over-expressed in at least 25% of the thyroid cancer samples in this anaplastic thyroid cancer cluster. Importantly, these 73 E2F-responsive genes were not over-expressed in those thyroid cancer samples that were not part of the anaplastic thyroid cancer cluster identified by PCA. Furthermore, fifty-one percent (51%) of these 73 E2F-responsive genes were identical to the over-expressed E2F-responsive genes that are characteristic of the ERGO breast cancer tumors identified by refined PCA (Fig. 15). A profile of selected over-expressed genes in thyroid cancer is provided in Fig. 16. There is also a group of E2F-responsive genes that was over-expressed in both anaplastic and papillary thyroid cancers, although the over-expression occurred at higher levels in the anaplastic thyroid cancer tumors which clearly identifies the papillary thyroid cancers as precursors of the ERGO anaplastic thyroid cancers. This conclusion is further supported by the observation that large numbers of both E2F-responsive and non-E2F-responsive genes were over-expressed in both tumor types, but without clear differences in levels of gene over-expression between the ERGO anaplastic thyroid cancers and papillary thyroid cancers (Fig. 16).

Importantly, the analyses here of thyroid and lung tumors show the frequency of over-expression of E2F-responsive genes that affect the G1/S cell cycle phase transition, and those that affect G2M were preserved in all ERGO tumors, regardless of the site of origin (*e.g.* breast, lung, or thyroid tissue) (Fig. 17). For example, in ERGO breast cancer tumors and ERGO thyroid cancer tumors, G2M-associated E2F-responsive genes were over-expressed more frequently than E2F-responsive genes associated with the G1/S phases. However, in ERGO lung cancer tumors identified by refined PCA the over-expression of G2M-associated E2F-responsive genes was less common and over-expression of E2F-responsive genes associated with DNA repair, was more common.

Example 3

Analysis of the Role of LINC Multiprotein Gene Transcription Repression Complex Function and FOXM1 Function in ERGO Tumors

The analyses above revealed that specific E2F-responsive genes were highly over-expressed in the ERGO tumors identified and that these specific E2F-responsive genes were over-expressed with high frequency among the different ERGO tumors identified. It was observed that many of these E2F responsive genes are targets of a multiprotein gene transcription repressing complex comprising both the Rb and E2F proteins that has been evolutionary conserved in *Caenorhabditis elegans* as the dRM protein complex, *Drosophila melanogaster* as the dREAM protein complex, and in mammals as the LINC protein complex. In *C. elegans* the dRM multiprotein complex represses transcription of genes that are required for DNA synthesis and mitosis, and produces controlled chromosomal aneuploidy to stop cell division and produce aneuploid differentiated cells as part of normal tissue differentiation of the hindgut in this organism.

Aberrations in at least four protein components of the dRM/dREAM/LINC multiprotein gene transcription repressing complex account for the majority of the abnormally over-expressed E2F-responsive genes in the ERGO tumors identified, and the over-expressed genes associated with DNA replication and mitosis. The downstream consequences of aberrations of the four components of this complex are shown in Fig. 5 and would produce a gene expression profile consistent with that observed in the ERGO tumors identified.

When the various components of these multiprotein repressor complexes, such as lin54, are lost these complexes fail to form correctly and no longer repress G2M-associated genes. Importantly, loss of TESMIN--the human homolog of the *C. Elegans* lin54 protein--results in the up-regulation of a number of known G2M-associated genes (Kittler 2007). Analysis of the complete Dai human breast cancer microarray set (s3) which consists of the entire group of 311 patients in the breast cancer microarray dataset revealed that TESMIN expression is deficient and apparently lost. This loss of TESMIN expression was observed in 25 out of 37 (68%) of ERGO tumors identified by refined PCA in the complete Dai human breast cancer microarray set and 25 out of 41 (61%) non-ERGO basal-like tumors identified. However, this loss of TESMIN expression occurred infrequently in the non-basal-like tumors and only 28 of 231 (12%) of the non-basal-like tumors identified by PCA of this microarray set had an apparent loss of TESMIN expression. Importantly, TESMIN-controlled genes account for 21 of the 107 E2F-responsive genes that are over-expressed in the ERGO tumors identified by refined PCA in

the complete Dai human breast cancer microarray set, and almost all of these 21 E2F-responsive genes are associated with mitosis.

The Rb protein is a component of the dRM/dREAM/LINC multiprotein gene transcription repressing complex. Loss of Rb expression in *Mus musculus* results in the over-expression of genes that are responsible for DNA replication and mitotic transit (Black and Nevins). Importantly, the analyses here found that RB1 is under-expressed in 19 of 37 (51%) ERGO tumors identified by refined PCA of the complete Dai human breast cancer microarray set, in 4 of 41 (10%) non-ERGO basal-like tumors identified, and in 23 of 231 (10%) of non-basal-like tumors identified in this microarray set. Twenty-four (24) of the genes that are over-expressed as a result of loss of Rb expression were also among the most highly over-expressed E2F-responsive genes in the ERGO tumors identified. These genes included mitosis-associated genes, and DNA replication-associated genes.

Some components of the dRM/dREAM/LINC multiprotein gene transcription repressing complex are associated with the complex only in quiescent cells. Examples of such proteins are E2F4 and p130 which is a "pocket" protein related to Rb. In proliferating cells the E2F4 and p130 components are shuttled out of the dRM/dREAM/LINC multiprotein gene transcription repressing complex and replaced by p107 which is another Rb-related protein, and B-Myb. When this occurs dRM/dREAM/LINC multiprotein complex becomes a gene transcription activating complex, and induces the transcription of genes that are associated predominantly with the G2M portion of the cell cycle. These induced genes minimally overlap with those induced by Rb loss.

B-myb induces transcription of cyclins A2, B1, and B2 which are also regulated by Rb. The analyses here found that B-myb is constitutively over-expressed in 10 of 37 (27%) ERGO tumors identified by refined PCA of the complete Dia human breast cancer microarray set, 4 of 41 (10%) non-ERGO basal-like tumors identified, and 8 of 231 (3%) of non-basal-like tumors identified. The analyses here also found that A-myb, another closely related member of the vertebrate myb gene family, is over-expressed in 12 of 37 (32%) ERGO tumors identified by refined PCA of the complete Dia human breast cancer microarray set, 2 of 41 (5%) of non-ERGO basal-like tumors identified, and 13 of 231 (6%) of non-basal-like tumors identified. Seven (7) genes that are regulated by B-myb were also over-expressed in the ERGO tumors identified and included cyclins A2, B1 and B2.

Over-expression of E2F1 and E2F2 by transfection of mouse embryo fibroblasts resulted in the identification of specific genes that are directly induced by E2F over-expression

(unlike a host of other E2F-responsive genes that might be indirectly induced as a result of downstream E2F-related effects on other genes) (Ishida *et al.*). The specific genes which are directly induced by E2F over-expression are predominantly genes associated with DNA replication and mitosis. The analyses here found that 15 of 37 (41%) ERGO tumors identified by refined PCA of the complete Dai human breast cancer microarray set over-expressed E2F1 and/or E2F2 (41%), while only 7 of 41 (17%) of non-ERGO basal-like tumors identified, and only 9 of 231 (4%) of non-basal-like tumors identified over-expressed E2F1 and/or E2F2. Twenty-one (21) genes that are governed by E2F are over-expressed in ERGO tumors and included cyclins A2, B1 and B2. This set of 21 genes had substantial overlap with those genes over-expressed as a result of an apparent loss of Rb expression.

Cyclins A2, B1, and B2 are over-expressed in response to derangement of multiple components of the human LINC multiprotein gene transcription repressing complex. These cyclins phosphorylate and activate the transcription factor FOXM1 (Major ML). FOXM1 is an E2F-responsive gene that is highly over-expressed in ERGO tumors, but is not a component of the LINC multiprotein repressor complex. Importantly, FOXM1 induces several DNA replication-associated and mitotic genes that do not overlap with those induced by derangements in components of the LINC multiprotein complex (Fig. 5). Activated FOXM1 does induce expression of cyclin A2, B1 and B2 which establishes a positive feedback loop between the cyclins and FOXM1. The analyses here found that FOXM1 is over-expressed in 23 of 37 (62%) ERGO tumors identified by refined PCA of the complete Dai human breast cancer microarray set, in 6 of 41 (15%) non-ERGO basal-like tumors identified, and in 2 of 231 (1%) non-basal-like tumors identified in this microarray set. Importantly, there is a direct relationship between the average level of FOXM1 gene expression per tumor and the number of over-expressed FOXM1-associated DNA replication genes and mitotic genes in that tumor (Fig. 6). Furthermore the highest average levels of FOXM1 and the greatest numbers of over-expressed FOXM1-associated genes per tumor are observed in ERGO tumors (Fig. 6).

Several additional over-expressed mitotic and DNA replication-associated genes that are over-expressed by the ERGO tumors identified have also been linked to the derangement of grouped components of LINC multiprotein repressor complex (Georlette). These four genes are identified in Fig. 5 by four short horizontal arrows.

The foregoing clearly indicates that derangements in four of the components of the LINC multiprotein gene transcription repressing complex and/or FOXM1 account for 55 out of 107 (51%) of the over-expressed E2F-responsive genes associated with ERGO tumors

identified in the complete Dai human breast cancer microarray set, and 50 of 67 (75%) of the mitotic and DNA replication-associated E2F-responsive genes that are over-expressed in these ERGO tumors. Most of the ERGO tumor-associated E2F-responsive genes that are aberrantly over-expressed in breast cancers, lung cancers, and thyroid cancers are DNA replication and mitosis associated genes that are linked to the Rb/E2F-containing multiprotein repressive complex. Together, these observations indicate that derangements of the human LINC multiprotein gene transcription repressing complex play a central role in the development of aggressive malignancies at multiple organ sites such as human breast, lung, and thyroid.

Example 4

Identification of E2F Responsive Gene Over-Expressing (ERGO) Tumors in a Prostate Cancer Microarray Set.

Prostate cancer is common among men over 60 years in age, but only about 15% of patients with invasive prostate cancer ultimately die of their disease. "Watchful waiting" is one option for management of prostate cancer, and could be more safely elected if robust markers for distinguishing aggressive prostate cancers from non-aggressive prostate cancers were available for patients with low to intermediate grade tumors (*e.g.* Gleason score of 4-7). Published studies also indicate that E2F3 over-expression may play some role in the development of prostate and bladder cancers. Here, prostate cancers were analyzed to determine if at least some prostate cancer tumors are ERGO tumors.

The prostate cancer microarray set published by Chandran *et al.* was used to investigate E2F-responsive gene expression in human prostate cancers and metastatic human prostate cancer samples. Gene expression data from tumor sample probed gene spots this microarray set was normalized to data from normal human prostate tissue sample probed gene spots that were included in the microarray set. The GSE6919 microarray set available from the NCBI GEO site was analyzed.

The Chandran microarray set includes multiple samples from metastatic prostate cancer tumors and androgen ablation-resistant prostate cancer tumors. Metastatic cancer samples in the same patient are known to be heterogeneous in their overall gene expression patterns, and this was confirmed in the Chandran microarray set. However, all metastatic cancer tumor samples in the Chandran microarry set showed fully developed ERGO tumor-associated gene expression patterns, and the homogeneity of ERGO gene expression patterns among different samples in each patient was striking. *See* Fig. 20. There is substantial overlap between the top

100 over-expressed E2F-responsive genes in metastatic prostate cancer, and the E2F-responsive genes over-expressed in ERGO tumors of the breast, lung, thyroid, and ovary.

In particular, E2F3 was over-expressed in most metastatic prostate cancer samples, as were cyclin A2, and cyclin E2. Cyclin B2 was was also prominently over-expressed. Many prostate cancer tumor samples also over-expressed EZH2 and FOXM1, as well as MYBL2 (B-MYB). It is noteworthy, that the cyclins FOXM1 and EZH2 are over-expressed, because these genes are members of potential positive feedback loops in the cascade of changes associated with dysregulation of the members of the Syn/MULVB/DRM/DREAM/LINC multiprotein repressor/activator complex. These potential positive feedback loops are shown in a larger context in Fig. 5, and are shown separately with more detail in Fig. 21.

This metastatic prostate cancer derived data indicates that these positive feedback loops are active in dangerous, advanced metastatic cancer, but not in the large subset of patients with non-metastatic primary tumors. Additionally, although the total number of cases included in the Chandran microarray set is relatively small, the fact that every one of these cases of metastatic prostate cancer exhibits over-expression of large numbers of over-expressed ERGO tumor-associated genes shows that E2F3-driven ERGO tumor development is a feature of most dangerous, advanced prostate cancers.

Identification of ERGO Tumors in Prostate by PCA.

The human prostate cancer microarray set of Chandran was analyzed by PCA. When PCA is applied to the primary prostate cancers without metastases identified in the Chandran microarray set using the limited subset of 325 E2F-responsive genes, a distinctive tumor cluster is apparent in which very few ERGO tumor-associated genes are over-expressed, but in which basal cytokeratin marker over-expression is relatively common. *See* Fig. 22 (spheres with crosses).

Among the remaining primary prostate cancer without metastases, there is a subset of primary prostate cancer tumors that exhibits many of the same features present in metastatic tumor samples. *See* Fig. 22 (clear white spheres). The primary prostate cancer tumors in this subset over-express large numbers of ERGO tumor-associated E2F responsive genes and frequently over-express E2F2 and E2F3, cyclin E2, cyclin A2, cyclin B2, EZH2, FOXM1 and MYBL2, suggesting that activation of the same positive feedback loops present in metastatic tumors. *See* Fig. 20 (tumors listed under "Advanced ERGO PCA Pattern"). Additionally, like the metastatic prostate cancer tumors identified, these tumors express basal cytokeratins only rarely. This subset of primary prostate cancer tumors also exhibits a wide range of Gleason

scores, ranging from 4 to 9. Consequently, patients with primary prostate cancer tumors in this subset should not be offered the "watchful waiting" option to manage their prostate cancer, and should instead be treated intensively at the time of diagnosis because the analyses here indicate these subsets of tumors have such extensive similarity with the dangerous metastatic prostate cancer tumors and are also ERGO tumors.

Example 5

Identification of E2F Responsive Gene Over-Expressing (ERGO) Tumors in a Ovarian Cancer Microarray Set.

Ovarian cancer, like breast cancer, arises in large proportions of patients with hereditary BRCA1 mutation (~ 50% of cases by age 70). Serous carcinomas is the predominant histological type of ovarian cancer occuring in BRCA1 patients. Patients carrying BRCA1 mutations that undergo prophylactic surgery are also frequently found to have occult serous cancers of the fallopian tube, suggesting that this is a preferred site of tumor formation in patients carrying BRCA1 mutations. Studies of normal fallopian tube epithelium and high grade serous fallopian tube and ovarian carcinomas in both patients carrying BRCA1 gene mutations and patients that do not carry such mutations were performed by microarray, and found that the gene expression profiles of the normal fallopian tube tissue in BRCA1 carriers clustered with the those of serous carcinomas not with normal fallopian tube epithelium from patients who do not carry BRCA1 mutations.

We have analyzed the normal fallopian tube epithelium, high grade serous fallopian tube and ovarian carcinoma microarray sets from these studies. These microarray sets are available as the GSE10971 series in the NCBI GEO data repository.

Theses analyses showed that high grade serous carcinomas from fallopian tube and ovary of both BRCA1 and non-BRCA1 mutation carriers were all advanced ERGO tumors. Results are shown in Fig. 23. The top 50 ERGO tumor-associated E2F-responsive genes were over-expressed in essentially every tumor. Every tumor over-expressed both E2F1 and E2F3, and also over-expressed CDKN2A and indicated a functional Rb defect. Essentially every tumor over-expressed at least one basal cytokeratin, and all but one expressed at least 2 basal cytokeratins, indicating that these cancers started out as basal like tumors, and that they retained their basal-like status in advanced malignancy--unlike the prostate cancers. All tumors over-expressed both EZH2 and FOXM1 plus at least two cyclins, indicating the activation of positive

feedback loops involving derangements of these components of the SYNMULVB/DRM/DREAM/LINC multiprotein repressor/activator complex. See Fig. 21.

In contrast, 10 of the 12 fallopian tube samples from the patients carrying BRCA1 mutations showed none of these patterns of gene over-expression. In the remaining two fallopian tube samples, approximately half of the top 50 ERGO tumor associated genes were over-expressed, and one over-expressed EZH2 and two cyclins. The findings in these two samples are interpreted as transitional evolutionary pattern phenotypes indicative of cells on the way toward developing into cells having an aggressive cancer phenotype in BRCA1 carriers.

The results here lead to the conclusion that all high grade serous ovarian and fallopian tube cancers, whether from patients carrying BRCA1 carriers or patients who do not carry such a mutation, are advanced ERGO tumors having patterns of gene over-expression consistent with the activation of positive feedback loops involving over-expression of EZH2, FOXM1, MYB2L (B-MYB), and mitotic cyclins. A minority of fallopian tube samples (<20%) from patients carrying BRCA1 mutation exhibit gene expression patterns consistent with early ERGO tumor-associated changes.

Example 6

Identification of ERGO Tumor Associated Over-Expressed Genes

A scoring system was developed to compile definitive master lists of ERGO tumor-associated over-expressed genes which took into account both the frequency of over-expression of a particular gene at any given organ site and the number of organ sites at which a particular gene is over-expressed. In this scoring system the "individual gene score" was determined using the following formula:

"Individual Gene Score" = fraction of ERGO breast cancers over-expressing the gene
+ fraction of ERGO lung cancers over-expressing the gene
+ fraction of ERGO thyroid cancers over-expressing the gene
+ fraction of ERGO ovarian cancers over-expressing the gene
+ fraction of metastatic ERGO prostate cancers over-expressing the gene.

A cutoff "individual gene score" of >1.2 was used to assign over-expressed E2F-responsive genes to the ERGO-tumor associated list. Genes with an "individual gene score" of greater than 1.2 were included in the list, and genes with an "individual gene score" of less than 1.2

were not included in the list. This insured that the gene was over-expressed in at least two organ sites, and that a frequency of over-expression of at least 0.6 was present at at least one organ site. Details concerning the frequencies of gene over-expression at each site and the individual gene scores for genes over-expressed in at least 20 percent of tumors at each site is shown in Table 5 below.

Table 5
ERGO tumor associated genes based on score cutoff > 1.2

	breast	lung	thyroid	ovary	prostate met	sum
BUB1	0.81081081	0.5	1	0.84615385	0.68	3.83696466
TPX2/C20ORF1	0.48648649	0.55555556	0.71428571	0.92307692	1	3.67940468
AURKA/STK15	0.45945946	0.5	0.71428571	1	1	3.67374517
CENPA	0.72972973	0.44444444	0.71428571	1	0.76	3.64845989
CKS2	0.32432432	0.33333333	1	1	0.92	3.57765766
AURKB/STK12	0.78378378	0.5	0.85714286	0.84615385	0.52	3.5070804[illegible]
UBE2C/UBCH10	0.62162162	0.38888889	0.28571429	0.92307692	0.96	3.17930172
KIF2C/KNSL6	0.75675676	0.38888889	0.71428571	0.76923077	0.48	3.10916213
STMN1	0.51351351	0.83333333	0.71428571	0.69230769	0.28	3.03344025
CDC45L	0.56756757	0.27777778	0.85714286	0.92307692	0.4	3.02556513
LMNB1	0.40540541		0.85714286	1	0.76	3.02254826
MAD2L1	0.48648649	0.66666667	0.71428571	0.53846154	0.56	2.96590041
KIFC1/KNSL2	0.81081081		0.57142857	0.92307692	0.56	2.86531631
HMMR	0.21621622	0.44444444	0.71428571	0.92307692	0.56	2.8580233
PTTG1	0.37837838	0.77777778		0.92307692	0.72	2.79923308
KIF11/KNSL1	0.32432432	0.5	0.42857143	0.92307692	0.6	2.77597268
CCNA2	0.62162162		0.71428571	0.76923077	0.64	2.74513811
UNG	0.24324324	0.72222222	0.57142857	0.61538462	0.52	2.67227865
CENPF	0.56756757	0.83333333	0.85714286	0.38461538		2.64265914
TTK	0.56756757	0.5	0.71428571	0.84615385		2.62800713
CCNB2	0.62162162	0.5	0.85714286		0.64	2.61876448
CDC2	0.37837838	0.61111111		0.92307692	0.68	2.59256641
EZH2	0.7027027			1	0.84	2.5427027
CDKN3		0.61111111	0.42857143	0.76923077	0.64	2.44891331

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	breast	lung	thyroid	ovary	prostate met	sum
BUB1B			0.71428571	0.92307692	0.76	2.39736264
ASF1B/FLJ10604		0.44444444	1	0.92307692		2.36752137
MKI67			0.71428571	0.84615385	0.8	2.36043956
NDC80/HEC	0.59459459		0.42857143	0.92307692	0.4	2.34624295
FOXM1	0.62162162			1	0.72	2.34162162
BIRC5	0.54054054	0.38888889		0.92307692	0.48	2.33250635
CDC20/p55CDC	0.7027027			0.92307692	0.68	2.30577963
CDC25B	0.45945946	0.44444444	0.42857143	0.92307692		2.25555226
BLM	0.54054054		0.28571429	0.84615385	0.56	2.2324086
TIMELESS		0.66666667	0.28571429	1	0.24	2.19238095
MCM2	0.51351351		0.71428571	0.92307692		2.15087615
CENPE	0.21621622		0.71428571	0.92307692	0.28	2.13357885
KPNA2	0.43243243	0.33333333		1	0.36	2.12576577
TMPO		0.83333333		0.76923077	0.52	2.1225641
MCM7	0.43243243	0.5		0.84615385	0.32	2.09858628
RAD54L	0.64864865	0.55555556		0.69230769	0.2	2.0965119
CDC6			1	0.69230769	0.4	2.09230769
CHEK1	0.45945946		0.28571429	0.76923077	0.56	2.07440451
ANLN	0.43243243		0.85714286	0.76923077		2.05880606
CCNB1	0.40540541			0.92307692	0.72	2.04848233
TK1	0.40540541		1		0.64	2.04540541
TOP2A		0.94444444		0.23076923	0.84	2.01521368
NUSAP1/BM037	0.2972973		0.71428571	1		2.01158301
RFC4	0.43243243	0.72222222		0.84615385		2.0008085
DEK	0.43243243	0.72222222		0.84615385		2.0008085
SMC2/SMC2L1	0.21621622	0.66666667		0.61538462	0.48	1.9782675
TYMS	0.2972973	0.55555556	0.42857143	0.23076923	0.44	1.95219351

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	breast	lung	thyroid	ovary	prostate met	sum
PBK			1	0.92307692		1.92307692
CCNE2	0.27027027			0.76923077	0.88	1.91950104
H2AFX	0.32432432		0.28571429	0.53846154	0.76	1.90850015
MCM6	0.43243243	0.27777778	0.42857143	0.76923077		1.90801241
ECT2	0.35135135	0.55555556		1		1.90690691
MELK/KIAA0175	0.62162162			0.92307692	0.36	1.90469854
CDC25C	0.24324324		0.57142857	0.46153846	0.6	1.87621028
NEK2	0.2972973	0.66666667		0.61538462	0.28	1.85934858
TOPBP1	0.21621622	0.66666667		0.61538462	0.36	1.8582675
CHAF1A	0.32432432	0.55555556		0.61538462	0.36	1.8552645
E2F1	0.35135135	0.57142857		0.92307692		1.84585685
PCNA	0.27027027	0.72222222		0.84615385		1.83864634
PRC1	0.40540541	0.5		0.92307692		1.82848233
HMGB3/HMG4	0.35135135	0.33333333		0.61538462	0.52	1.8200693
MSH2	0.27027027	0.38888889		0.69230769	0.44	1.79146685
E2F3				1	0.76	1.76
SRGAP2/KIAA0456	0.5		0.28571429		0.96	1.74571429
NUP155	0.21621622	0.27777778		0.76923077	0.48	1.74322476
RRM2			0.28571429	1	0.44	1.72571429
CHAF1B	0.48648649	0.61111111		0.61538462		1.71298221
UBE2T/HSPC150	0.21621622	0.77777778		0.92307692		1.7008547
RFC2		0.44444444		0.76923077	0.48	1.69367521
CDKN2C	0.21621622	0.72222222		0.30769231	0.4	1.64613075
SMC4/SMC4L1	0.37837838	0.33333333	0.28571429	0.30769231	0.30769231	1.61281061
UHRF1/ICBP90			0.57142857	1		1.57142857
PLAU			0.85714286	0.69230769		1.54945055
KIF20A/RAB6KIFL	0.62162162			0.92307692		1.54469854

	breast	lung	thyroid	ovary	prostate met	sum
GCH1		0.38888889	0.42857143	0.46153846	0.24	1.51899878
PARP1/ADPRT		0.72222222		0.76923077		1.49145299
TCF19		0.55555556		0.92307692		1.47863248
DNMT1	0.24324324	0.44444444		0.76923077		1.45691846
RACGAP1/ID-GAP	0.43243243			1		1.43243243
CCNF		0.55555556	0.85714286			1.41269841
DCK		0.38888889		0.61538462	0.4	1.4042735
TEAD4	0.45945946			0.92307692		1.38253638
MCM3		0.44444444		0.92307692		1.36752137
FEN1	0.40540541			0.92307692		1.32848233
GINS1/KIAA0186				0.92307692	0.4	1.32307692
RRM1			0.28571429	0.30769231	0.72	1.31340659
POLE2		0.38888889		0.92307692		1.31196581
BARD1	0.21621622	0.5		0.38461538	0.2	1.3008316
RAD51AP1/PIR51	0.2972973			1		1.2972973
PLK4/STK18	0.24324324	0.61111111			0.44	1.29435435
SERPINE1			0.85714286	0.23076923	0.2	1.28791209
POLA2	0.27027027			0.69230769	0.32	1.28257796
CDCA4/FLJ20764			0.42857143	0.84615385		1.27472527
CCND1			0.71428571		0.56	1.27428571
DTYMK				0.46153846	0.8	1.26153846
CCNE1	0.24324324			1		1.24324324
MCM4	0.27027027			0.76923077	0.2	1.23950104
H2AFZ		0.5		0.53846154	0.2	1.23846154
HIST1H2BF/H2BFG			0.57142857	0.46153846	0.2	1.23296703
LHX2	0.24324324	0.66666667			0.32	1.22990991
CKS1	0.37837838			0.84615385		1.22453222

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Rejected based on score cutoff of 1.2 or less

	breast	lung	tyroid	ovary	Prostate met	sum
PMAIP1		0.38888889			0.8	1.18888889
MRE11A				0.69230769	0.48	1.17230769
USP1	0.35135135	0.27777778		0.53846154		1.16759067
SFPQ		0.44444444			0.72	1.16444444
ORC6L	0.37837838			0.76923077		1.14760915
MYC	0.56756757		0.57142857			1.13899614
CDC7L1	0.24324324			0.84615385		1.08939709
UMPS				0.76923077	0.32	1.08923077
PRIM2A	0.45945946			0.61538462		1.07484407
VRK1		0.33333333		0.53846154	0.2	1.07179487
DNA2L	0.37837838			0.69230769		1.07068607
VEGF	0.40540541			0.61538462		1.02079002
SLBP				0.61538462	0.4	1.01538462
MCL1				0.76923077	0.24	1.00923077
CDCA7L/DKFZp762L0311	0.2972973			0.69230769		0.98960499
DUT		0.5			0.48	0.98
AR					0.96	0.96
HMGB2/HMG2	0.21621622				0.72	0.93621622
PRIM1				0.69230769	0.24	0.93230769
RAD51				0.69230769	0.24	0.93230769
FANCL/FLJ10335	0.24324324				0.68	0.92324324
BAK1				0.92307692		0.92307692
KIF4A	0.21621622			0.69230769		0.90852391

	breast	lung	tyroid	ovary	Prostate met	sum
CDK2		0.44444444		0.46153846		0.90598291
RAD51C		0.66666667		0.23076923		0.8974359
MPHOSPH1				0.69230769	0.2	0.89230769
FGFR1OP					0.88	0.88
PRKAR2B				0.38461538	0.48	0.86461538
APOE				0.46153846	0.4	0.86153846
PBX3		0.5			0.36	0.86
DMRT1	0.24324324			0.61538462		0.85862786
HRK	0.56756757		0.28571429			0.85328185
FIGNL1				0.84615385		0.84615385
SHCBP1/FLJ22009				0.84615385		0.84615385
ORC3L	0.21621622	0.38888889		0.23076923		0.83587434
TP53BP2	0.48648649			0.30769231		0.79417879
ARHGAP4			0.28571429	0.30769231	0.2	0.79340659
MTHFD1	0.21621622		0.57142857			0.78764479
MAPK1				0.76923077		0.76923077
DHFR				0.76923077		0.76923077
CITED2					0.76	0.76
PRG4				0.46153846	0.28	0.74153846
RPA3				0.46153846	0.28	0.74153846
CSTF1				0.53846154	0.2	0.73846154
HOXA7		0.5		0.23076923		0.73076923
BTG3	0.48648649				0.24	0.72648649
MMP16			0.28571429		0.44	0.72571429
PLK1			0.71428571			0.71428571
INHBA			0.71428571			0.71428571
EED	0.24324324			0.46153846		0.7047817
SSX2IP/KIAA0923		0.38888889		0.30769231		0.6965812

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	breast	lung	tyroid	ovary	Prostate met	sum
RFC3				0.69230769		0.69230769
FKSG14				0.69230769		0.69230769
NUP107				0.69230769		0.69230769
CASP8		0.44444444			0.24	0.68444444
ORC2L				0.46153846	0.2	0.66153846
FST			0.42857143	0.23076923		0.65934066
RPA1			0.42857143	0.23076923		0.65934066
COL11A1					0.64	0.64
DBF4/ASK				0.30769231	0.32	0.62769231
RDC1				0.61538462		0.61538462
BID	0.21621622			0.38461538		0.6008316
HIST1H2AE					0.6	0.6
PLK2/SNK			0.28571429	0.30769231		0.59340659
SPHK1			0.57142857			0.57142857
MCM5	0.56756757					0.56756757
EGR1			0.28571429		0.28	0.56571429
NPAT		0.55555556				0.55555556
PLSCR1	0.54054054					0.54054054
CSRP2	0.54054054					0.54054054
H2AFL				0.53846154		0.53846154
LSM5				0.53846154		0.53846154
H2AFA				0.53846154		0.53846154
RBL1					0.52	0.52
CBX5				0.23076923	0.28	0.51076923
		0.5				0.5
LIG1					0.48	0.48
PDGFRA					0.48	0.48
H3FB				0.46153846		0.46153846

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	breast	lung	tyroid	ovary	Prostate met	sum
H2BFH				0.46153846		0.46153846
APBB2				0.46153846		0.46153846
SMARCA5		0.44444444				0.44444444
HIST1H3D					0.44	0.44
SOX9	0.43243243					0.43243243
NASP	0.43243243					0.43243243
HIST1H2BN/H2BFD			0.42857143			0.42857143
BACH1			0.42857143			0.42857143
TGFA	0.40540541					0.40540541
ROD1					0.4	0.4
KIF22					0.4	0.4
PTPNS1	0.37837838					0.37837838
CSDA	0.37837838					0.37837838
BMP2					0.36	0.36
SNAPC1					0.36	0.36
RAD52					0.36	0.36
PAWR					0.36	0.36
ANXA8	0.35135135					0.35135135
PRPS1		0.33333333				0.33333333
BUB3		0.33333333				0.33333333
HSP90B1					0.32	0.32
RECQL5					0.32	0.32
CFLAR					0.32	0.32
FGFR3				0.30769231		0.30769231
RFC5				0.30769231		0.30769231
BMPR1A				0.30769231		0.30769231
HNRPC				0.30769231		0.30769231
CD58				0.30769231		0.30769231

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	breast	lung	tyroid	ovary	Prostate met	sum
PEX19/PXF				0.30769231		0.30769231
GAB2				0.30769231		0.30769231
NRP1				0.30769231		0.30769231
GMNN/GEM			0.28571429			0.28571429
RECQL			0.28571429			0.28571429
ADAMTS1			0.28571429			0.28571429
TGFB3			0.28571429			0.28571429
SERPINF2			0.28571429			0.28571429
HMGB1					0.28	0.28
HIST1H2AC					0.28	0.28
CASP3					0.28	0.28
ACOX1					0.28	0.28
MAP3K14	0.27027027					0.27027027
BCL2L11					0.24	0.24
SKP2					0.24	0.24
E2F2					0.24	0.24
SLPI					0.24	0.24
BBC3					0.24	0.24
PPP1R13B					0.24	0.24
MAP2K1				0.23076923		0.23076923
CASP7				0.23076923		0.23076923
ENO3				0.23076923		0.23076923
CALR				0.23076923		0.23076923
INCENP				0.23076923		0.23076923
YY1				0.23076923		0.23076923
NOLC1				0.23076923		0.23076923
H2BFN				0.23076923		0.23076923
H2BFR				0.23076923		0.23076923

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	breast	lung	tyroid	ovary	Prostate met	sum
PMS2L1				0.23076923		0.23076923
POLD1					0.2	0.2
CDC7					0.2	0.2
ATM					0.2	0.2
SULT2A1					0.2	0.2

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The working premise underlying the scoring system is that derangements of one or more of the components of the SYNMULVB/DRM/DREAM/LINC repressor/activator complex produces a cascade of gene over-expression that can occur at many different organ sites and produce ERGO tumors.

The final list of ERGO tumor associated over-expressed genes identified and their scores are summarized in Table 6 below.

Table 6

ERGO Gene List

gene/protein name	score
BUB1	3.83696466
TPX2/C20ORF1	3.67940468
AURKA/STK15	3.67374517
CENPA	3.64845989
CKS2	3.57765766
AURKB/STK12	3.50708049
UBE2C/UBCH10	3.17930172
KIF2C/KNSL6	3.10916213
STMN1	3.03344025
CDC45L	3.02556513
LMNB1	3.02254826
MAD2L1	2.96590041
KIFC1/KNSL2	2.86531631
HMMR	2.8580233
PTTG1	2.79923308
KIF11/KNSL1	2.77597268
CCNA2	2.74513811
UNG	2.67227865
CENPF	2.64265914
TTK	2.62800713
CCNB2	2.61876448
CDC2	2.59256641
EZH2	2.5427027
CDKN3	2.44891331
BUB1B	2.39736264
ASF1B/FLJ10604	2.36752137
MKI67	2.36043956
NDC80/HEC	2.34624295
FOXM1	2.34162162
BIRC5	2.33250635
CDC20/p55CDC	2.30577963
CDC25B	2.25555226

gene/protein name	score
BLM	2.23240867
TIMELESS	2.19238095
MCM2	2.15087615
CENPE	2.13357885
KPNA2	2.12576577
TMPO	2.1225641
MCM7	2.09858628
RAD54L	2.0965119
CDC6	2.09230769
CHEK1	2.07440451
ANLN	2.05880606
CCNB1	2.04848233
TK1	2.04540541
TOP2A	2.01521368
NUSAP1/BM037	2.01158301
RFC4	2.0008085
DEK	2.0008085
SMC2/SMC2L1	1.9782675
TYMS	1.95219351
PBK	1.92307692
CCNE2	1.91950104
H2AFX	1.90850015
MCM6	1.90801241
ECT2	1.90690691
MELK/KIAA0175	1.90469854
CDC25C	1.87621028
NEK2	1.85934858
TOPBP1	1.8582675
CHAF1A	1.8552645
E2F1	1.84585685
PCNA	1.83864634
PRC1	1.82848233
HMGB3/HMG4	1.8200693
MSH2	1.79146685
E2F3	1.76
SRGAP2/KIAA0456	1.74571429
NUP155	1.74322476
RRM2	1.72571429
CHAF1B	1.71298221
UBE2T/HSPC150	1.7008547
RFC2	1.69367521
CDKN2C	1.64613075
SMC4/SMC4L1	1.61281061
UHRF1/ICBP90	1.57142857
PLAU	1.54945055
KIF20A/RAB6KIFL	1.54469854

gene/protein name	score
GCH1	1.51899878
PARP1/ADPRT	1.49145299
TCF19	1.47863248
DNMT1	1.45691846
RACGAP1/ID-GAP	1.43243243
CCNF	1.41269841
DCK	1.4042735
TEAD4	1.38253638
MCM3	1.36752137
FEN1	1.32848233
GINS1/KIAA0186	1.32307692
RRM1	1.31340659
POLE2	1.31196581
BARD1	1.3008316
RAD51AP1/PIR51	1.2972973
PLK4/STK18	1.29435435
SERPINE1	1.28791209
POLA2	1.28257796
CDCA4/FLJ20764	1.27472527
CCND1	1.27428571
DTYMK	1.26153846
CCNE1	1.24324324
MCM4	1.23950104
H2AFZ	1.23846154
HIST1H2BF/H2BFG	1.23296703
LHX2	1.22990991
CKS1	1.22453222

This list of 105 ERGO tumor associated genes includes the nucleic acid sequences shown in SEQ ID NO:s 12-14, 20-21, 35, 37, 43-44, 46-47, 49-51, 54, 56, 58-67, 69-71, 75, 79-84, 86, 88, 91, 93-95, 103-105, 107-110, 112, 116, 118-120, 122, 125-126, 128-129, 131, 145-146, 148-149, 151, 154, 156-157, 163, 165-166, 171, 173, 176-177, 180, 184, 186, 188, 193, 196, 198, 200-201, 203, 205, 209, 246-247, 249, 254, 267, 269, 274-275, 292-294, 311, 316, 231-323, and 333; and splice variants or nucleic acids encoding different peptide chain isoforms derived from these nucleic acids that are capable of hybridizing to the nucleic acid sequences shown in these SEQ ID NO:s, or the complement thereof, under the hybridization conditions of a microarray experiment. This list accounts for a common list, or basic "mosaic" of over-expressed genes that are observed in ERGO tumors including ERGO tumors occurring at different organ sites. Table 7 below provides a key and identifies the gene or protein name as appropriate, the accession number of each amino acid sequence or nucleic acid sequence as

appropriate, the SEQ ID NO:s for the 325 E2F response genes used in the analyses here and the SEQ ID NO:s for the final list of 105 ERGO tumor associated over-expressed genes identified. Astericks ("*") are used in Table 7 to identify the final list of 105 ERGO tumor associated over-expressed genes identified. Daggers ("†") are used in Table 7 to identify a refined list of 125 ERGO tumor associated over-expressed genes that were also identified. Double daggers ("‡") are used in Table 7 to identify housekeeping genes with transcript levels that do not appreciably vary in either normal or malignant tissue, such as normal or cancerous prostate tissue, and are useful for normalization of indicator values and references values. Genes having the sequences shown in SEQ ID NO:s 68 and 335-336 are E2F responsive genes with high sequence identity, or sequence similarity, to other ERGO genes identified. Genes having the sequences shown in SEQ ID NO:s 39, 72, 102, 123, 160, 164, 174, 217, 259, 295, 298, 307, 331 and 337-340 are E2F responsive genes that were identified by analyses of microarray data from prostate tissue samples and have been found to be useful in discriminating aggressive prostate cancers from non-aggressive prostate cancers.

Table 7

gene/protein name	accession number	SEQ ID NO:
BCL2L11	NM_006538	10
FOXO1//FOXO1A	NM_002015	11
CCNE2*,†	NM_057749	12
CDKN2C*,†	NM_001262	13
CCNE1*,†	NM_001238	14
MYC	NM_002467	15
FGFR3	NM_000142	16
MAP3K5	NM_005923	17
BMP2	NM_001200	18
MYB	NM_005375	19
LHX2*,†	NM_004789	20
GCH1*,†	NM_000161	21
MAPK9	NM_002752	22
MAPK8	NM_002750	23
MAPK3	X60188	24
MAPK1	NM_002745	25
MAPK4	NM_002747	26
MAP2K1	NM_002755	27
MAP2K2	NM_030662	28
FOXO3//FOXO3A	NM_001455	29

gene/protein name	accession number	SEQ ID NO:
GADD45B	NM_015675	30
MCL1	L08246	31
BCL2	NM_000633	32
CCND3	NM_00176	33
FOXN3//CHES1	NM_005197	34
MKI67*,†	NM_002417	35
CDKN1C	NM_000076	36
KIFC1*,†	D14678	37
PRG4	NM_005807	38
PMS2†	NM_000535	39
PLK2//SNK	NM_006622	40
HRK	NM_003806	41
CASP8	NM_001228	42
TYMS*,†	NM_001071	43
TK1*,†	NM_003258	44
DUT	NM_001948	45
RRM1*,†	NM_001033	46
RRM2*,†	NM_001034	47
CDK2	NM_001798	48
MCM3*,†	NM_002388	49
MCM7*,†	D55716	50
PCNA*,†	NM_002592	51
RFC3	NM_002915	52
PRIM1	NM_000946	53
TOP2A*,†	NM_001067	54
LIG1	NM_000234	55
FEN1*,†	NM_004111	56
RAD51	NM_002875	57
CDC20*,†	NM_001255	58
CDC2*,†	NM_001786	59
CCNA2*,†	NM_001237	60
CCNB1*,†	NM_031966	61
CCNB2*,†	NM_004701	62
SMC2//SMC2L1*,†	NM_006444	63
STMN1*,†	NM_005563	64
NDC80//HEC*,†	NM_006101	65
BUB1*,†	NM_004336	66
KPNA2*,†	NM_002266	67
HMGB2†	NM_001130688	68
EZH2*,†	NM_004456	69
AURKB//STK12*,†	NM_004217	70
PTTG1*,†	NM_004219	71
SLBP†	NM_006527	72
RB1	NM_000321	73
ANXA8	NM_001040084	74

gene/protein name	accession number	SEQ ID NO:
DCK*,†	NM_000788	75
CDC25A	NM_001789	76
EPS8	NM_004447	77
FST	NM_013409	78
TMPO*,†	NM_003276	79
RAD51AP1//PIR51*,†	NM_006479	80
ASF1B*,†	NM_018154	81
CDCA4*,†	NM_017955	82
RFC4*,†	NM_002916	83
BLM*,†	NM_000057	84
VRK1	NM_003384	85
BARD1*,†	NM_000465	86
BTG3	NM_006806	87
CHAF1A*,†	NM_005483	88
NPAT	NM_002519	89
HUNK	NM_014586	90
DEK*,†	NM_003472	91
EED	AF099032	92
MCM4*,†	X74794	93
MELK*,†	NM_014791	94
TCF19*,†	NM_007109	95
FANCL	NM_018062	96
PBX3	NM_006195	97
EGR1	NM_001964	98
CDCA7L	NM_001127370	99
SKP2	NM_005983	100
CTGF	NM_001901	101
CITED2†	NM_006079	102
SERPINE1*,†	M16006	103
CCND1*,†	NM_053056	104
UHRF1//ICBP90*,†	NM_013282	105
MCM5	NM_006739	106
HMGB3*,†	NM_005342	107
MCM6*,†	NM_005915	108
CDC45L*,†	NM_003504	109
CDC6*,†	NM_001254	110
ORC6L	NM_014321	111
CKS2*,†	NM_001827	112
GMNN	NM_015895	113
PRIM2	NM_000947	114
CENPK//FKSG14	NM_022145	115
NUP155*,†	NM_004298	116
FIGNL1	NM_001042762	117
MAD2L1*,†	NM_002358	118
CCNF*,†	NM_001761	119

gene/protein name	accession number	SEQ ID NO:
DNMT1*,†	NM_001379	120
RPA1	NM_002945	121
PRC1*,†	NM_003981	122
RBL1†	NM_002895	123
BRCA1	NM_007294	124
H2AFZ*,†	NM_002106	125
DTYMK*,†	NM_012145	126
PLK1	NM_005030	127
POLA2*,†	NM_002689	128
PBK*,†	NM_018492	129
CASP7	NM_001227	130
MCM2*,†	NM_004526	131
RPA3	NM_002947	132
GJC1//GJA7	NM_005497	133
USP1	NM_003368	134
DNA2L	D42046	135
CITED1	NM_004143	136
NASP	NM_002482	137
RFC5†	NM_007370, NM_001130112	138, 340
SMARCA5	NM_003601	139
SHCBP1//FLJ22009	NM_024745	140
SSX2IP	NM_014021	141
MFAP1	NM_005926	142
ROD1	NM_005156	143
BMPR1A	NM_004329	144
E2F3*,†	NM_001949	145
UNG*,†	NM_003362	146
ENO3	NM_001976	147
MSH2*,†	NM_000251	148
PLK4*,†	NM_014264	149
ACTA2	NM_001613	150
TIMELESS*,†	NM_003920	151
BOK	NM_032515	152
KBTBD10//SARCOSIN	NM_006063	153
BUB1B*,†	NM_001211	154
NUP107	NM_020401	155
KIF2C//KNSL6*,†	NM_006845	156
LMNB1*,†	NM_005573	157
RPA2	NM_002946	158
CHEK2//CDS1	NM_007194	159
COL11A1†	NM_001854	160
TGFB3	NM_003239	161
CALR‡	NM_004343	162
TTK*,†	NM_003318	163

gene/protein name	accession number	SEQ ID NO:
E2F2†	NM_004091	164
CKS1B//CKS1*†	NM_001826	165
RFC2*†	NM_002914	166
UMPS	NM_000373	167
DBF4//ASK	NM_006716	168
CHEK1*†	NM_001274	169
BUB3	NM_004725	170
CENPE*†	NM_001813	171
CSTF1	NM_001324	172
RAD54L*†	NM_003579	173
POLD1†	NM_002691	174
MLH1	NM_000249	175
CENPA*†	NM_001809	176
SMC4//SMC4L1*†	NM_005496	177
HMGB1//HMG1†	AL110194, NM_002128	178, 336
HIST1H3D//H3FB	NM_003530	179
H2AFX*†	NM_002105	180
CBX5	NM_012117	181
HIST1H2AC//H2AFL	NM_003512	182
KIF22//KNSL4	NM_007317	183
NEK2*†	NM_002497	184
KIF4A	NM_012310	185
HMMR*†	NM_012484	186
MTHFD1	NM_005956	187
GINS1*†	D80008	188
SFPQ	NM_005066	189
HSP90B1//TRA1	NM_003299	190
MAP3K7	NM_003188	191
PLSCR1	AB006746	192
ANLN*†	NM_018685	193
SFRS2	NM_003016	194
ID3	X69111	195
TEAD4*†	NM_003213	196
SRPR	NM_003139	197
UBE2T//HSPC150*†	NM_014176	198
INCENP	NM_020238	199
CDC25B*†	NM_004358	200
AURKA//STK15*†	NM_003600	201
DHFR	NM_000791	202
CDKN3*†	NM_005192	203
CDC7//CDC7L1	AF015592	204
RACGAP1//ID-GAP*†	NM_013277	205
CSRP2	NM_001321	206
MAF	NM_005360	207

gene/protein name	accession number	SEQ ID NO:
CBX3	NM_007276	208
CHAF1B*,†	NM_005441	209
ADAMTS1	NM_006988	210
TCOF1	NM_000356	211
LSM5	NM_012322	212
HNRNPC//HNRPC	NM_001077442	213
APAF1	NM_013229	214
ASH2L	NM_004674	215
BCL3	NM_005178	216
CASP3†	NM_004346	217
CAV1	AF070648	218
CD58	NM_001779	219
DMRT1	AF130728	220
DYRK1A	NM_001396	221
LIMA1//EPLIN	NM_016357	222
FGFR2	NM_000141	223
HEY1	NM_012258	224
INHBA	NM_002192	225
TBC1D2B//KIAA1055	AK000173	226
OSMR	NM_003999	227
FURIN//PACE	NM_002569	228
PRKAR2B	NM_002736	229
SIRPA//PTPNS1	NM_001040022	230
RANBP9	NM_005493	231
SOX9	NM_000346	232
SPHK1	AF238083	233
TACC1	NM_006283	234
TGFA	NM_003236	235
TGFB2	NM_003238	236
YY1	NM_003403	237
SNAPC1	NM_003082	238
CCNG2	NM_004354	239
HOXA7	NM_006896	240
HOXA9	NM_152739	241
PITX1	NM_002653	242
SMARCA2	NM_003070	243
BACH1	NM_001186	244
CBFB	NM_001755	245
BIRC5*,†	NM_001168	246
CDC25C*,†	NM_001790	247
ORC3L	NM_012381	248
TOPBP1*,†	NM_007027	249
MRE11A	NM_005590	250
ATM	NM_000051	251
XRCC4	NM_003401	252

gene/protein name	accession number	SEQ ID NO:
RECQL	NM_002907	253
CENPF*†	NM_016343	254
CENPH//PMF1	NM_022909	255
NOLC1	NM_004741	256
KIF20B//MPHOSPH1	NM_016195	257
BMI1	NM_005180	258
HIST1H2AE//H2AFA†	NM_021052	259
HIST1H2AD//H2AFG	NM_021065	260
HIST1H2BN//H2BFD	NM_003520	261
HIST1H2BE//H2BFH	NM_003523	262
HIST1H2BO//H2BFN	NM_003527	263
HIST1H2BJ//H2BFR	NM_021058	264
HIST1H3B//H3FL	NM_003537	265
HIST2H4A//H4F2	NM_003548	266
HIST1H2BF//H2BFG*†	NM_003522	267
HIST1H3E//H3FD	NM_003532	268
KIF20A//RAB6KIFL*†	NM_005733	269
FGFR1OP//FOP†	AL117608, NM_007045	270, 337
DHPS	NM_013406	271
PEX19//PXF	NM_002857	272
PPM1D	NM_003620	273
E2F1*†	M96577	274
PARP1//ADPRT*†	NM_001618	275
ORC2L	NM_006190	276
VEGFA//VEGF	NM_003376	277
APOE	NM_000041	278
PRPS1	NM_002764	279
TGFB1I1	NM_015927	280
CXCR7//RDC1	U67784	281
PDGFRA	X76079	282
SLPI	NM_003064	283
FAS//TNFRSF6	NM_000043	284
CPT1A	NM_001876	285
PDCD4	NM_014456	286
TANK	NM_004180	287
APBB2	NM_173075	288
GADD45A	NM_001924	289
ACOX1	NM_007292	290
CSDA	NM_003651	291
UBE2C//UBCH10*†	NM_007019	292
TPX2//C20orf1*†	AB024704	293
NUSAP1//BM037*†	NM_016359	294
SULT2A1†	NM_003167	295
INMT	NM_006774	296

gene/protein name	accession number	SEQ ID NO:
ARHGAP4	X78817	297
RAD52†	NM_134424	298
TNFSF9	NM_003811	299
BAD	U66879	300
BAK1	NM_001188	301
BID	NM_001196	302
CFLAR	NM_003879	303
MAP3K14	NM_003954	304
PAWR	NM_002583	305
FGF2	NM_002006	306
MMP16†	NM_005941	307
TP53BP2	NM_005426	308
VEGFB	NM_003377	309
IFNA2	M54886	310
SRGAP2//KIAA0456*,†	AK000885	311
DIP//KIAA0767	AB018310	312
SERPINF2	D00174	313
CCNO//UNG2	NM_021147	314
TP73	NM_005427	315
POLE2*,†	NM_002692	316
RAD51C	NM_002876	317
PMS2L1	D38435	318
DDB2	NM_000107	319
NFKB2	NM_002502	320
KIF11//KNSL1*,†	NM_004523	321
FOXM1*,†	U74612	322
PLAU*,†	NM_002658	323
BBC3	U82987	324
PMAIP1	D90070	325
GAB2	NM_012296	326
SIVA1//SIVA	NM_006427	327
PPP1R13B	AB018314	328
AXIN2	NM_004655	329
DIABLO//SMAC	NM_019887	330
AR†	NM_000044	331
NRP1	NM_003873	332
ECT2*,†	NM_018098	333
ISYNA1	NM_016368	334
MYBL1†	NM_001080416	335
MYBL2†	NM_002466	338
HIST1H2BK†	NM_080593	339
CUL4B‡	NM_001079872	341
OAZ2‡	NM_002537	342
TBCC‡	NM_003192	343
NUP214‡	NM_005085	344

gene/protein name	accession number	SEQ ID NO:
FBXW11‡	NM_012300	345
POP4‡	NM_006627	346
LPCAT3‡	NM_005768	347
ARSE‡	NM_000047	348
ARC‡	NM_015193	349
POLR3D‡	NM_001722	350
DLGAP4‡	NM_001042486	351
SLC22A5‡	NM_003060	352
BRMS1‡	NM_001024957	353
ZFAND5‡	NM_001102420	354
THOP1‡	NM_003249	355
DNPEP‡	NM_012100	356
USP20‡	NM_001008563	357
HMGN2‡	NM_005517	358
ARF3‡	NM_001659	359
PSMB1‡	NM_002793	360
CFL1‡	NM_005507	361
RPS25‡	NM_001028	362
MANF‡	NM_006010	363
HADHB‡	NM_000183	364
RPL22‡	NM_000983	365

Example 7

Bladder Cancer is an ERGO Tumor

Studies by Olsson *et al.* (2007) have indicated that E2F3 overexpression may play a role in the development of bladder cancers. We examined dataset GSE3167 (Dyrskjøt *et al.*, (2004)), available from the NCBI GEO site, which contains gene expression microarray data from patient samples of normal bladder tissues which were used for data normalization, patient samples of localized bladder cancers, and patient samples of muscle-invasive bladder cancers. Among 33 tumor samples that were histopathologically grade 3 or 4, 32 of these 33 samples simultaneously overexpressed at least 20 of a list of 93 E2F-responsive genes included in these analyses. *See* Fig. 26. All of the genes in the list were overexpressed in a least 20 percent of the 33 tumors. Fifty-five of these 93 E2F-responsive genes, or 59% of the 93 E2F-responsive genes, were amoung the 125 genes identified in the generic ERGO gene list shown in Table 8. In contrast, only 2 of 8 grade 2 bladder cancer samples, and none of the 7 normal bladder samples, overexpressed at least 20 of these 93 E2F responsive genes. *See* Fig. 26. These results demonstrate that bladder cancers are an ERGO tumor and that the overexpression of ERGO tumor genes is correlated to increasing bladder cancer grade.

Example 8

Hepatoma is an ERGO Tumor

Heptomas have been reported by Kalinichenko *et al.*, (2004) to overexpress FOXM1 which we know to be an ERGO tumor-associated gene. We examined dataset GSE1898, available from the NCBI GEO site, which contained gene expression microarray data from 182 patient samples of hepatoma. Sixty (60) of these samples simultaneously overexpressed at least 20% of the genes in a list of 107 E2F-responsive genes included in these analyses. *See* Fig. 27. Moreover, each one of the individual E2F-responsive genes in this list of 107 E2F-responsive genes was also overexpressed in at least 20% of the tumors. In fact, 58% of these genes were included in the list of 125 genes identified in the generic ERGO gene list shown in Table 8. These results demonstrate that approximately one third of hepatomas, or 60 out of 182 patient samples of hepatoma, are ERGO tumors.

All references (*e.g.* journal articles, patent documents, and accession numbers) cited herein are incorporated by reference in their entirety.

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Claims

What is claimed is:

1. A method of identifying a tumor as an ERGO tumor comprising the steps of:

a) providing a tumor sample;

b) providing a reference;

c) measuring an indicator of gene transcript levels in the tumor sample to produce an indicator value for each of the following gene transcripts having the nucleic acid sequences shown in SEQ ID NO:s 12-14, 20-21, 35, 37, 39, 43-44, 46-47, 49-51, 54, 56, 58-72, 75, 79-84, 86, 88, 91, 93-95, 102-105, 107-110, 112, 116, 118-120, 122-123, 125-126, 128-129, 131, 145-146, 148-149, 151, 154, 156-157, 160, 163-166, 169, 171, 173-174, 176-177, 180, 184, 186, 188, 193, 196, 198, 200-201, 203, 205, 209, 217, 246-247, 249, 254, 259, 267, 269, 274-275, 292-295, 298, 307, 311, 316, 321-323, 331, 333, and 335-340;

d) measuring the reference to produce a reference value; and

e) comparing the indicator value to the reference value to determine which of the gene transcripts is over-expressed;

whereby the tumor is identified as an ERGO tumor if at least 21 of these gene transcripts are over-expressed.

2. The method of claim 1 wherein the tumor sample is from lung tissue.

3. The method of claim 1 wherein the tumor sample is from thyroid tissue.

4. The method of claim 1 wherein the tumor sample is from ovarian tissue.

5. The method of claim 1 wherein the tumor sample is from prostate tissue.

6. The method of claim 1 wherein the indicator value is at least 1.8 times greater than the reference value for each of the gene transcripts.

7. A method of determining the odds that an individual ERGO tumor patient will survive to a future date comprising the steps of:

a) providing a tumor sample from an individual patient;

b) providing a reference;

c) measuring an indicator of gene transcript levels in the tumor sample to produce an indicator value for each of the following gene transcripts having the nucleic acid sequences shown in SEQ ID NO:s 12-14, 20-21, 35, 37, 39, 43-44, 46-47, 49-51, 54, 56, 58-72, 75, 79-84, 86, 88, 91, 93-95, 102-105, 107-110, 112, 116, 118-120, 122-123, 125-126, 128-129, 131, 145-146, 148-149, 151, 154, 156-157, 160, 163-166, 169, 171, 173-174, 176-177, 180, 184, 186, 188, 193, 196, 198, 200-201, 203, 205, 209, 217, 246-247, 249, 254, 259, 267, 269, 274-275, 292-295, 298, 307, 311, 316, 321-323, 331, 333, and 335-340;

d) measuring the reference to produce a reference value; and

e) comparing the indicator value to the reference value to determine which of the gene transcripts is over-expressed, whereby the tumor is identified as an ERGO tumor and the individual patient is diagnosed as an ERGO tumor patient if at least 21 of these gene transcripts are over-expressed;

f) plotting the fraction of surviving patients in a population of patients diagnosed as ERGO tumor patients as a function of the time since diagnosis of the ERGO tumor to generate a survival plot; and

g) selecting a future date after the individual patient is diagnosed as an ERGO tumor patient and determining the fraction of surviving patients in the population from the survival plot;

whereby the fraction of surviving patients on the survival plot at the future date predicts the odds that an individual tumor patient will survive to the future date.

8. The method of claim 7 wherein the tumor sample is from lung tissue and the population of patients is diagnosed as ERGO lung tumor patients.

9. The method of claim 7 wherein the tumor sample is from thyroid tissue and the population of patients is diagnosed as ERGO thyroid tumor patients.

10. The method of claim 7 wherein the tumor sample is from ovarian tissue and the population of patients is diagnosed as ERGO ovarian tumor patients.

11. The method of claim 7 wherein the tumor sample is from prostate tissue and the population of patients is diagnosed as ERGO prostate tumor patients.

12. The method of claim 7 wherein the indicator value is at least 1.8 times greater than the reference value for each of the gene transcripts.

13. A method of treating an ERGO tumor in a patient comprising the steps of:

a) providing a tumor sample from a patient;

b) providing a reference;

c) measuring an indicator of gene transcript levels in the tumor sample to produce an indicator value for each of the following gene transcripts having the nucleic acid sequences shown in SEQ ID NO:s 12-14, 20-21, 35, 37, 39, 43-44, 46-47, 49-51, 54, 56, 58-72, 75, 79-84, 86, 88, 91, 93-95, 102-105, 107-110, 112, 116, 118-120, 122-123, 125-126, 128-129, 131, 145-146, 148-149, 151, 154, 156-157, 160, 163-166, 169, 171, 173-174, 176-177, 180, 184, 186, 188, 193, 196, 198, 200-201, 203, 205, 209, 217, 246-247, 249, 254, 259, 267, 269, 274-275, 292-295, 298, 307, 311, 316, 321-323, 331, 333, and 335-340;

d) measuring the reference to produce a reference value; and

e) comparing the indicator value to the reference value to determine which of the gene transcripts is over-expressed, whereby the tumor is identified as an ERGO tumor if at least 21 of these gene transcripts are over-expressed;

f) selecting a drug capable of killing or inhibiting division of an ERGO tumor cell expressing at least one protein encoded by at least one gene transcript selected from the group consisting of the following gene transcripts having the nucleic acid sequences shown in SEQ ID NO:s 12-14, 20-21, 35, 37, 39, 43-44, 46-47, 49-51, 54, 56, 58-72, 75, 79-84, 86, 88, 91, 93-95, 102-105, 107-110, 112, 116, 118-120, 122-123, 125-126, 128-129, 131, 145-146, 148-149, 151, 154, 156-157, 160, 163-166, 169, 171, 173-174, 176-177, 180, 184, 186, 188,

193, 196, 198, 200-201, 203, 205, 209, 217, 246-247, 249, 254, 259, 267, 269, 274-275, 292-295, 298, 307, 311, 316, 321-323, 331, 333, and 335-340; and

g) administering a pharmaceutically acceptable amount of the drug to the patient;

whereby the ERGO tumor in the patient is treated.

14. The method of claim 13 wherein the drug is an aurora kinase antagonist.

15. The method of claim 14 wherein the aurora kinase antagonist is at least one molecule selected from the group consisting of VX-680, MLN8237, MLN8054, AZD1152, hesperadin, and ZM-447439.

16. The method of claim 13 wherein the drug is a survivin antagonist.

17. The method of claim 16 wherein the survivin antagonist is YM155.

18. The method of claim 13 wherein the drug is a FOXM1 antagonist.

19. The method of claim 18 wherein the FOXM1 antagonist is the $(D\text{-}Arg)_9$-p19ARF 26-44 peptide.

20. The method of claim 13 wherein the drug is an E2F antagonist.

21. The method of claim 20 wherein the E2F antagonist is eugenol.

22. The method of claim 13 wherein the drug is a LINC protein complex agonist.

23. The method of claim 13 wherein the indicator value is at least 1.8 times greater than the reference value for each of the gene transcripts.

24. A method of identifying an individual tumor in a population of tumors as an ERGO tumor comprising the steps of:

a) providing a population of tumor samples;

b) providing a reference;

c) measuring gene transcript levels in the tumor samples to produce a transcript value for each of the following gene transcripts having the nucleic acid sequences shown in SEQ ID NO:s 10-340;

d) comparing the transcript value to the reference value for each tumor to identify the gene transcripts over-expressed by each tumor;

e) ranking the tumors in the population with a rank ordering algorithm to order the tumors according to the number of the gene transcripts over-expressed by each tumor; and

f) removing individual tumors from the population that over-express the smallest number of each gene transcript per cell and that have the lowest levels of over-expression of each gene transcript per cell until at least 20% of the individual tumors remaining in the population over-express at least 20% of the gene transcripts;

whereby an individual tumor remaining in the population of tumors is identified as an ERGO tumor.

25. The method of claim 24 wherein the indicator value is at least 1.8 times greater than the reference value for each of the gene transcripts.

26. A method of identifying an individual tumor in a population of tumors as an ERGO tumor comprising the steps of:

a) providing a population of tumor samples;

b) providing a reference;

c) measuring gene transcript levels in the tumor samples to produce a transcript value for each of the following gene transcripts having the nucleic acid sequence shown in SEQ ID NO:s 10-340;

d) comparing the transcript value to the reference value for each tumor to identify the gene transcripts over-expressed by each tumor; and

e) applying a principle component analysis algorithm in which the analyzed gene set is restricted to each gene transcript having the nucleic acid sequence shown in SEQ ID NO:s 10-340 to identify a tumor cluster over-expressing these E2F-responsive genes;

whereby an individual tumor in the population of tumors in the cluster is identified as an ERGO tumor.

27. The method of claim 26 wherein the indicator value is at least 1.8 times greater than the reference value for each of the gene transcripts.

28. A method of selecting treatment for a prostate cancer patient comprising the steps of:

a) providing a tumor sample from a prostate cancer patient;

b) providing a reference;

c) measuring an indicator of gene transcript levels in the tumor sample to produce an indicator value for each of the following gene transcripts having the nucleic acid sequences shown in SEQ ID NO:s 12-14, 20-21, 35, 37, 39, 43-44, 46-47, 49-51, 54, 56, 58-72, 75, 79-84, 86, 88, 91, 93-95, 102-105, 107-110, 112, 116, 118-120, 122-123, 125-126, 128-129, 131, 145-146, 148-149, 151, 154, 156-157, 160, 163-166, 169, 171, 173-174, 176-177, 180, 184, 186, 188, 193, 196, 198, 200-201, 203, 205, 209, 217, 246-247, 249, 254, 259, 267, 269, 274-275, 292-295, 298, 307, 311, 316, 321-323, 331, 333, and 335-340;

d) measuring the reference to produce a reference value; and

e) comparing the indicator value to the reference value to determine which of the gene transcripts is over-expressed, whereby the tumor is identified as an ERGO tumor and the prostate cancer patient is diagnosed as an ERGO tumor prostate cancer patient if at least 21 of these gene transcripts are over-expressed; and

f) choosing at least one treatment selected from the group consisting of removal of at least one tumor and adjuvant therapy, if the patient is diagnosed as an ERGO tumor prostate cancer patient;

whereby a treatment is selected for the prostate cancer patient.

29. The method of claim 28, wherein the removal of at least one tumor is performed using at least one therapy selected from the group consisting of using focused energy, cryoablation, and radiation therapy.

30. The method of claim 29, wherein the adjuvant therapy is at least one therapy selected from the group consisting of chemotherapy, hormone therapy, and immunotherapy.

31. A method as in claims 5, 11, 28, 29 or 30 further comprising measuring an indicator of gene transcript levels in at least one selected from the group consisting of the tumor sample and the reference to produce a housekeeping value for at least one gene transcript selected from the group consisting of the nucleic acid sequences shown in SEQ ID NO:s 162, 341-364 and 365; and normalizing at least one selected from the group consisting of the indicator value and the reference value to the housekeeping value.

32. The use of an aurora kinase antagonist in the manufacture of a medicament for the treatment of an ERGO tumor identified according to the method of claim 1.

33. The use of VX-680 in the manufacture of a medicament for the treatment of an ERGO tumor identified according to the method of claim 1.

34. The use of MLN8237 in the manufacture of a medicament for the treatment of an ERGO tumor identified according to the method of claim 1.

35. The use of MLN8054 in the manufacture of a medicament for the treatment of an ERGO tumor identified according to the method of claim 1.

36. The use of AZD1152 in the manufacture of a medicament for the treatment of an ERGO tumor identified according to the method of claim 1.

37. The use of hesperadin in the manufacture of a medicament for the treatment of an ERGO tumor identified according to the method of claim 1.

38. The use of ZM-447439 in the manufacture of a medicament for the treatment of an ERGO tumor identified according to the method of claim 1.

39. The use of a survivin antagonist in the manufacture of a medicament for the treatment of an ERGO tumor identified according to the method of claim 1.

40. The use of YM155 in the manufacture of a medicament for the treatment of an ERGO tumor identified according to the method of claim 1.

41. The use of a FOXM1 antagonist in the manufacture of a medicament for the treatment of an ERGO tumor identified according to the method of claim 1.

42. The use of the $(D\text{-}Arg)_9$-p19ARF 26-44 peptide in the manufacture of a medicament for the treatment of an ERGO tumor identified according to the method of claim 1.

43. The use of an E2F antagonist in the manufacture of a medicament for the treatment of an ERGO tumor identified according to the method of claim 1.

44. The use of eugenol in the manufacture of a medicament for the treatment of an ERGO tumor identified according to the method of claim 1.

45. The use of a LINC protein complex agonist in the manufacture of a medicament for the treatment of an ERGO tumor identified according to the method of claim 1.

46. An apparatus comprising:

a) a specifically programmed computer in communication with a nucleic acid array analyzer and an output display,

wherein the specifically programmed computer is adapted to compare indicator values to reference values and to determine which gene transcripts are over-expressed in a tumor sample;

b) a nucleic acid array comprising at least 21 of the nucleic acid sequences shown in SEQ ID NO:s 12-14, 20-21, 35, 37, 39, 43-44, 46-47, 49-51, 54, 56,

58-72, 75, 79-84, 86, 88, 91, 93-95, 102-105, 107-110, 112, 116, 118-120, 122-123, 125-126, 128-129, 131, 145-146, 148-149, 151, 154, 156-157, 160, 163-166, 169, 171, 173-174, 176-177, 180, 184, 186, 188, 193, 196, 198, 200-201, 203, 205, 209, 217, 246-247, 249, 254, 259, 267, 269, 274-275, 292-295, 298, 307, 311, 316, 321-323, 331, 333, and 335-340 adapted for hybridization to nucleic acids in a tumor sample;

c) a memory containing an indicator value for each of the following gene transcripts having the nucleic acid sequences shown in SEQ ID NO:s 12-14, 20-21, 35, 37, 39, 43-44, 46-47, 49-51, 54, 56, 58-72, 75, 79-84, 86, 88, 91, 93-95, 102-105, 107-110, 112, 116, 118-120, 122-123, 125-126, 128-129, 131, 145-146, 148-149, 151, 154, 156-157, 160, 163-166, 169, 171, 173-174, 176-177, 180, 184, 186, 188, 193, 196, 198, 200-201, 203, 205, 209, 217, 246-247, 249, 254, 259, 267, 269, 274-275, 292-295, 298, 307, 311, 316, 321-323, 331, 333, and 335-340 produced by hybridization of the nucleic acid array to the nucleic acids in the tumor sample, and containing reference values for the gene transcripts; and

d) an output display which shows the tumor sample is an ERGO tumor when the specifically programmed computer determines at least 21 of the gene transcripts are over-expressed in a tumor sample.

47. The method of claim 1 wherein the tumor sample is from liver tissue.

48. The method of claim 1 wherein the tumor sample is from bladder tissue.

49. The method of claim 7 wherein the tumor sample is from liver tissue and the population of patients is diagnosed as ERGO hepatoma tumor patients.

50. The method of claim 7 wherein the tumor sample is from bladder tissue and the population of patients is diagnosed as ERGO bladder tumor patients.

51. The method of claim 13 wherein the ERGO tumor is from a tissue selected from the group consisting of lung tissue, thyroid tissue, ovarian tissue, prostate tissue, liver tissue and bladder tissue.

52. The method of claim 24 wherein the tumor sample is from a tissue selected from the group consisting of lung tissue, thyroid tissue, ovarian tissue, prostate tissue, liver tissue and bladder tissue.

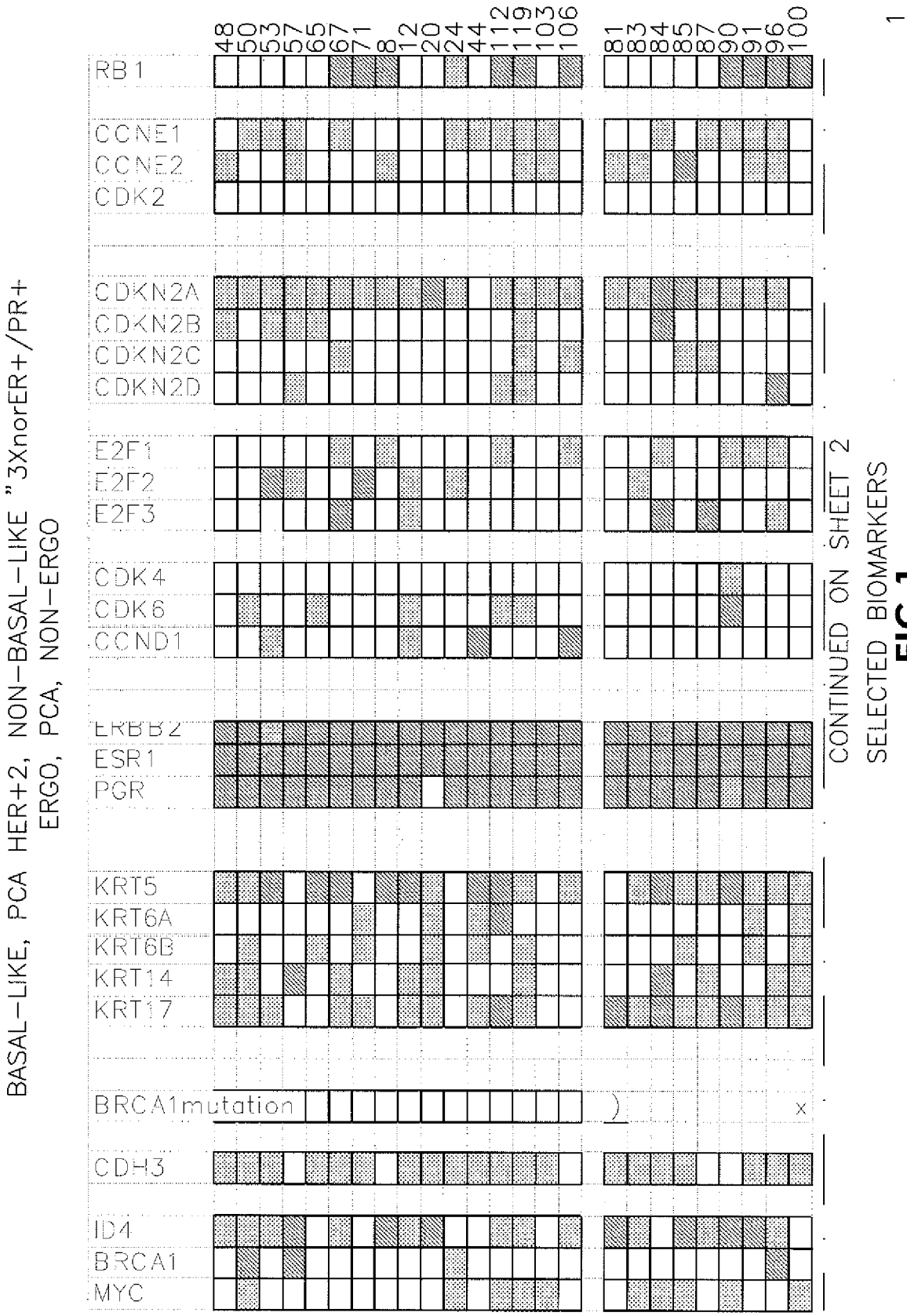

BASAL-LIKE, PCA HER+2, NON-BASAL-LIKE "3XnorER+/PR+
ERGO, PCA, NON-ERGO
48 50 53 57 65 67 71 8 12 20 24 44 112 119 103 106
81 83 84 85 87 90 91 96 100
RB1
CCNE1
CCNE2
CDK2
CDKN2A
CDKN2B
CDKN2C
CDKN2D
E2F1
E2F2
E2F3
CDK4
CDK6
CCND1
ERBB2
ESR1
PGR
KRT5
KRT6A
KRT6B
KRT14
KRT17
BRCA1mutation
CDH3
ID4
BRCA1
MYC
CONTINUED ON SHEET 2
SELECTED BIOMARKERS
1

FIG.1

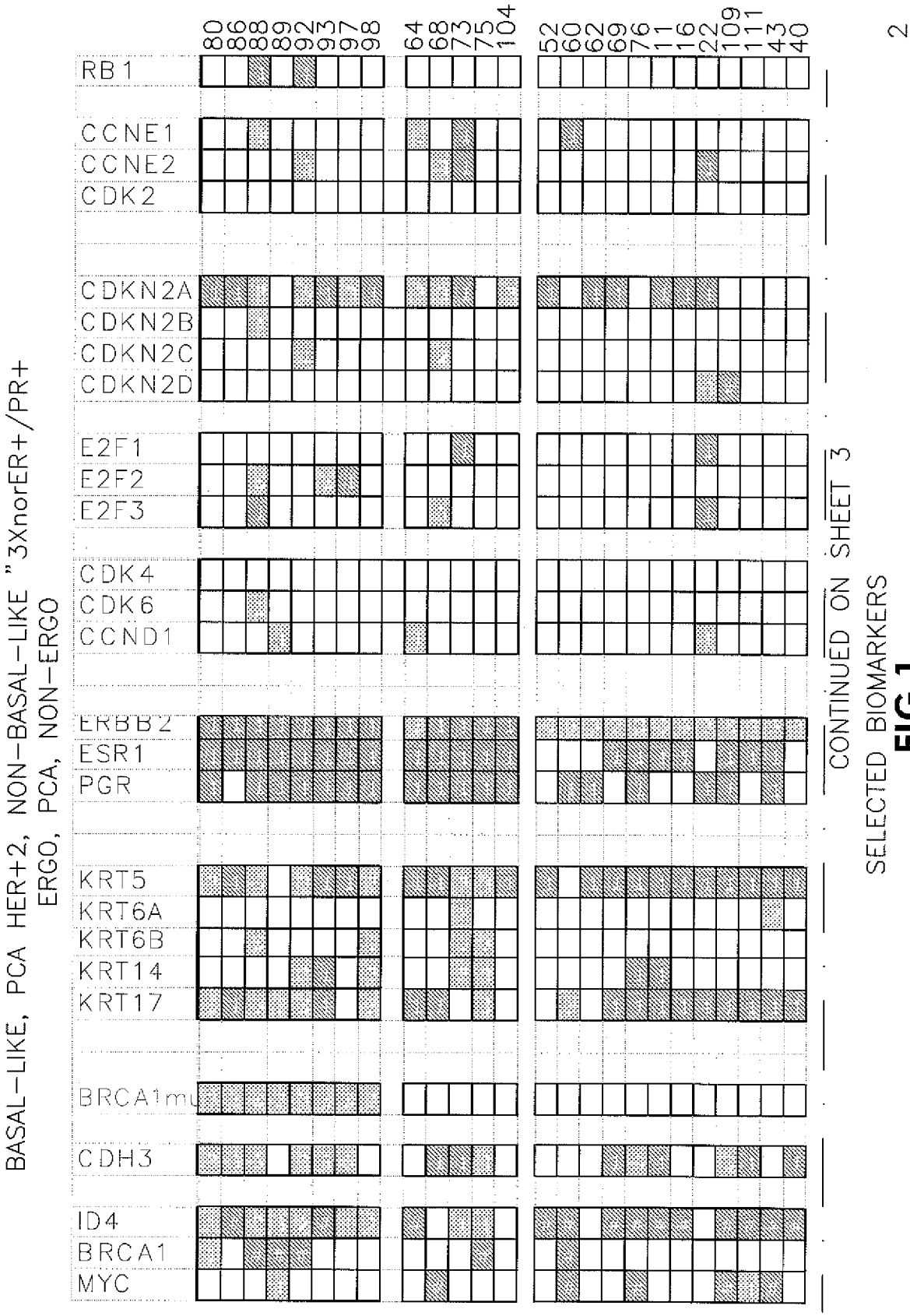

BASAL-LIKE, PCA HER+2, NON-BASAL-LIKE "3XnorER+/PR+
ERGO, PCA, NON-ERGO
80 86 88 89 92 93 97 98
64 68 73 75 104
52 60 62 69 76 11 16 22 109 111 43 40
RB1
CCNE1
CCNE2
CDK2
CDKN2A
CDKN2B
CDKN2C
CDKN2D
E2F1
E2F2
E2F3
CDK4
CDK6
CCND1
ERBB2
ESR1
PGR
KRT5
KRT6A
KRT6B
KRT14
KRT17
BRCA1mu
CDH3
ID4
BRCA1
MYC
CONTINUED ON SHEET 3
SELECTED BIOMARKERS

FIG.1

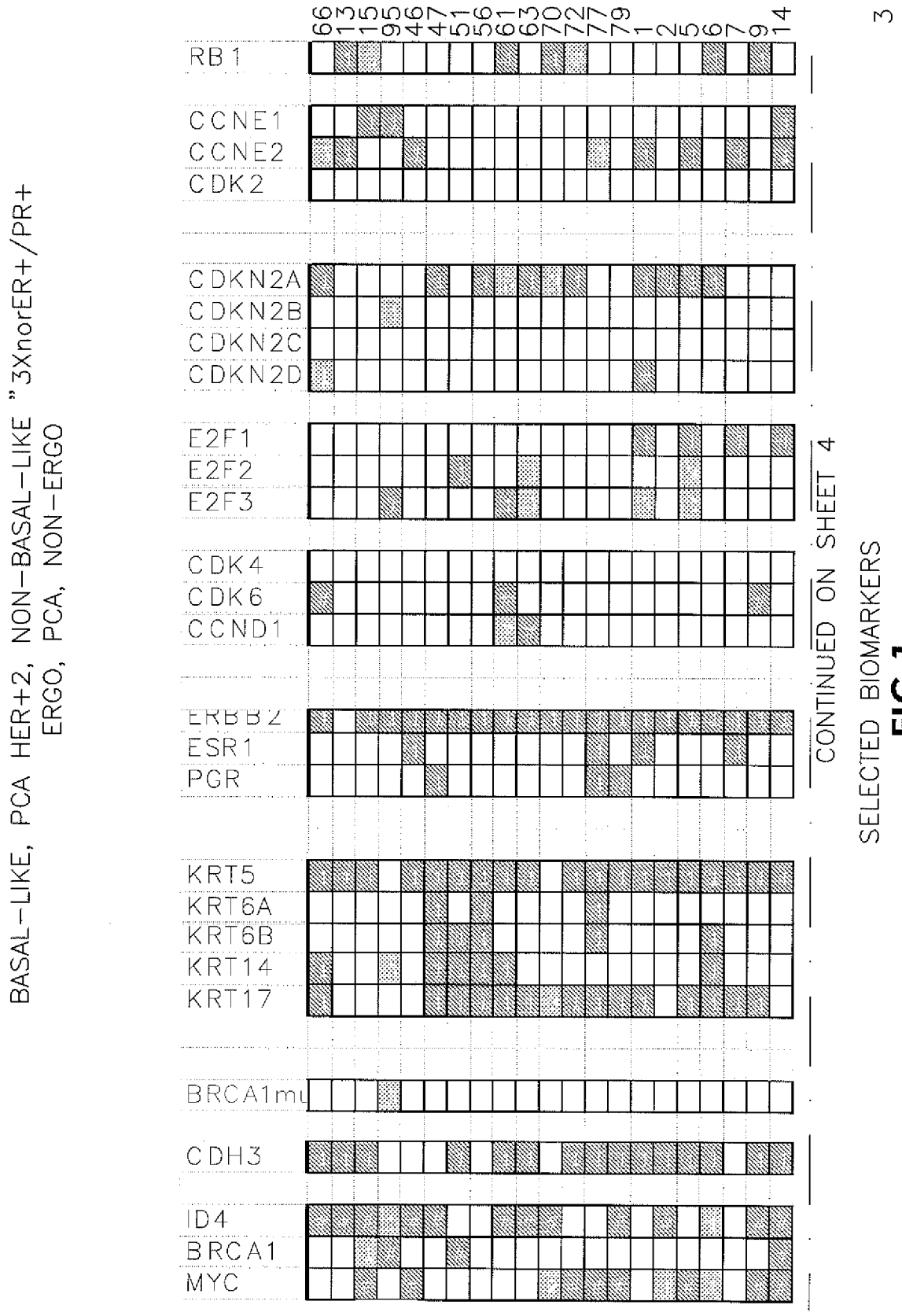

BASAL-LIKE, PCA HER+2, NON-BASAL-LIKE "3XnorER+/PR+
ERGO, PCA, NON-ERGO
66 13 15 95 46 47 51 56 61 63 70 72 77 79 1 2 5 6 7 9 14
RB1
CCNE1
CCNE2
CDK2
CDKN2A
CDKN2B
CDKN2C
CDKN2D
E2F1
E2F2
E2F3
CDK4
CDK6
CCND1
ERBB2
ESR1
PGR
KRT5
KRT6A
KRT6B
KRT14
KRT17
BRCA1mu
CDH3
ID4
BRCA1
MYC
CONTINUED ON SHEET 4
SELECTED BIOMARKERS
3

FIG. 1

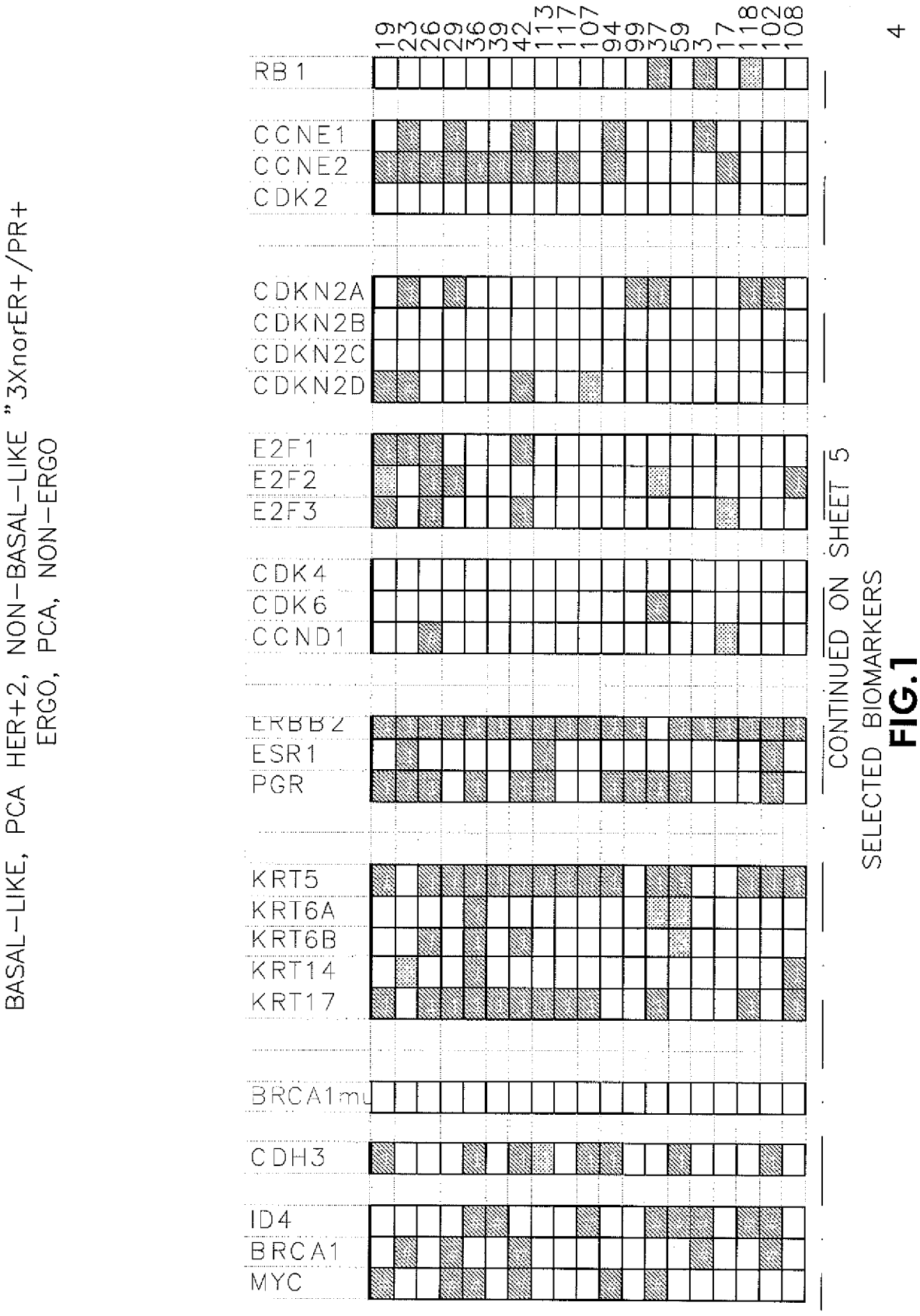

BASAL-LIKE, PCA HER+2, NON-BASAL-LIKE "3XnorER+/PR+
ERGO, PCA, NON-ERGO
19 23 26 29 36 39 42 113 117 107 94 99 37 59 3 17 118 102 108
RB1
CCNE1
CCNE2
CDK2
CDKN2A
CDKN2B
CDKN2C
CDKN2D
E2F1
E2F2
E2F3
CDK4
CDK6
CCND1
ERBB2
ESR1
PGR
KRT5
KRT6A
KRT6B
KRT14
KRT17
BRCA1mu
CDH3
ID4
BRCA1
MYC
CONTINUED ON SHEET 5
SELECTED BIOMARKERS

FIG.1

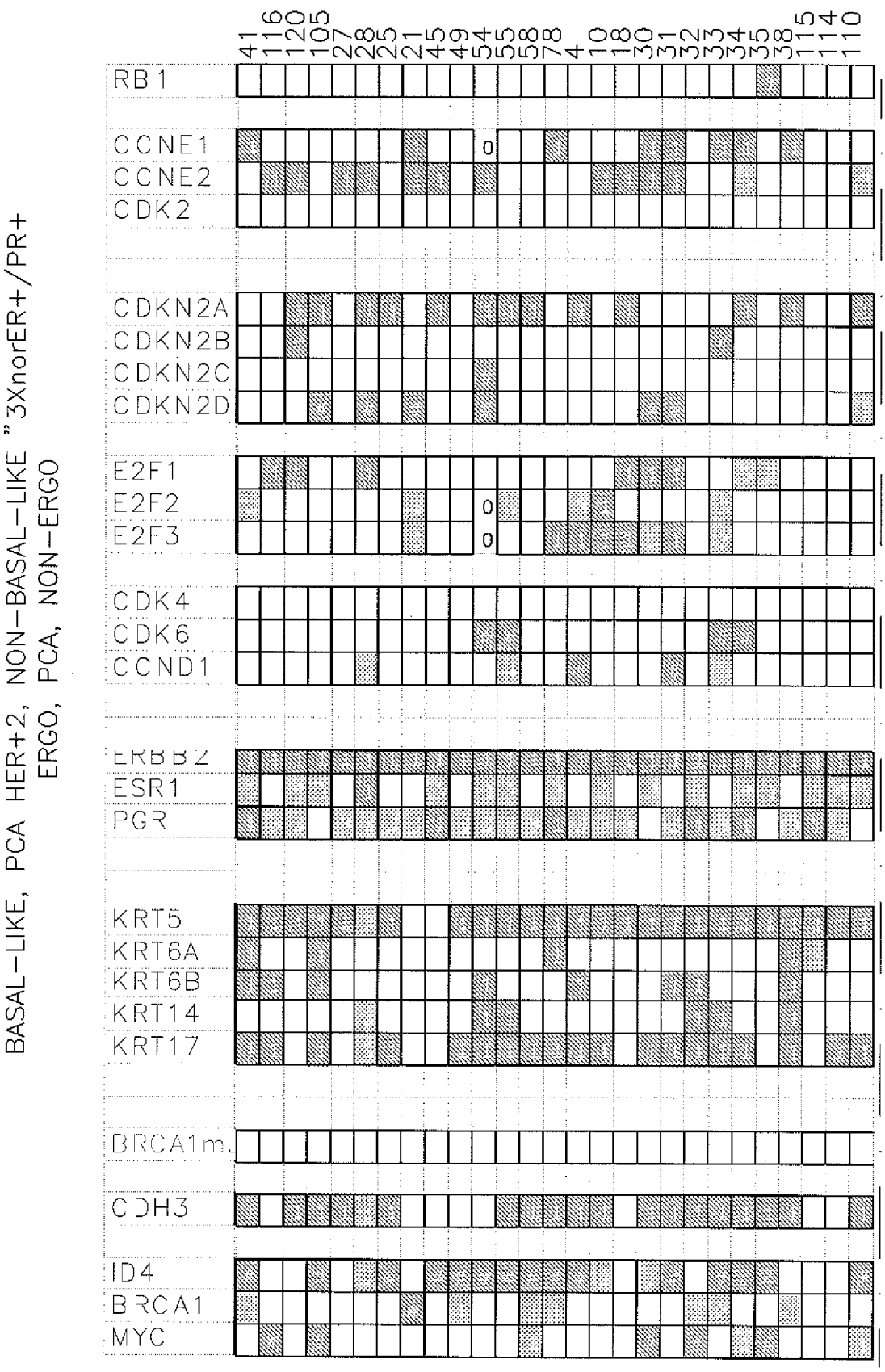

BASAL-LIKE, PCA HER+2, NON-BASAL-LIKE "3XnorER+/PR+
ERGO, PCA, NON-ERGO
41 116 120 105 27 28 25 21 45 49 54 55 58 78 4 10 18 30 31 32 33 34 35 38 115 114 110
RB1
CCNE1
CCNE2
CDK2
CDKN2A
CDKN2B
CDKN2C
CDKN2D
E2F1
E2F2
E2F3
CDK4
CDK6
CCND1
ERBB2
ESR1
PGR
KRT5
KRT6A
KRT6B
KRT14
KRT17
BRCA1mL
CDH3
ID4
BRCA1
MYC
END OF ROW
SELECTED BIOMARKERS

FIG.1

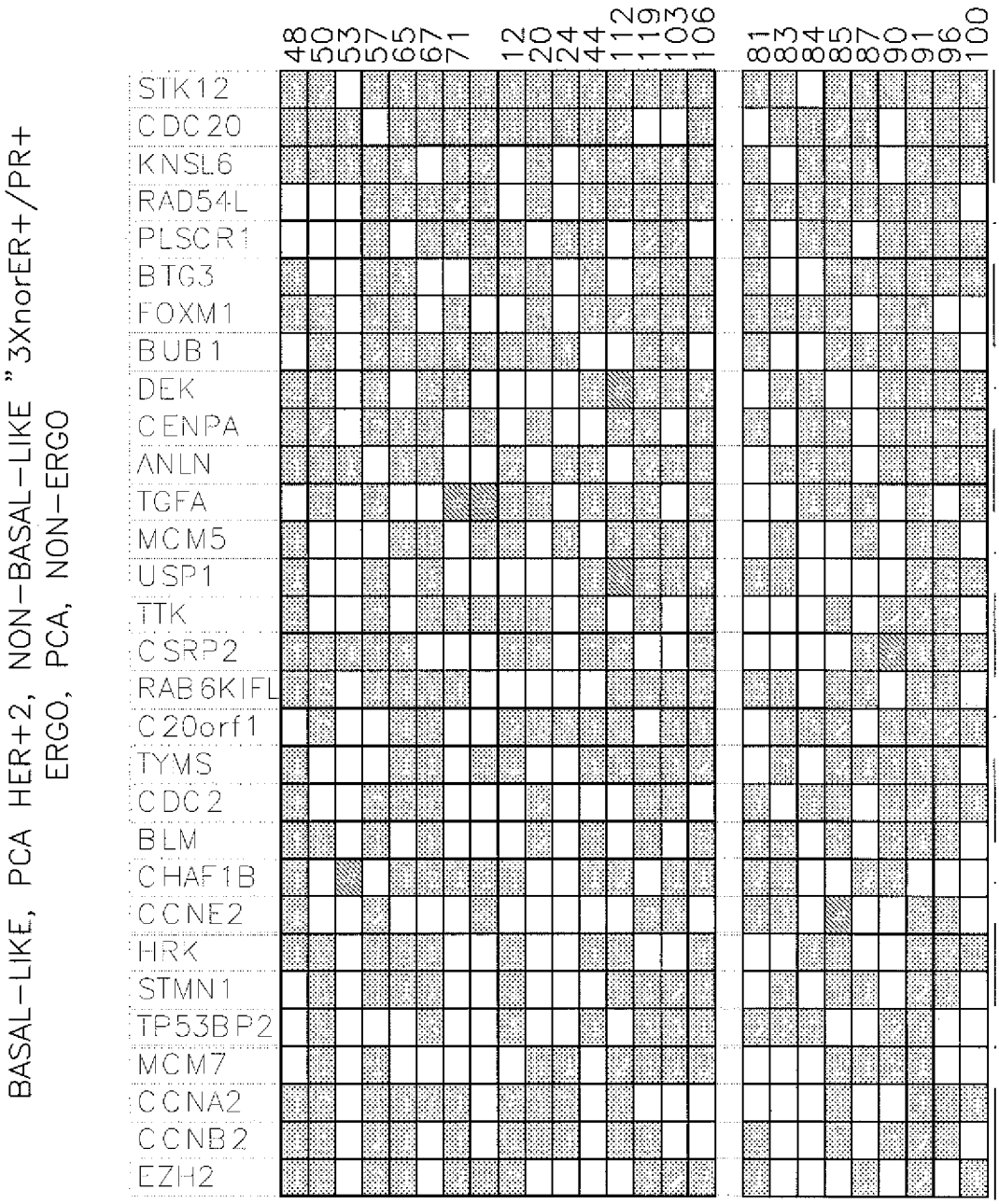

BASAL-LIKE, PCA HER+2, NON-BASAL-LIKE "3XnorER+/PR+
ERGO, PCA, NON-ERGO
48 50 53 57 65 67 71 12 20 24 44 112 119 103 106 81 83 84 85 87 90 91 96 100
STK12
CDC20
KNSL6
RAD54L
PLSCR1
BTG3
FOXM1
BUB1
DEK
CENPA
ANLN
TGFA
MCM5
USP1
TTK
CSRP2
RAB6KIFL
C20orf1
TYMS
CDC2
BLM
CHAF1B
CCNE2
HRK
STMN1
TP53BP2
MCM7
CCNA2
CCNB2
EZH2
CONTINUED ON SHEET 7
TOP 30 OVEREXPRESSED ERGO GENES

FIG.1

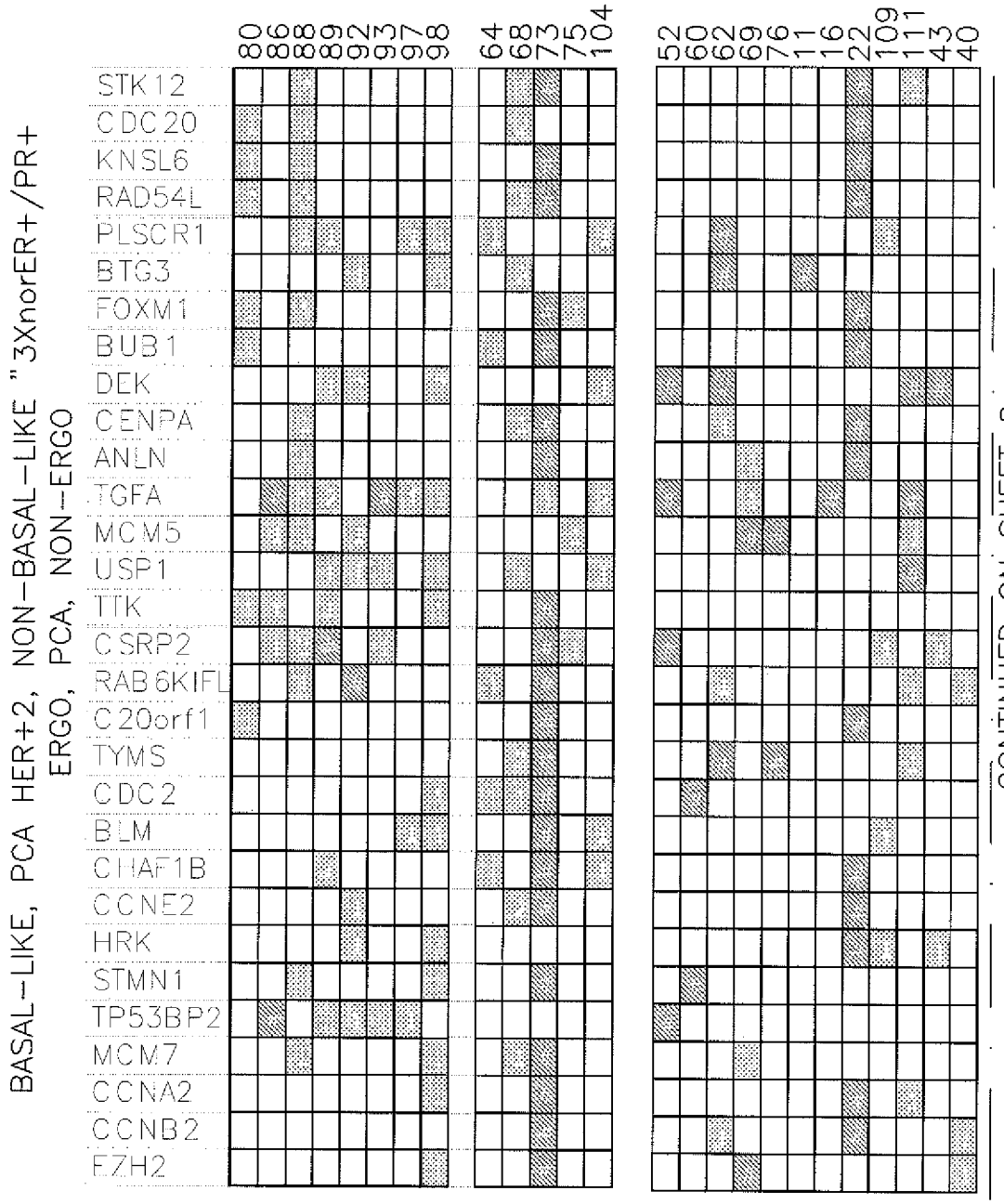
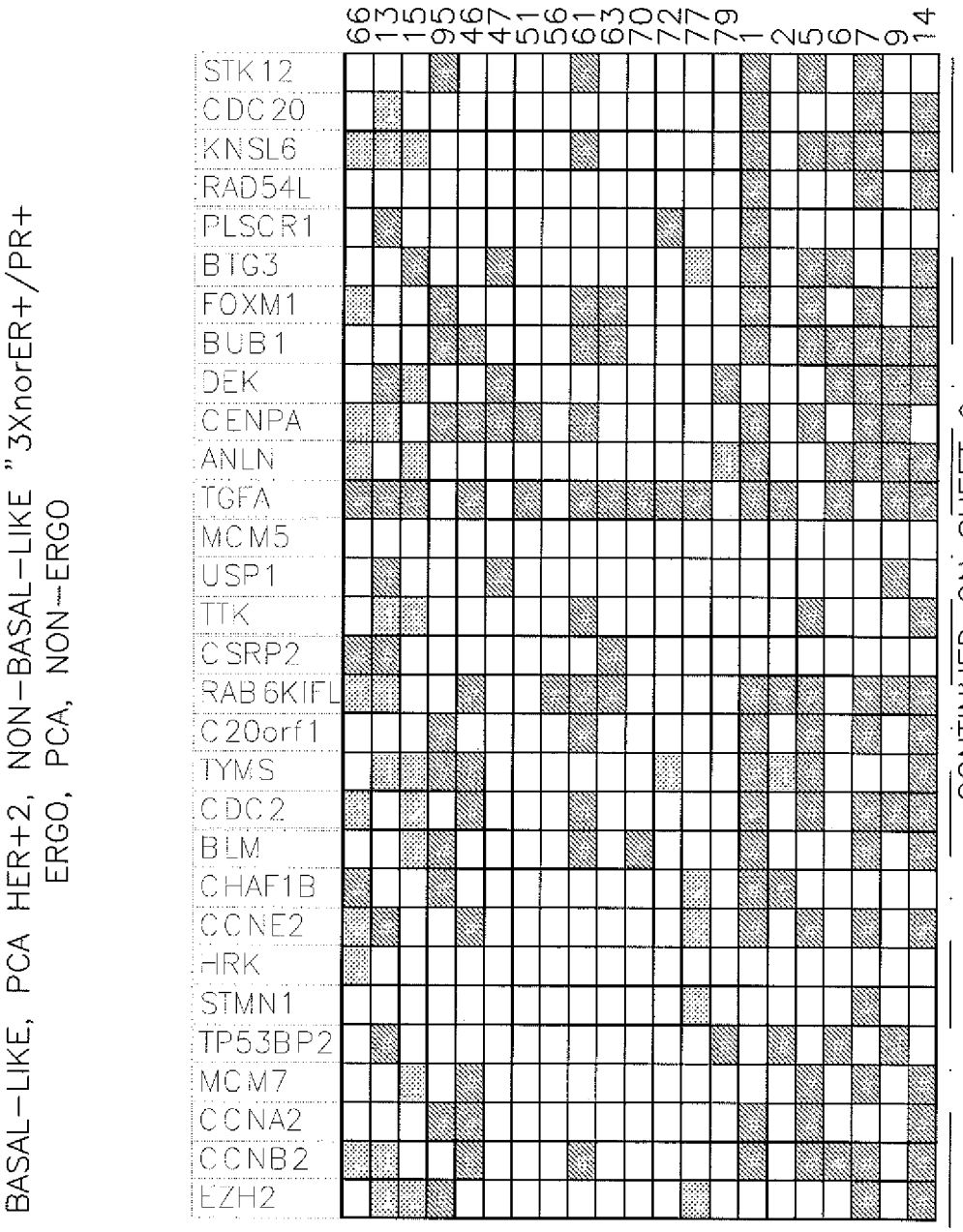

BASAL-LIKE, PCA HER+2, NON-BASAL-LIKE "3XnorER+/PR+
ERGO, PCA, NON-ERGO
80 86 88 89 92 93 97 98 64 68 73 75 104 52 60 62 69 76 11 16 22 109 111 43 40
STK12
CDC20
KNSL6
RAD54L
PLSCR1
BTG3
FOXM1
BUB1
DEK
CENPA
ANLN
TGFA
MCM5
USP1
TTK
CSRP2
RAB6KIFL
C20orf1
TYMS
CDC2
BLM
CHAF1B
CCNE2
HRK
STMN1
TP53BP2
MCM7
CCNA2
CCNB2
EZH2
CONTINUED ON SHEET 8
TOP 30 OVEREXPRESSED ERGO GENES

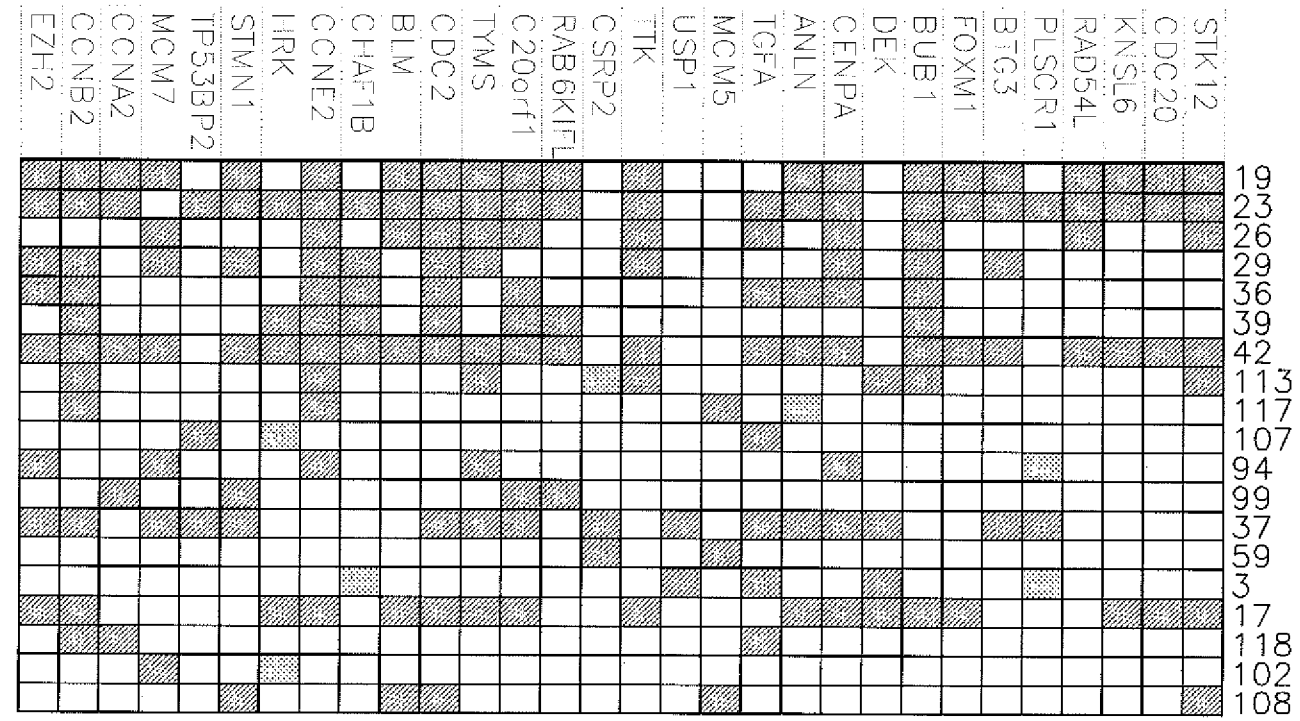
FIG.1



TOP 30 OVEREXPRESSED ERGO GENES

FIG.1

BASAL–LIKE, PCA HER+2, NON–BASAL–LIKE "3XnorER+/PR+
ERGO, PCA, NON–ERGO



CONTINUED ON SHEET 10

TOP 30 OVEREXPRESSED ERGO GENES

FIG.1

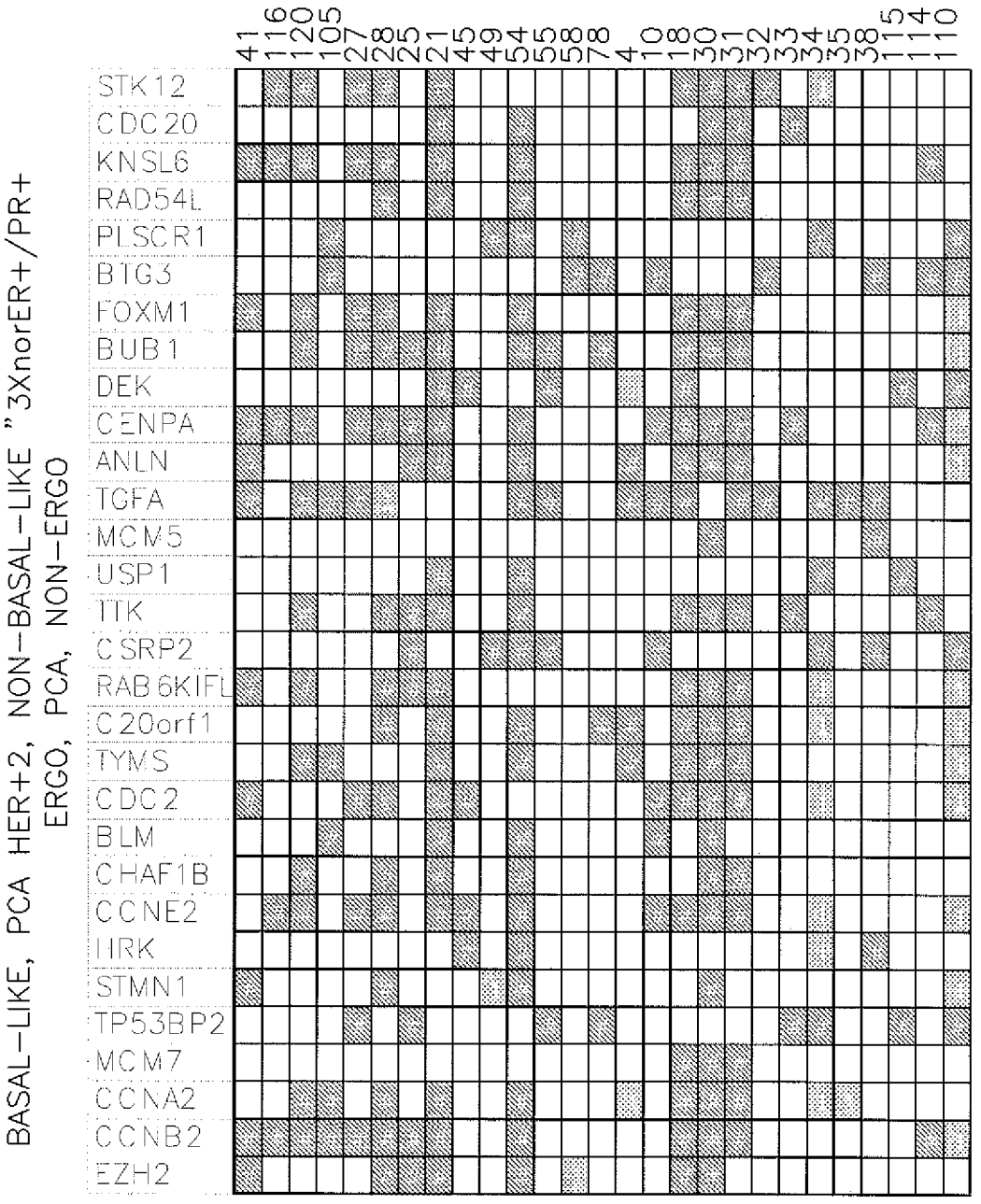
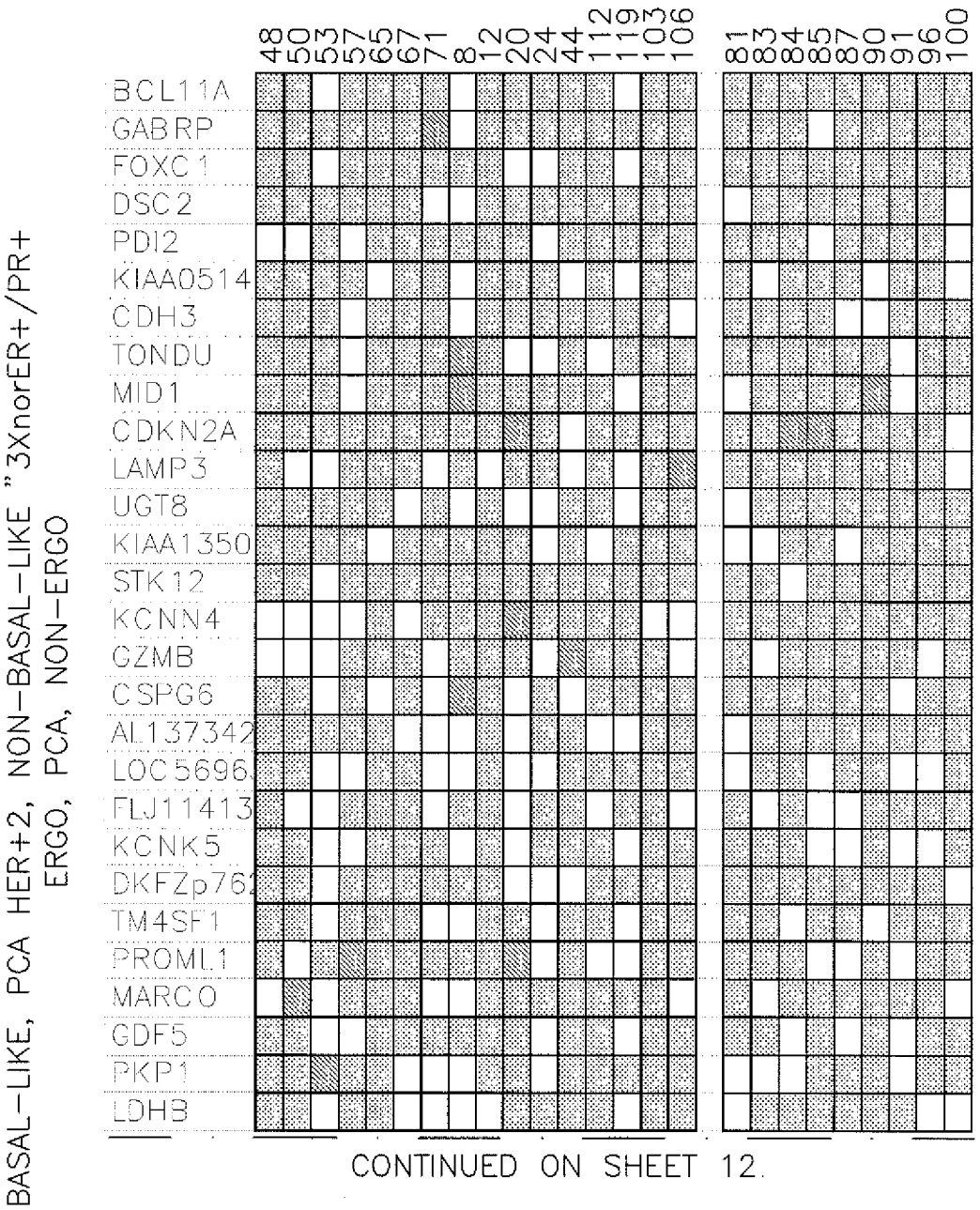

BASAL-LIKE, PCA HER+2, NON-BASAL-LIKE "3XnorER+/PR+
ERGO, PCA, NON-ERGO
41 116 120 105 27 28 25 21 45 49 54 55 58 78 4 10 18 30 31 32 33 34 35 38 115 114 110
STK12
CDC20
KNSL6
RAD54L
PLSCR1
BTG3
FOXM1
BUB1
DEK
CENPA
ANLN
TGFA
MCM5
USP1
ITK
CSRP2
RAB6KIFL
C20orf1
TYMS
CDC2
BLM
CHAF1B
CCNE2
IIRK
STMN1
TP53BP2
MCM7
CCNA2
CCNB2
EZH2
END OF ROW
TOP 30 OVEREXPRESSED ERGO GENES

FIG.1

10



TOP 50 OVEREXPRESSED BASAL-LIKE GENES

FIG.1

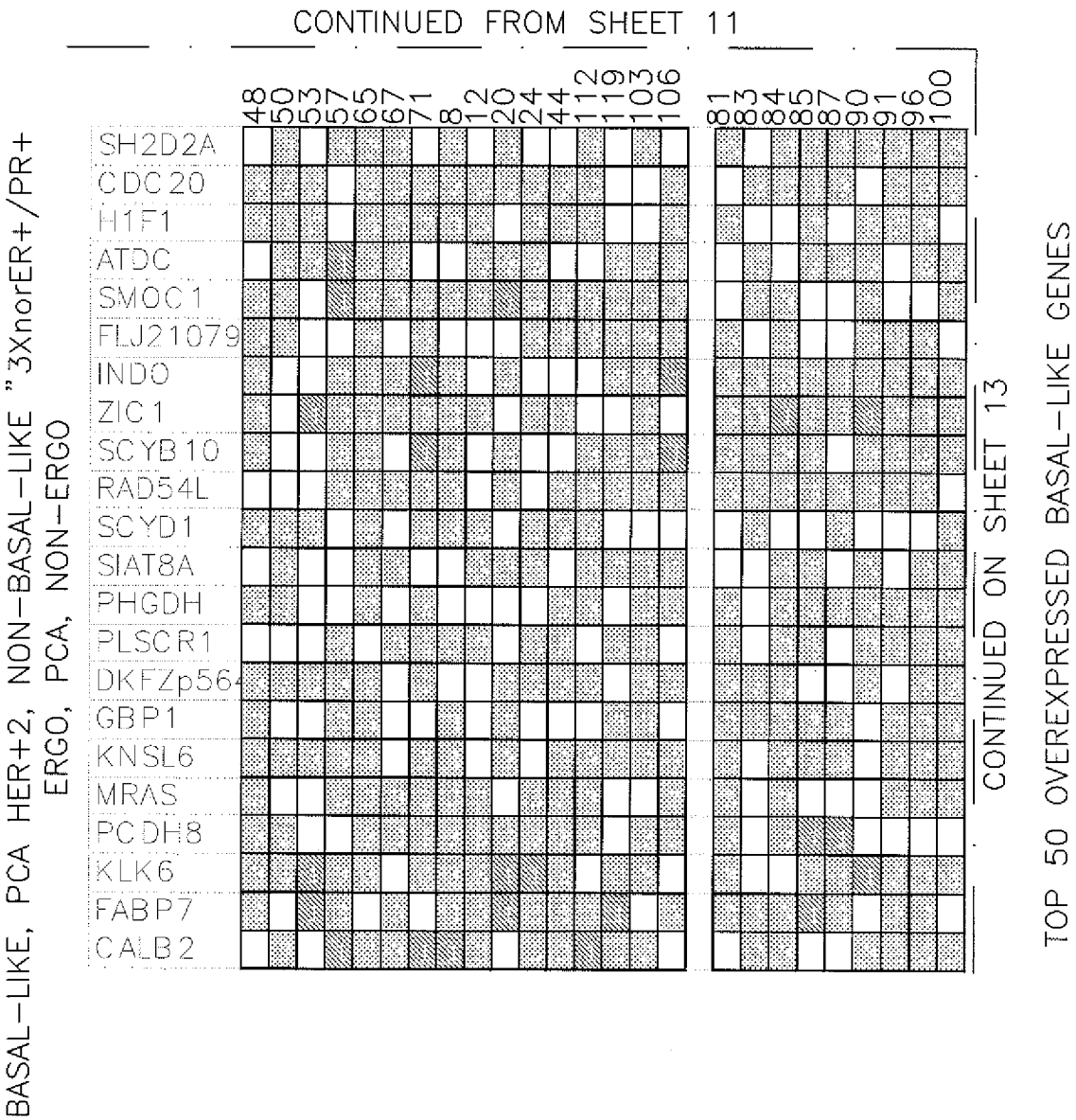
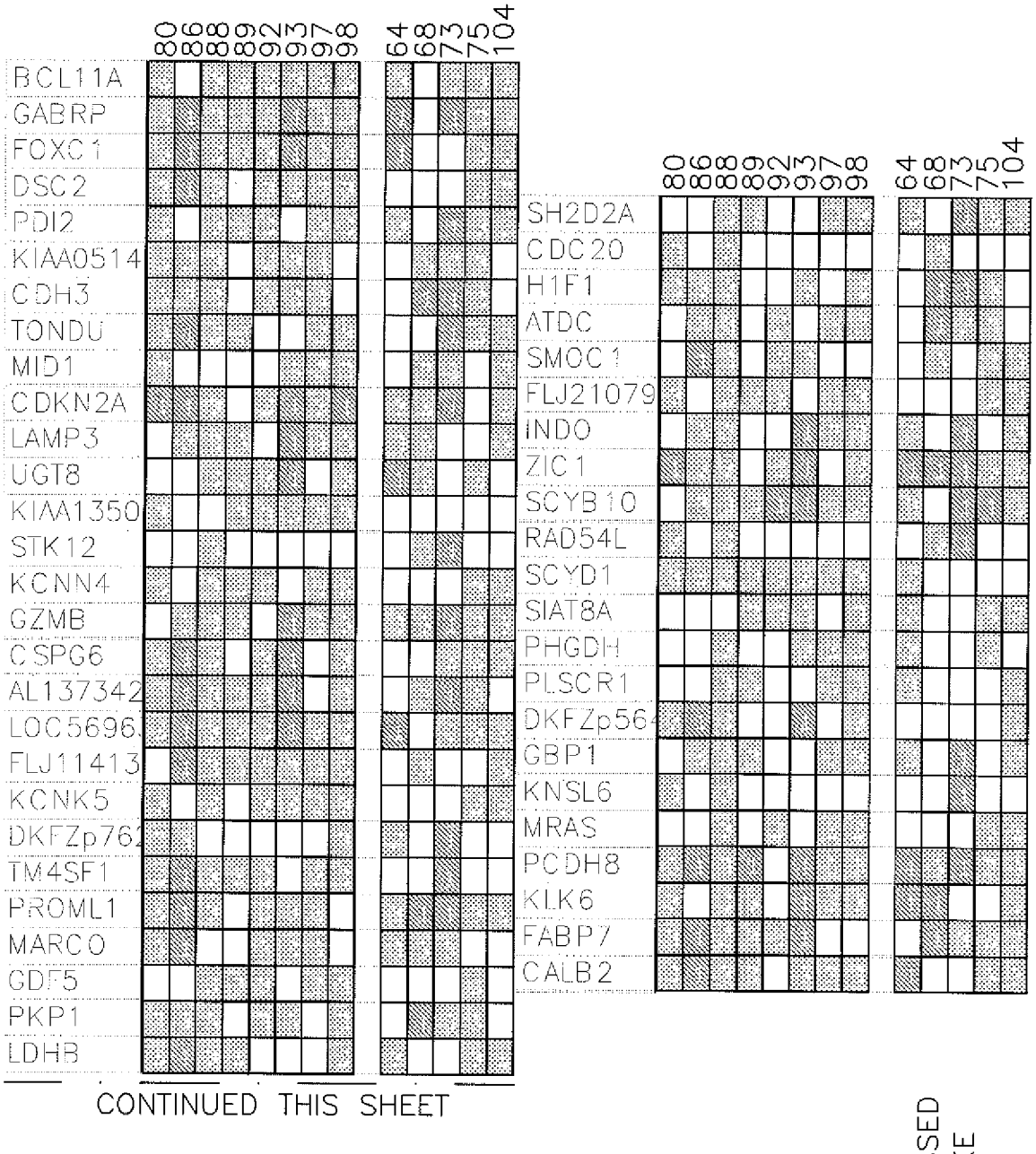

CONTINUED FROM SHEET 11
BASAL-LIKE, PCA HER+2, NON-BASAL-LIKE "3XnorER+/PR+ ERGO, PCA, NON-ERGO
48 50 53 57 65 67 71 8 12 20 24 44 112 119 103 106 81 83 84 85 87 90 91 96 100
SH2D2A
CDC20
H1F1
ATDC
SMOC1
FLJ21079
INDO
ZIC1
SCYB10
RAD54L
SCYD1
SIAT8A
PHGDH
PLSCR1
DKFZp564
GBP1
KNSL6
MRAS
PCDH8
KLK6
FABP7
CALB2
CONTINUED ON SHEET 13
TOP 50 OVEREXPRESSED BASAL-LIKE GENES

FIG.1



TOP 50 OVEREXPRESSED BASAL-LIKE GENES

FIG.1

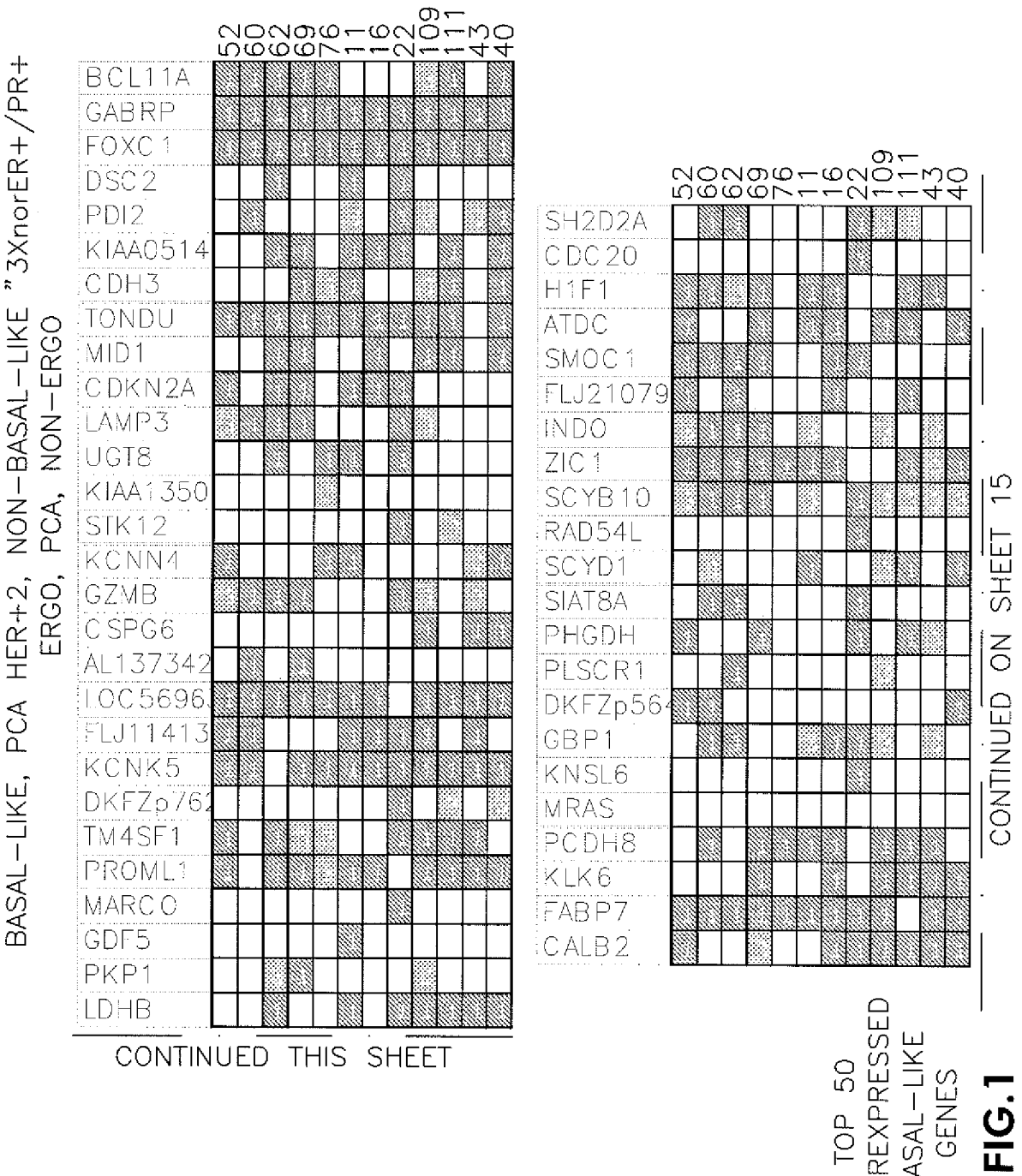

BASAL-LIKE, PCA HER+2, NON-BASAL-LIKE "3XnorER+/PR+
ERGO, PCA, NON-ERGO
52 60 62 69 76 11 16 22 109 111 43 40
BCL11A
GABRP
FOXC1
DSC2
PDI2
KIAA0514
CDH3
TONDU
MID1
CDKN2A
LAMP3
UGT8
KIAA1350
STK12
KCNN4
GZMB
CSPG6
AL137342
IOC5696
FLJ11413
KCNK5
DKFZp762
TM4SF1
PROML1
MARCO
GDF5
PKP1
LDHB
CONTINUED THIS SHEET
SH2D2A
CDC20
H1F1
ATDC
SMOC1
FLJ21079
INDO
ZIC1
SCYB10
RAD54L
SCYD1
SIAT8A
PHGDH
PLSCR1
DKFZp564
GBP1
KNSL6
MRAS
PCDH8
KLK6
FABP7
CALB2
CONTINUED ON SHEET 15
TOP 50 OVEREXPRESSED BASAL-LIKE GENES

FIG.1

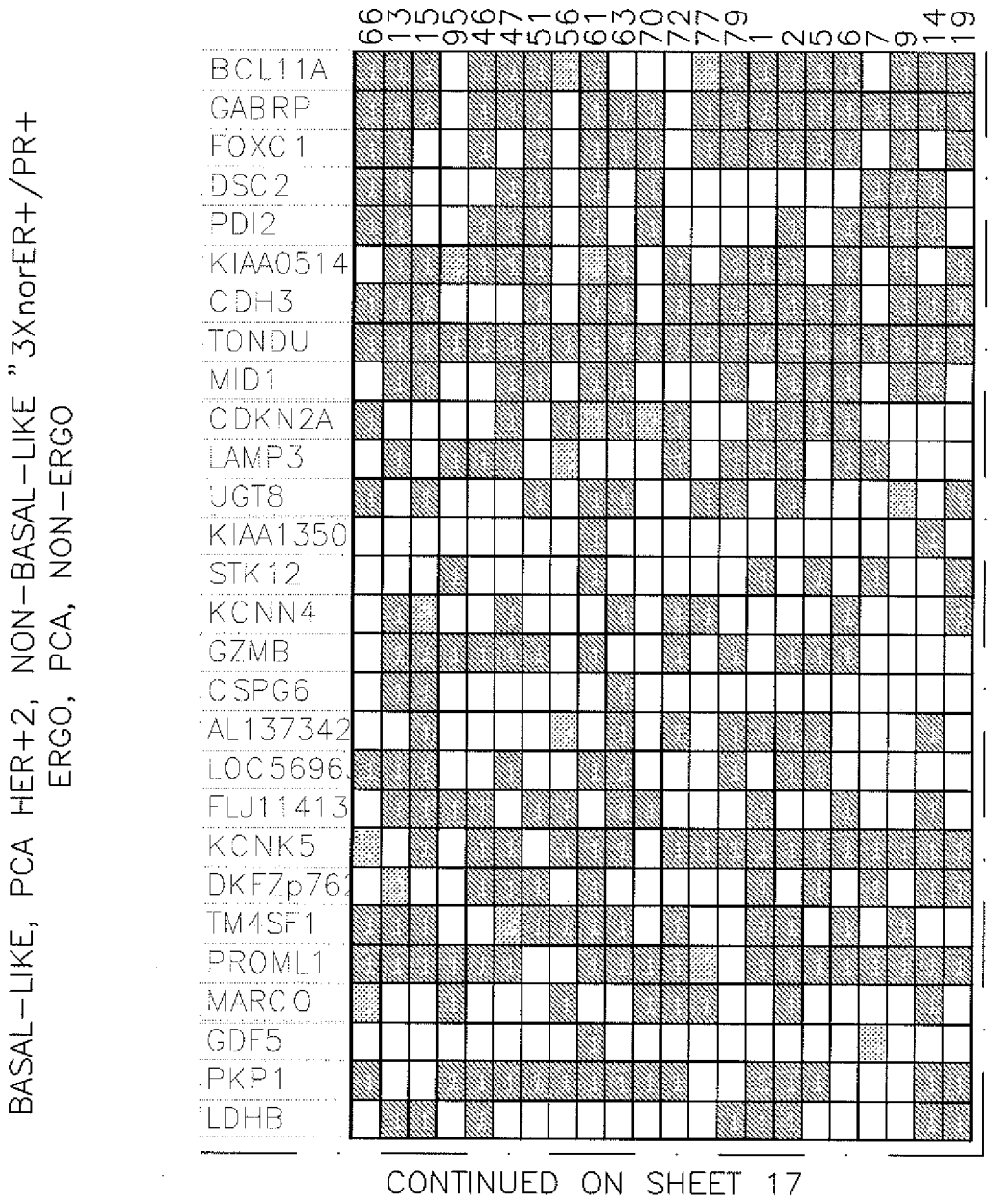
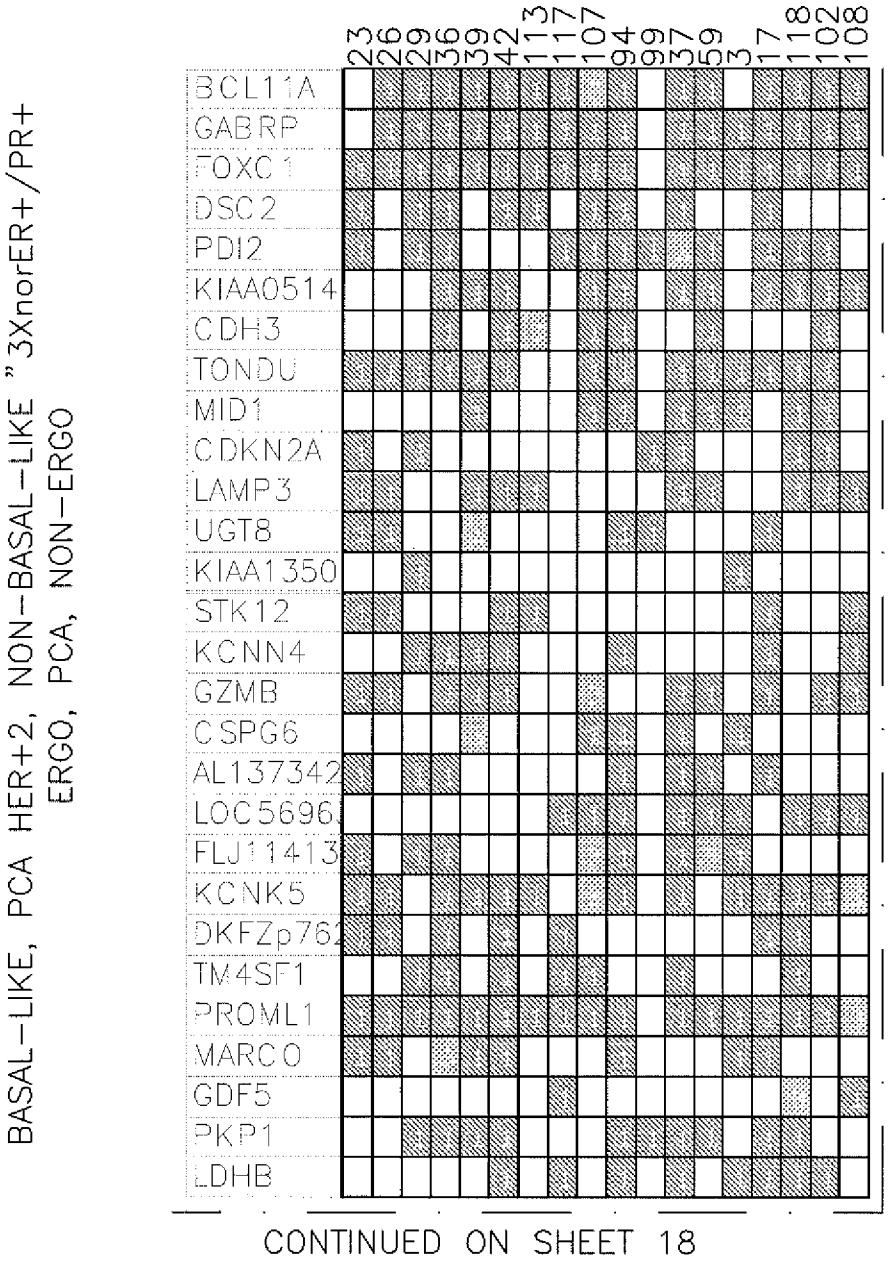

BASAL-LIKE, PCA HER+2, NON-BASAL-LIKE "3XnorER+/PR+
ERGO, PCA, NON-ERGO
66 13 15 95 46 47 51 56 61 63 70 72 77 79 1 2 5 6 7 9 14 19
BCL11A
GABRP
FOXC1
DSC2
PDI2
KIAA0514
CDH3
TONDU
MID1
CDKN2A
LAMP3
UGT8
KIAA1350
STK12
KCNN4
GZMB
CSPG6
AL137342
LOC5696
FLJ11413
KCNK5
DKFZp76
TM4SF1
PROML1
MARCO
GDF5
PKP1
LDHB
CONTINUED ON SHEET 16
CONTINUED ON SHEET 17
TOP 50 OVEREXPRESSED BASAL-LIKE GENES

FIG.1



TOP 50 OVEREXPRESSED BASAL-LIKE GENES

FIG.1

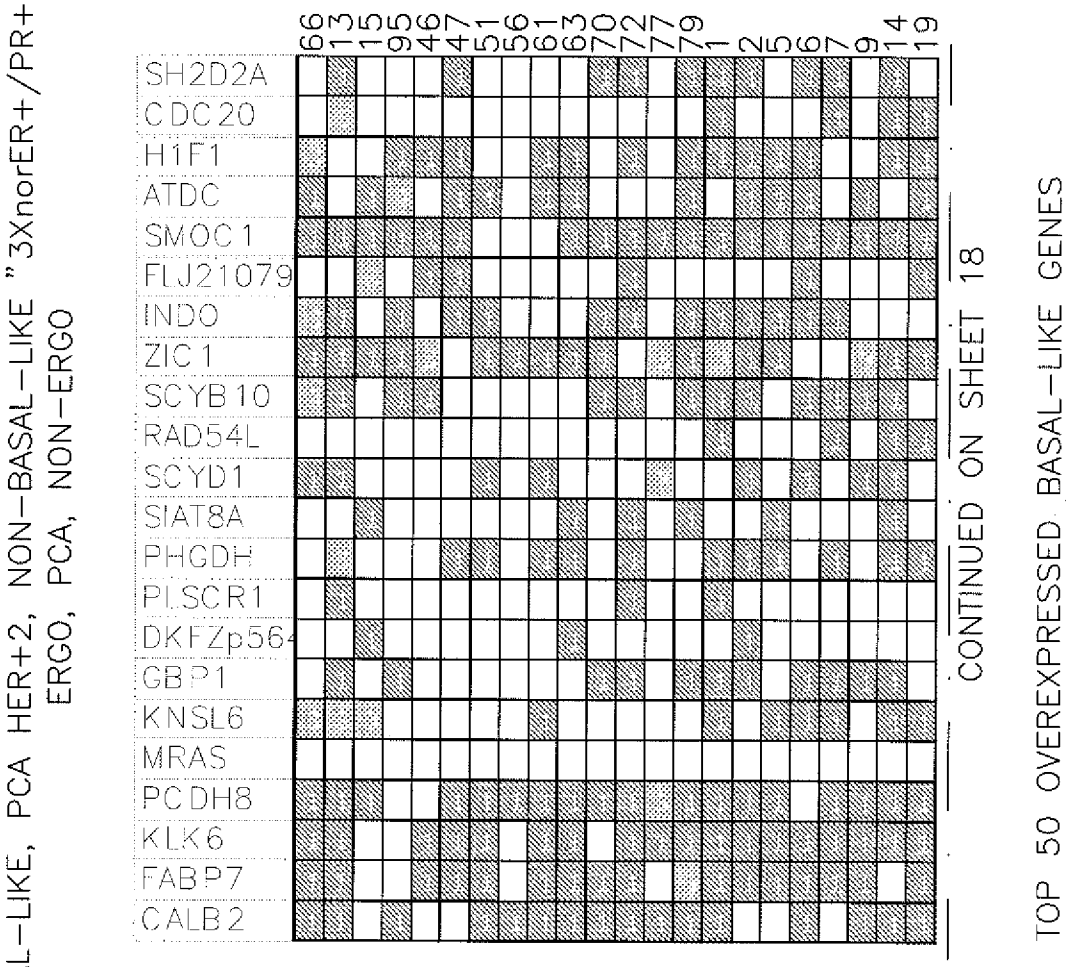
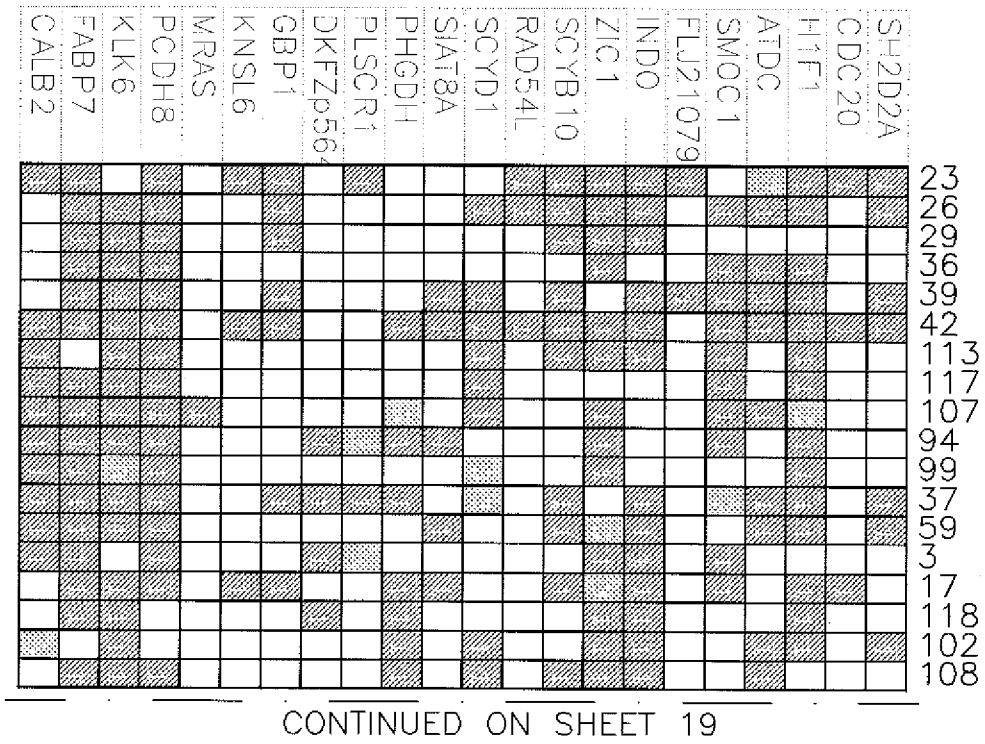

BASAL-LIKE, PCA HER+2, NON-BASAL-LIKE "3XnorER+/PR+
ERGO, PCA, NON-ERGO
66 13 15 95 46 47 51 56 61 63 70 72 77 79 1 2 5 6 7 9 14 19
SH2D2A
CDC20
H1F1
ATDC
SMOC1
FLJ21079
INDO
ZIC1
SCYB10
RAD54L
SCYD1
SIAT8A
PHGDH
PLSCR1
DKFZp56
GBP1
KNSL6
MRAS
PCDH8
KLK6
FABP7
CALB2
CONTINUED ON SHEET 18
TOP 50 OVEREXPRESSED BASAL-LIKE GENES

FIG.1

BASAL–LIKE, PCA HER+2, NON–BASAL–LIKE "3XnorER+/PR+
ERGO, PCA, NON–ERGO



CONTINUED ON SHEET 19

TOP 50 OVEREXPRESSED BASAL–LIKE GENES

FIG.1

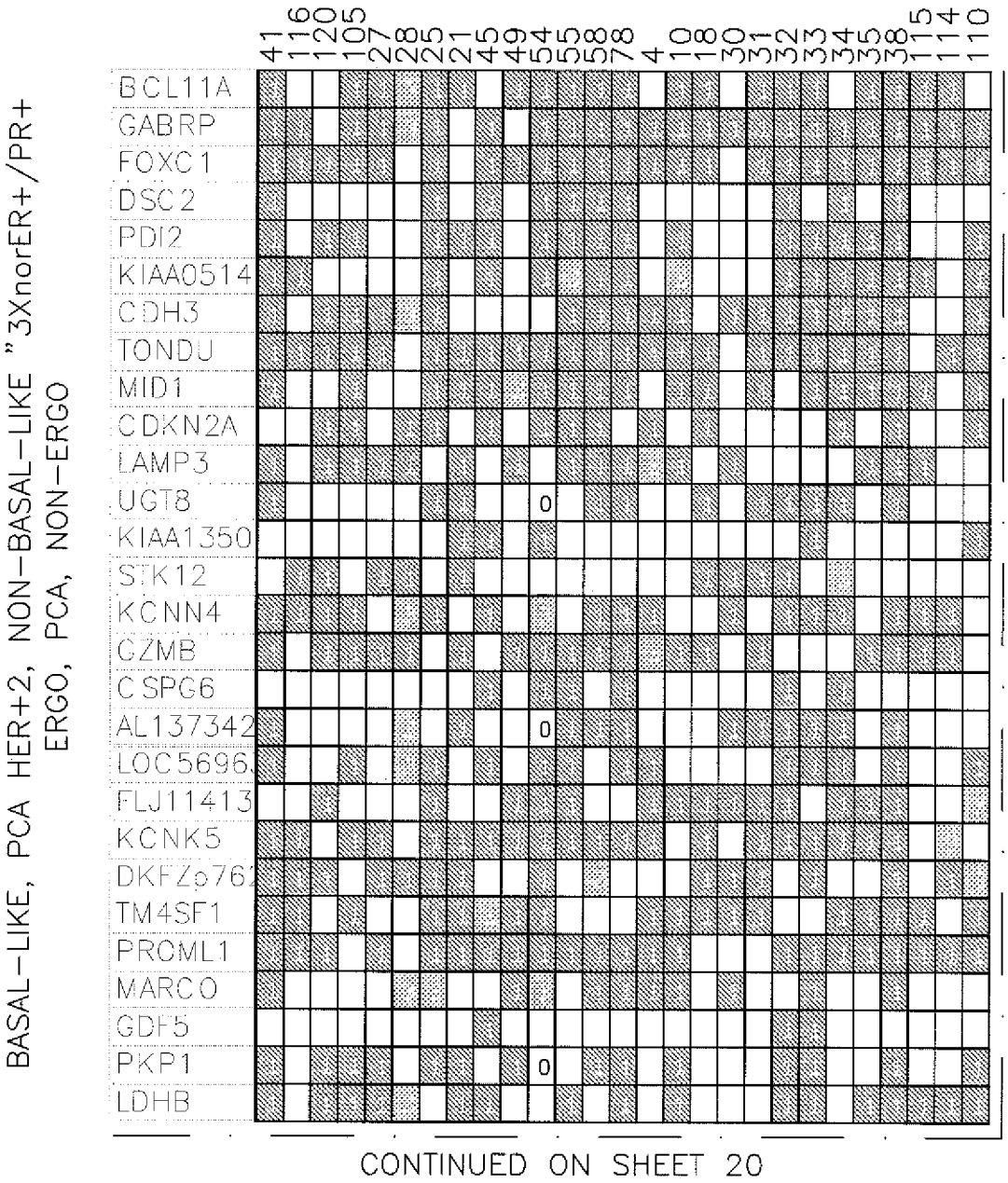

BASAL-LIKE, PCA HER+2, NON-BASAL-LIKE "3XnorER+/PR+
ERGO, PCA, NON-ERGO
41 116 120 105 27 28 25 21 45 49 54 55 58 78 4 10 18 30 31 32 33 34 35 38 115 114 110
BCL11A
GABRP
FOXC1
DSC2
PDI2
KIAA0514
CDH3
TONDU
MID1
CDKN2A
LAMP3
UGT8
KIAA1350
STK12
KCNN4
CZMB
CSPG6
AL137342
LOC5696
FLJ11413
KCNK5
DKFZp76
TM4SF1
PROML1
MARCO
GDF5
PKP1
LDHB
0
0
0
END OF ROW
TOP 50 OVEREXPRESSED BASAL-LIKE GENES
CONTINUED ON SHEET 20

FIG.1

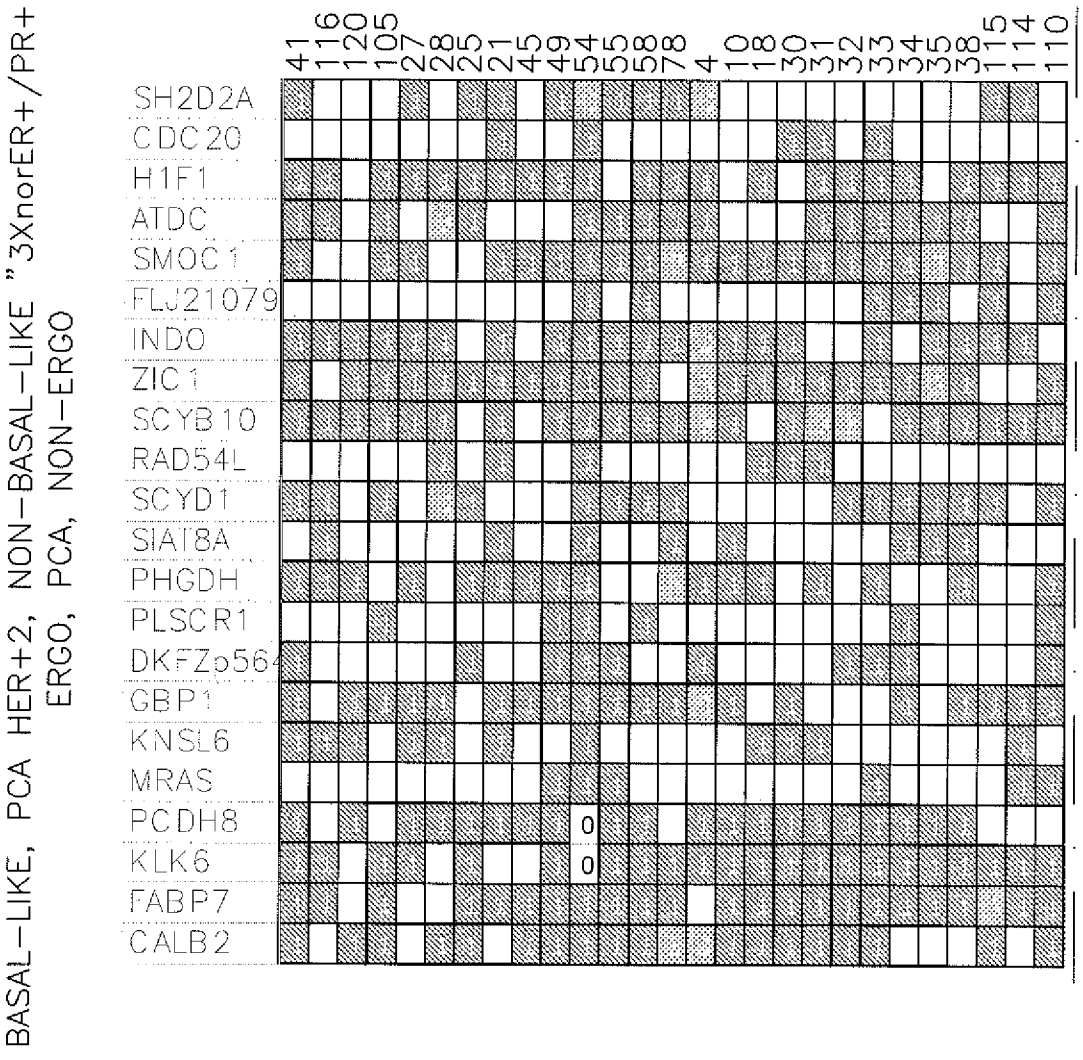

BASAL-LIKE, PCA HER+2, NON-BASAL-LIKE "3XnorER+/PR+
ERGO, PCA, NON-ERGO
41 116 120 105 27 28 25 21 45 49 54 55 58 78 4 10 18 30 31 32 33 34 35 38 115 114 110
SH2D2A
CDC20
H1F1
ATDC
SMOC1
FLJ21079
INDO
ZIC1
SCYB10
RAD54L
SCYD1
SIAT8A
PHGDH
PLSCR1
DKFZp564
GBP1
KNSL6
MRAS
PCDH8
KLK6
FABP7
CALB2
END OF ROW
TOP 50 OVEREXPRESSED BASAL-LIKE GENES

FIG. 1

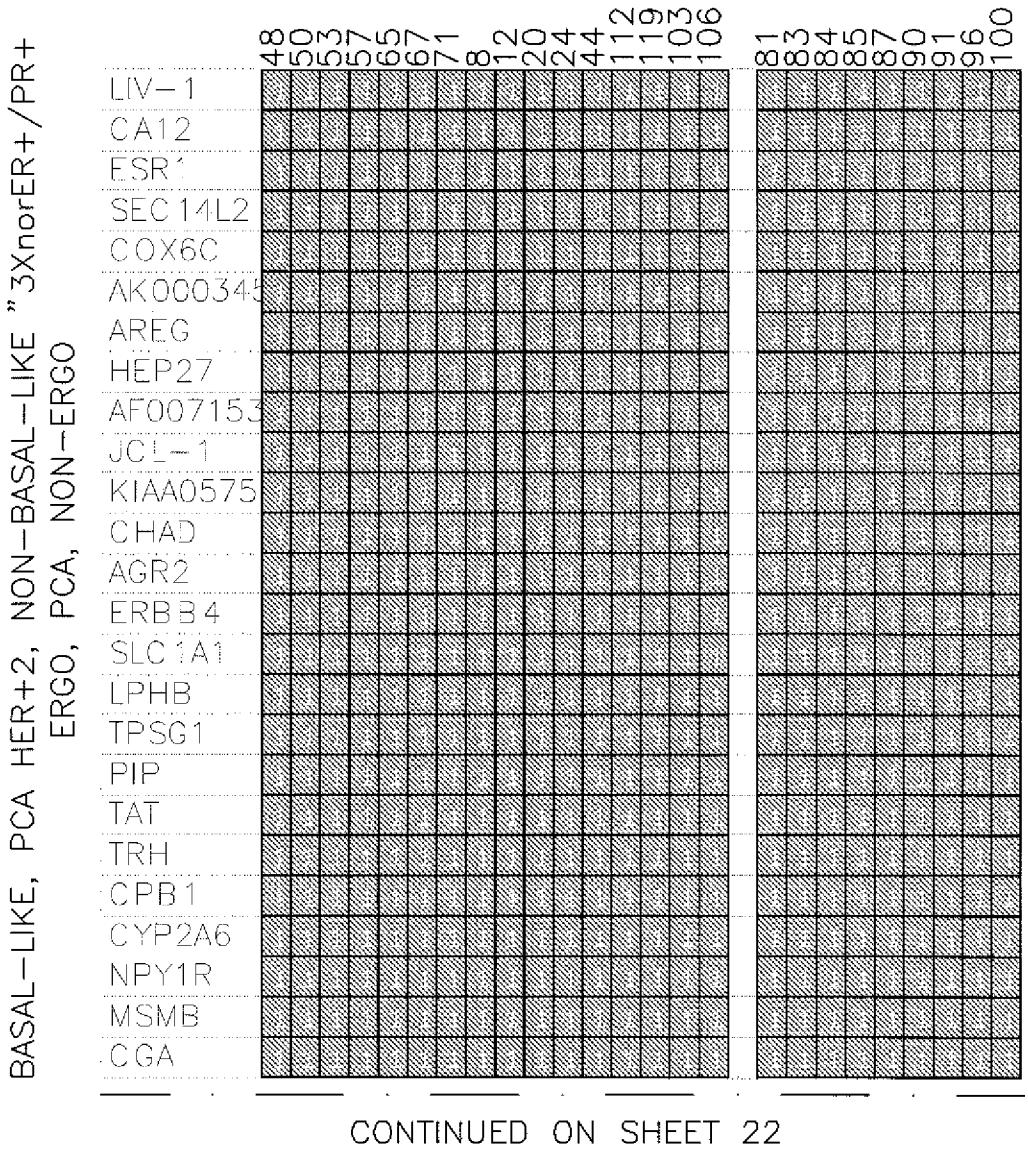
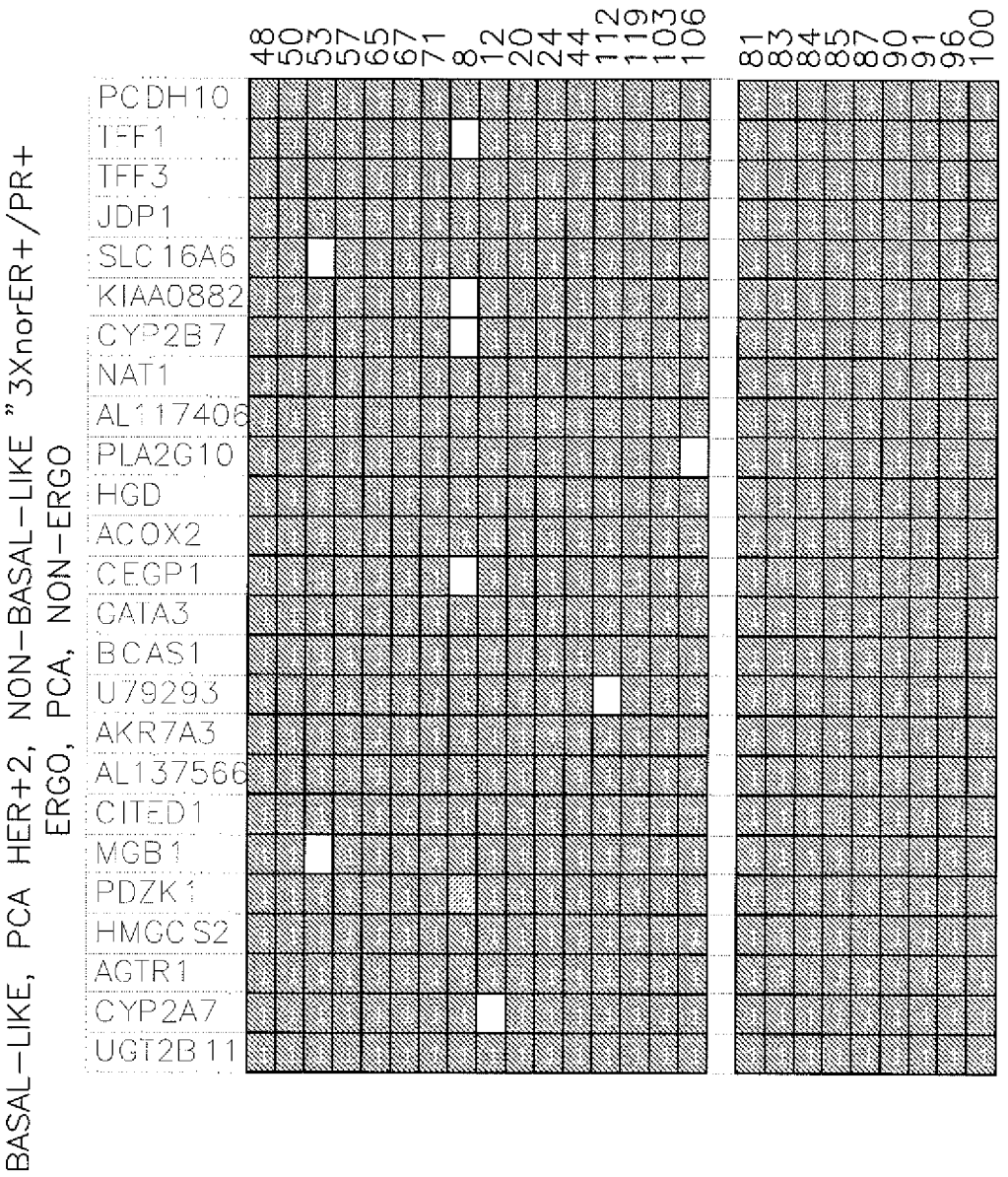


FIG.1

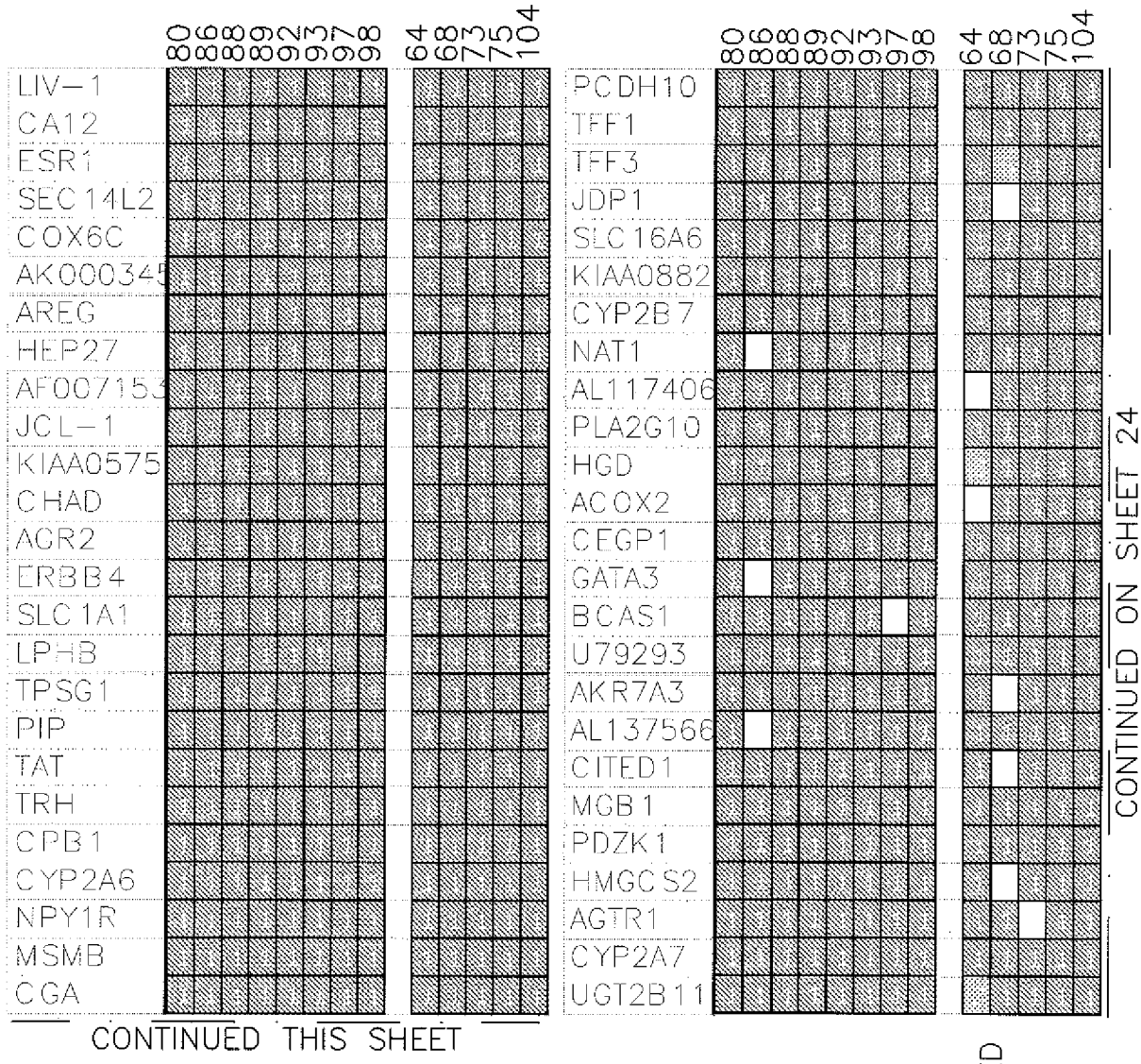
CONTINUED ON SHEET 22



TOP 50 UNDEREXPRESSED BASAL−LIKE GENES

FIG.1

BASAL–LIKE, PCA HER+2, NON–BASAL–LIKE "3XnorER+/PR+
ERGO, PCA, NON–ERGO



TOP 50 UNDEREXPRESSED BASAL–LIKE GENES

FIG.1

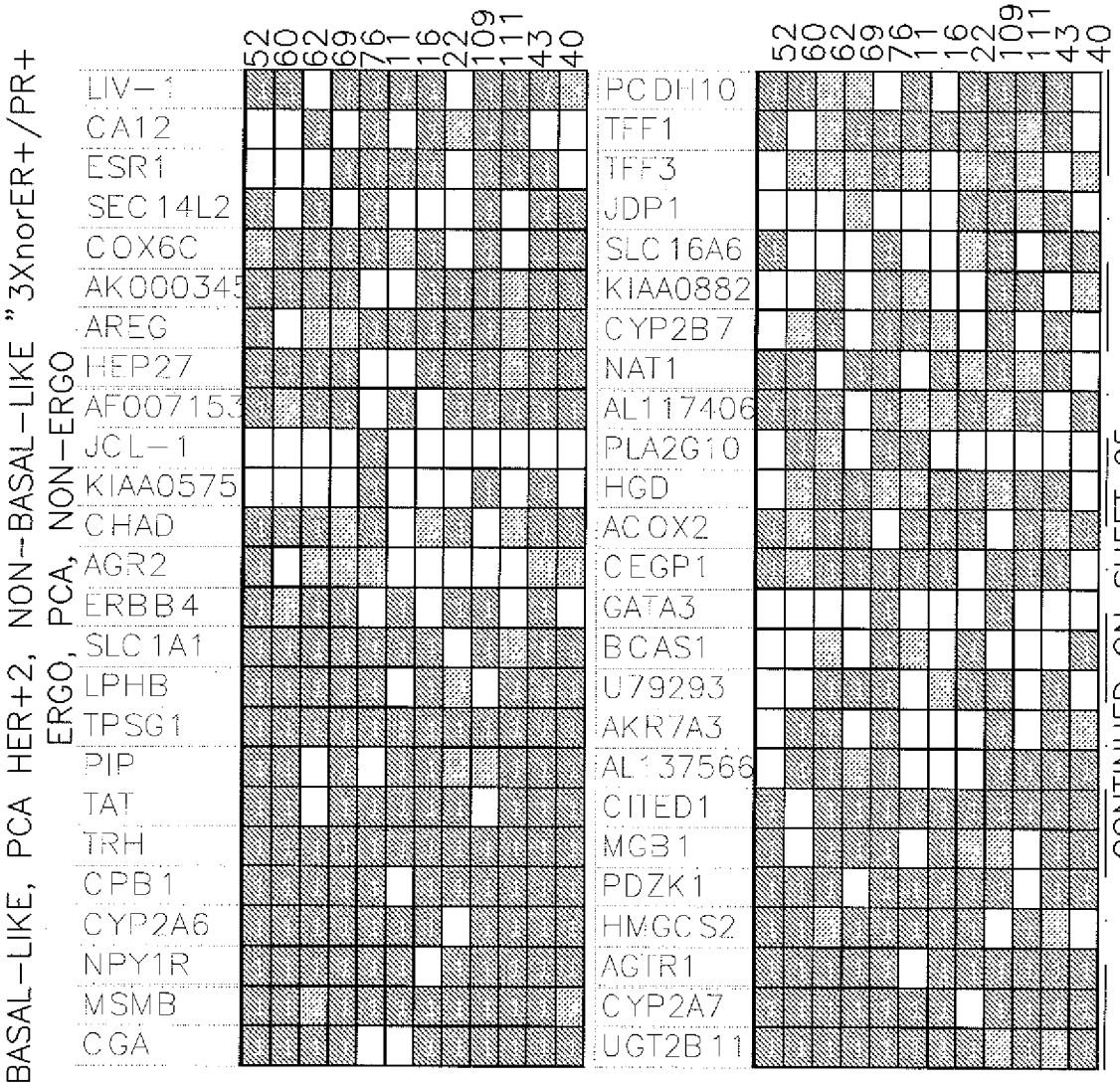
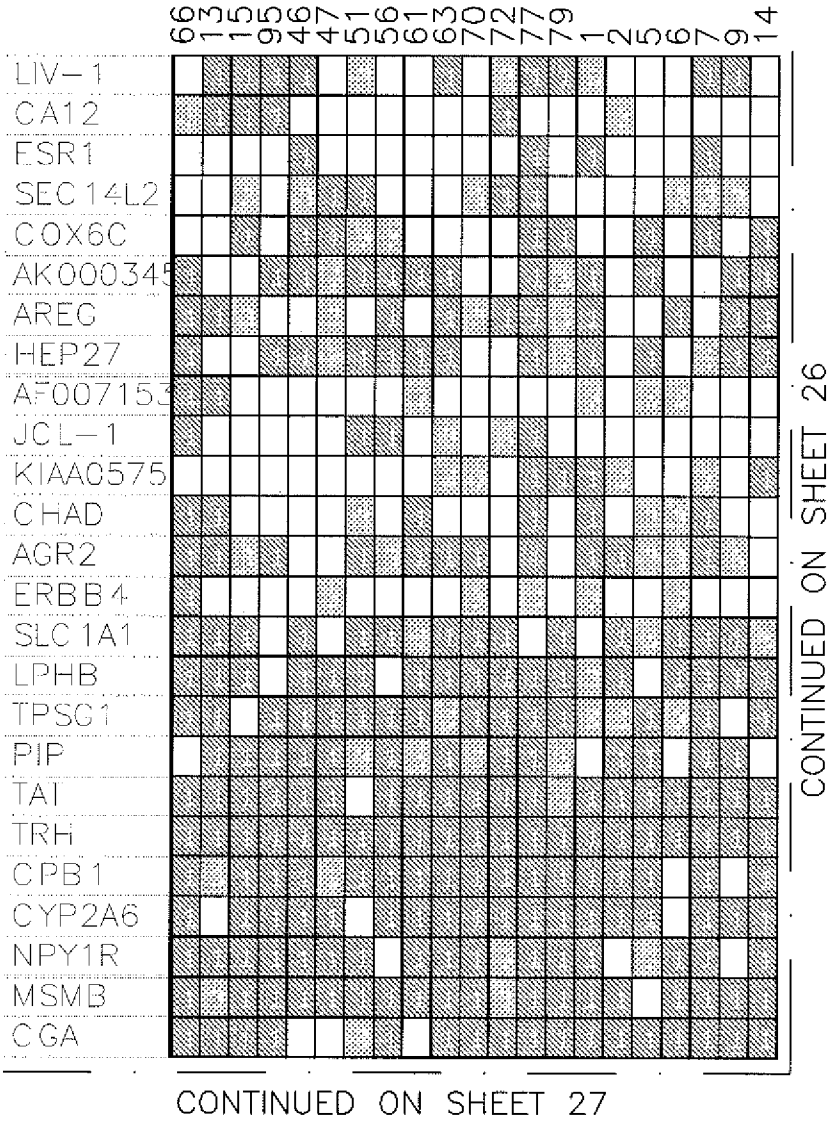

BASAL-LIKE, PCA HER+2, NON-BASAL-LIKE "3XnorER+/PR+ ERGO, PCA, NON-ERGO
52 60 62 69 76 11 16 22 109 111 43 40
LIV-1
CA12
ESR1
SEC14L2
COX6C
AK000345
AREG
HEP27
AF007153
JCL-1
KIAA0575
CHAD
AGR2
ERBB4
SLC1A1
LPHB
TPSG1
PIP
TAT
TRH
CPB1
CYP2A6
NPY1R
MSMB
CGA
PCDH10
TFF1
TFF3
JDP1
SLC16A6
KIAA0882
CYP2B7
NAT1
AL117406
PLA2G10
HGD
ACOX2
CEGP1
GATA3
BCAS1
U79293
AKR7A3
AL137566
CITED1
MGB1
PDZK1
HMGCS2
AGTR1
CYP2A7
UGT2B11
CONTINUED ON SHEET 25
TOP 50 UNDEREXPRESSED BASAL-LIKE GENES

FIG.1



TOP 50 UNDEREXPRESSED BASAL-LIKE GENES

FIG.1

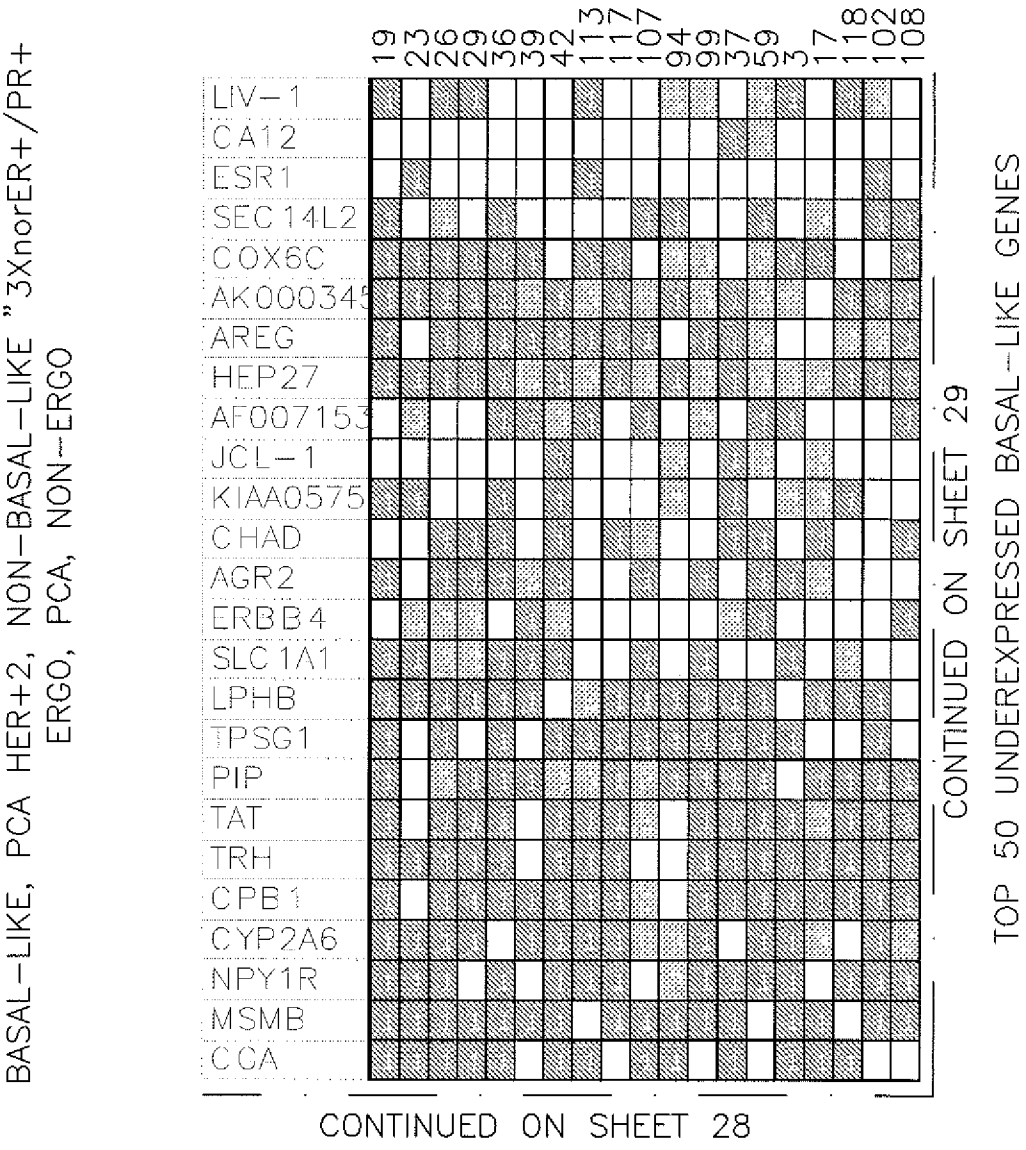
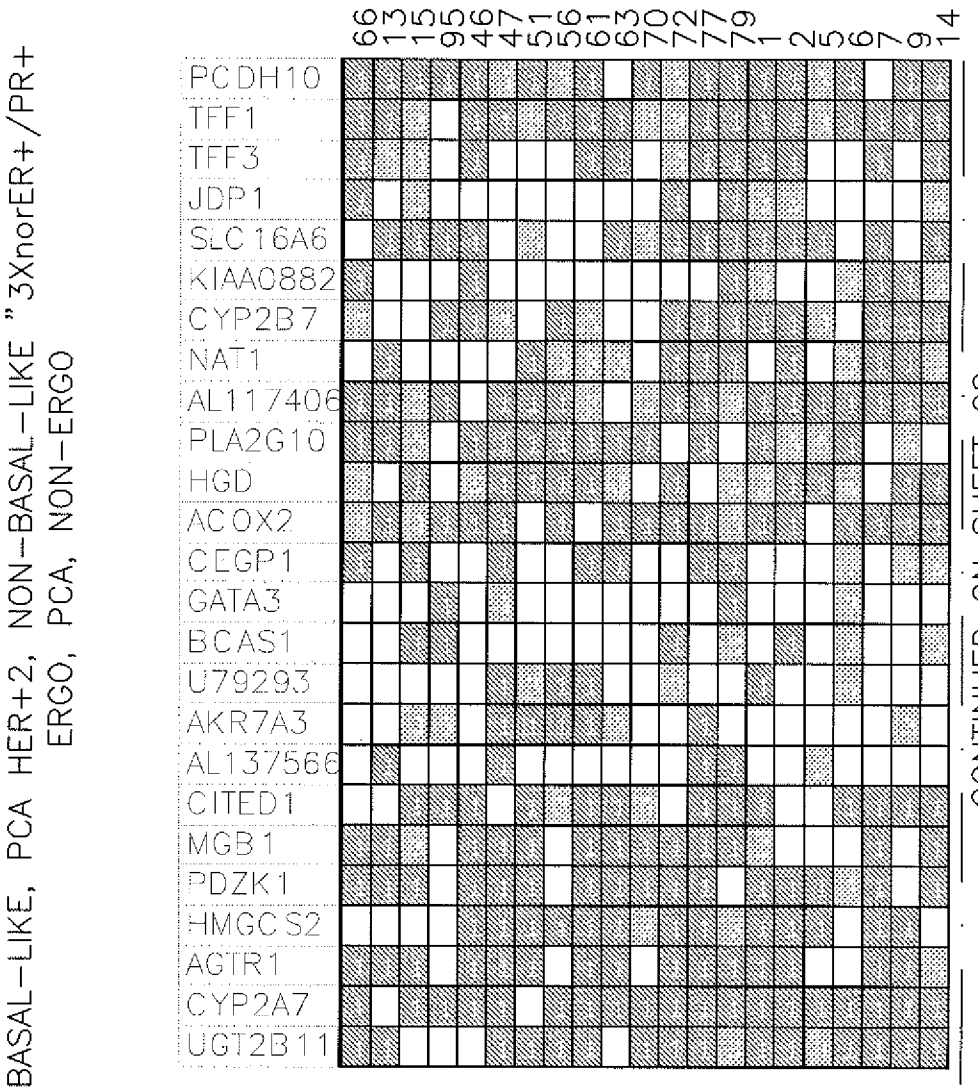

BASAL-LIKE, PCA HER+2, NON-BASAL-LIKE "3XnorER+/PR+
ERGO, PCA, NON-ERGO
19 23 26 29 36 39 42 113 117 107 94 99 37 59 3 17 118 102 108
LIV-1
CA12
ESR1
SEC14L2
COX6C
AK00034
AREG
HEP27
AF007153
JCL-1
KIAA0575
CHAD
AGR2
ERBB4
SLC1A1
LPHB
TPSG1
PIP
TAT
TRH
CPB1
CYP2A6
NPY1R
MSMB
CCA
CONTINUED ON SHEET 28
CONTINUED ON SHEET 29
TOP 50 UNDEREXPRESSED BASAL-LIKE GENES

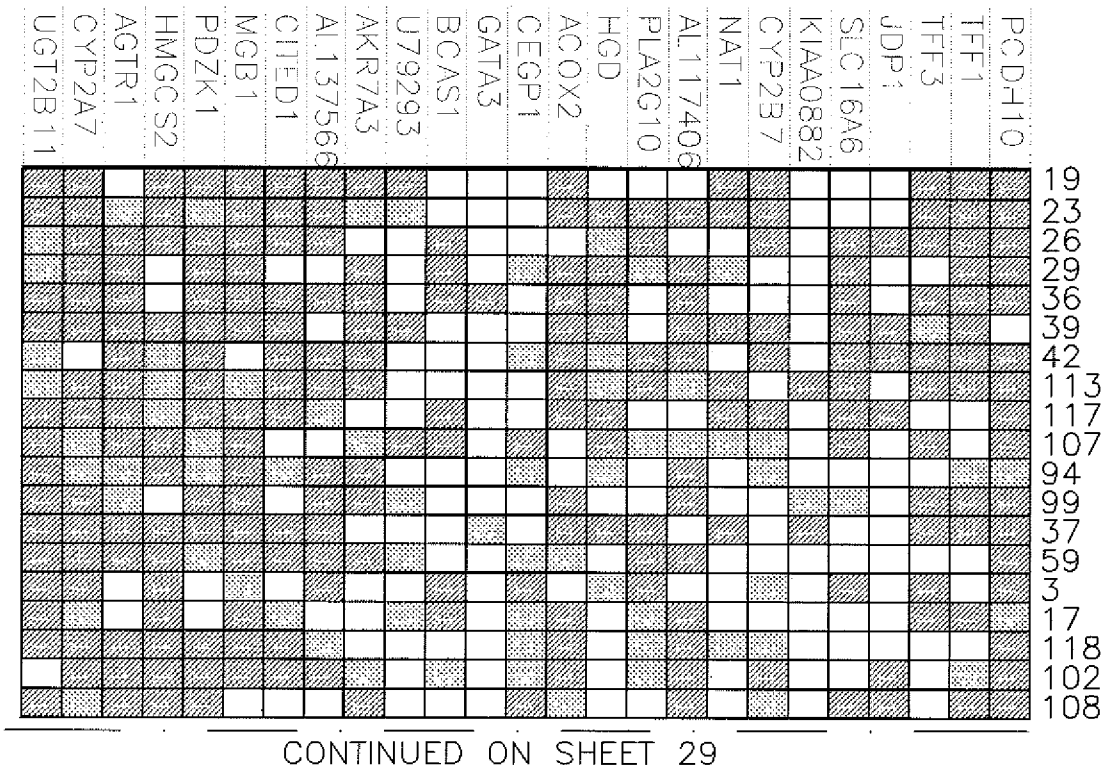
FIG.1



TOP 50 UNDEREXPRESSED BASAL-LIKE GENES

FIG. 1

BASAL-LIKE, PCA HER+2, NON-BASAL-LIKE "3XnorER+/PR+
ERGO, PCA, NON-ERGO



CONTINUED ON SHEET 29

TOP 50 UNDEREXPRESSED BASAL-LIKE GENES

FIG.1

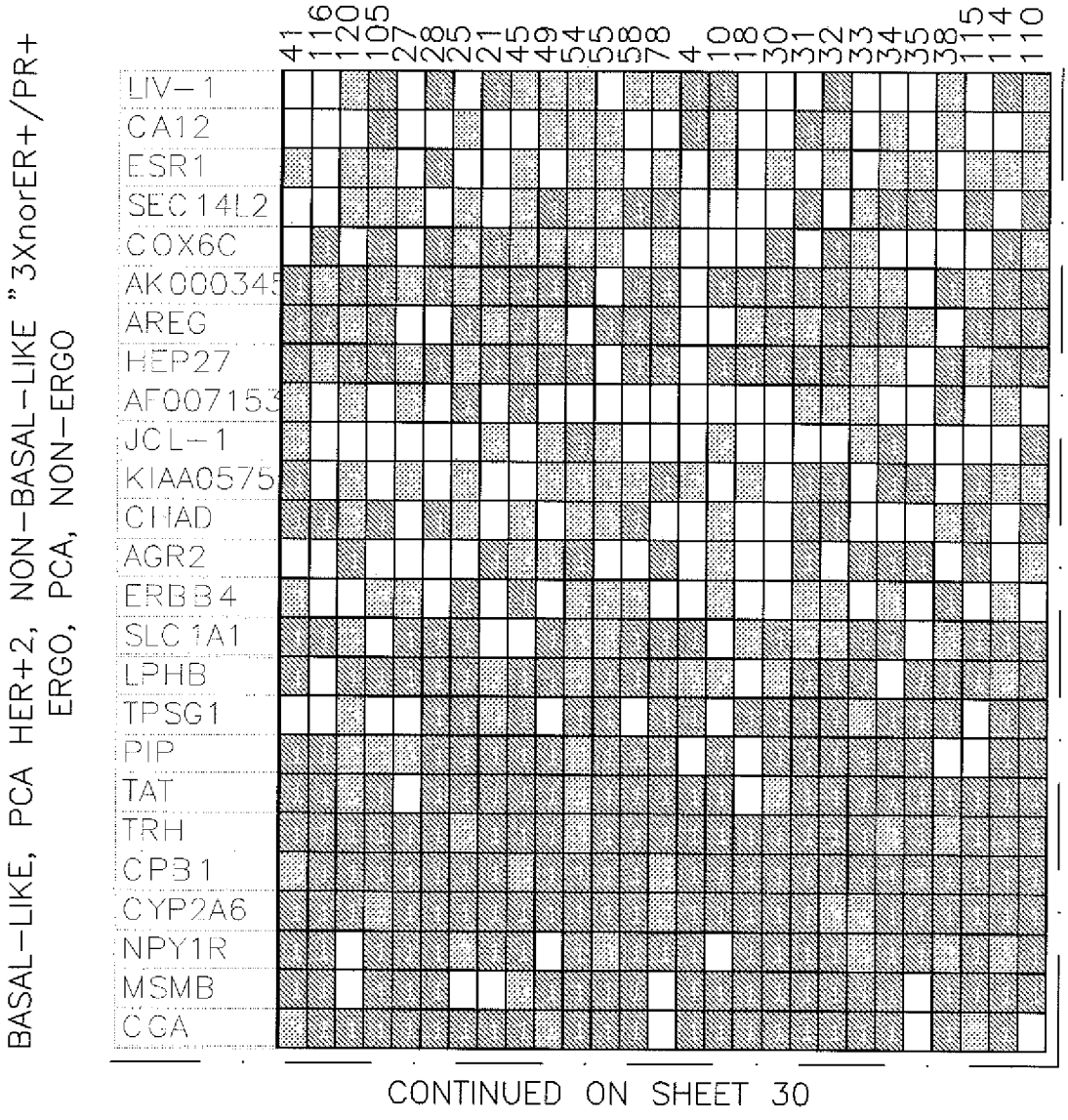

BASAL-LIKE, PCA HER+2, NON-BASAL-LIKE "3XnorER+/PR+
ERGO, PCA, NON-ERGO
41 116 120 105 27 28 25 21 45 49 54 55 58 78 4 10 18 30 31 32 33 34 35 38 115 114 110
LIV-1
CA12
ESR1
SEC14L2
COX6C
AK000345
AREG
HEP27
AF007153
JCL-1
KIAA0575
CHAD
AGR2
ERBB4
SLC1A1
LPHB
TPSG1
PIP
TAT
TRH
CPB1
CYP2A6
NPY1R
MSMB
CGA
END OF ROW
TOP 50 UNDEREXPRESSED BASAL-LIKE GENES
CONTINUED ON SHEET 30

FIG.1

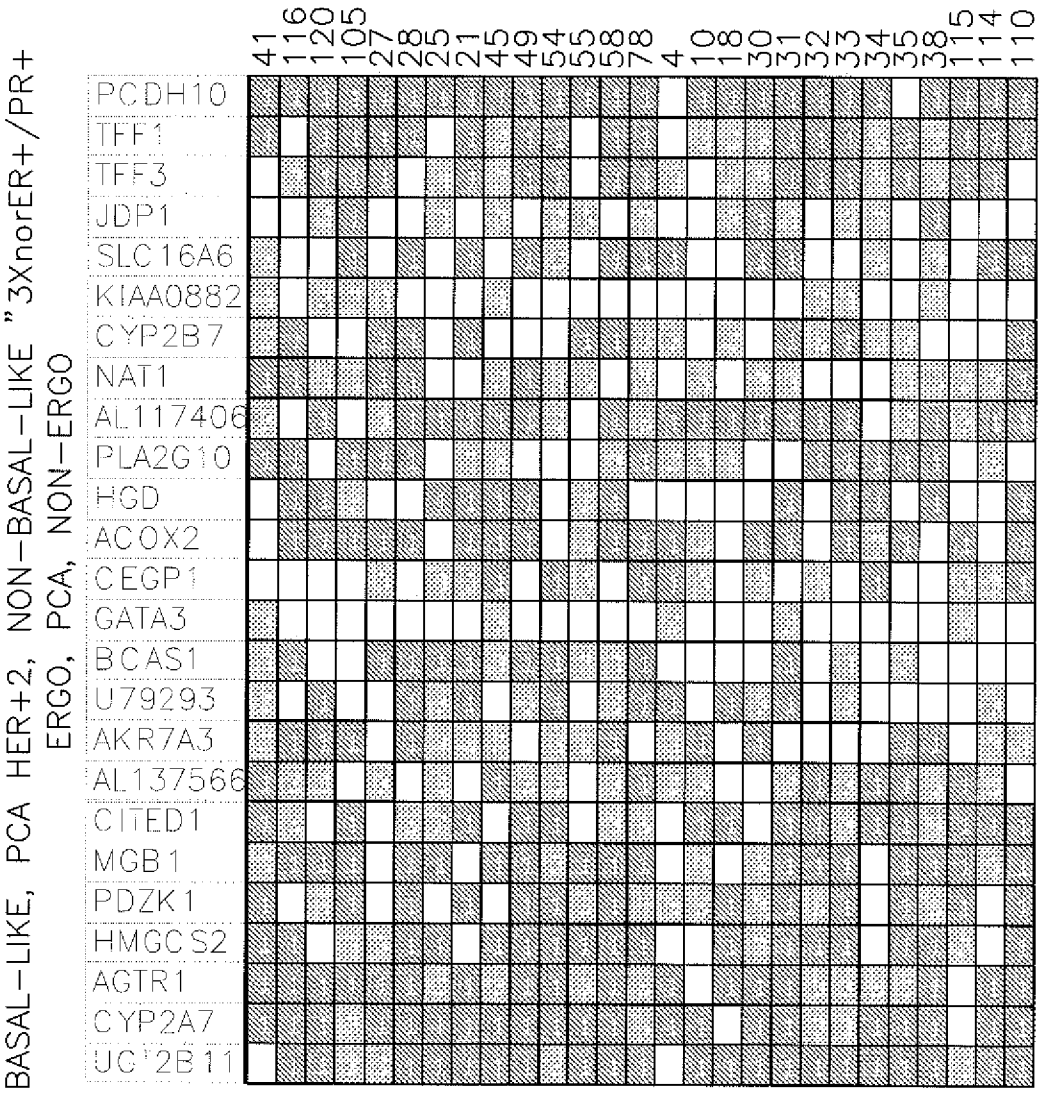

BASAL-LIKE, PCA HER+2, NON-BASAL-LIKE "3XnorER+/PR+
ERGO, PCA, NON-ERGO
41 116 120 105 27 28 25 21 45 49 54 55 58 78 4 10 18 30 31 32 33 34 35 38 115 114 110
PCDH10
TFF1
TFF3
JDP1
SLC16A6
KIAA0882
CYP2B7
NAT1
AL117406
PLA2G10
HGD
ACOX2
CEGP1
GATA3
BCAS1
U79293
AKR7A3
AL137566
CITED1
MGB1
PDZK1
HMGCS2
AGTR1
CYP2A7
CYP2B11
END OF ROW
TOP 50 UNDEREXPRESSED BASAL-LIKE GENES

FIG.1

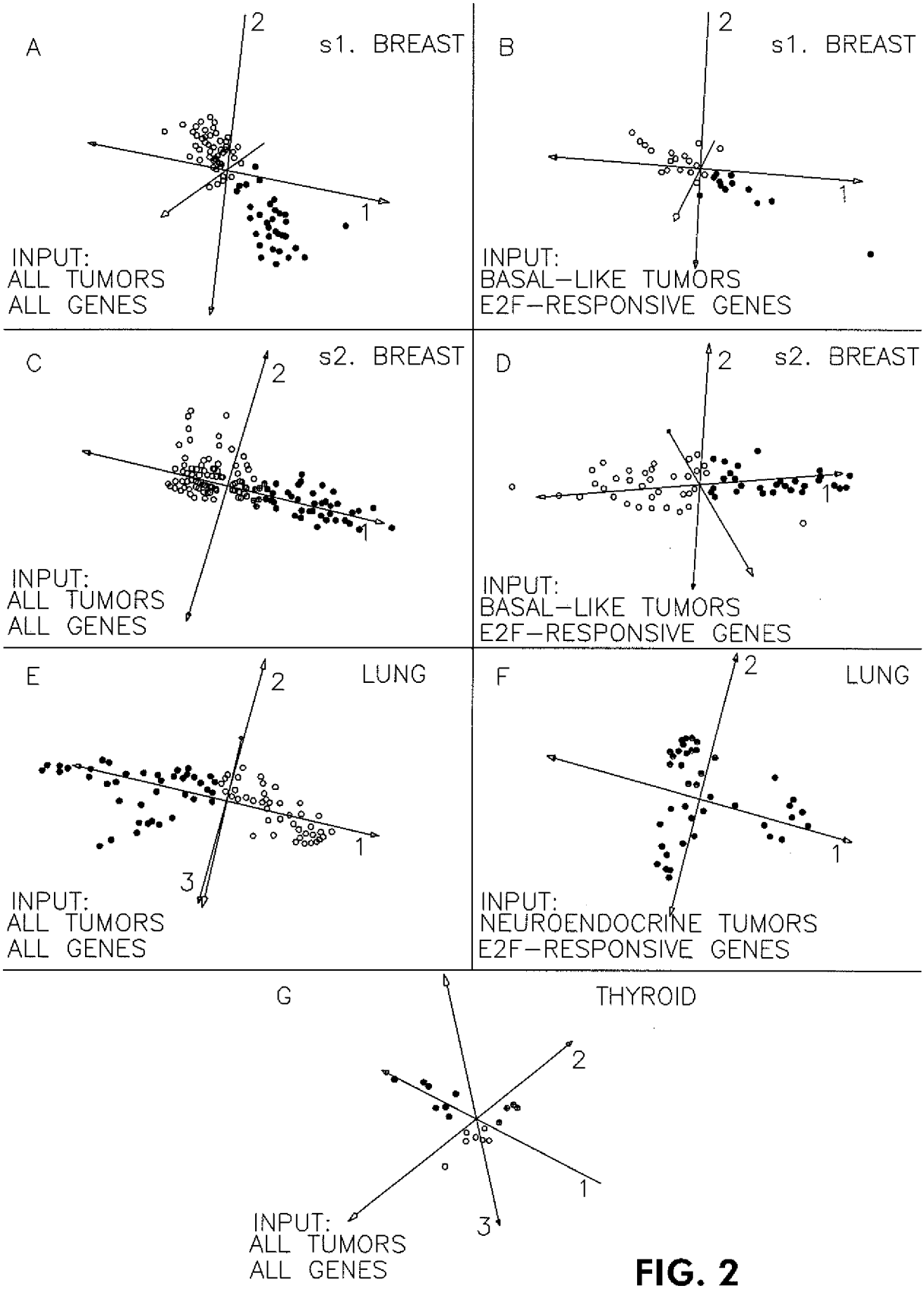

A
s1. BREAST
2
1
INPUT:
ALL TUMORS
ALL GENES
B
s1. BREAST
2
1
INPUT:
BASAL-LIKE TUMORS
E2F-RESPONSIVE GENES
C
s2. BREAST
2
1
INPUT:
ALL TUMORS
ALL GENES
D
s2. BREAST
2
1
INPUT:
BASAL-LIKE TUMORS
E2F-RESPONSIVE GENES
E
LUNG
2
1
3
INPUT:
ALL TUMORS
ALL GENES
F
LUNG
2
1
INPUT:
NEUROENDOCRINE TUMORS
E2F-RESPONSIVE GENES
G
THYROID
2
1
3
INPUT:
ALL TUMORS
ALL GENES

FIG. 2

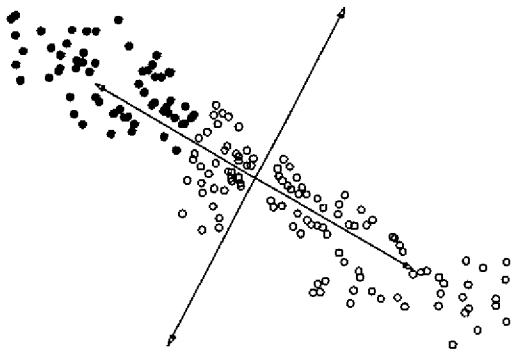


FIG. 3A

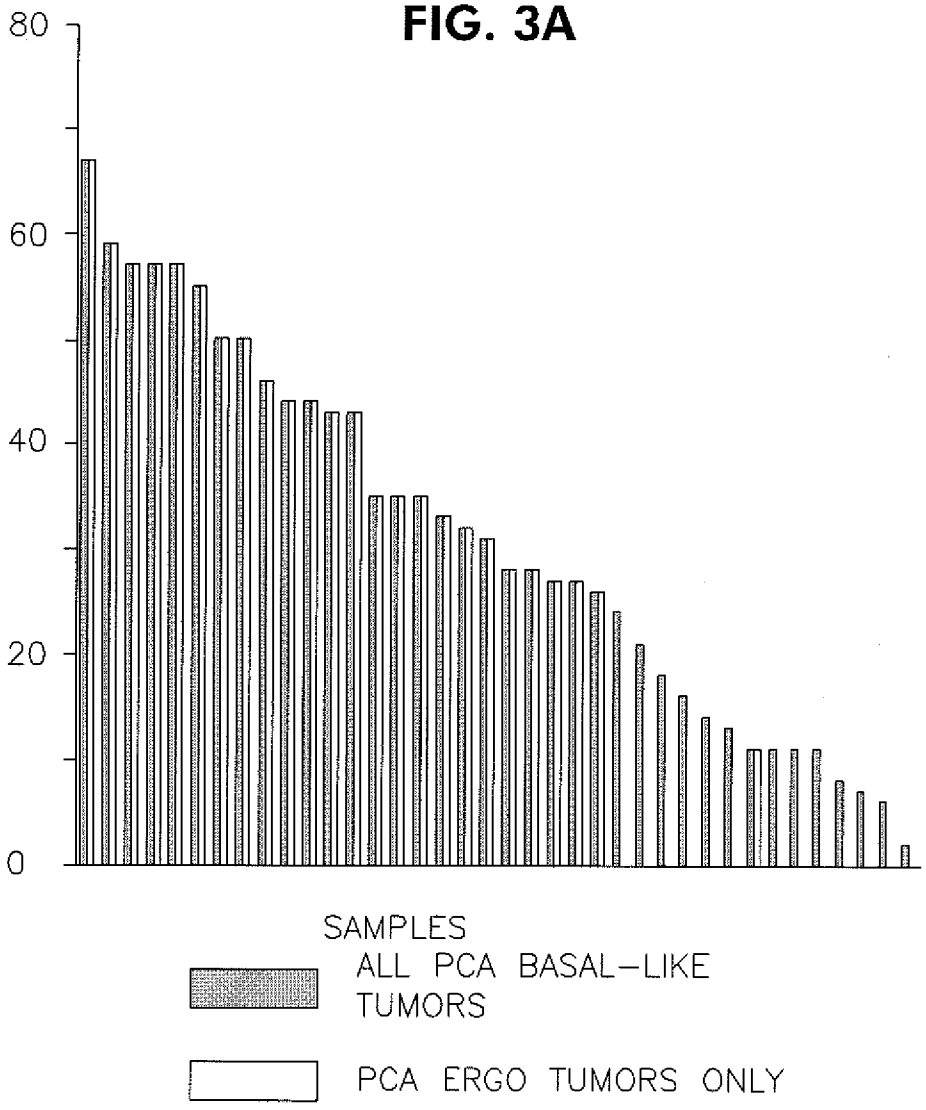

80
60
40
20
0
SAMPLES
ALL PCA BASAL–LIKE TUMORS
PCA ERGO TUMORS ONLY

FIG. 3C

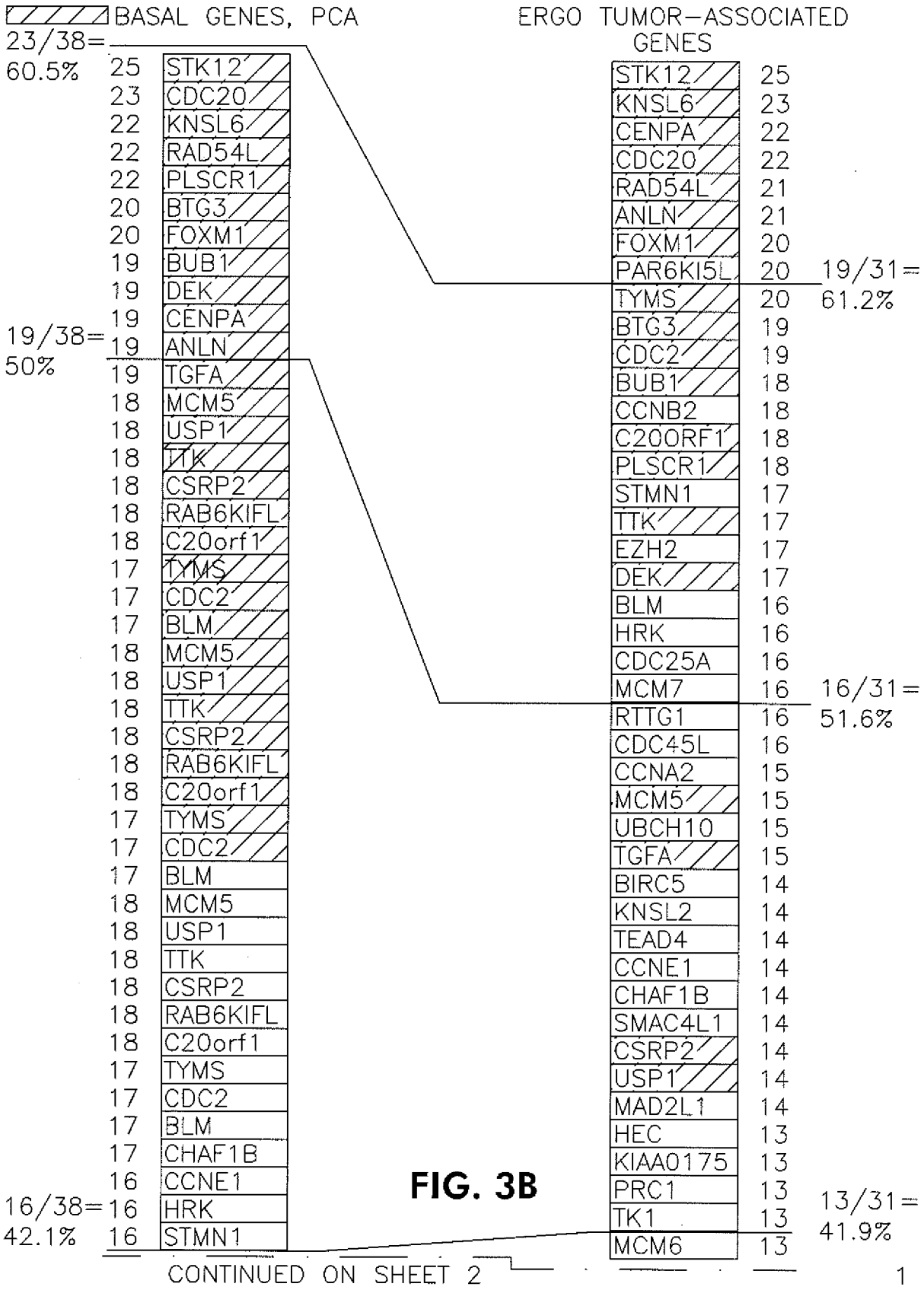

BASAL GENES, PCA
23/38= 60.5%
19/38= 50%
16/38= 42.1%
25 STK12
23 CDC20
22 KNSL6
22 RAD54L
22 PLSCR1
20 BTG3
20 FOXM1
19 BUB1
19 DEK
19 CENPA
19 ANLN
19 TGFA
18 MCM5
18 USP1
18 TTK
18 CSRP2
18 RAB6KIFL
18 C20orf1
17 TYMS
17 CDC2
17 BLM
18 MCM5
18 USP1
18 TTK
18 CSRP2
18 RAB6KIFL
18 C20orf1
17 TYMS
17 CDC2
17 BLM
18 MCM5
18 USP1
18 TTK
18 CSRP2
18 RAB6KIFL
18 C20orf1
17 TYMS
17 CDC2
17 BLM
17 CHAF1B
16 CCNE1
16 HRK
16 STMN1
CONTINUED ON SHEET 2
ERGO TUMOR-ASSOCIATED GENES
STK12 25
KNSL6 23
CENPA 22
CDC20 22
RAD54L 21
ANLN 21
FOXM1 20
PAR6KI5L 20
TYMS 20
BTG3 19
CDC2 19
BUB1 18
CCNB2 18
C20ORF1 18
PLSCR1 18
STMN1 17
TTK 17
EZH2 17
DEK 17
BLM 16
HRK 16
CDC25A 16
MCM7 16
RTTG1 16
CDC45L 16
CCNA2 15
MCM5 15
UBCH10 15
TGFA 15
BIRC5 14
KNSL2 14
TEAD4 14
CCNE1 14
CHAF1B 14
SMAC4L1 14
CSRP2 14
USP1 14
MAD2L1 14
HEC 13
KIAA0175 13
PRC1 13
TK1 13
MCM6 13
19/31= 61.2%
16/31= 51.6%
13/31= 41.9%

FIG. 3B

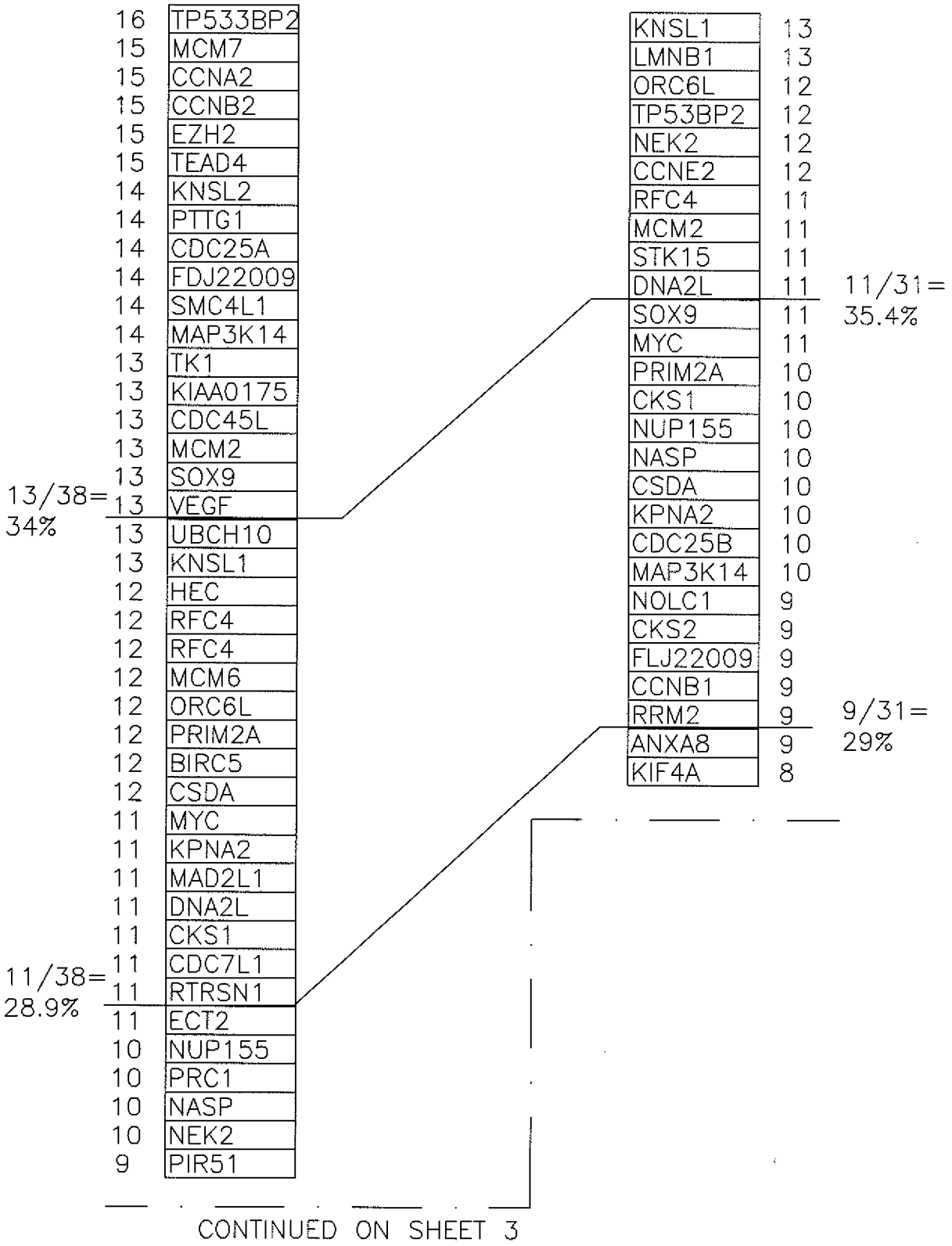

16 TP533BP2
15 MCM7
15 CCNA2
15 CCNB2
15 EZH2
15 TEAD4
14 KNSL2
14 PTTG1
14 CDC25A
14 FDJ22009
14 SMC4L1
14 MAP3K14
13 TK1
13 KIAA0175
13 CDC45L
13 MCM2
13 SOX9
13/38= 13 VEGF
34%
13 UBCH10
13 KNSL1
12 HEC
12 RFC4
12 RFC4
12 MCM6
12 ORC6L
12 PRIM2A
12 BIRC5
12 CSDA
11 MYC
11 KPNA2
11 MAD2L1
11 DNA2L
11 CKS1
11/38= 11 CDC7L1
28.9% 11 RTRSN1
11 ECT2
10 NUP155
10 PRC1
10 NASP
10 NEK2
9 PIR51
KNSL1 13
LMNB1 13
ORC6L 12
TP53BP2 12
NEK2 12
CCNE2 12
RFC4 11
MCM2 11
STK15 11
DNA2L 11
SOX9 11
MYC 11
PRIM2A 10
CKS1 10
NUP155 10
NASP 10
CSDA 10
KPNA2 10
CDC25B 10
MAP3K14 10
NOLC1 9
CKS2 9
FLJ22009 9
CCNB1 9
RRM2 9
ANXA8 9
KIF4A 8
11/31= 35.4%
9/31= 29%
CONTINUED ON SHEET 3

FIG. 3B

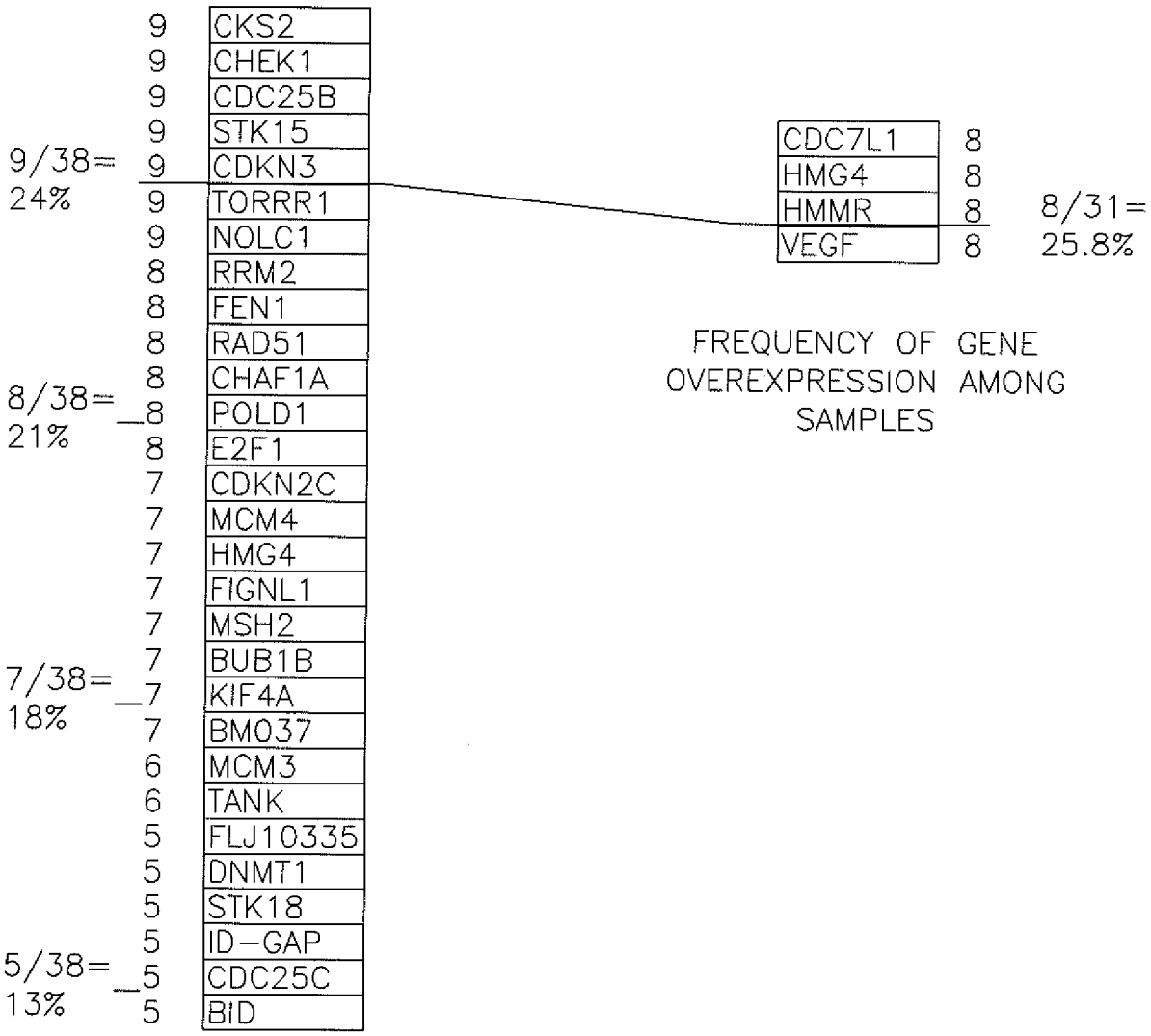
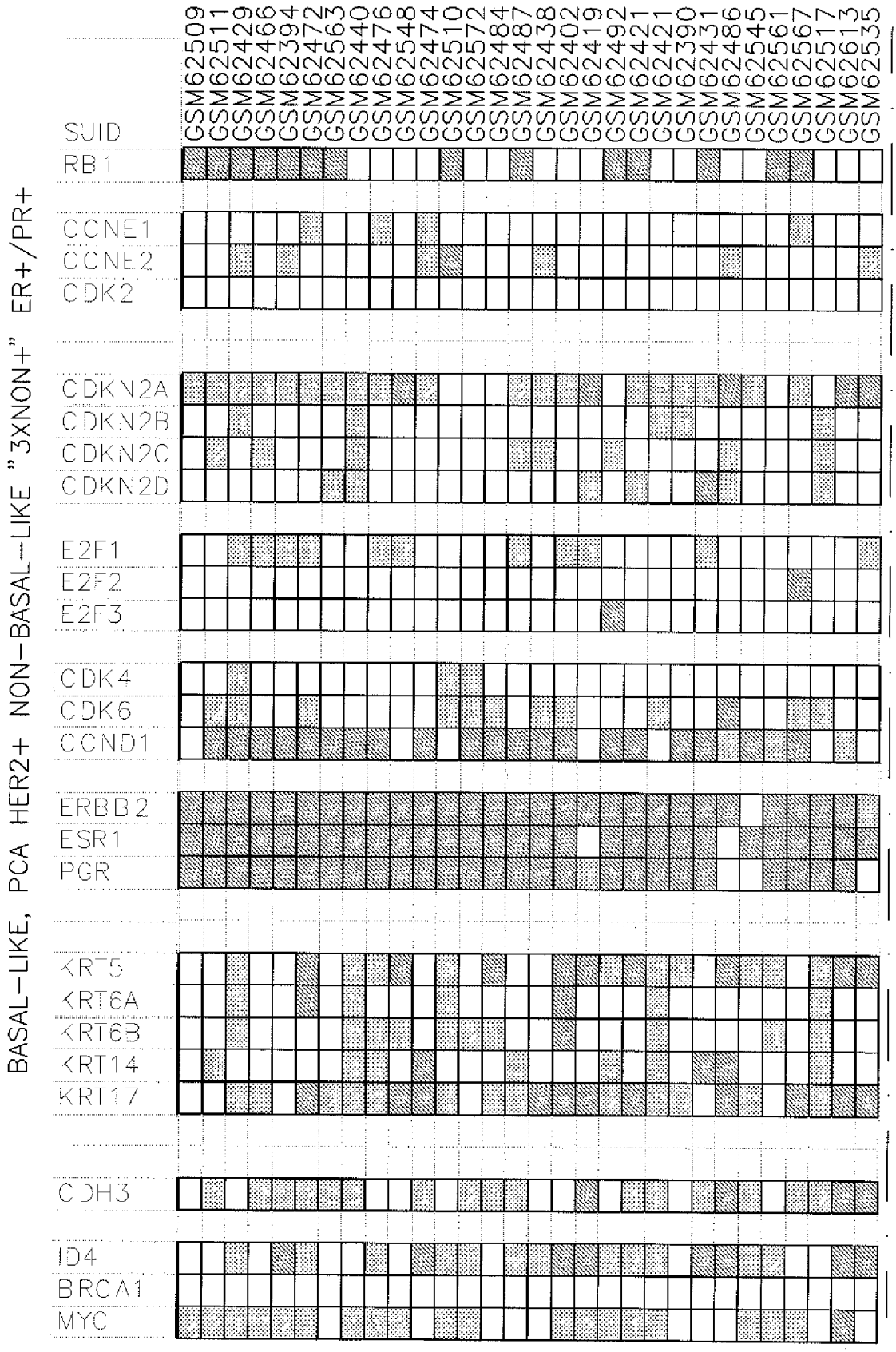
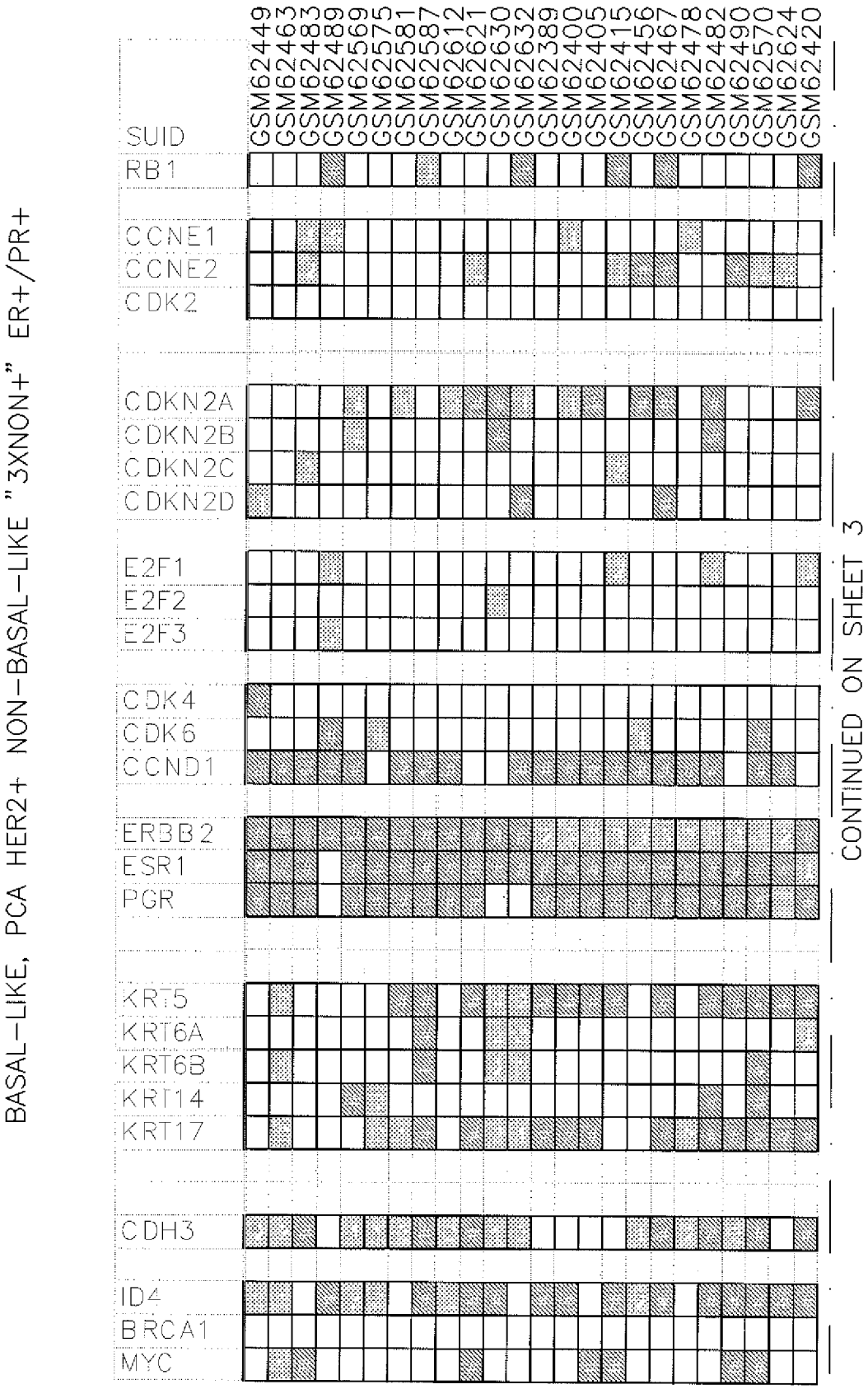
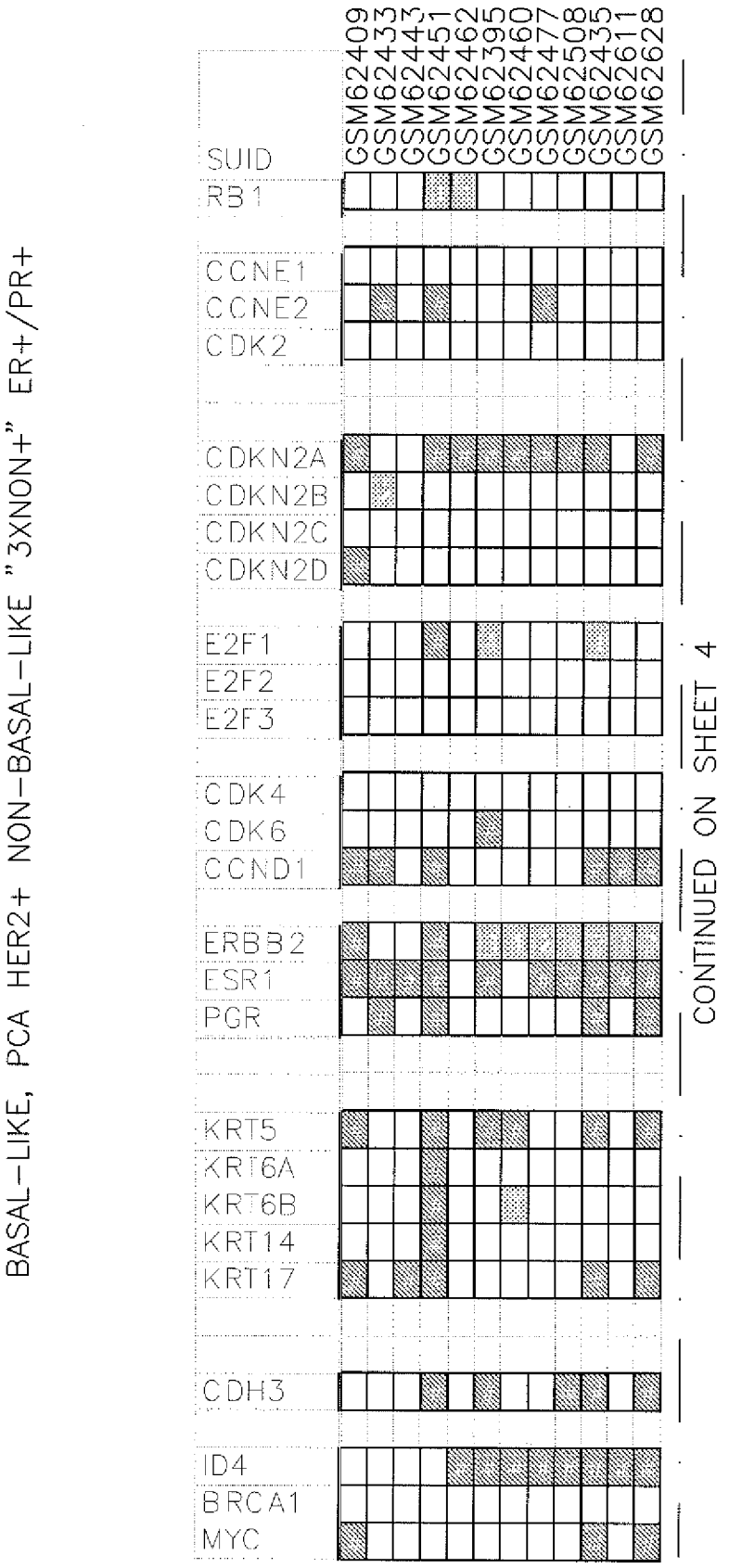

9 CKS2
9 CHEK1
9 CDC25B
9 STK15
9/38= 9 CDKN3
24% 9 TORRR1
9 NOLC1
8 RRM2
8 FEN1
8 RAD51
8 CHAF1A
8/38= 8 POLD1
21% 8 E2F1
7 CDKN2C
7 MCM4
7 HMG4
7 FIGNL1
7 MSH2
7 BUB1B
7/38= 7 KIF4A
18% 7 BM037
6 MCM3
6 TANK
5 FLJ10335
5 DNMT1
5 STK18
5 ID-GAP
5/38= 5 CDC25C
13% 5 BID
FREQUENCY OF GENE OVEREXPRESSION AMONG SAMPLES
CDC7L1 8
HMG4 8
HMMR 8
VEGF 8
8/31= 25.8%
FREQUENCY OF GENE OVEREXPRESSION AMONG SAMPLES

FIG. 3B

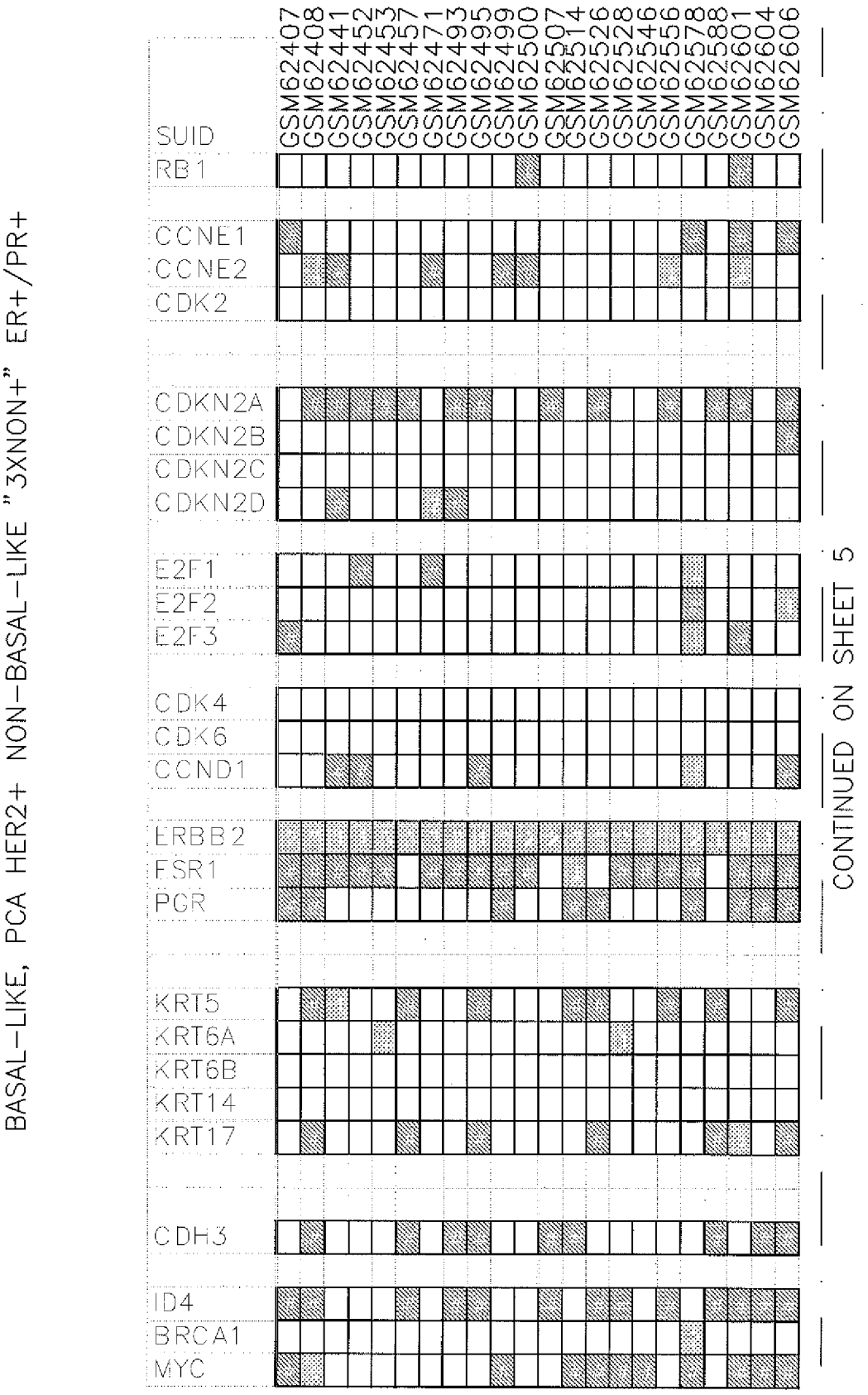

BASAL-LIKE, PCA HER2+ NON-BASAL-LIKE "3XNON+" ER+/PR+
SJID
RB1
CCNE1
CCNE2
CDK2
CDKN2A
CDKN2B
CDKN2C
CDKN2D
E2F1
E2F2
E2F3
CDK4
CDK6
CCND1
ERBB2
ESR1
PGR
KRT5
KRT6A
KRT6B
KRT14
KRT17
CDH3
ID4
BRCA1
MYC
GSM625091
GSM625111
GSM624291
GSM624661
GSM623941
GSM624721
GSM625631
GSM624401
GSM624761
GSM625481
GSM624741
GSM625101
GSM625721
GSM624841
GSM624871
GSM624381
GSM624021
GSM624191
GSM624921
GSM624211
GSM624211
GSM623901
GSM624311
GSM624861
GSM625451
GSM625611
GSM625671
GSM625171
GSM626131
GSM625351
CONTINUED ON SHEET 2
SELECTED BIOMARKERS FIG. 4
1



SELECTED BIOMARKERS **FIG. 4**



SELECTED BIOMARKERS **FIG. 4**



SELECTED BIOMARKERS **FIG. 4**

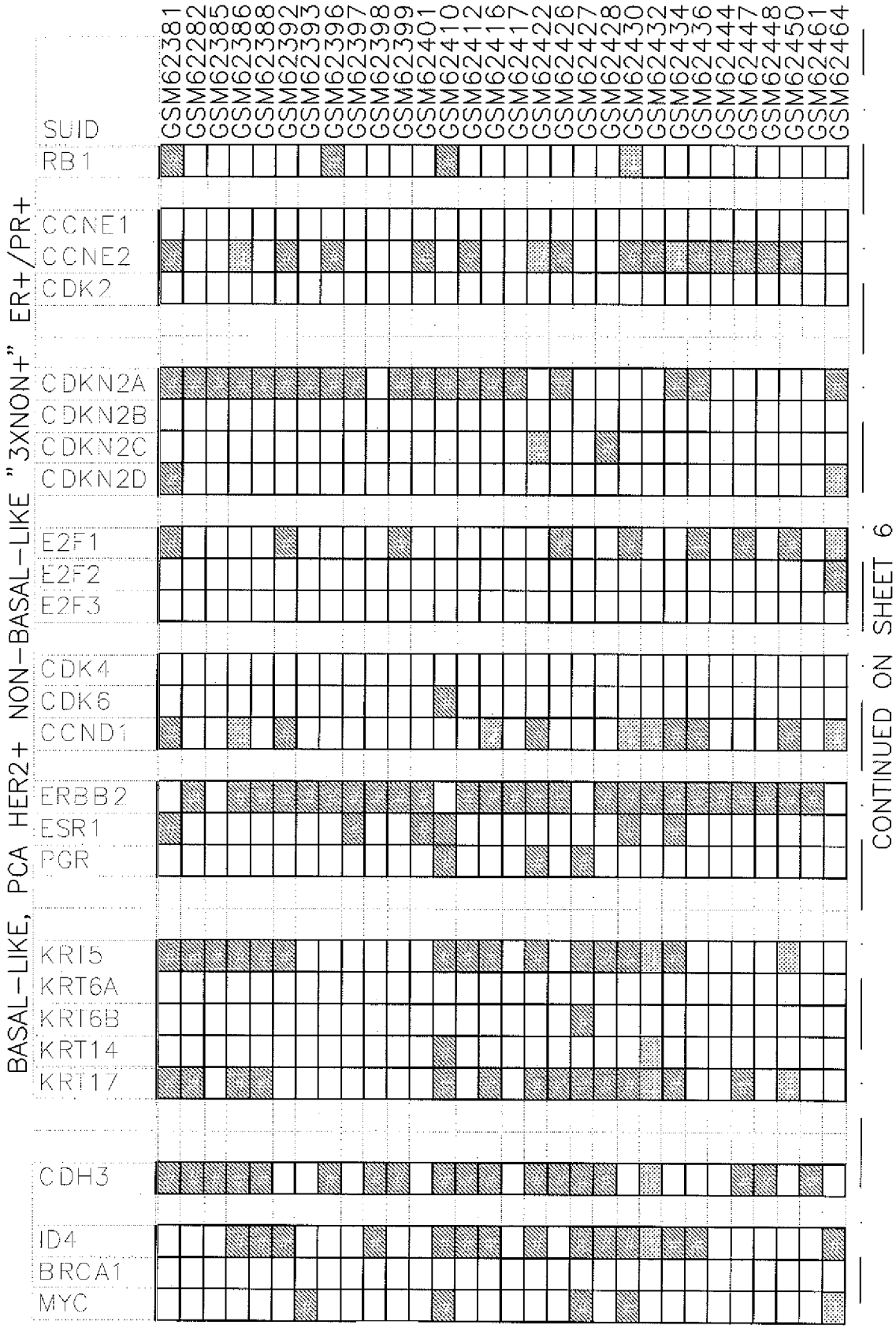
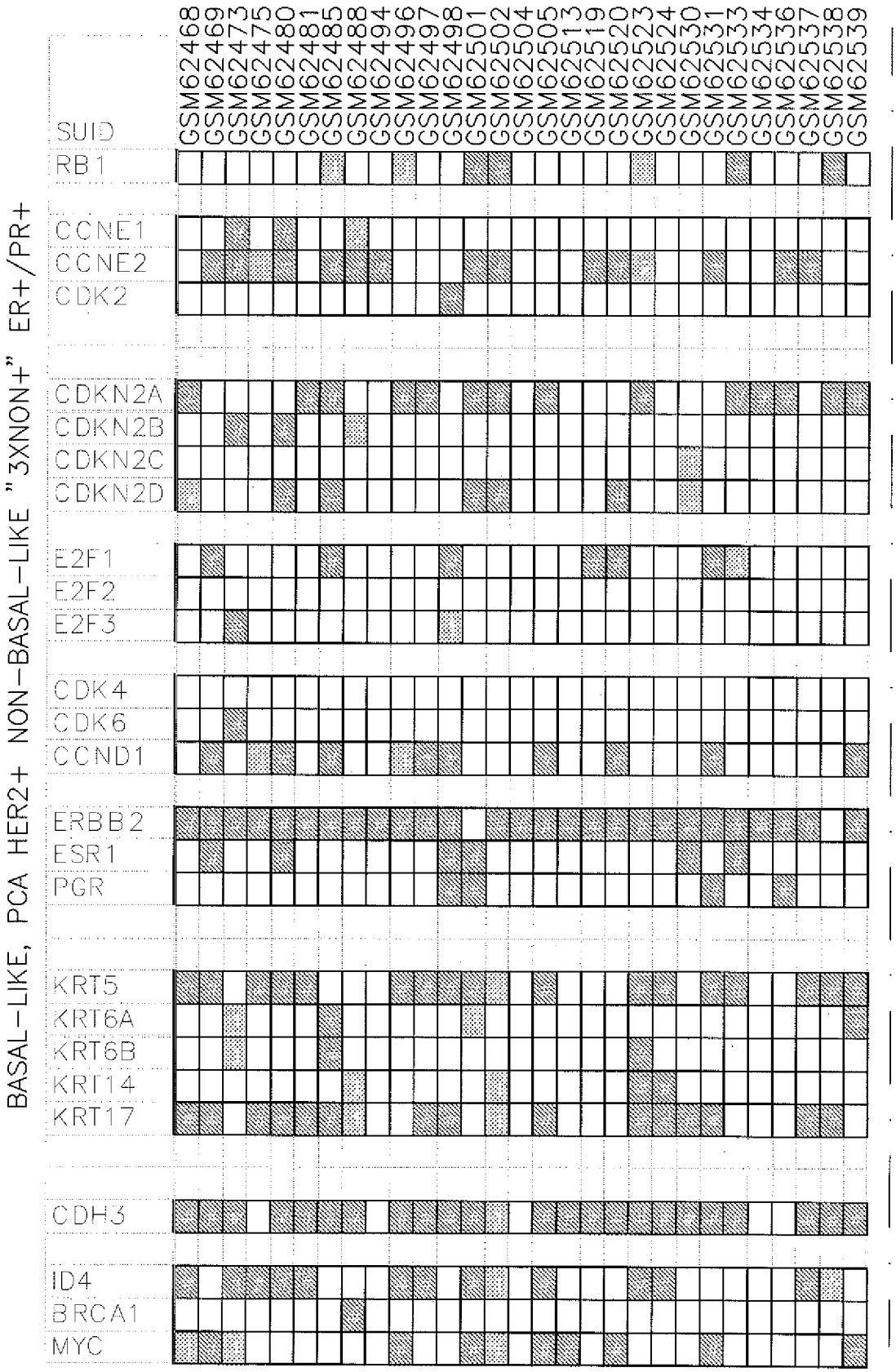
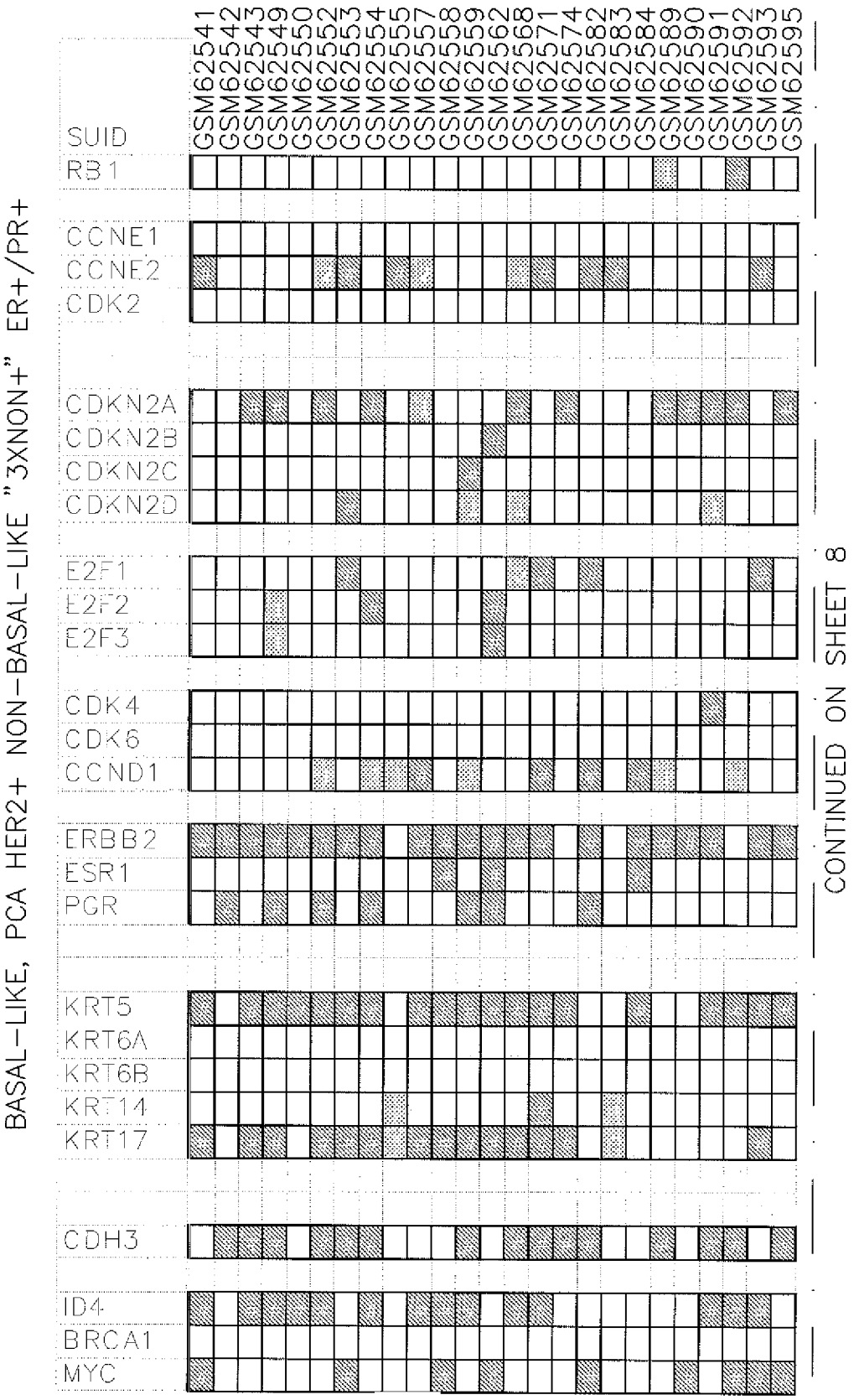

SUID
GSM62381
GSM62382
GSM62385
GSM62386
GSM62388
GSM62392
GSM62393
GSM62396
GSM62397
GSM62398
GSM62399
GSM62401
GSM62410
GSM62412
GSM62416
GSM62417
GSM62422
GSM62426
GSM62427
GSM62428
GSM62430
GSM62432
GSM62434
GSM62436
GSM62444
GSM62447
GSM62448
GSM62450
GSM62461
GSM62464
RB1
CCNE1
CCNE2
CDK2
CDKN2A
CDKN2B
CDKN2C
CDKN2D
E2F1
E2F2
E2F3
CDK4
CDK6
CCND1
ERBB2
ESR1
PGR
KRT5
KRT6A
KRT6B
KRT14
KRT17
CDH3
ID4
BRCA1
MYC
BASAL-LIKE, PCA HER2+ NON-BASAL-LIKE "3XNON+" ER+/PR+
CONTINUED ON SHEET 6
SELECTED BIOMARKERS

FIG. 4

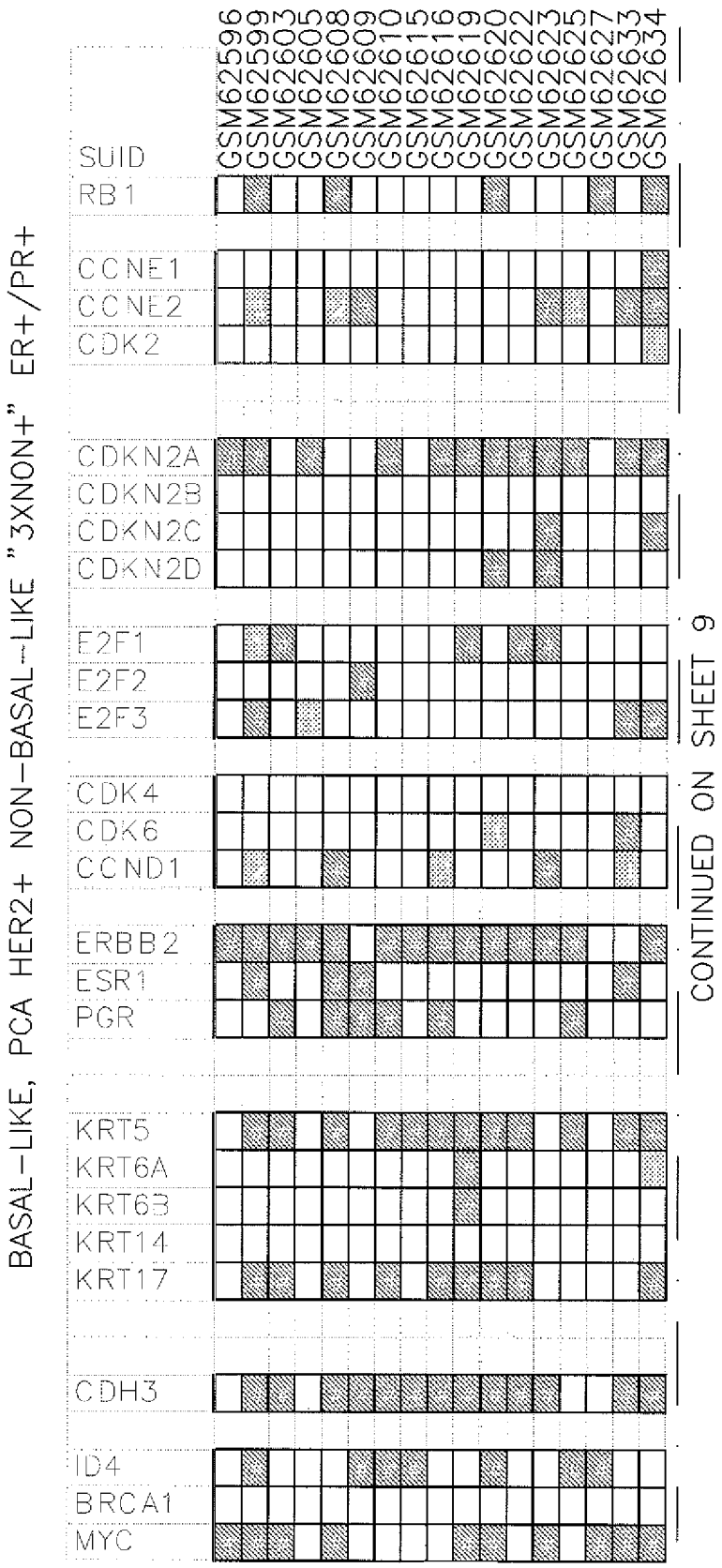


CONTINUED ON SHEET 7

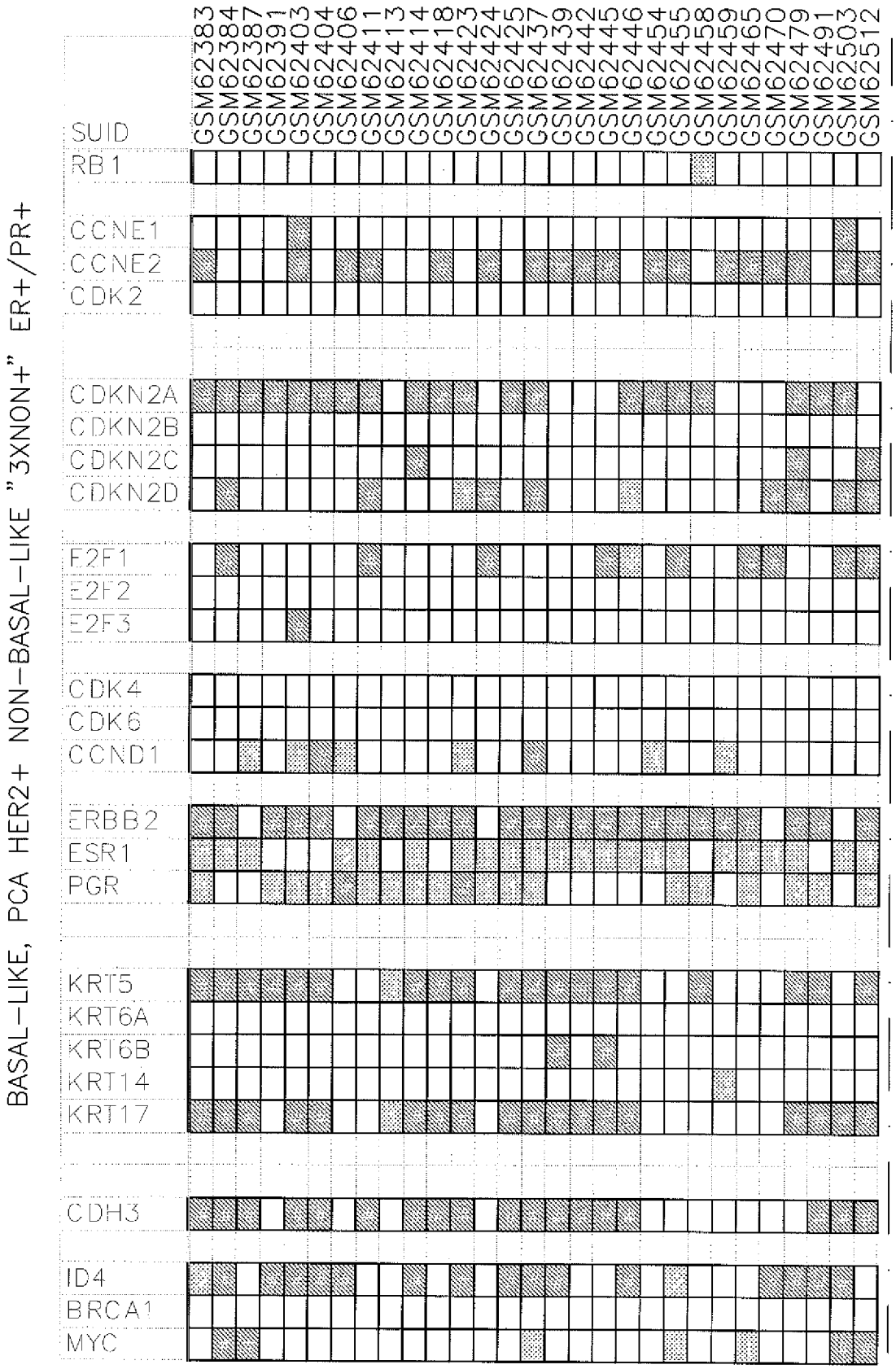
SELECTED BIOMARKERS **FIG. 4**



SELECTED BIOMARKERS **FIG. 4**



SELECTED BIOMARKERS **FIG. 4**



SELECTED BIOMARKERS **FIG. 4**

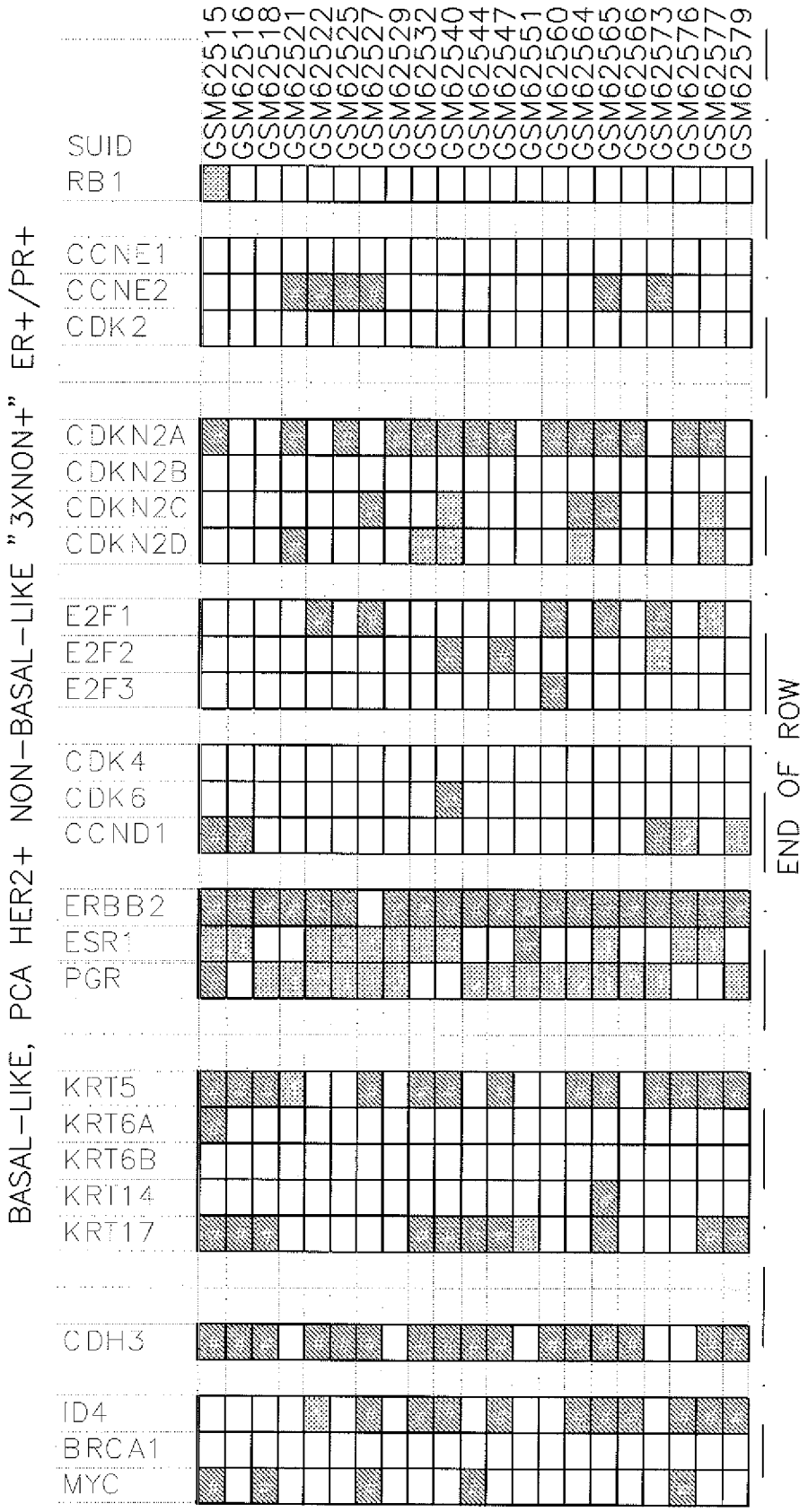
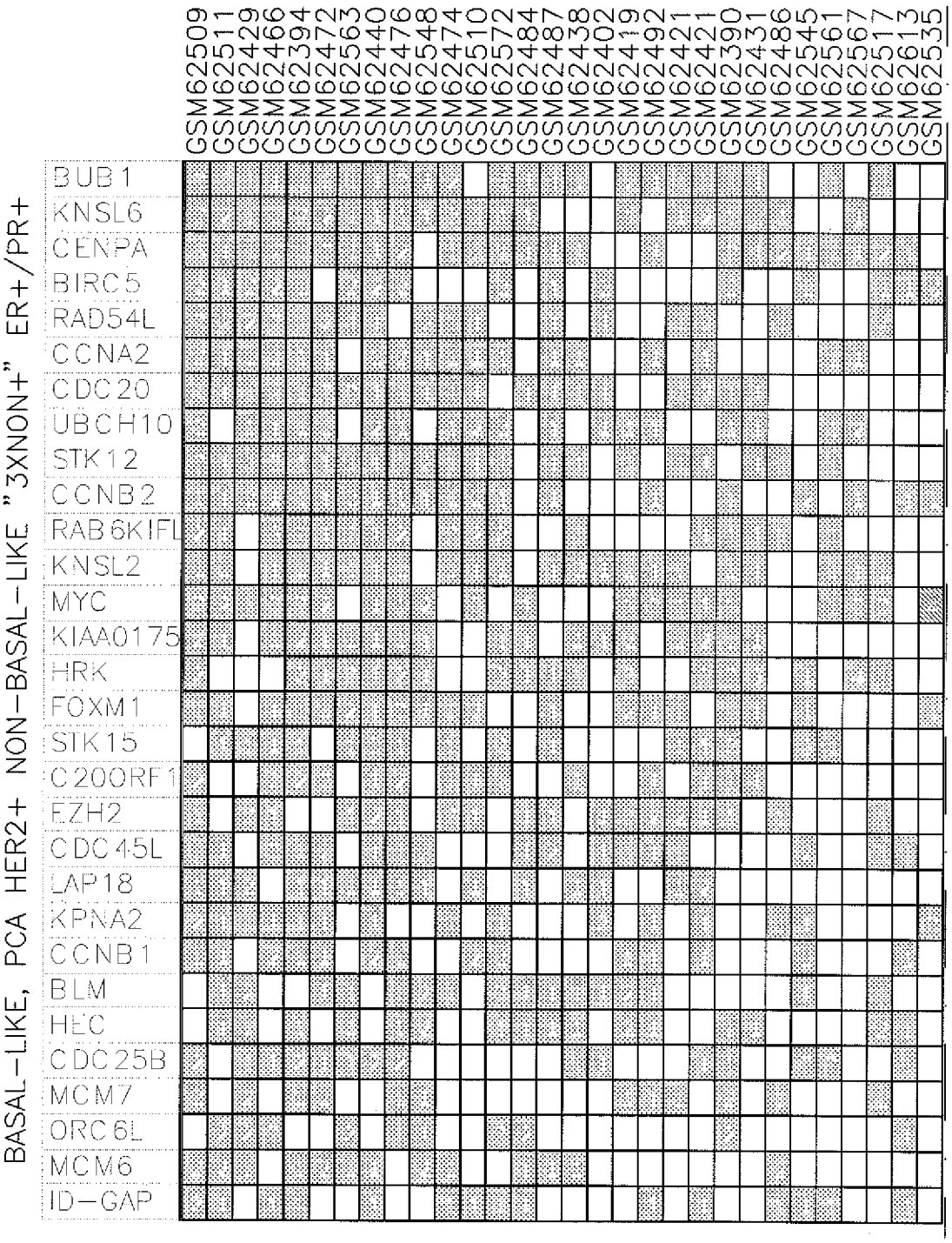


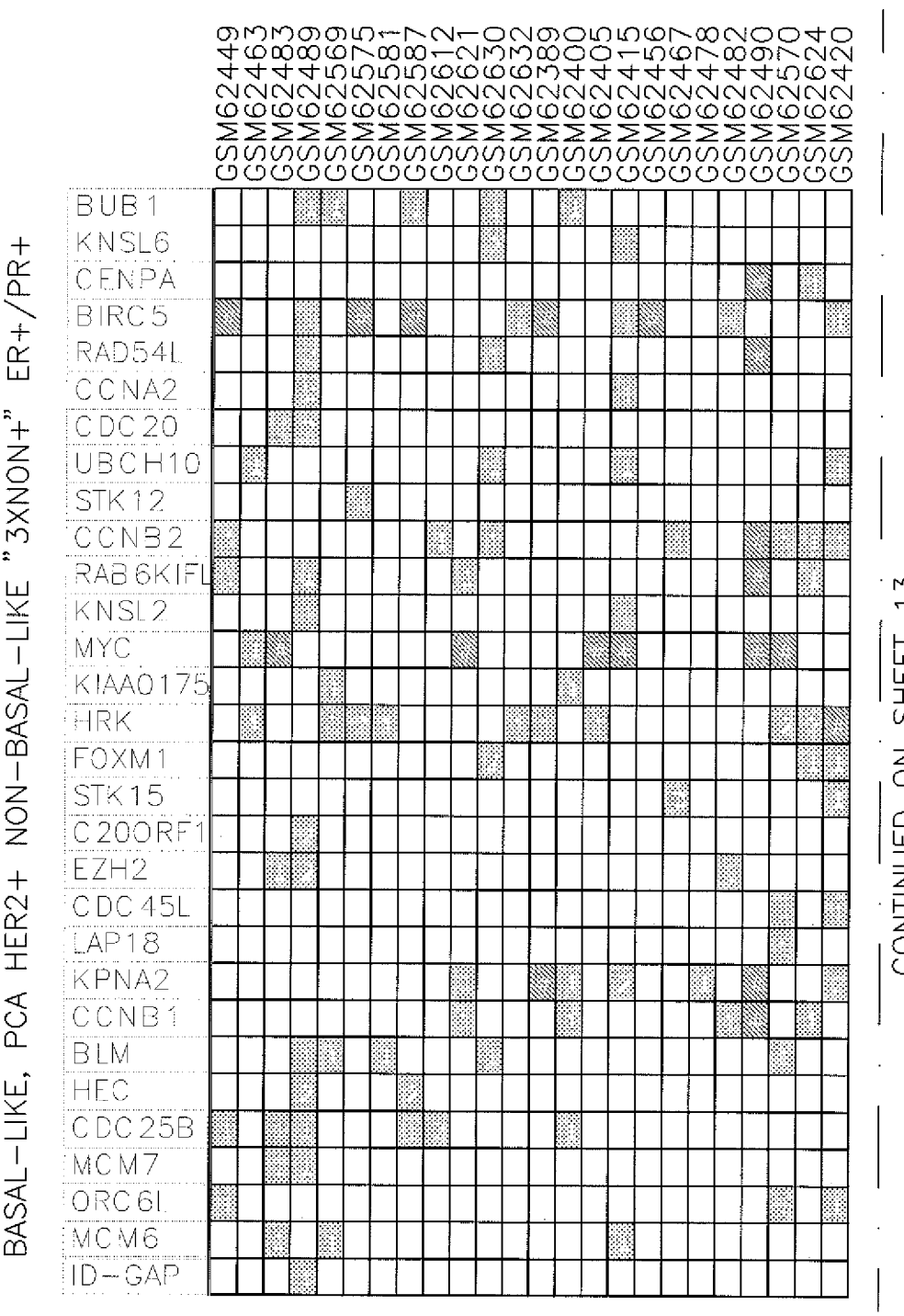
FIG. 4 SELECTED BIOMARKERS



TOP 30 OVEREXPRESSED ERGO GENES

CONTINUED ON SHEET 12

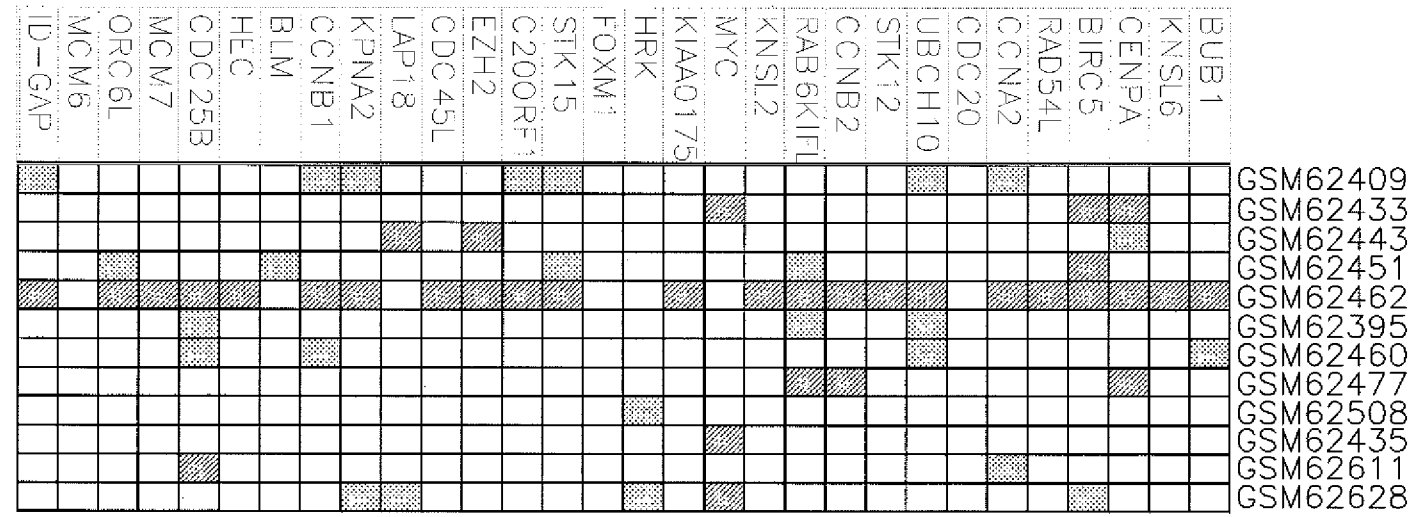
FIG. 4



TOP 30 OVEREXPRESSED ERGO GENES

FIG. 4

BASAL-LIKE, PCA HER2+ NON-BASAL-LIKE "3XNON+" ER+/PR+

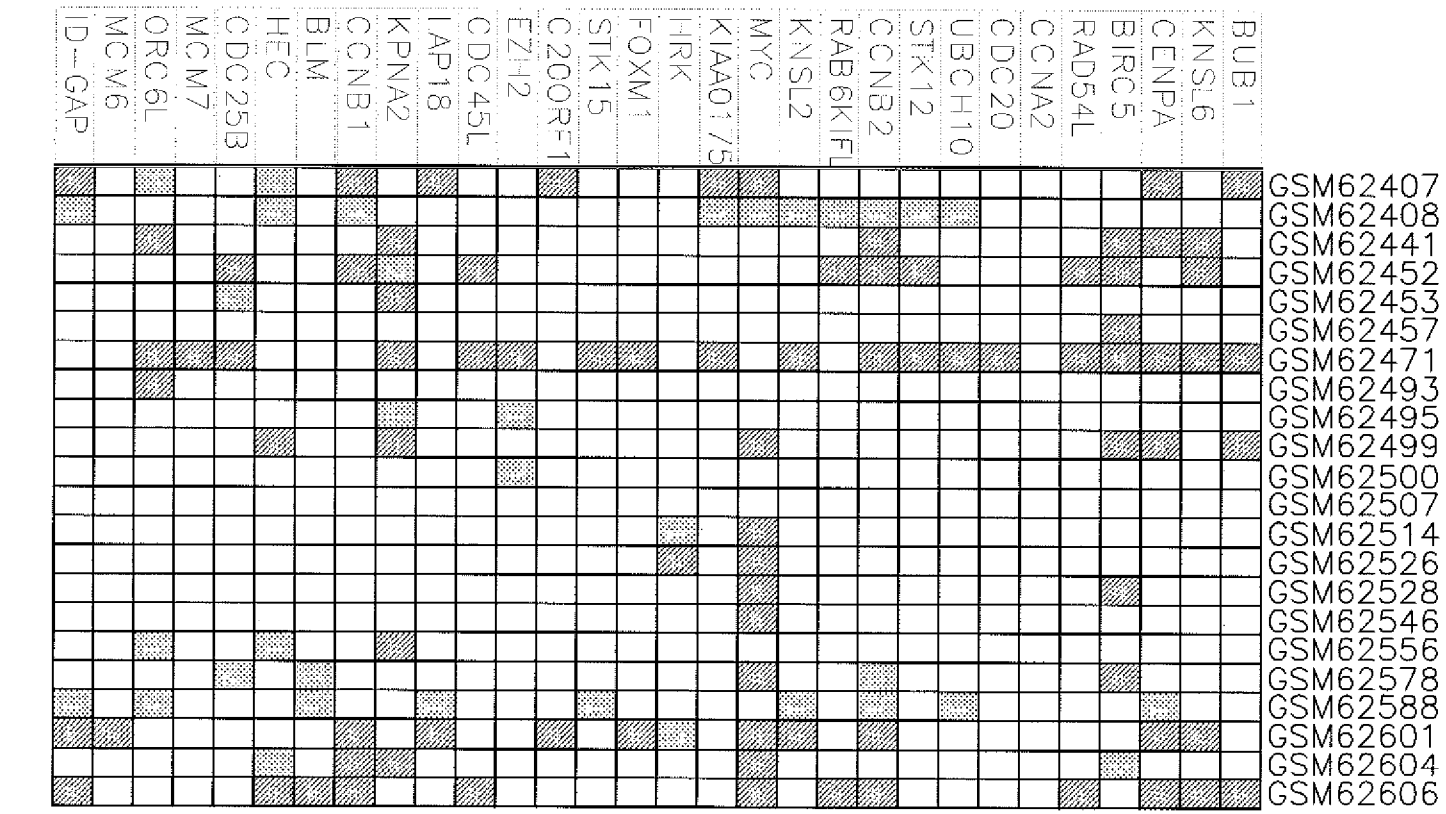


CONTINUED ON SHEET 14

TOP 30 OVEREXPRESSED ERGO GENES

FIG. 4

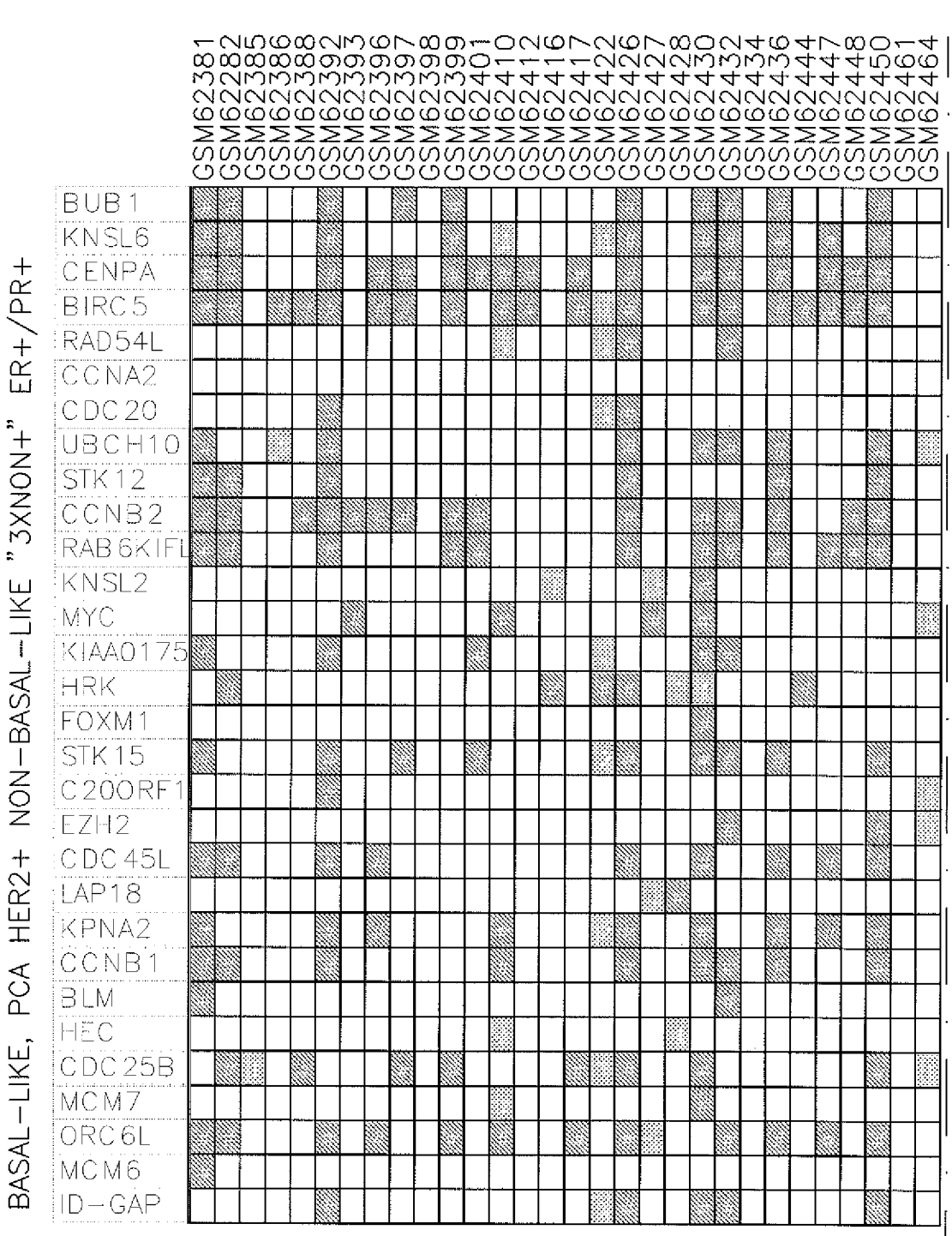
BASAL-LIKE, PCA HER2+ NON-BASAL-LIKE "3XNON+" ER+/PR+



CONTINUED ON SHEET 15

TOP 30 OVEREXPRESSED ERGO GENES

FIG. 4


BASAL-LIKE, PCA HER2+ NON-BASAL-LIKE "3XNON+" ER+/PR+
BUB1
KNSL6
CENPA
BIRC5
RAD54L
CCNA2
CDC20
UBCH10
STK12
CCNB2
RAB6KIFL
KNSL2
MYC
KIAA0175
HRK
FOXM1
STK15
C20ORF1
EZH2
CDC45L
LAP18
KPNA2
CCNB1
BLM
HEC
CDC25B
MCM7
ORC6L
MCM6
ID-GAP
GSM62381
GSM62382
GSM62385
GSM62386
GSM62388
GSM62392
GSM62393
GSM62396
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GSM62430
GSM62432
GSM62434
GSM62436
GSM62444
GSM62447
GSM62448
GSM62450
GSM62461
GSM62464
CONTINUED ON SHEET 15
TOP 30 OVEREXPRESSED ERGO GENES

FIG. 4

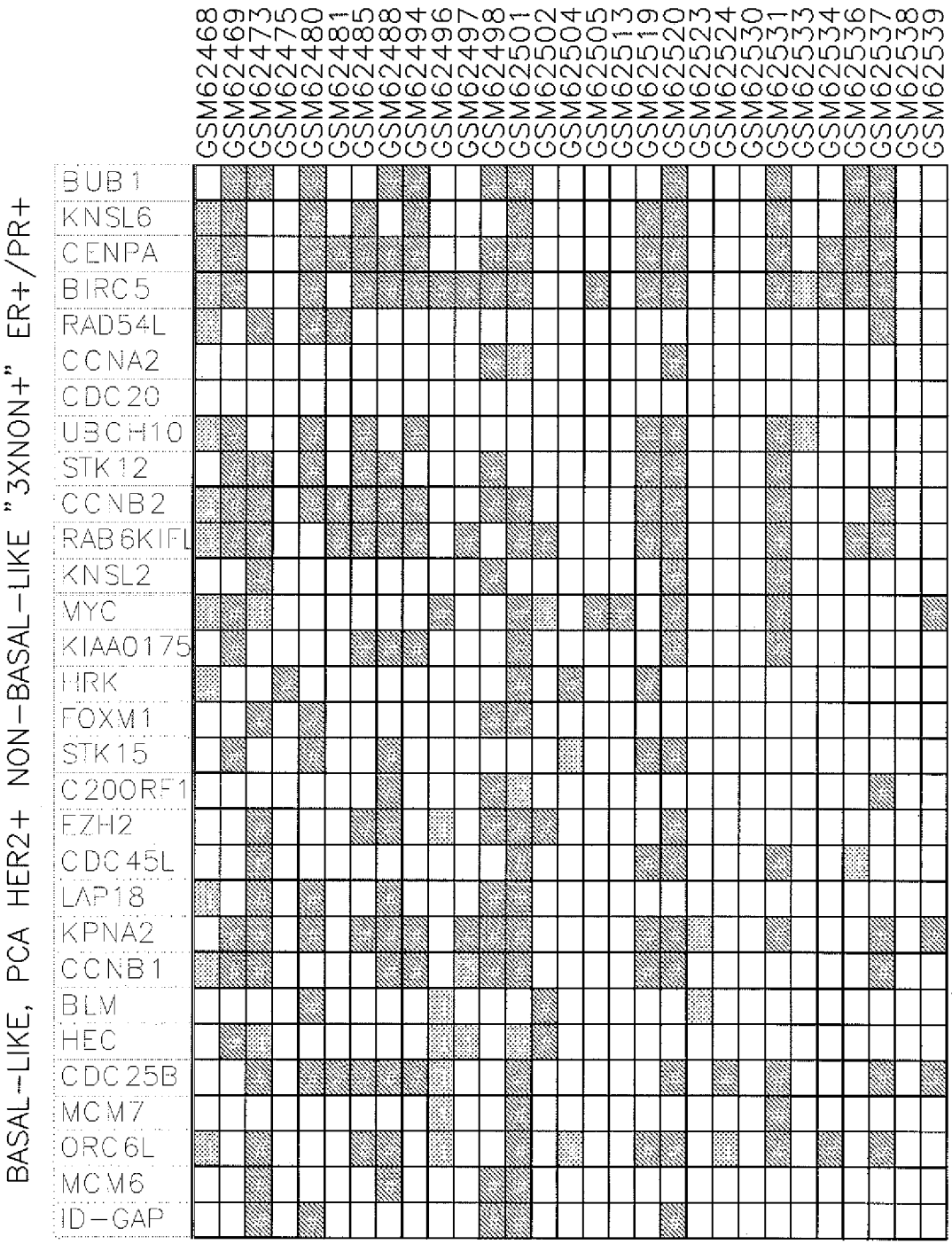
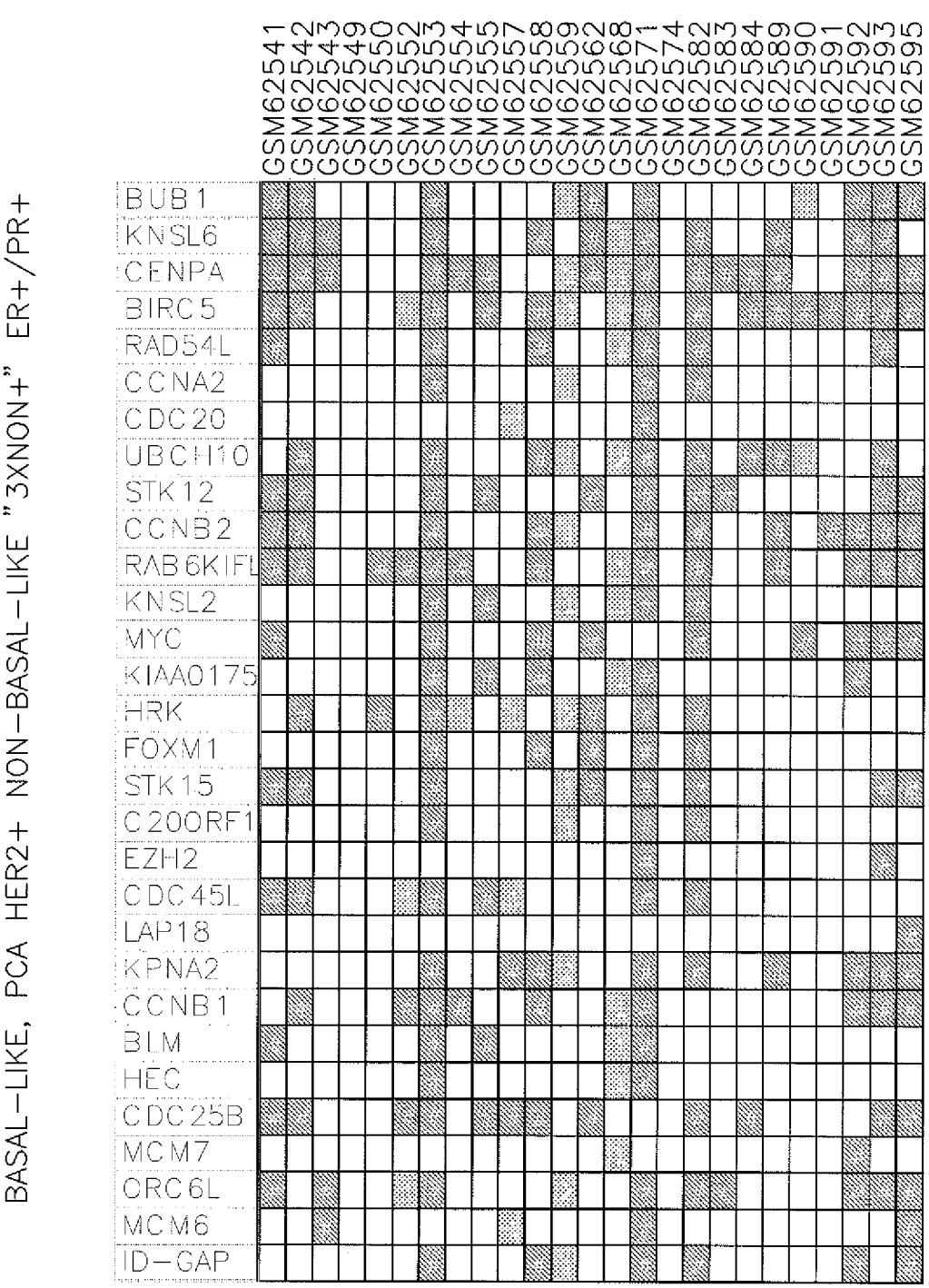


FIG. 4

TOP 30 OVEREXPRESSED ERGO GENES

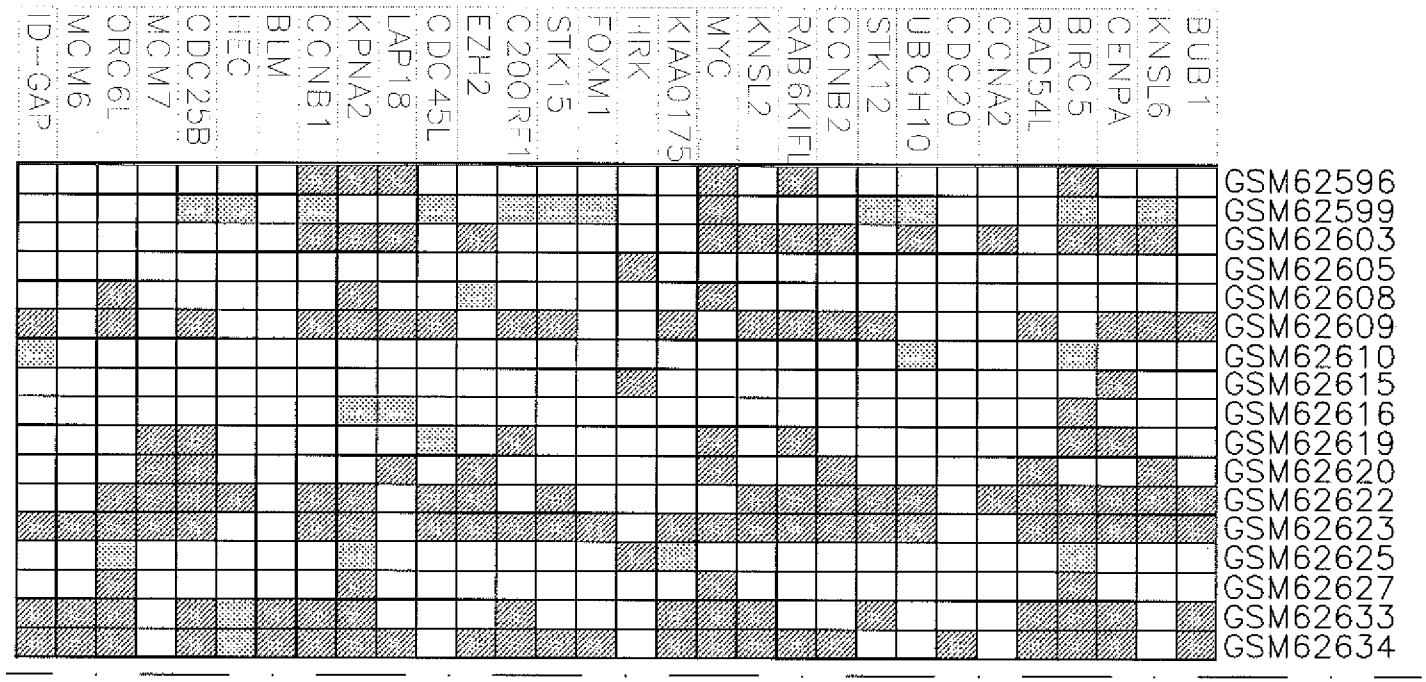


CONTINUED ON SHEET 18

TOP 30 OVEREXPRESSED ERGO GENES

FIG. 4

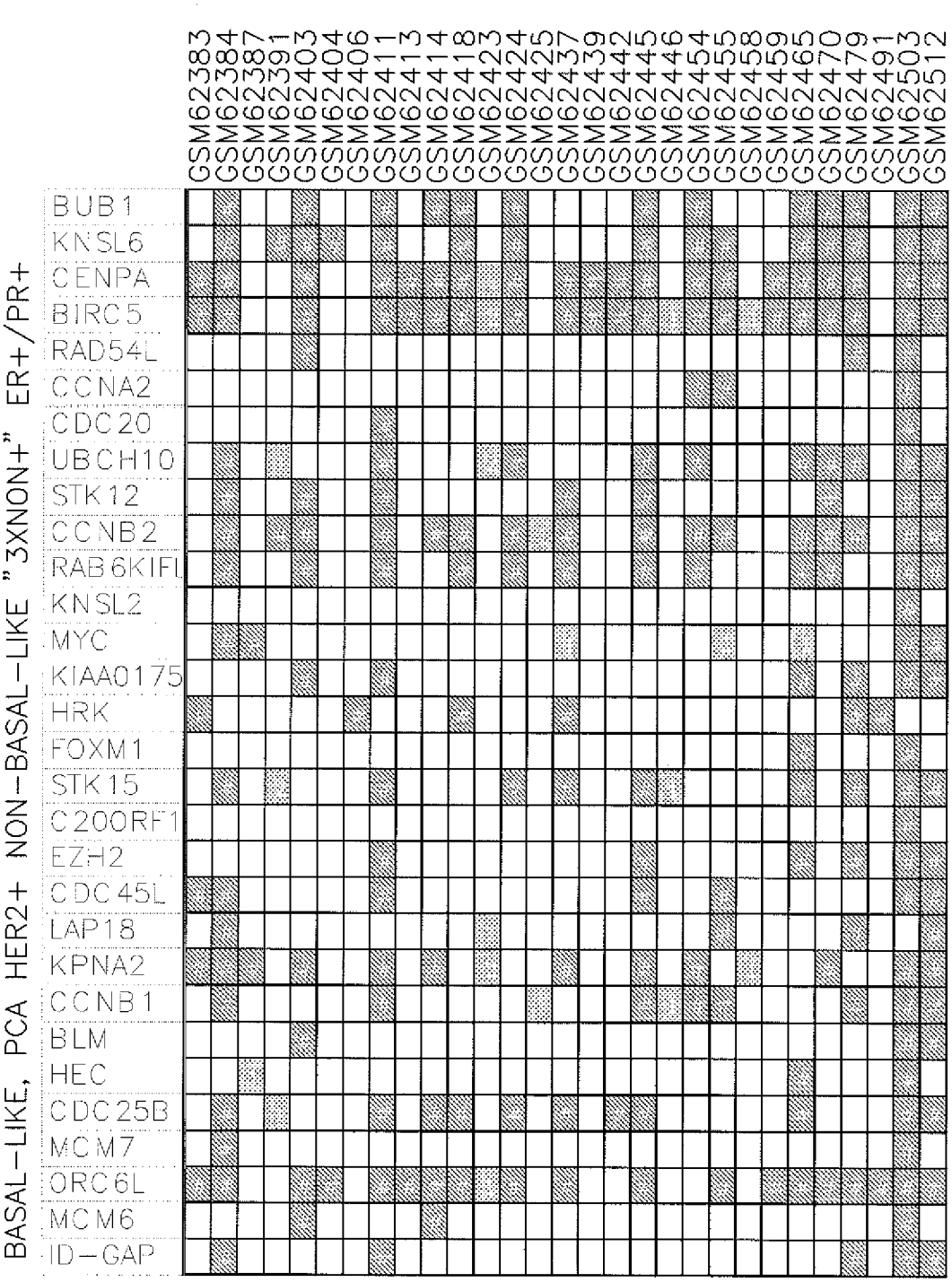
BASAL-LIKE, PCA HER2+ NON-BASAL-LIKE "3XNON+" ER+/PR+



CONTINUED ON SHEET 19

TOP 30 OVEREXPRESSED ERGO GENES

FIG. 4

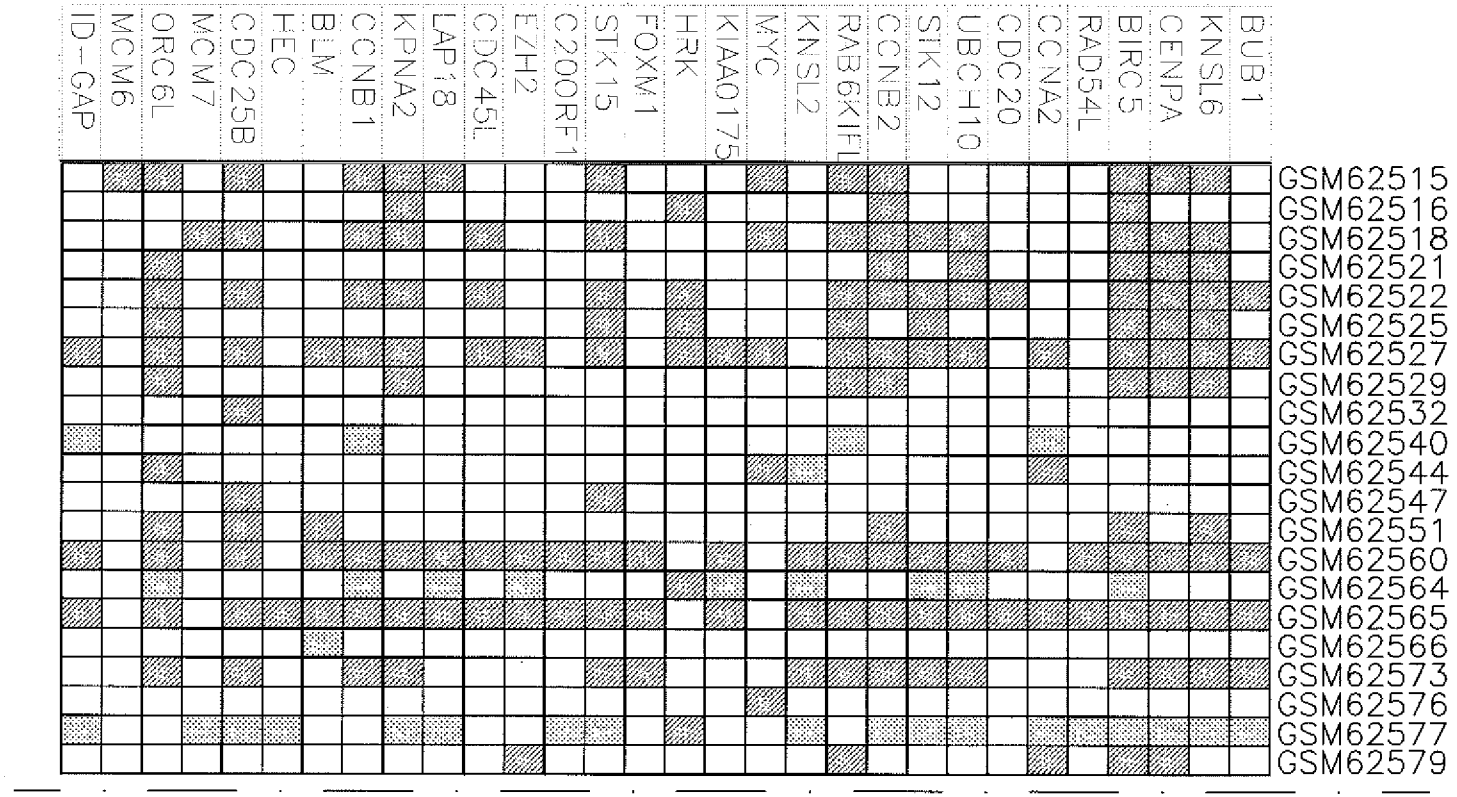


CONTINUED ON SHEET 20

TOP 30 OVEREXPRESSED ERGO GENES

FIG. 4

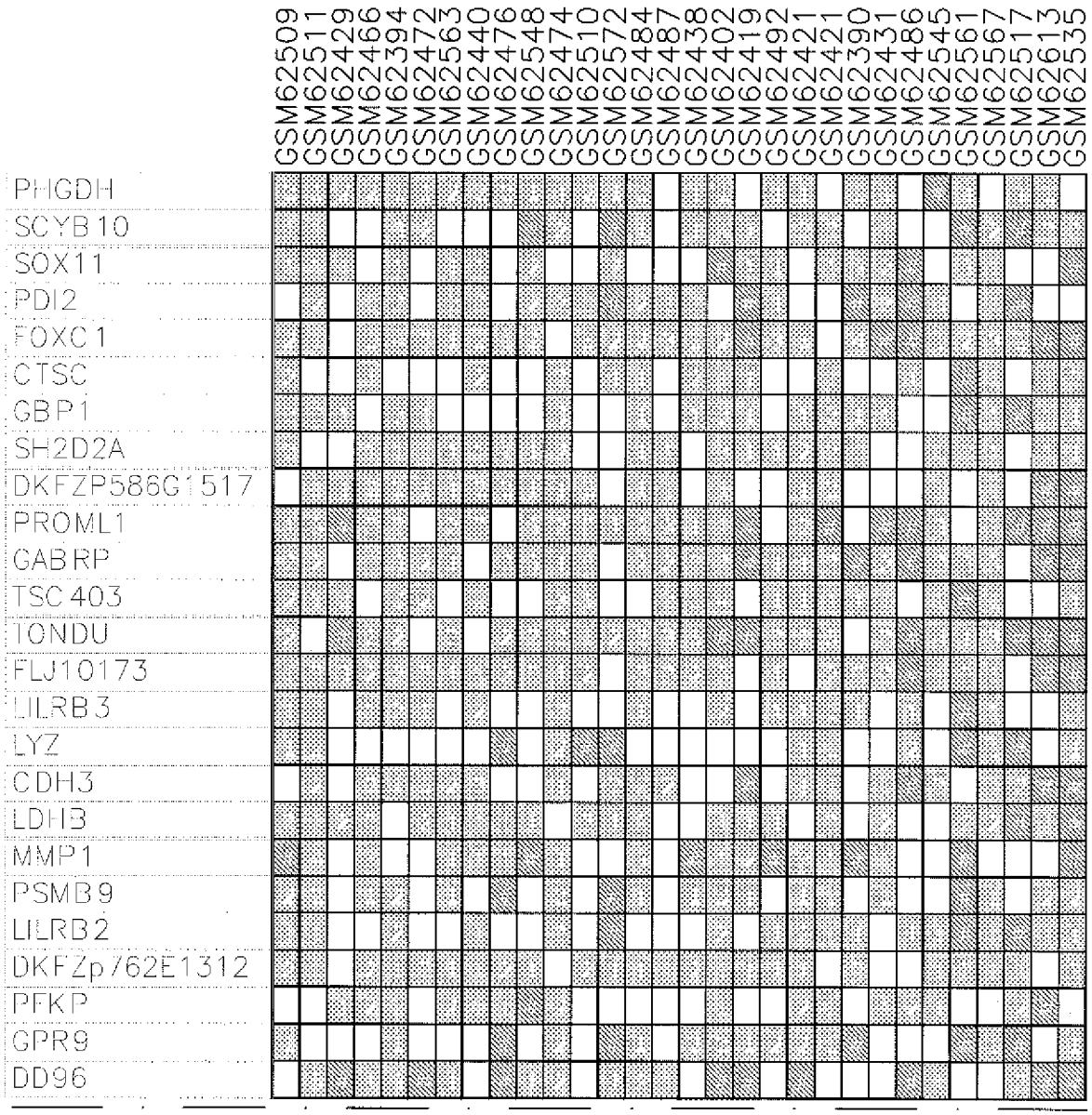
BASAL-LIKE, PCA HER2+ NON-BASAL-LIKE "3XNON+" ER+/PR+



CONTINUED ON SHEET 21

TOP 30 OVEREXPRESSED ERGO GENES

FIG. 4



CONTINUED ON SHEET 22

FIG. 4

BASAL-LIKE, PCA HER2+ NON-BASAL-LIKE "3XNON+" ER+/PR+
TOP 50 OVEREXPRESSED BASAL-LIKE GENES

CONTINUED FROM SHEET 21

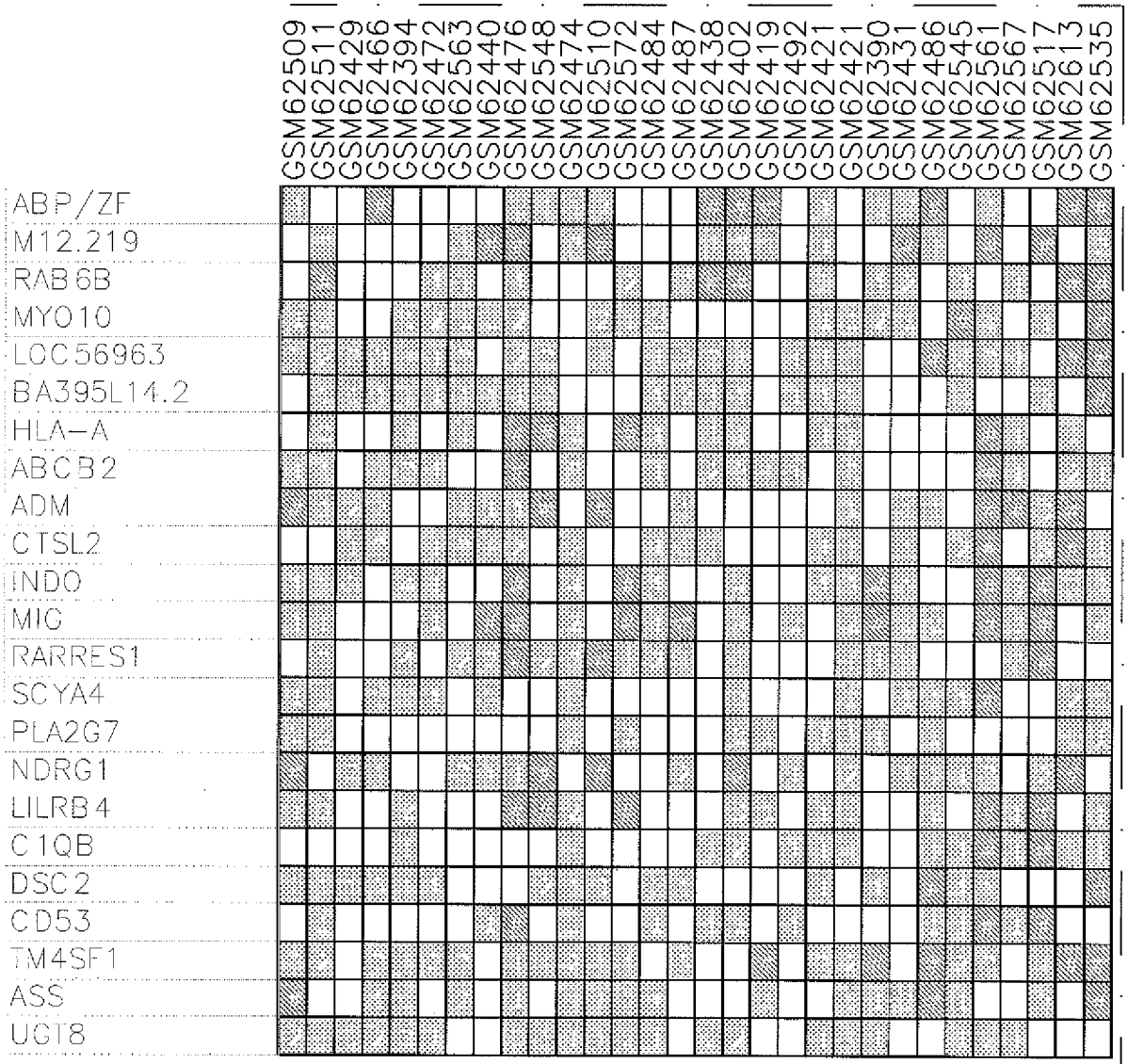
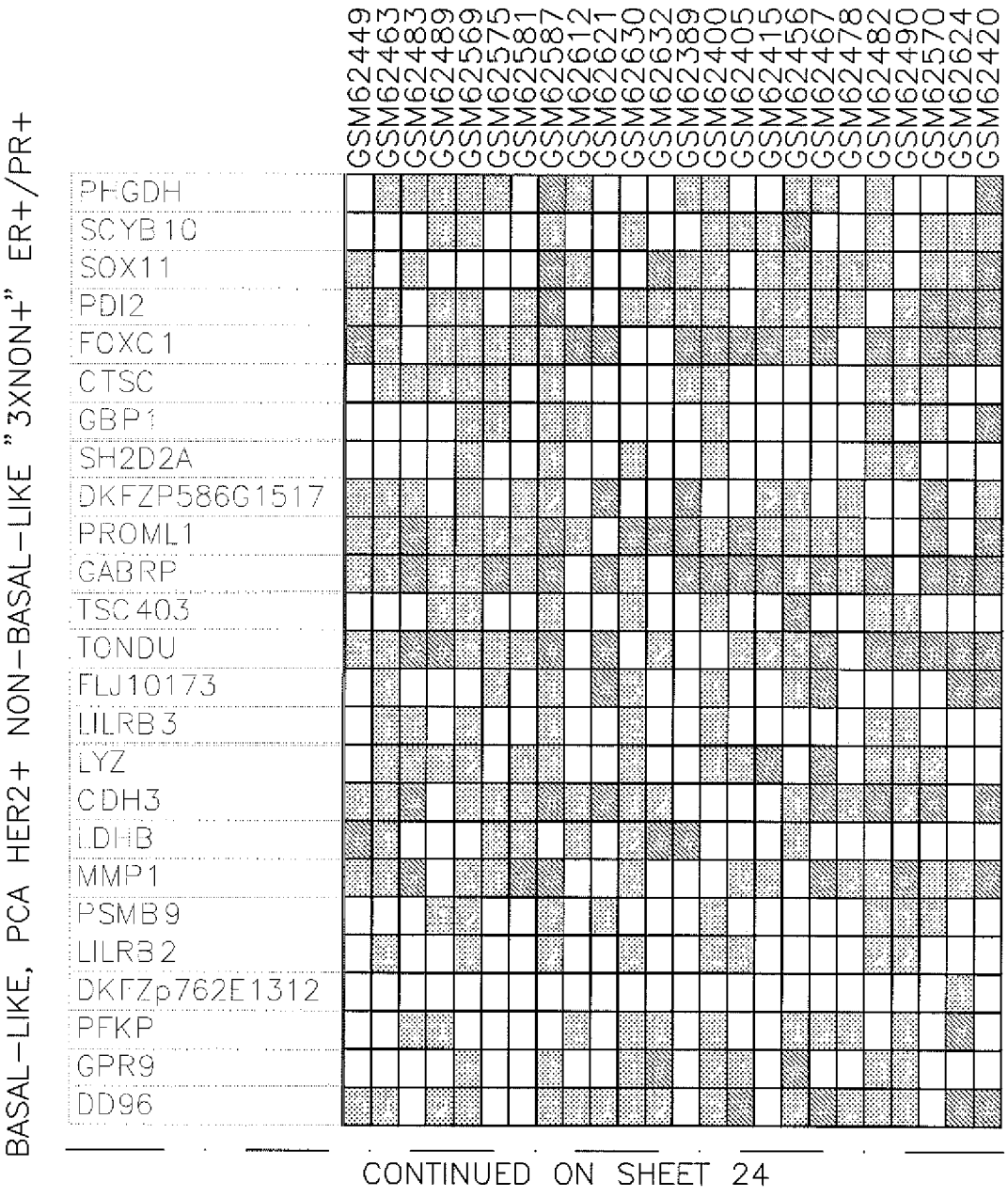


FIG. 4

CONTINUED ON SHEET 23

BASAL-LIKE, PCA HER2+ NON-BASAL-LIKE "3XNON+" ER+/PR+
TOP 50 OVEREXPRESSED BASAL-LIKE GENES



TOP 50 OVEREXPRESSED BASAL-LIKE GENES

FIG. 4

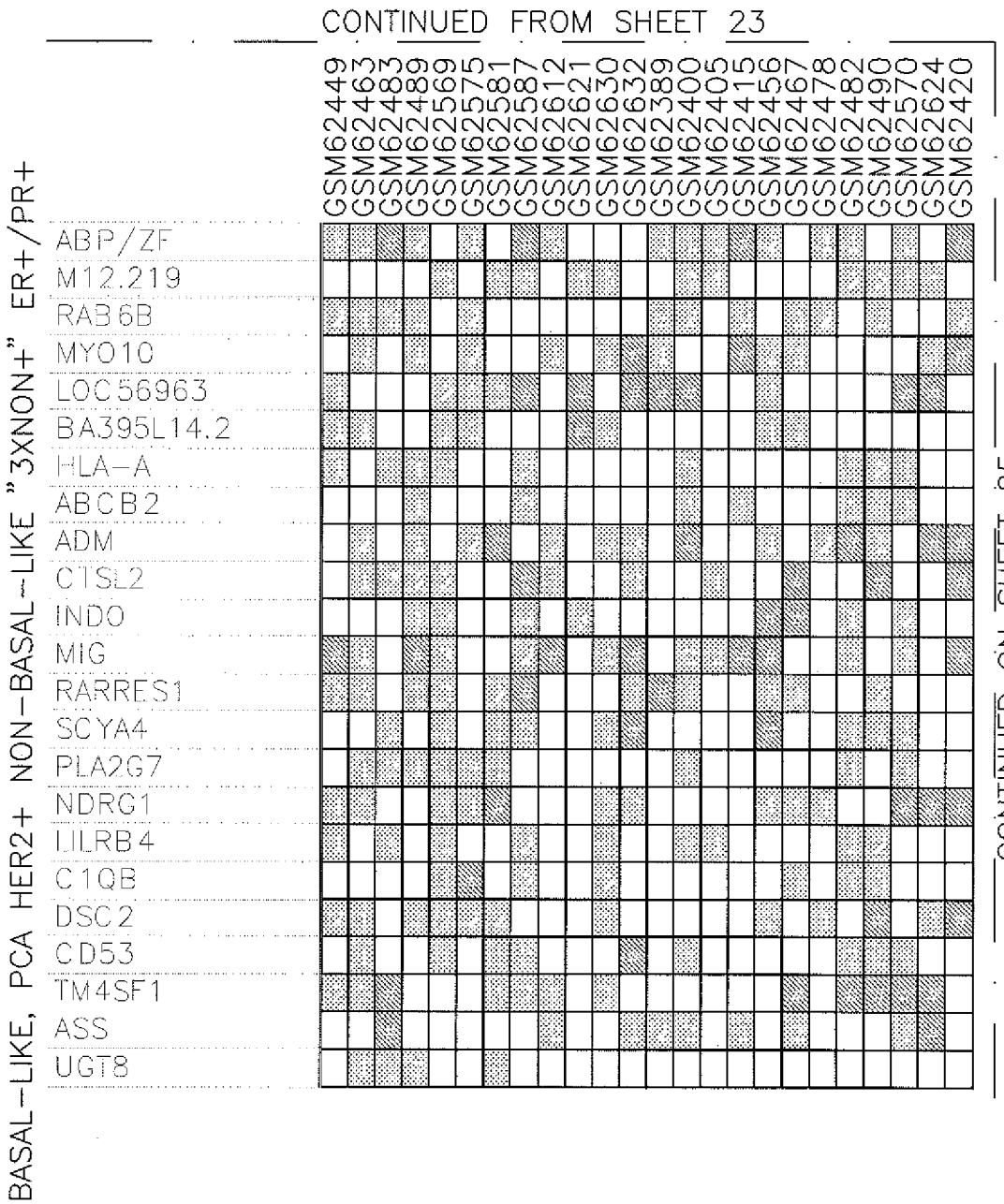
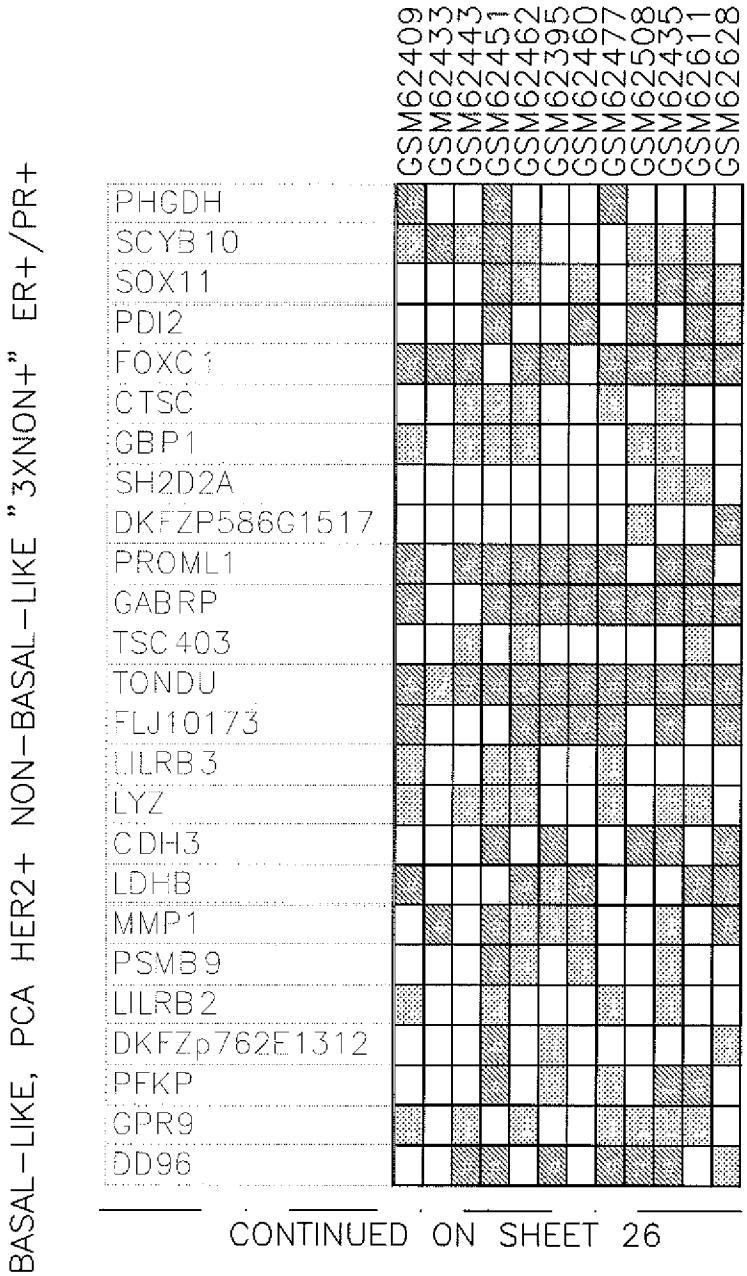

CONTINUED FROM SHEET 23
GSM62449
GSM62463
GSM62483
GSM62489
GSM62569
GSM62575
GSM62581
GSM62587
GSM62612
GSM62621
GSM62630
GSM62632
GSM62389
GSM62400
GSM62405
GSM62415
GSM62456
GSM62467
GSM62478
GSM62482
GSM62490
GSM62570
GSM62624
GSM62420
BASAL-LIKE, PCA HER2+ NON-BASAL-LIKE "3XNON+" ER+/PR+
ABP/ZF
M12.219
RAB6B
MYO1C
LOC56963
BA395L14.2
HLA-A
ABCB2
ADM
CTSL2
INDO
MIG
RARRES1
SCYA4
PLA2G7
NDRG1
LILRB4
C1QB
DSC2
CD53
TM4SF1
ASS
UGT8
CONTINUED ON SHEET 25
TOP 50 OVEREXPRESSED BASAL-LIKE GENES

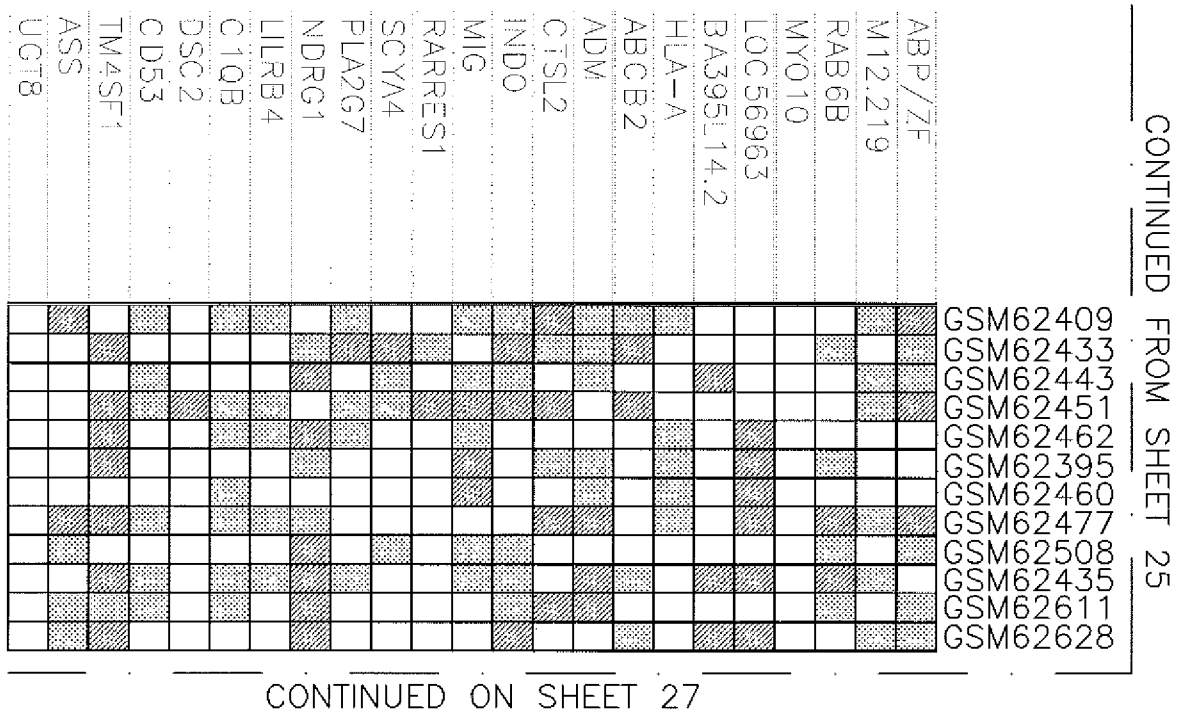
FIG. 4



TOP 50 OVEREXPRESSED BASAL-LIKE GENES

FIG. 4

BASAL-LIKE, PCA HER2+ NON-BASAL-LIKE "3XNON+" ER+/PR+



TOP 50 OVEREXPRESSED BASAL-LIKE GENES

FIG. 4

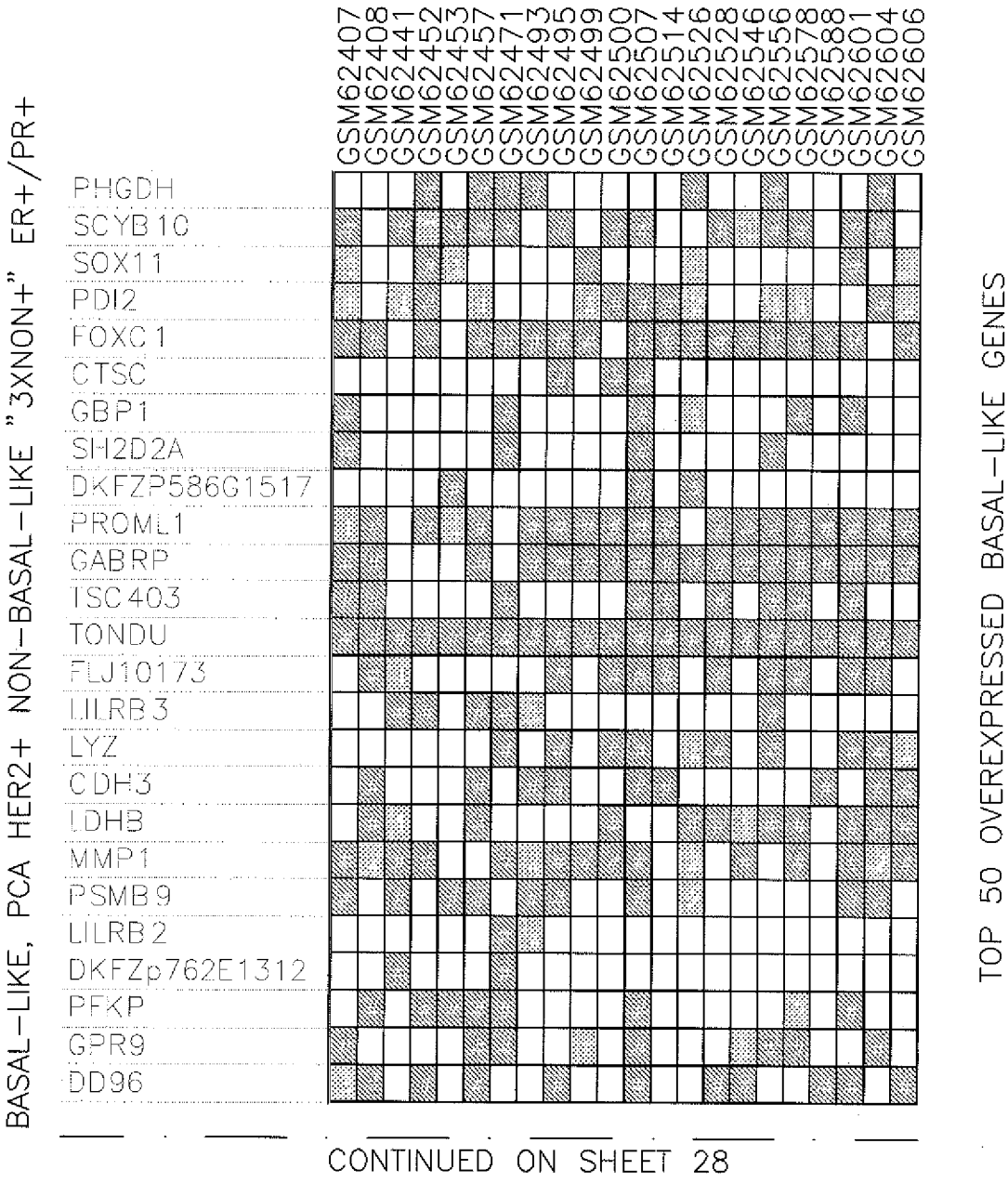
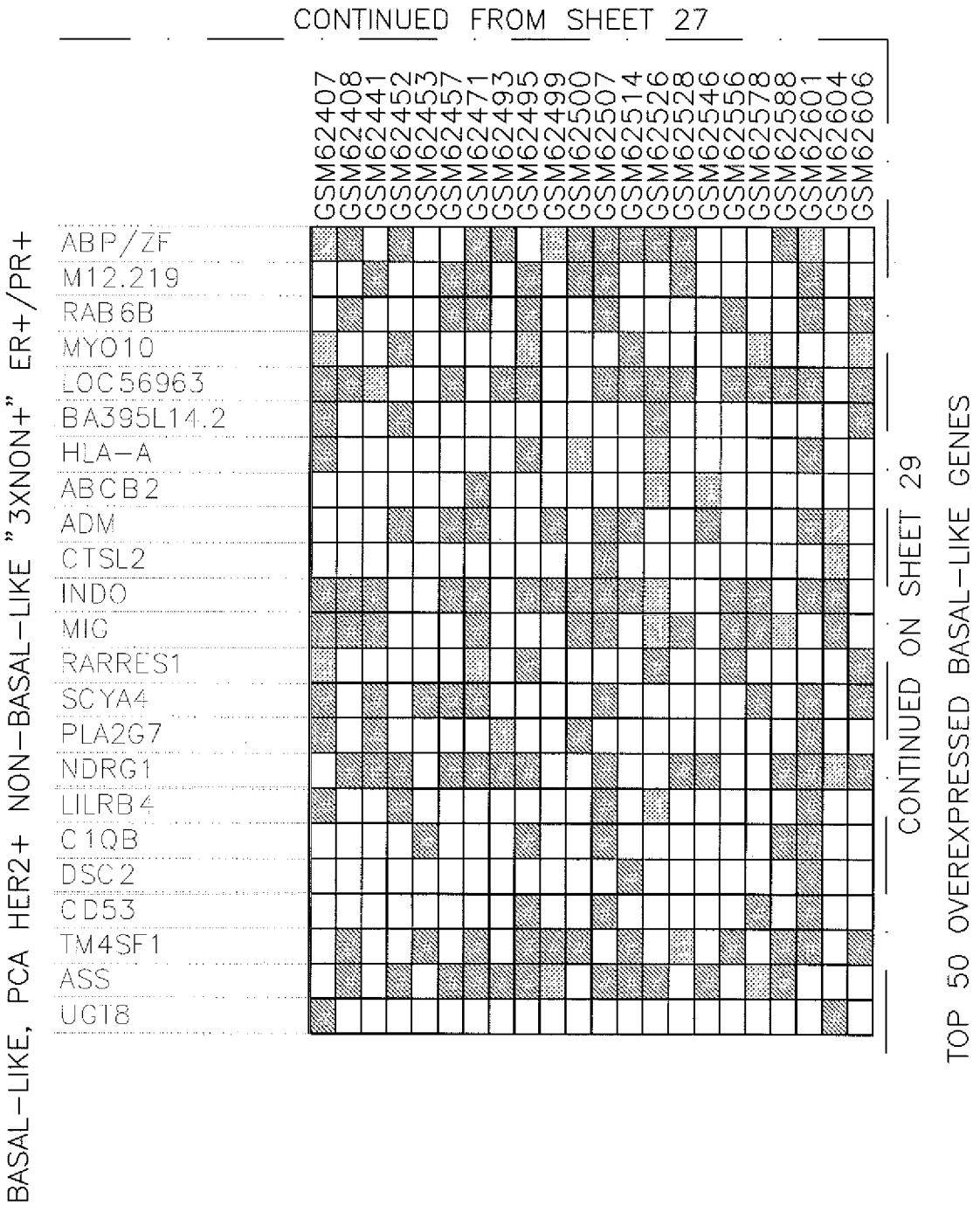

BASAL-LIKE, PCA HER2+ NON-BASAL-LIKE "3XNON+" ER+/PR+
GSM62407
GSM62408
GSM62441
GSM62452
GSM62453
GSM62457
GSM62471
GSM62493
GSM62495
GSM62499
GSM62500
GSM62507
GSM62514
GSM62526
GSM62528
GSM62546
GSM62556
GSM62578
GSM62588
GSM62601
GSM62604
GSM62606
PHGDH
SCYB10
SOX11
PDI2
FOXC1
CTSC
GBP1
SH2D2A
DKFZP586G1517
PROML1
GABRP
ISC403
TONDU
FLJ10173
LILRB3
LYZ
CDH3
LDHB
MMP1
PSMB9
LILRB2
DKFZp762E1312
PFKP
GPR9
DD96
TOP 50 OVEREXPRESSED BASAL-LIKE GENES
CONTINUED ON SHEET 28

FIG. 4


CONTINUED FROM SHEET 27
GSM62407
GSM62408
GSM62441
GSM62452
GSM62453
GSM62457
GSM62471
GSM62493
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GSM62499
GSM62500
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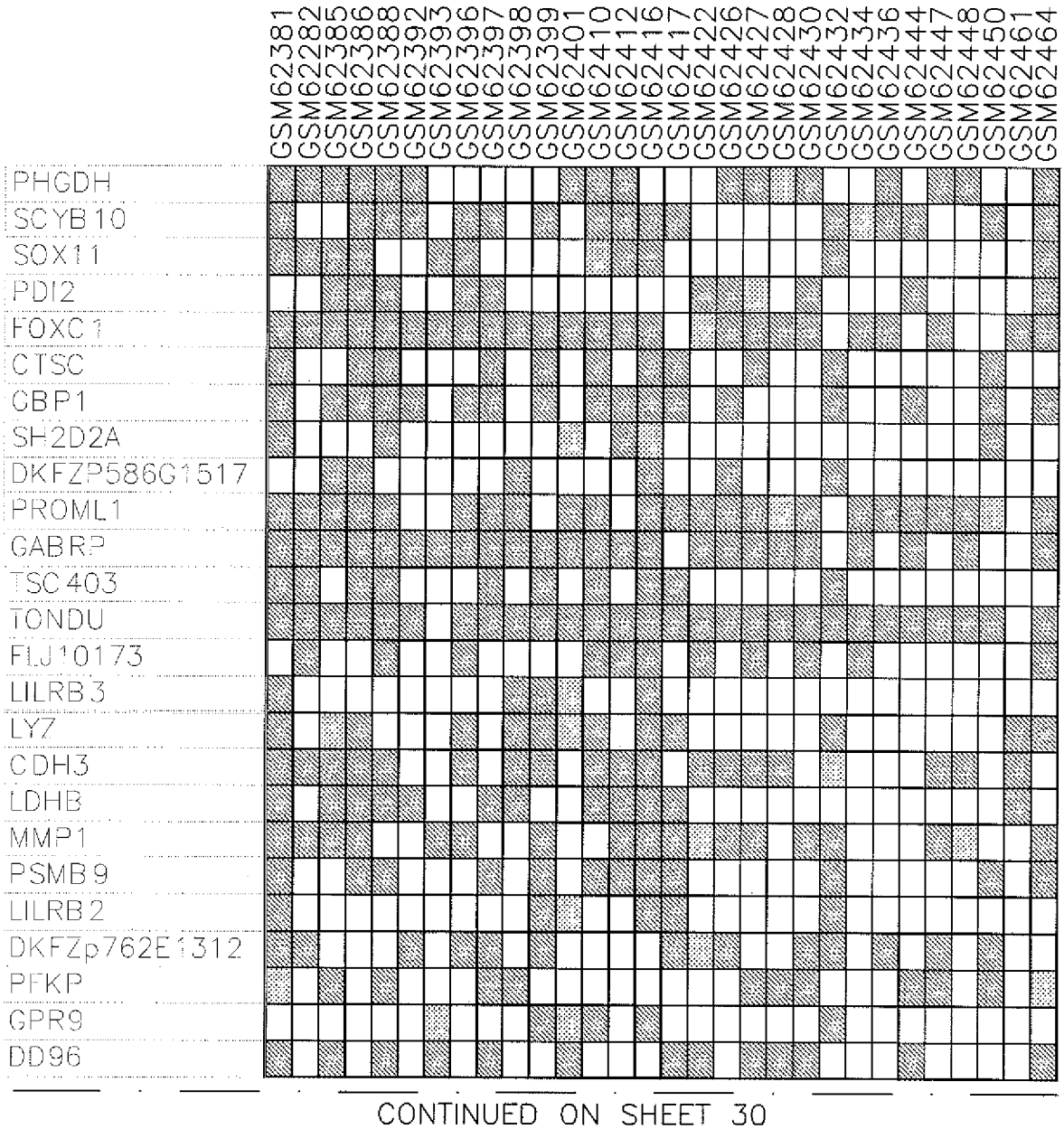
GSM62556
GSM62578
GSM62588
GSM62601
GSM62604
GSM62606
ABP/ZF
M12.219
RAB6B
MYO10
LOC56963
BA395L14.2
HLA-A
ABCB2
ADM
CTSL2
INDO
MIC
RARRES1
SCYA4
PLA2G7
NDRG1
LILRB4
C1QB
DSC2
CD53
TM4SF1
ASS
UGT8
BASAL-LIKE, PCA HER2+ NON-BASAL-LIKE "3XNON+" ER+/PR+
CONTINUED ON SHEET 29
TOP 50 OVEREXPRESSED BASAL-LIKE GENES

FIG. 4



CONTINUED ON SHEET 30

FIG. 4

BASAL-LIKE, PCA HER2+ NON-BASAL-LIKE "3XNON+" ER+/PR+
TOP 50 OVEREXPRESSED BASAL-LIKE GENES

CONTINUED FROM SHEET 29

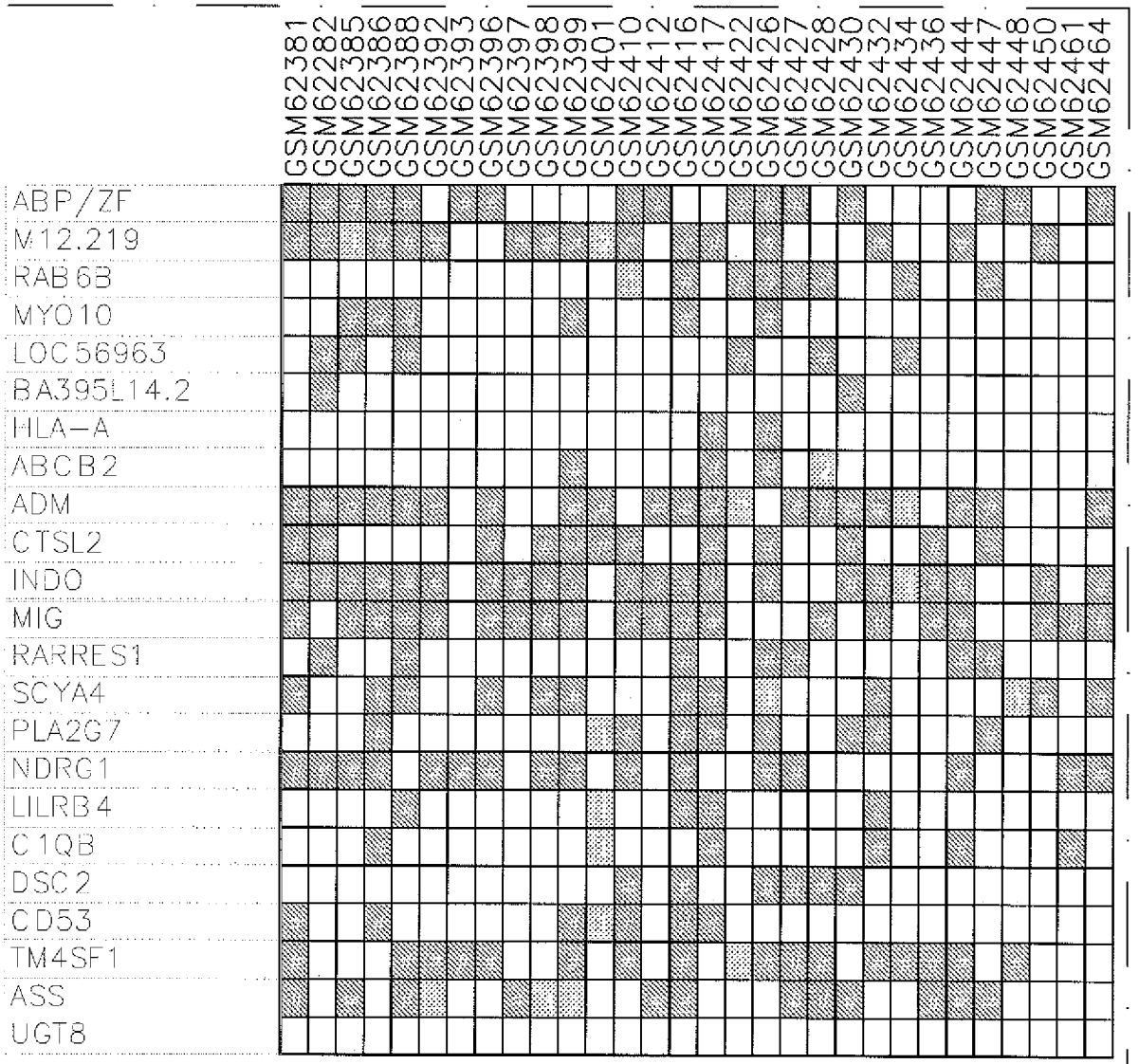


FIG. 4

CONTINUE ON SHEET 31

BASAL-LIKE, PCA HER2+ NON-BASAL-LIKE "3XNON+" ER+/PR+
TOP 50 OVEREXPRESSED BASAL-LIKE GENES

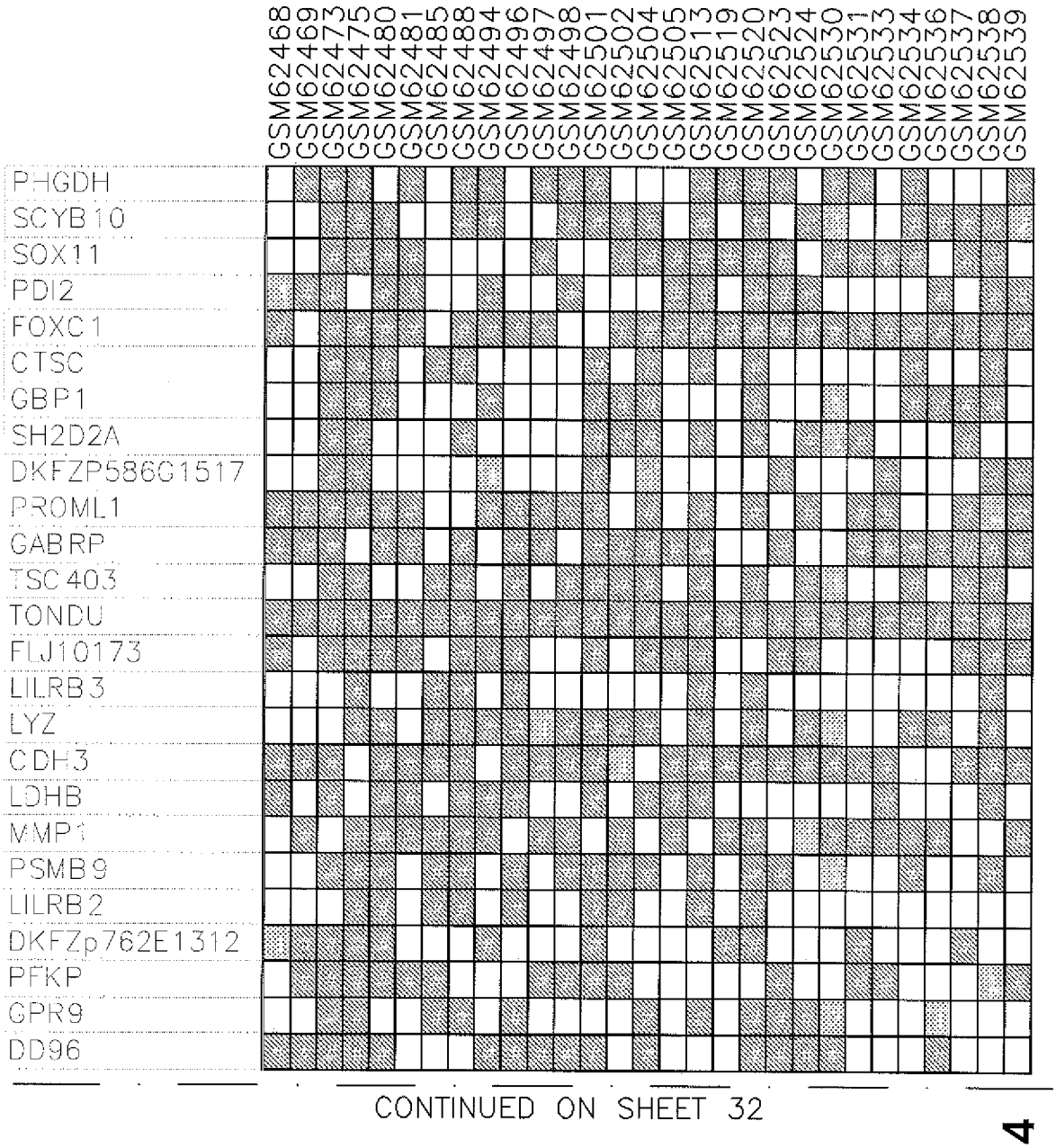


FIG. 4

BASAL-LIKE, PCA HER2+ NON-BASAL-LIKE "3XNON+" ER+/PR+
TOP 50 OVEREXPRESSED BASAL-LIKE GENES

CONTINUED FROM SHEET 31

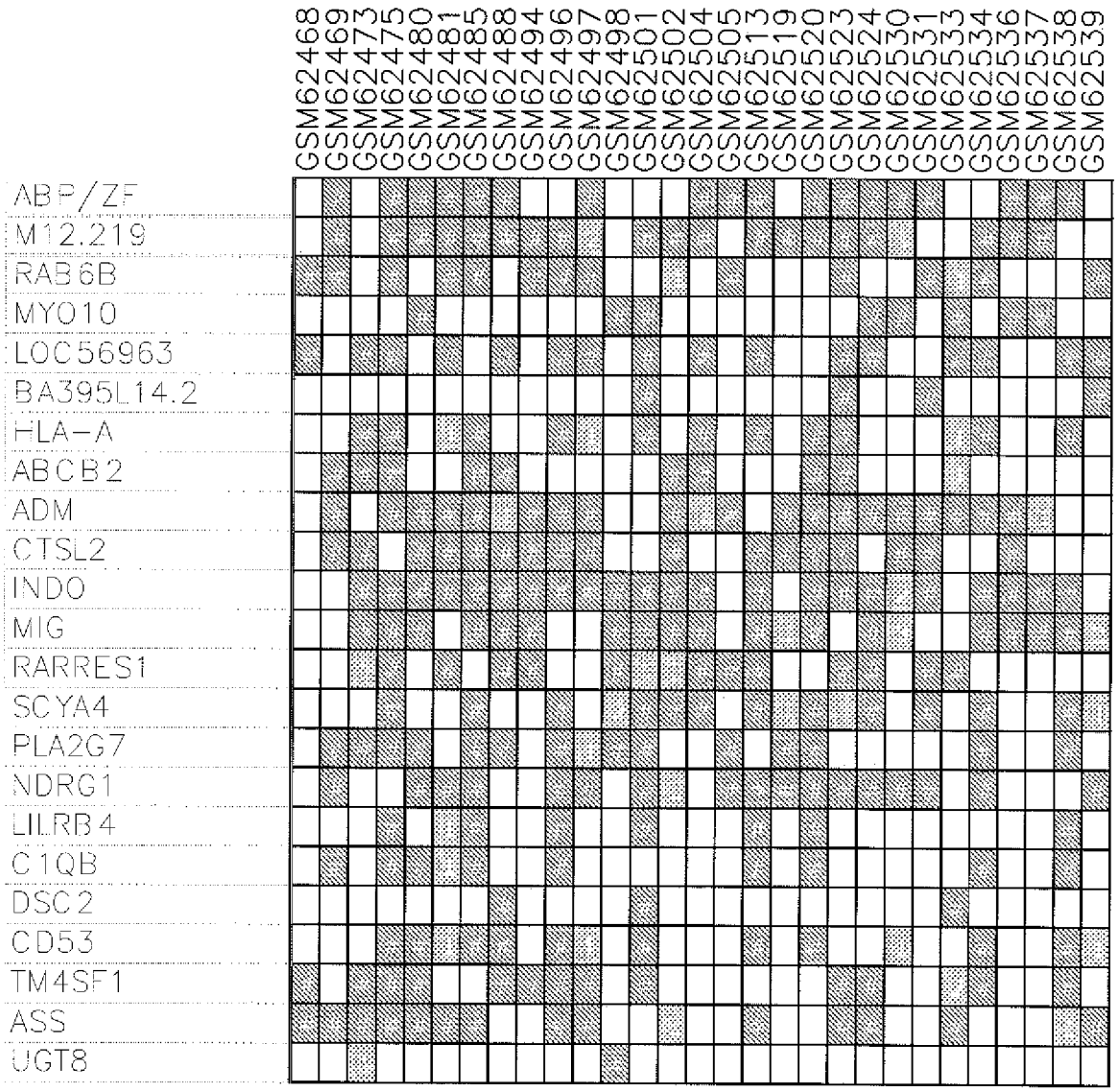
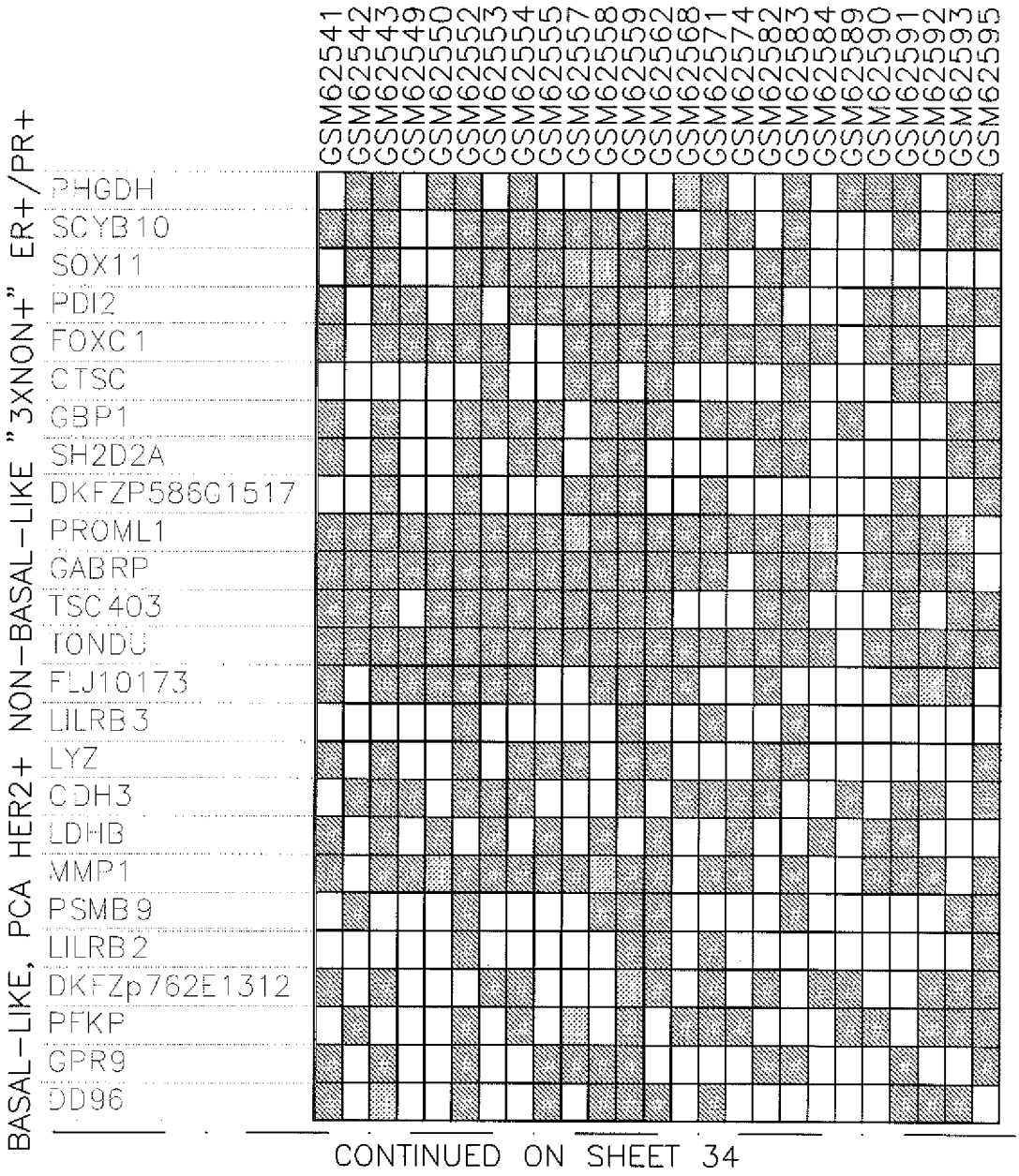


FIG. 4

CONTINUE ON SHEET 33

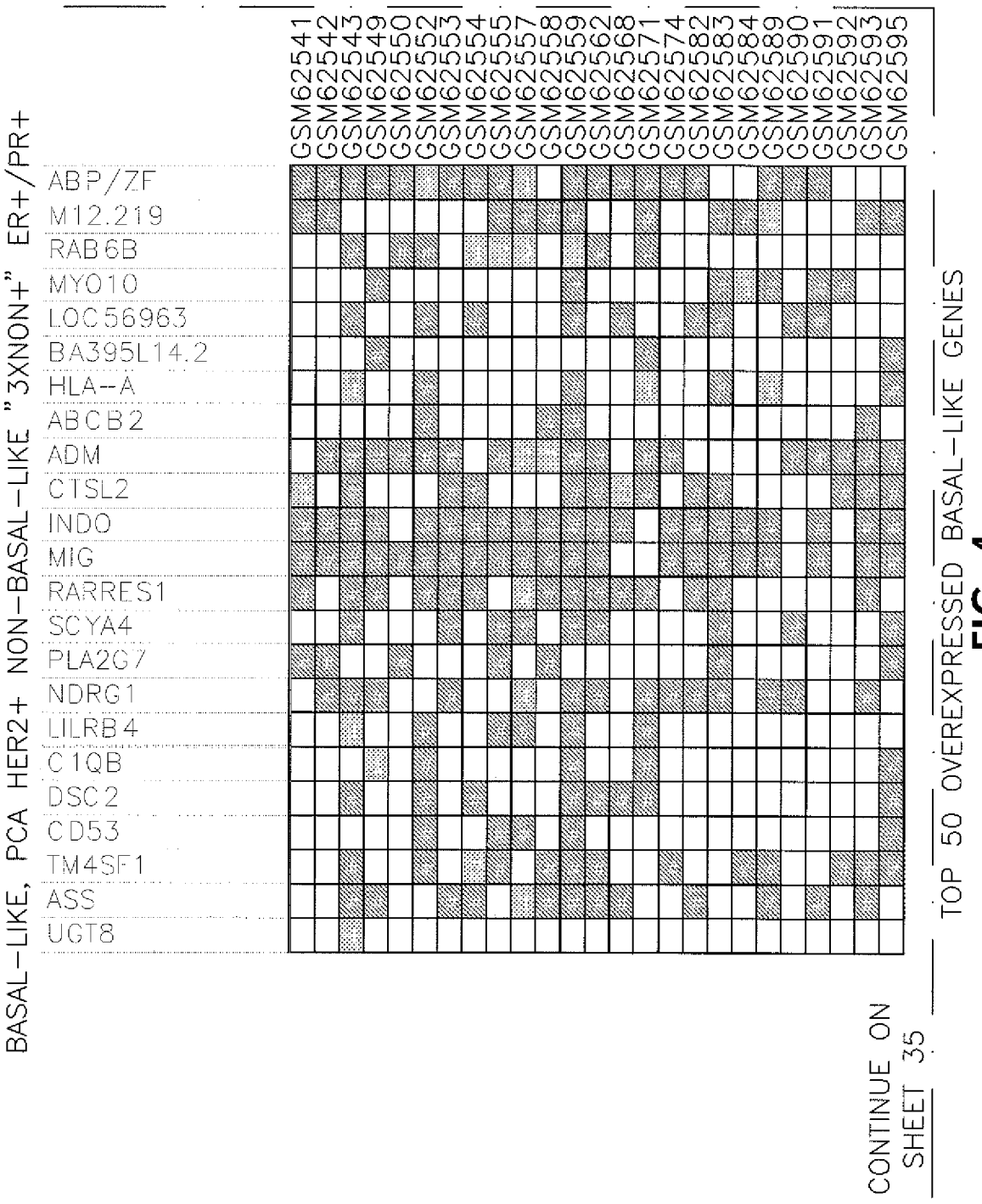
BASAL-LIKE, PCA HER2+ NON-BASAL-LIKE "3XNON+" ER+/PR+
TOP 50 OVEREXPRESSED BASAL-LIKE GENES



CONTINUED ON SHEET 34

TOP 50 OVEREXPRESSED BASAL-LIKE GENES

FIG. 4


CONTINUED FROM SHEET 33
GSM625541
GSM625542
GSM625543
GSM625549
GSM625550
GSM625552
GSM625553
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GSM625574
GSM625582
GSM625583
GSM625584
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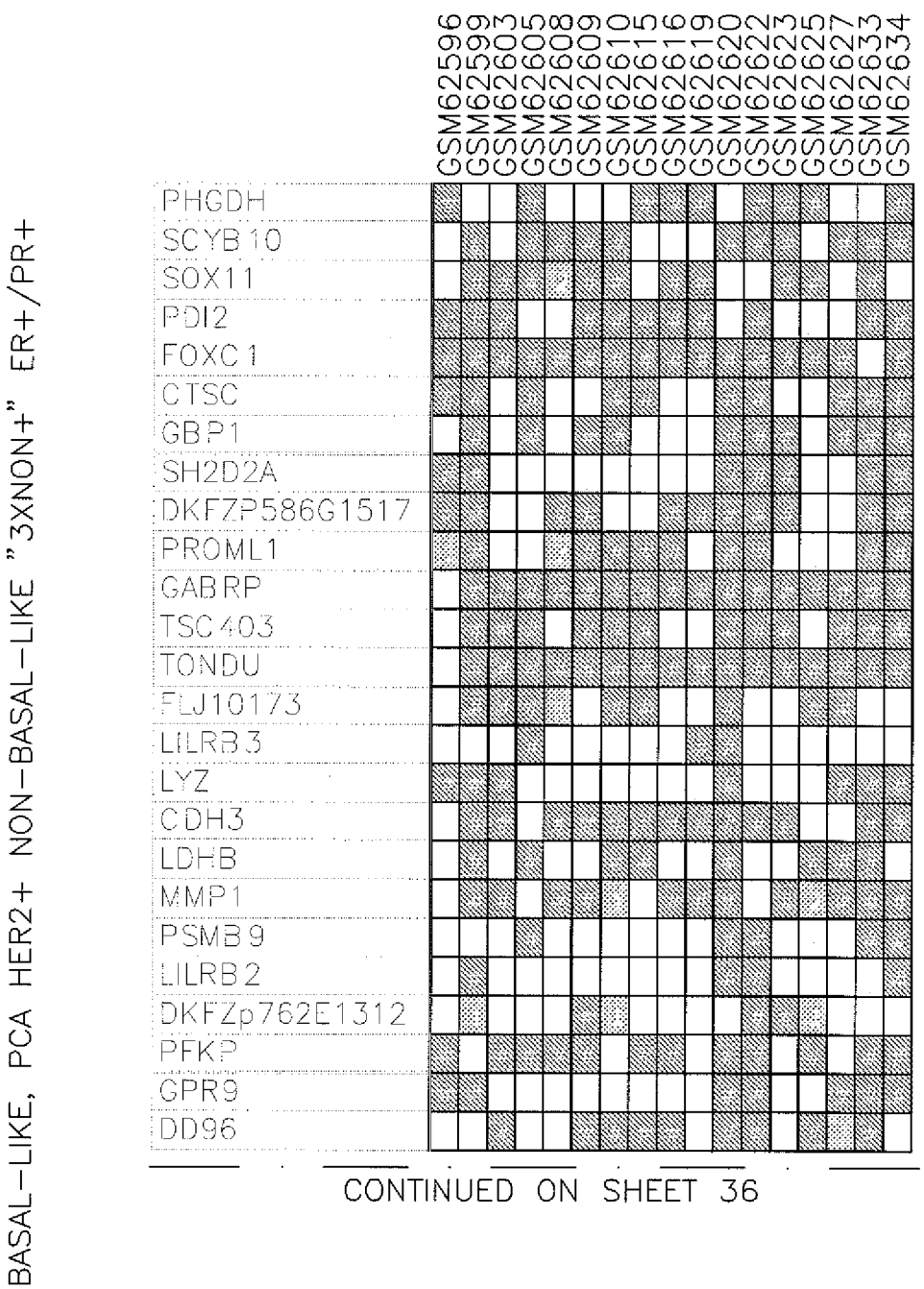
GSM625592
GSM625593
GSM625595
ABP/ZF
M12.219
RAB6B
MYO10
LOC56963
BA395L14.2
HLA--A
ABCB2
ADM
CTSL2
INDO
MIG
RARRES1
SCYA4
PLA2G7
NDRG1
LILRB4
C1QB
DSC2
CD53
TM4SF1
ASS
UGT8
BASAL-LIKE, PCA HER2+ NON-BASAL-LIKE "3XNON+" ER+/PR+
TOP 50 OVEREXPRESSED BASAL-LIKE GENES
CONTINUE ON SHEET 35

FIG. 4



TOP 50 OVEREXPRESSED BASAL-LIKE GENES

FIG. 4

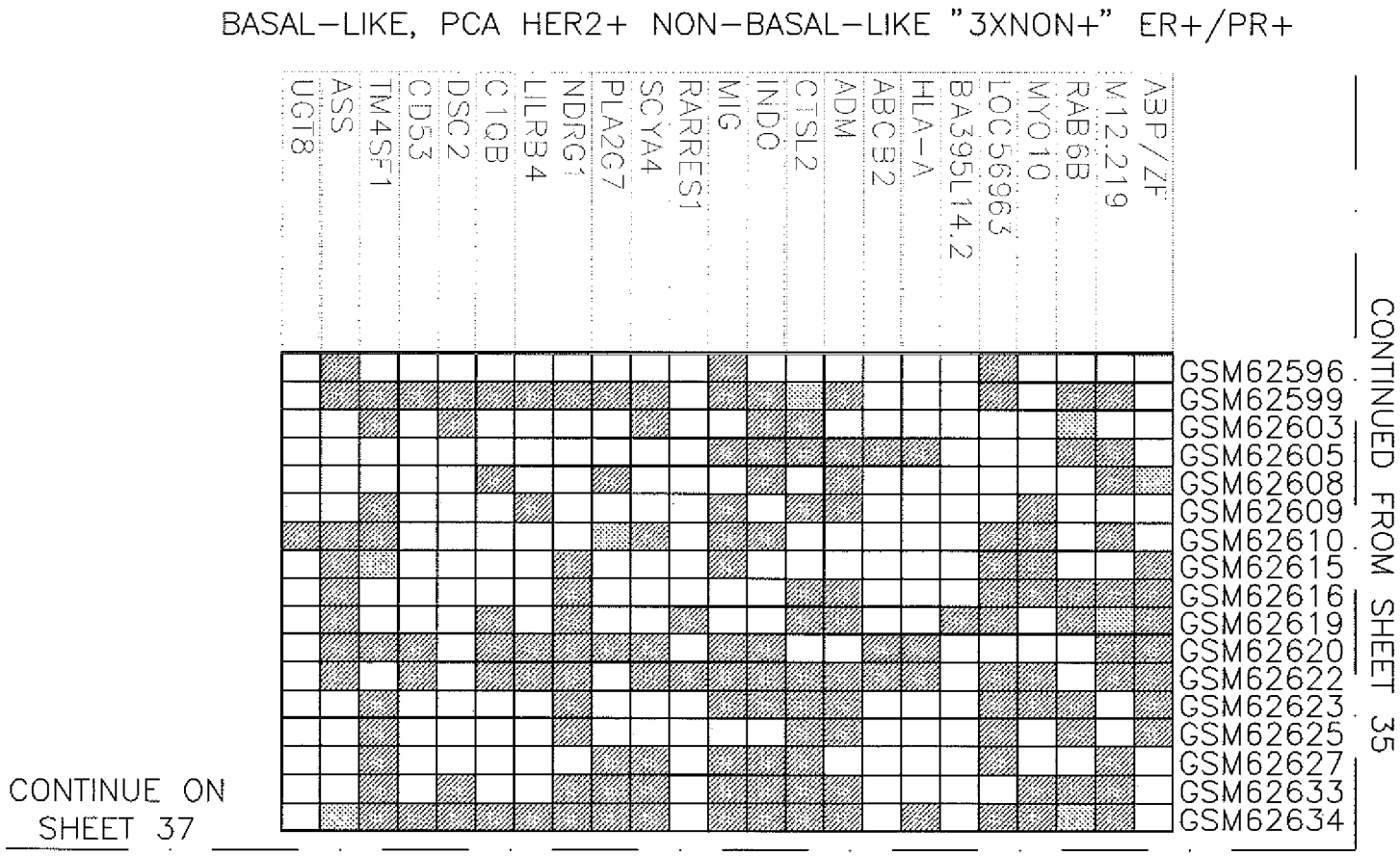
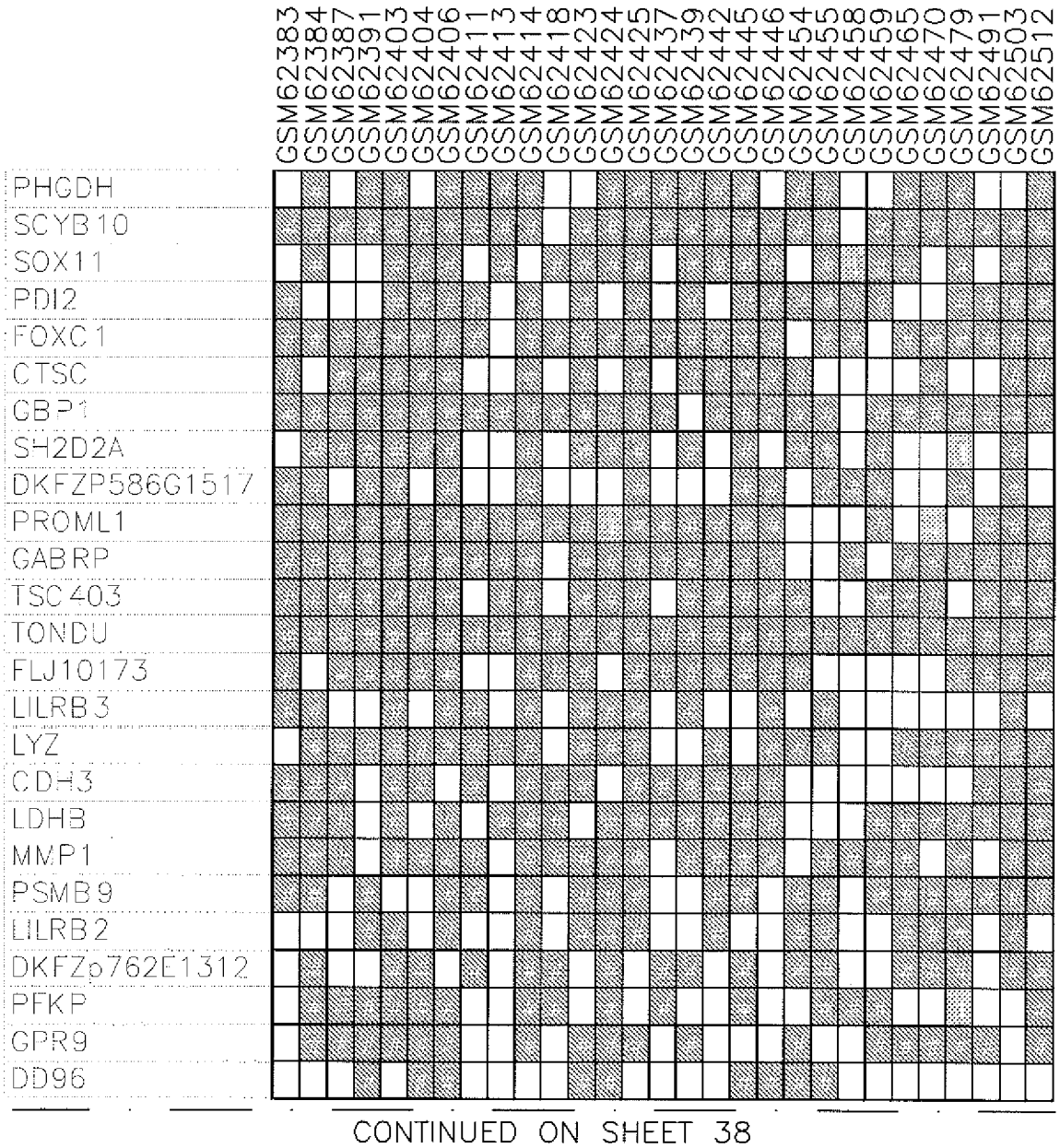

BASAL-LIKE, PCA HER2+ NON-BASAL-LIKE "3XNON+" ER+/PR+
A3P/ZF
M12.219
RAB6B
MYO10
LOC56963
BA395L14.2
HLA-A
ABCB2
ADM
CTSL2
INDO
MIG
RARRES1
SCYA4
PLA2G7
NDRG1
LILRB4
C1QB
DSC2
CD53
TM4SF1
ASS
UGT8
GSM62596
GSM62599
GSM62603
GSM62605
GSM62608
GSM62609
GSM62610
GSM62615
GSM62616
GSM62619
GSM62620
GSM62622
GSM62623
GSM62625
GSM62627
GSM62633
GSM62634
CONTINUED FROM SHEET 35
CONTINUE ON SHEET 37
TOP 50 OVEREXPRESSED BASAL-LIKE GENES

FIG. 4



CONTINUED ON SHEET 38

FIG. 4

BASAL-LIKE, PCA HER2+ NON-BASAL-LIKE "3XNON+" ER+/PR+
TOP 50 OVEREXPRESSED BASAL-LIKE GENES

CONTINUED FROM SHEET 37

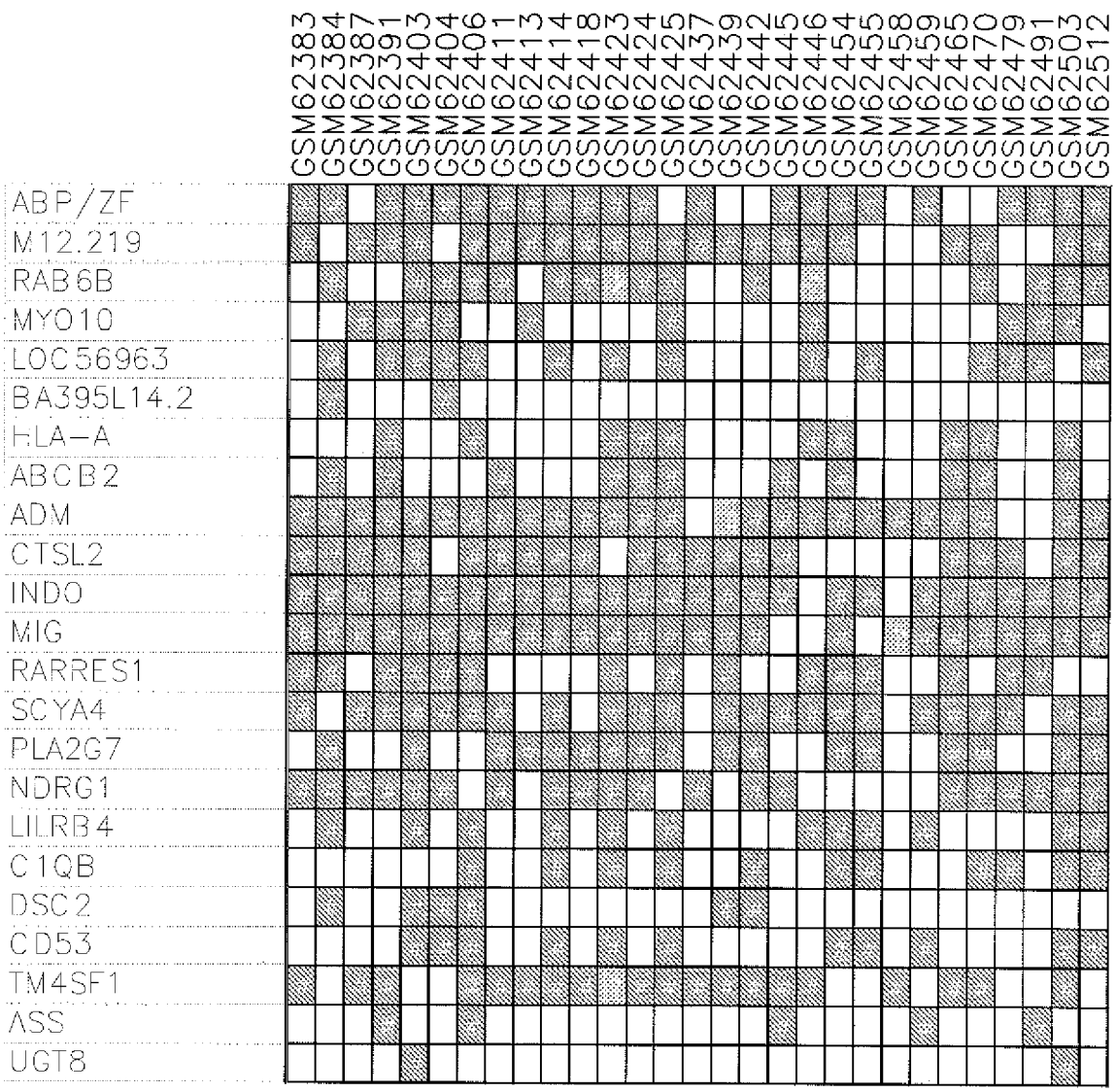
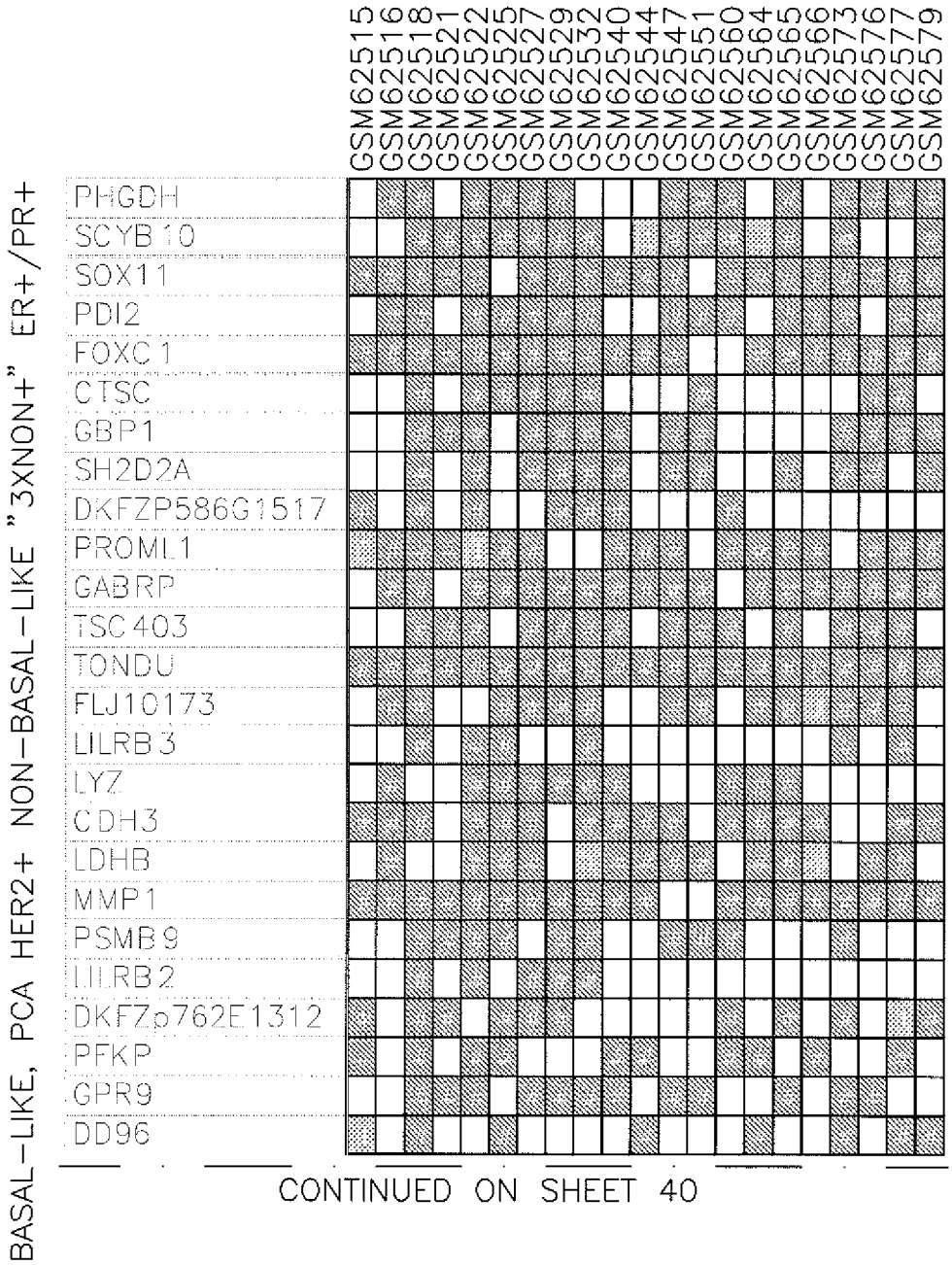


FIG. 4

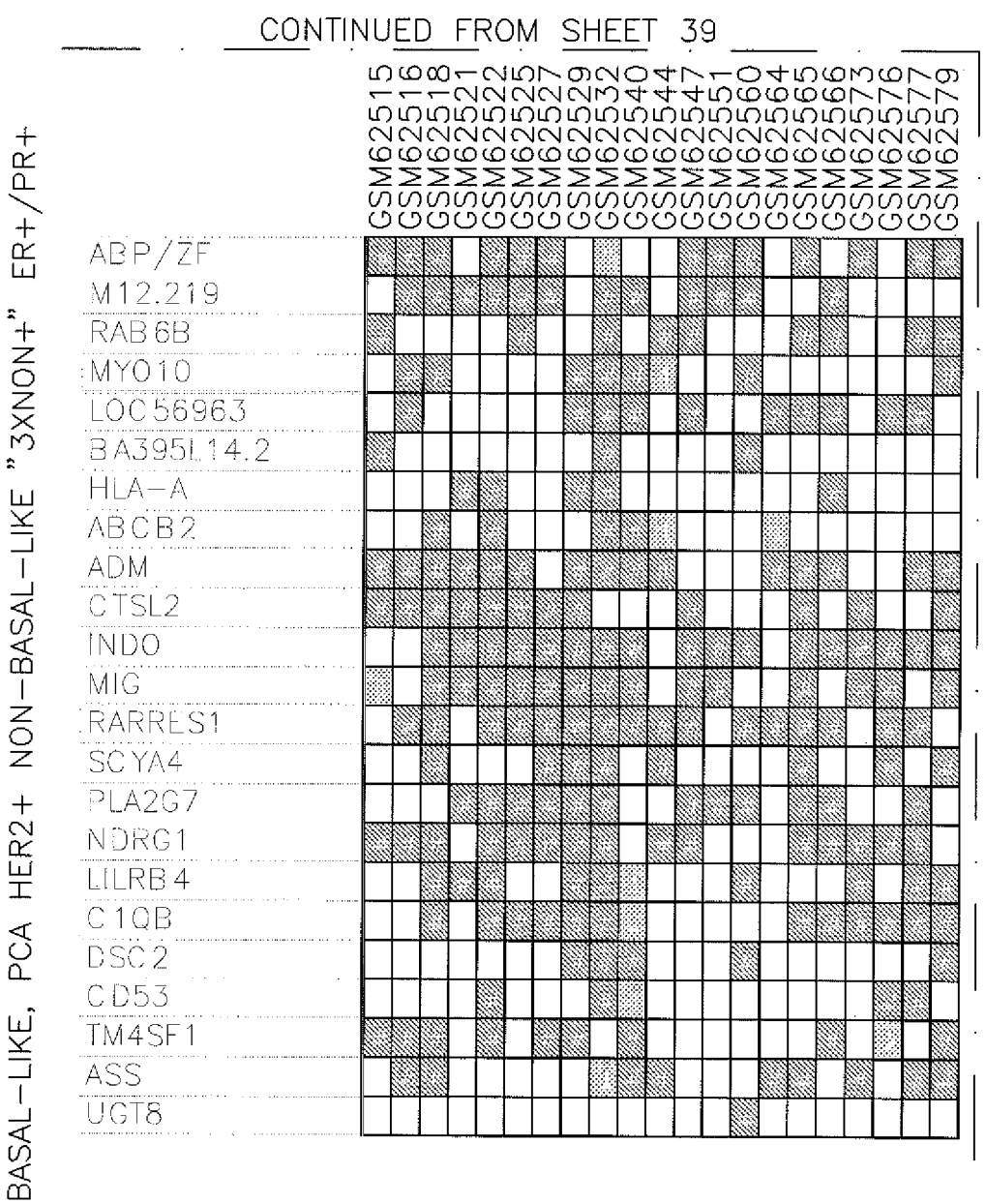
CONTINUE ON SHEET 39

BASAL-LIKE, PCA HER2+ NON-BASAL-LIKE "3XNON+" ER+/PR+
TOP 50 OVEREXPRESSED BASAL-LIKE GENES



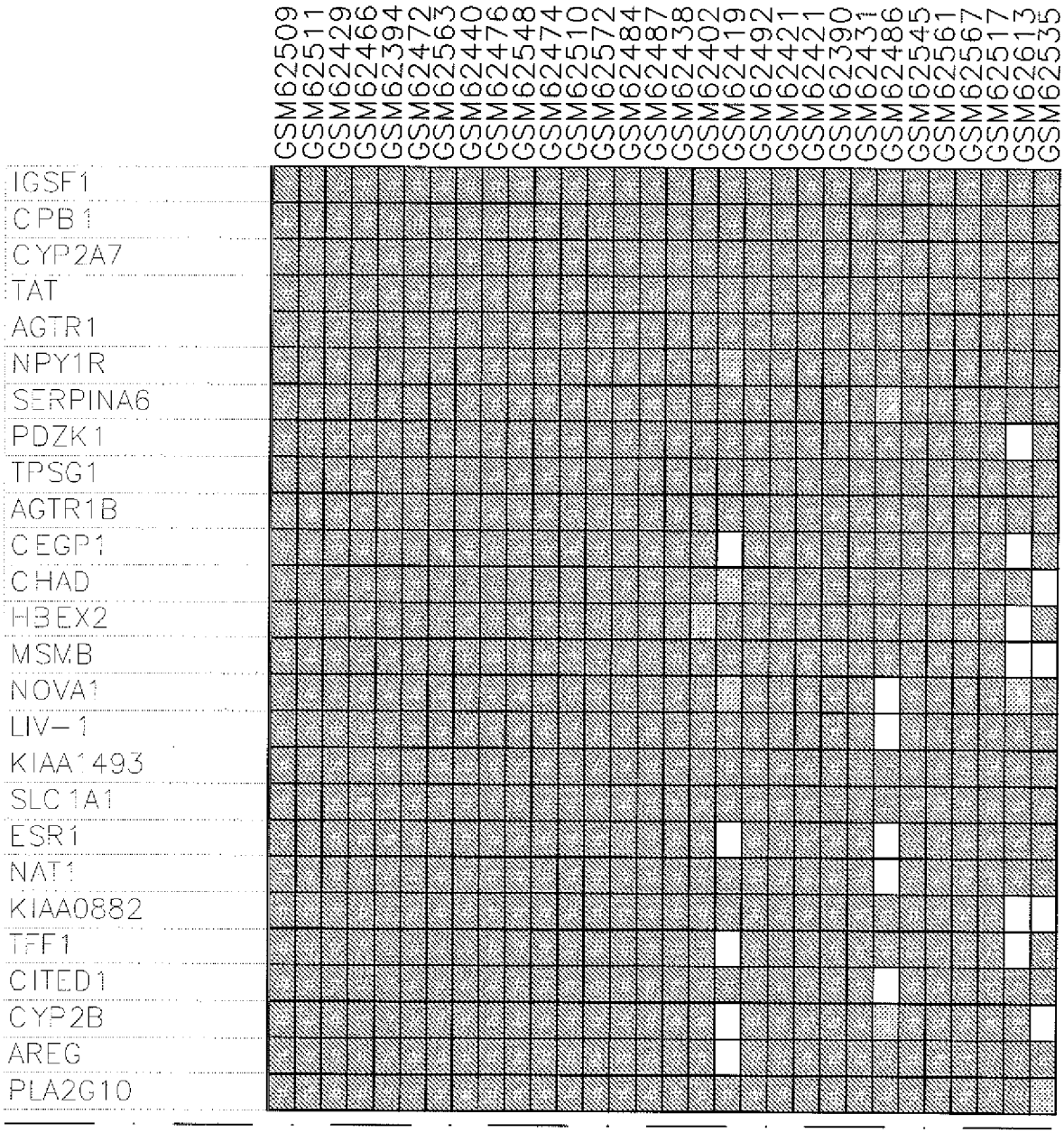
TOP 50 OVEREXPRESSED BASAL-LIKE GENES

FIG. 4



TOP 50 OVEREXPRESSED BASAL-LIKE GENES

FIG. 4



CONTINUED ON SHEET 42

FIG. 4

TOP 50 UNDEREXPRESSED BASAL-LIKE GENES
BASAL-LIKE, PCA HER2+ NON-BASAL-LIKE "3XNON+" ER+/PR+

CONTINUED FROM SHEET 41

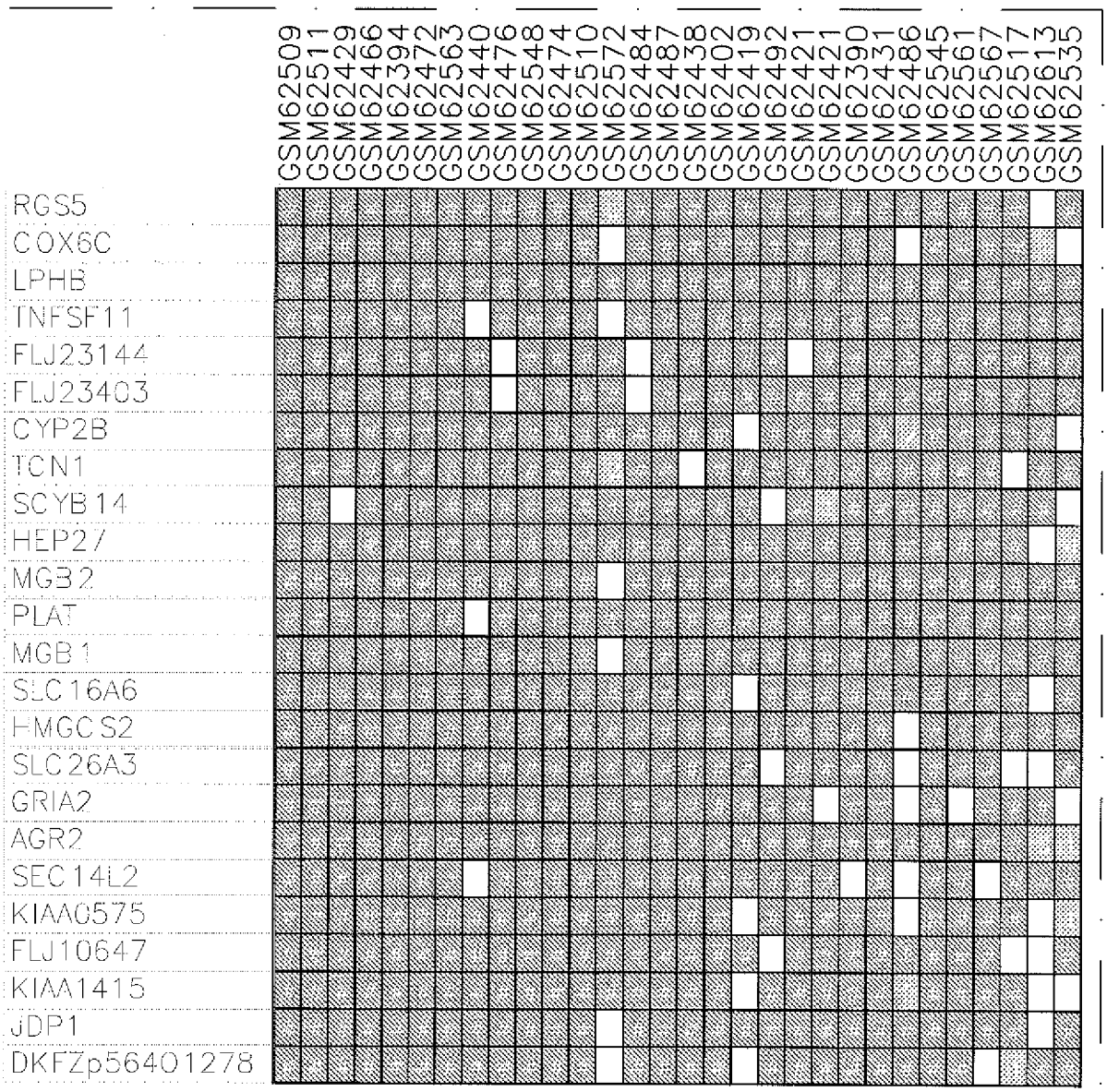
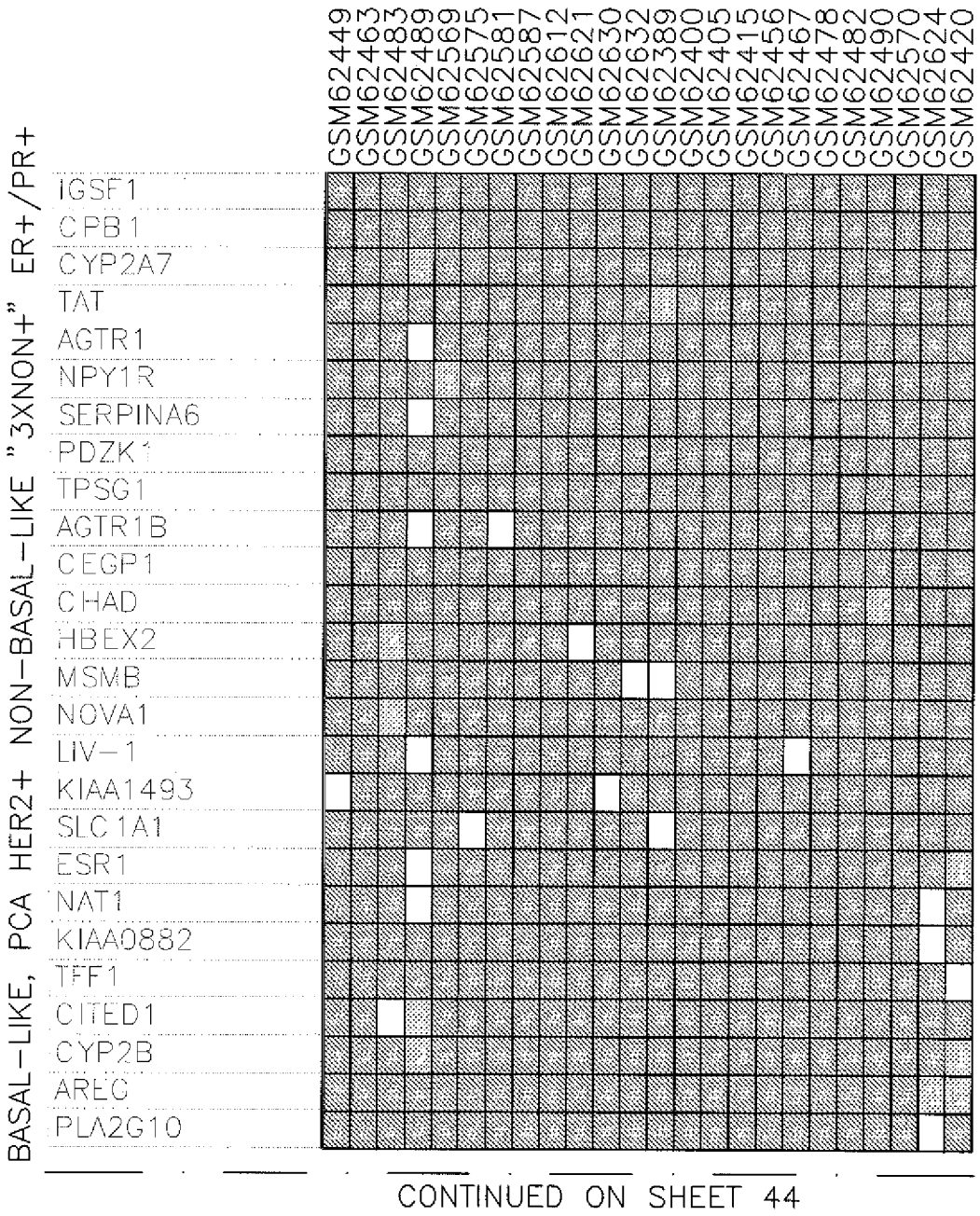


FIG. 4

CONTINUE ON SHEET 43

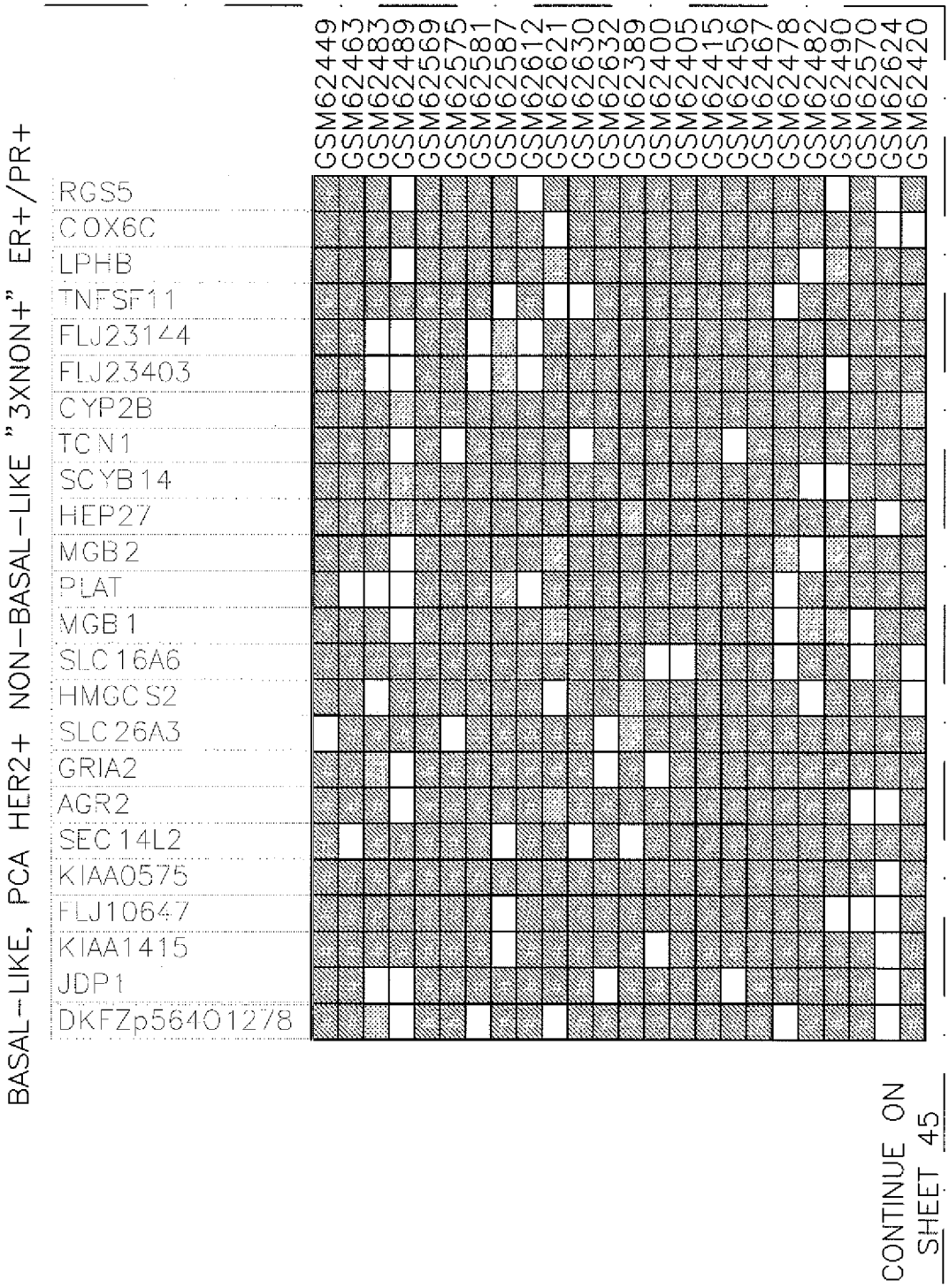
TOP 50 UNDEREXPRESSED BASAL-LIKE GENES
BASAL-LIKE, PCA HER2+ NON-BASAL-LIKE "3XNON+" ER+/PR+



CONTINUED ON SHEET 44

TOP 50 UNDEREXPRESSED BASAL-LIKE GENES

FIG. 4



TOP 50 UNDEREXPRESSED BASAL-LIKE GENES

FIG. 4

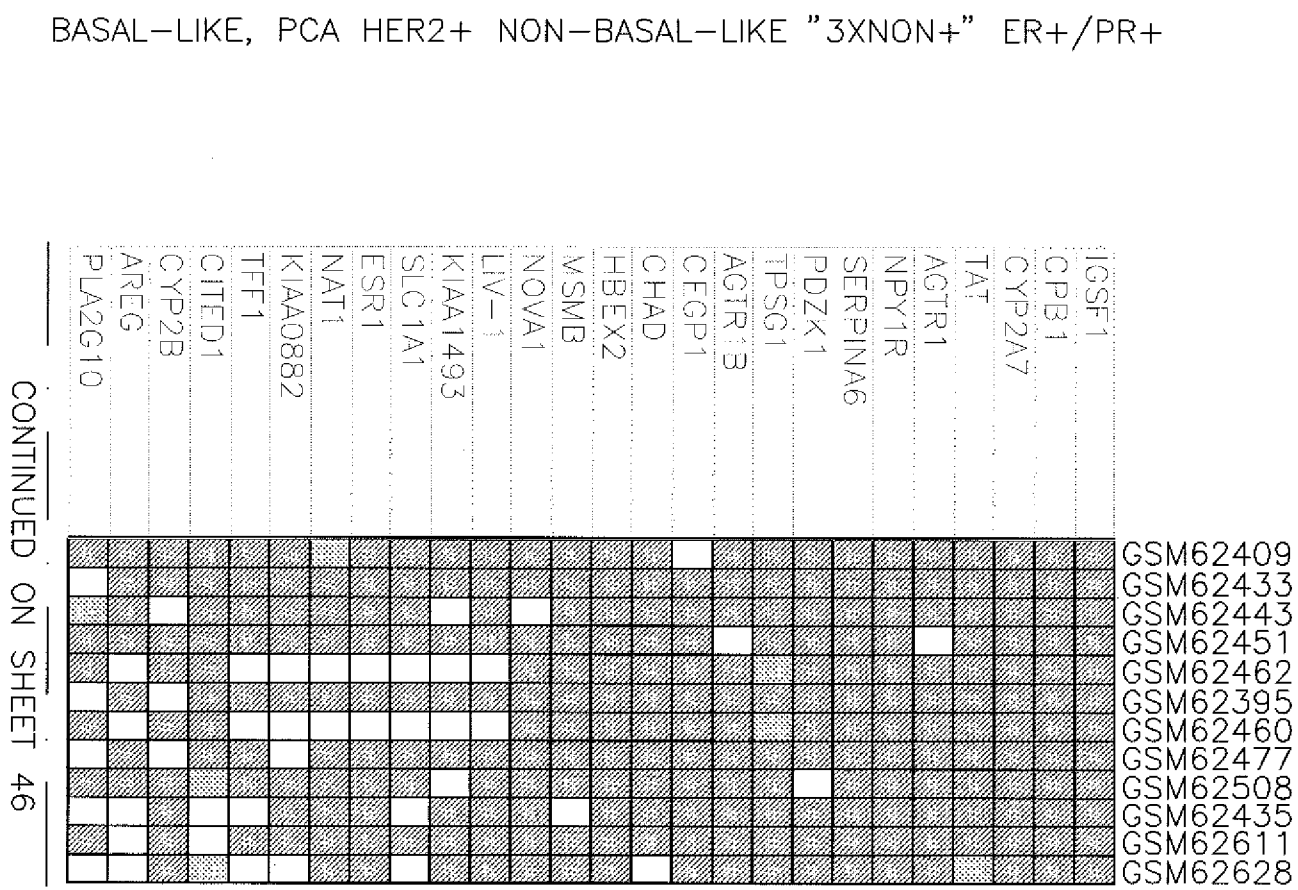
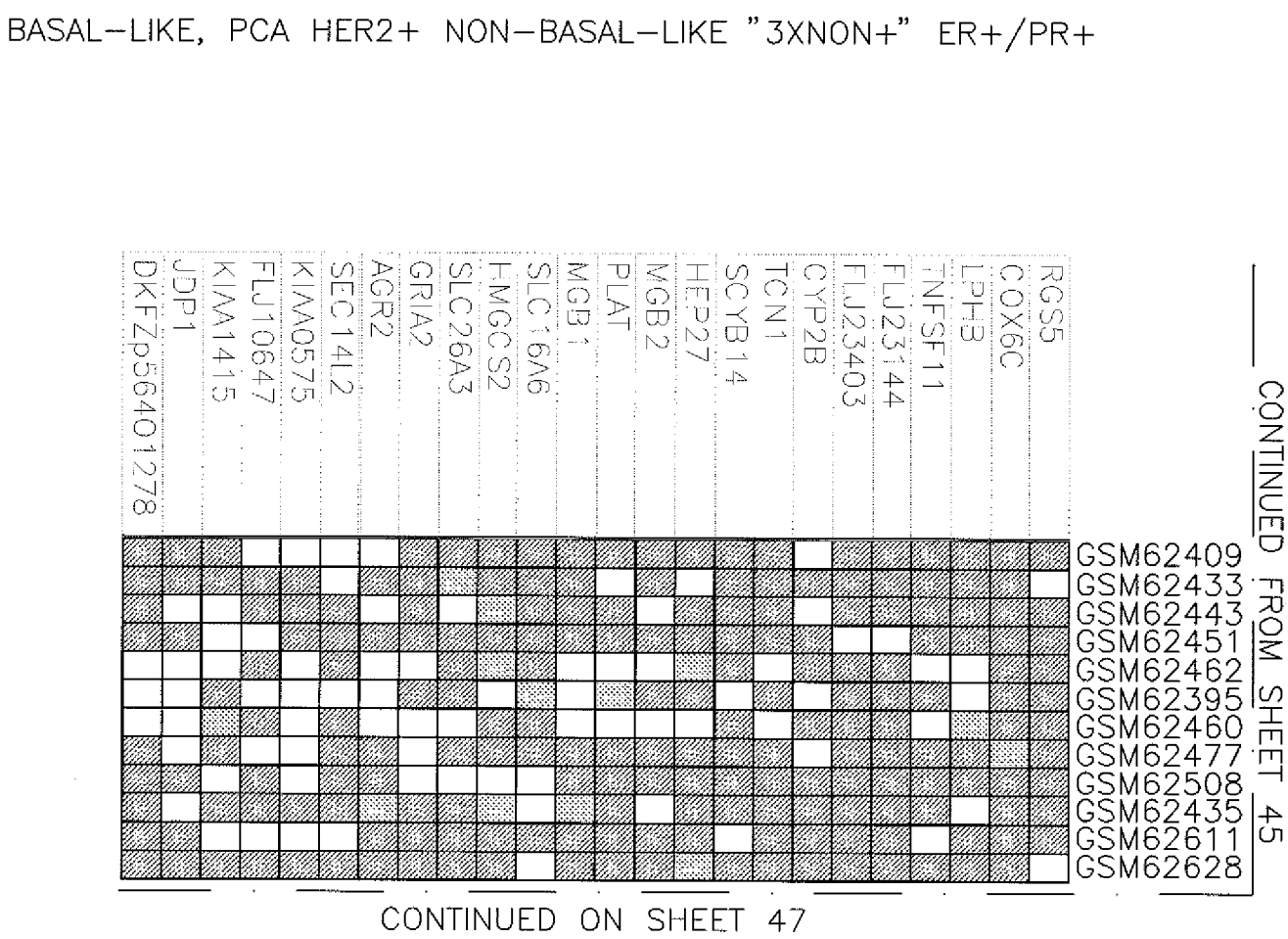
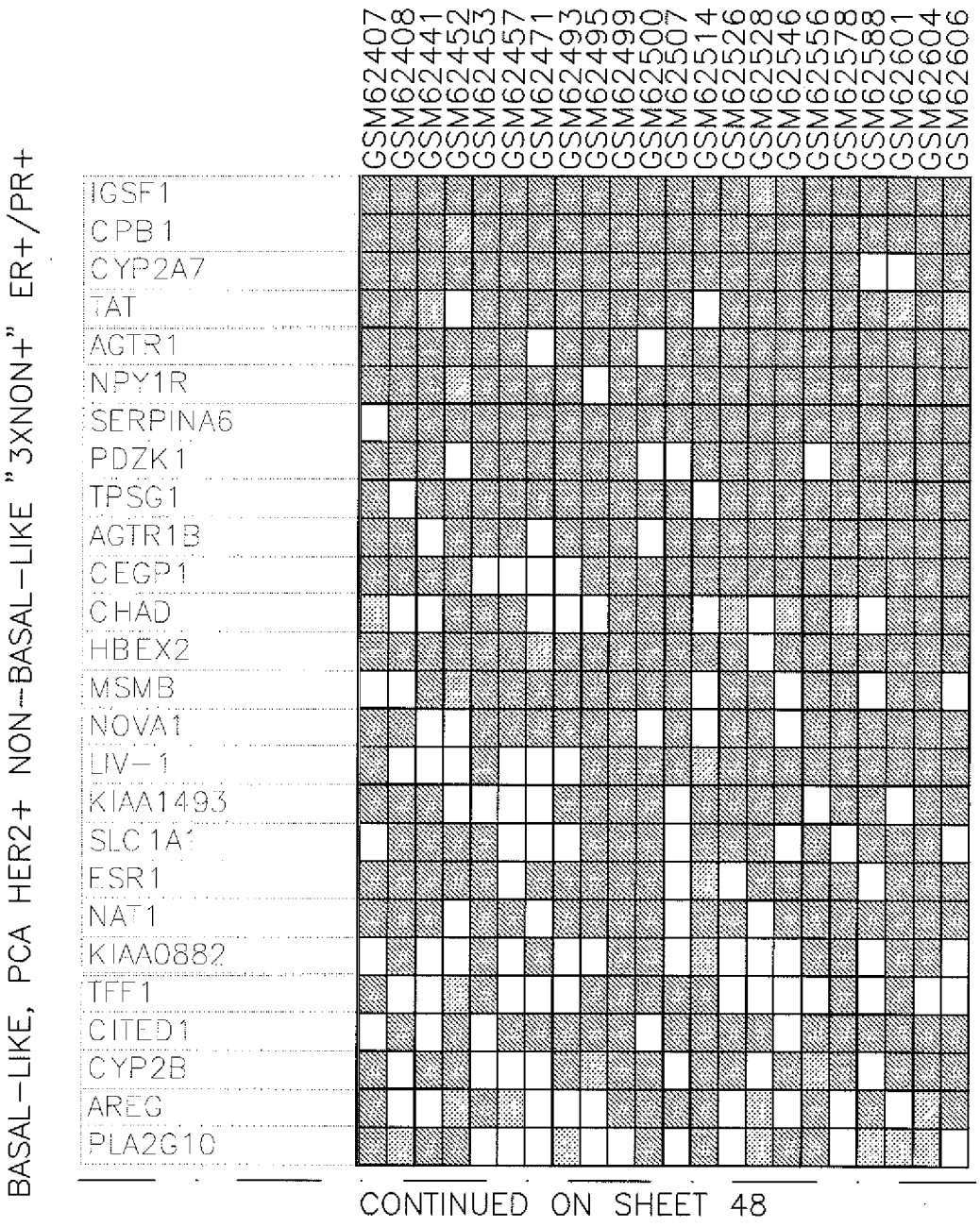

BASAL-LIKE, PCA HER2+ NON-BASAL-LIKE "3XNON+" ER+/PR+
IGSF1
CPB1
CYP2A7
TAT
AGTR1
NPY1R
SERPINA6
PDZK1
TPSG1
AGTR1 3
CFGP1
CHAD
HBEX2
VSMB
NOVA1
LIV-1
KIAA1493
SLC1A1
ESR1
NAT1
KIAA0882
TFF1
CITED1
CYP2B
AREG
PLA2G10
GSM62409
GSM62433
GSM62443
GSM62451
GSM62462
GSM62395
GSM62460
GSM62477
GSM62508
GSM62435
GSM62611
GSM62628
CONTINUED ON SHEET 46
TOP 50 UNDEREXPRESSED BASAL-LIKE GENES

FIG. 4



TOP 50 UNDEREXPRESSED BASAL-LIKE GENES

FIG. 4



TOP 50 UNDEREXPRESSED BASAL-LIKE GENES

FIG. 4

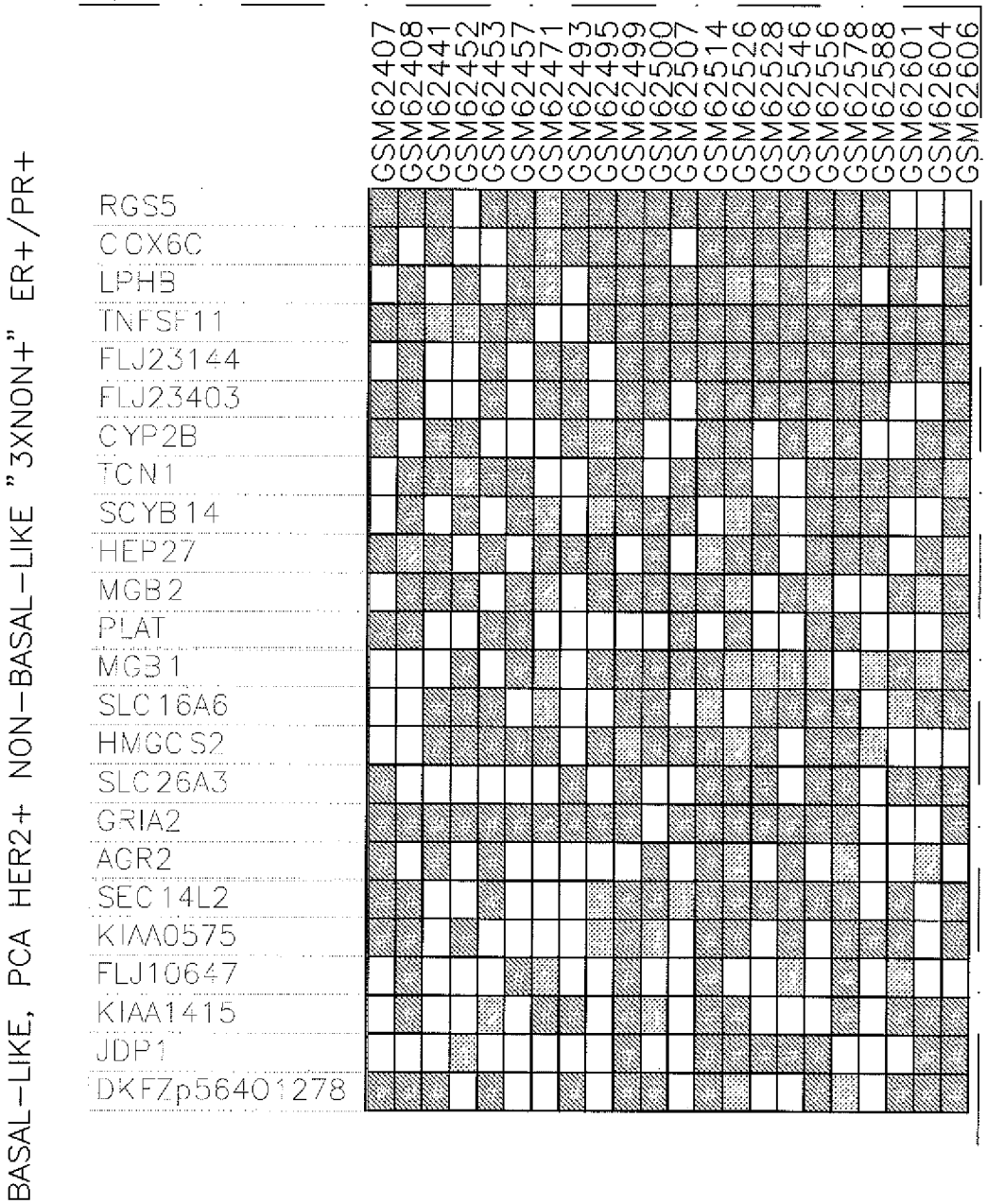
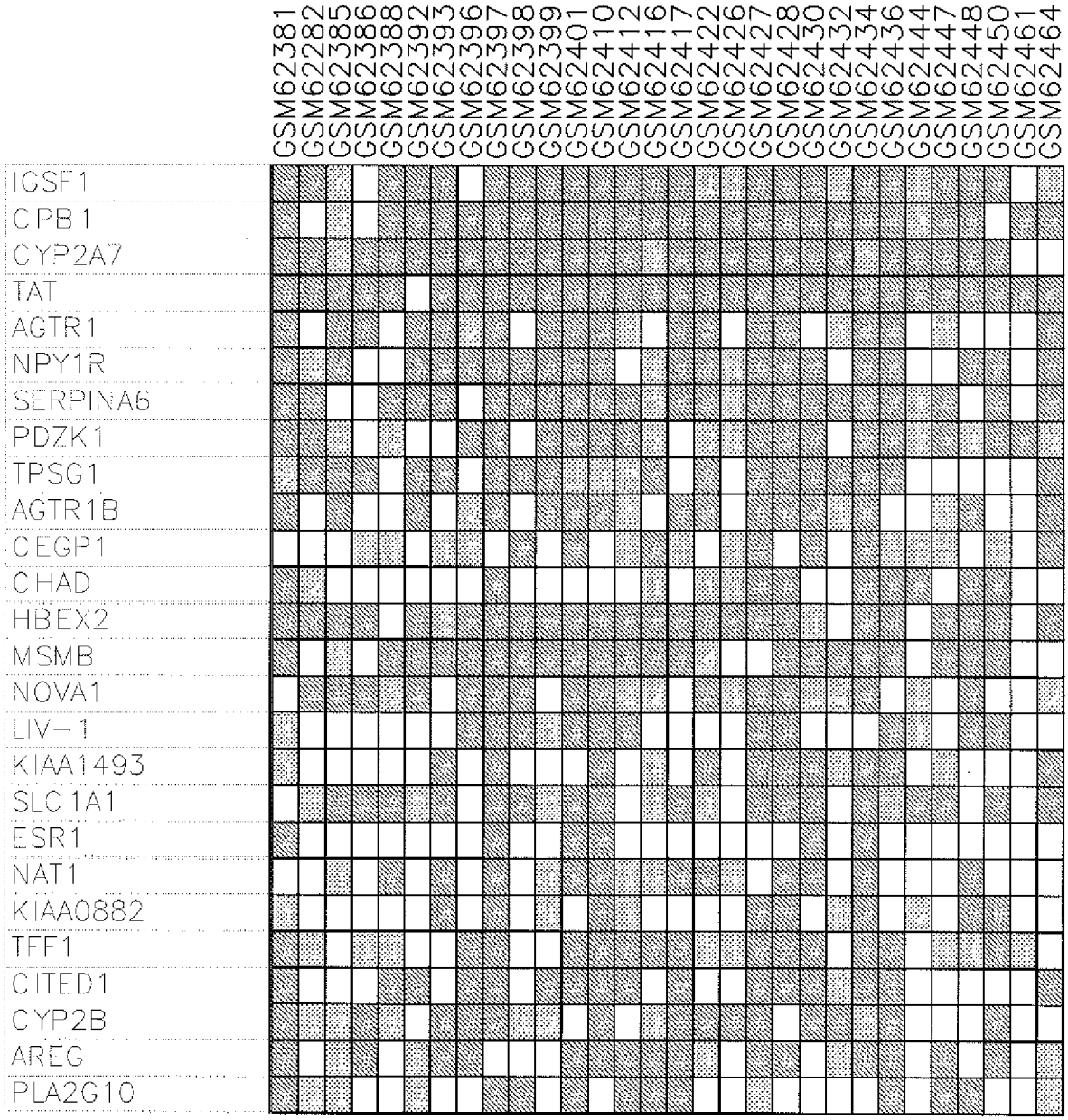

CONTINUED FROM SHEET 47
GSM62407
GSM62408
GSM62441
GSM62452
GSM62453
GSM62457
GSM62471
GSM62493
GSM62495
GSM62499
GSM62500
GSM62507
GSM62514
GSM62526
GSM62528
GSM62546
GSM62556
GSM62578
GSM62588
GSM62601
GSM62604
GSM62606
RGS5
COX6C
LPHB
TNFSF11
FLJ23144
FLJ23403
CYP2B
TCN1
SCYB14
HEP27
MGB2
PLAT
MGB1
SLC16A6
HMGCS2
SLC26A3
GRIA2
AGR2
SEC14L2
KIAA0575
FLJ10647
KIAA1415
JDP1
DKFZp564O1278
CONTINUED ON SHEET 49
TOP 50 UNDEREXPRESSED BASAL-LIKE GENES
BASAL-LIKE, PCA HER2+ NON-BASAL-LIKE "3XNON+" ER+/PR+

FIG. 4



CONTINUED ON SHEET 50

FIG. 4

TOP 50 UNDEREXPRESSED BASAL-LIKE GENES
BASAL-LIKE, PCA HER2+ NON-BASAL-LIKE "3XNON+" ER+/PR+

CONTINUED FROM SHEET 49

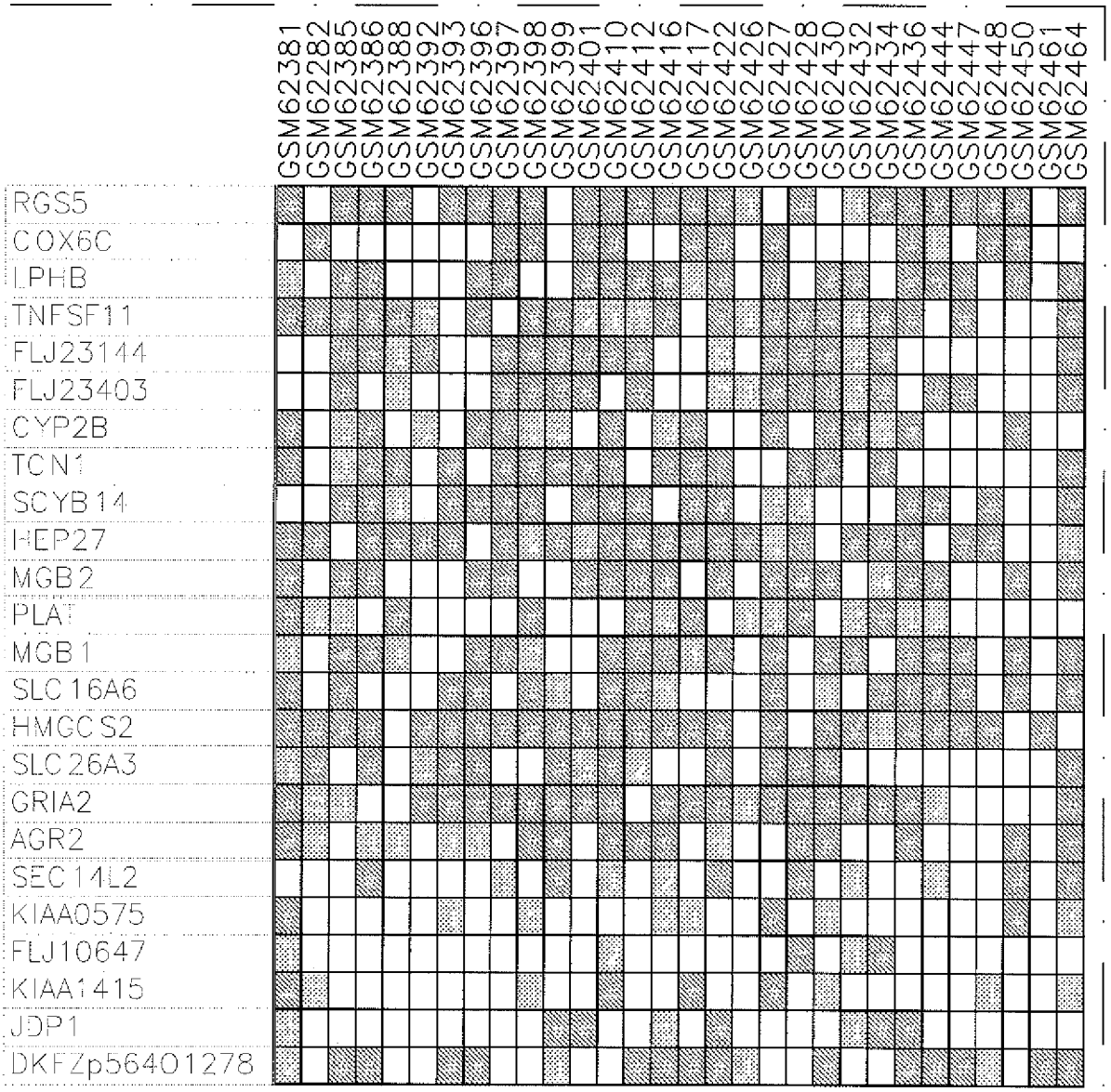
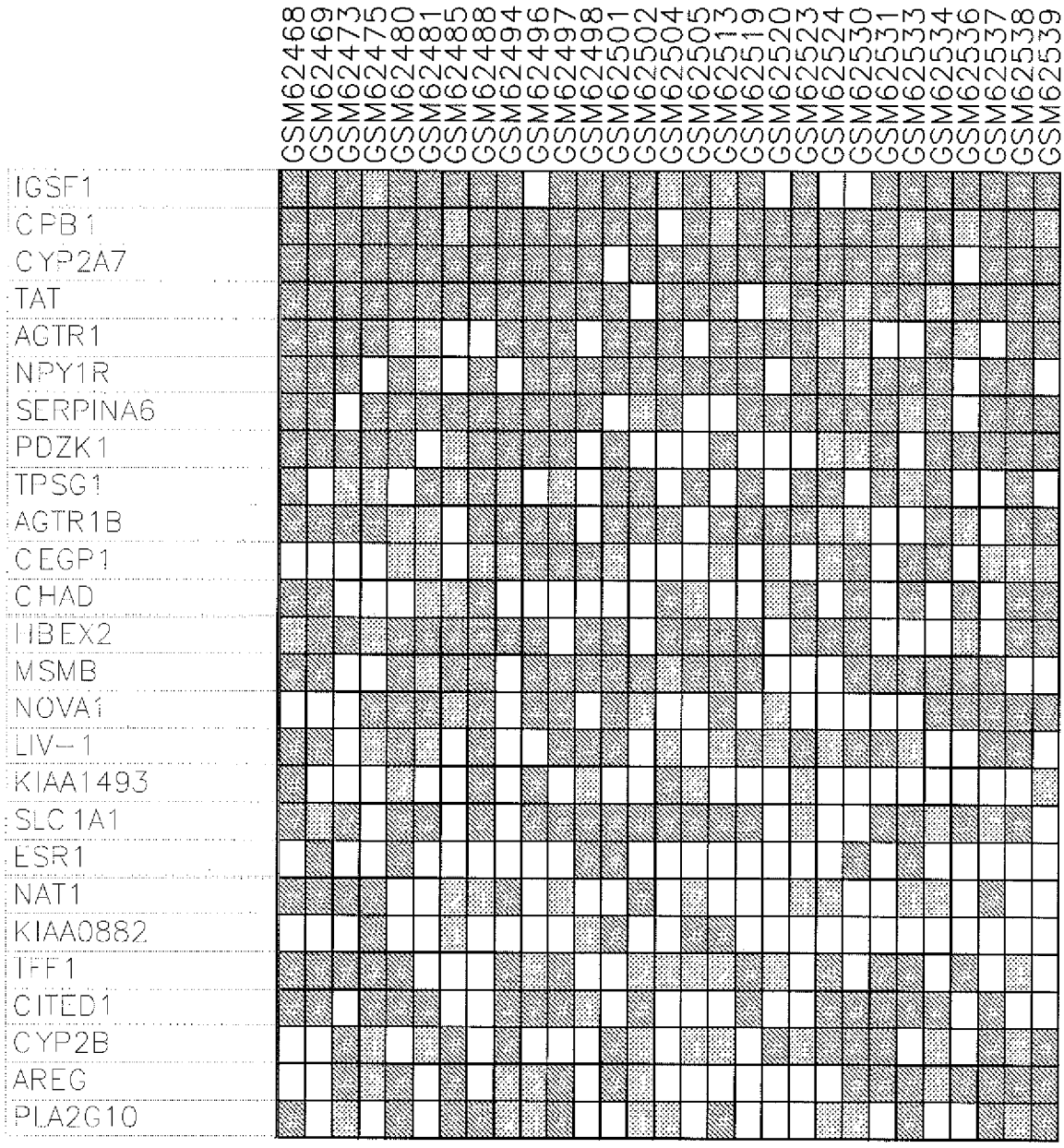


FIG. 4

CONTINUED ON SHEET 51

TOP 50 UNDEREXPRESSED BASAL-LIKE GENES
BASAL-LIKE, PCA HER2+ NON-BASAL-LIKE "3XNON+" ER+/PR+



CONTINUED ON SHEET 52

FIG. 4

TOP 50 UNDEREXPRESSED BASAL-LIKE GENES
BASAL-LIKE, PCA HER2+ NON-BASAL-LIKE "3XNON+" ER+/PR+

52

CONTINUED FROM SHEET 51

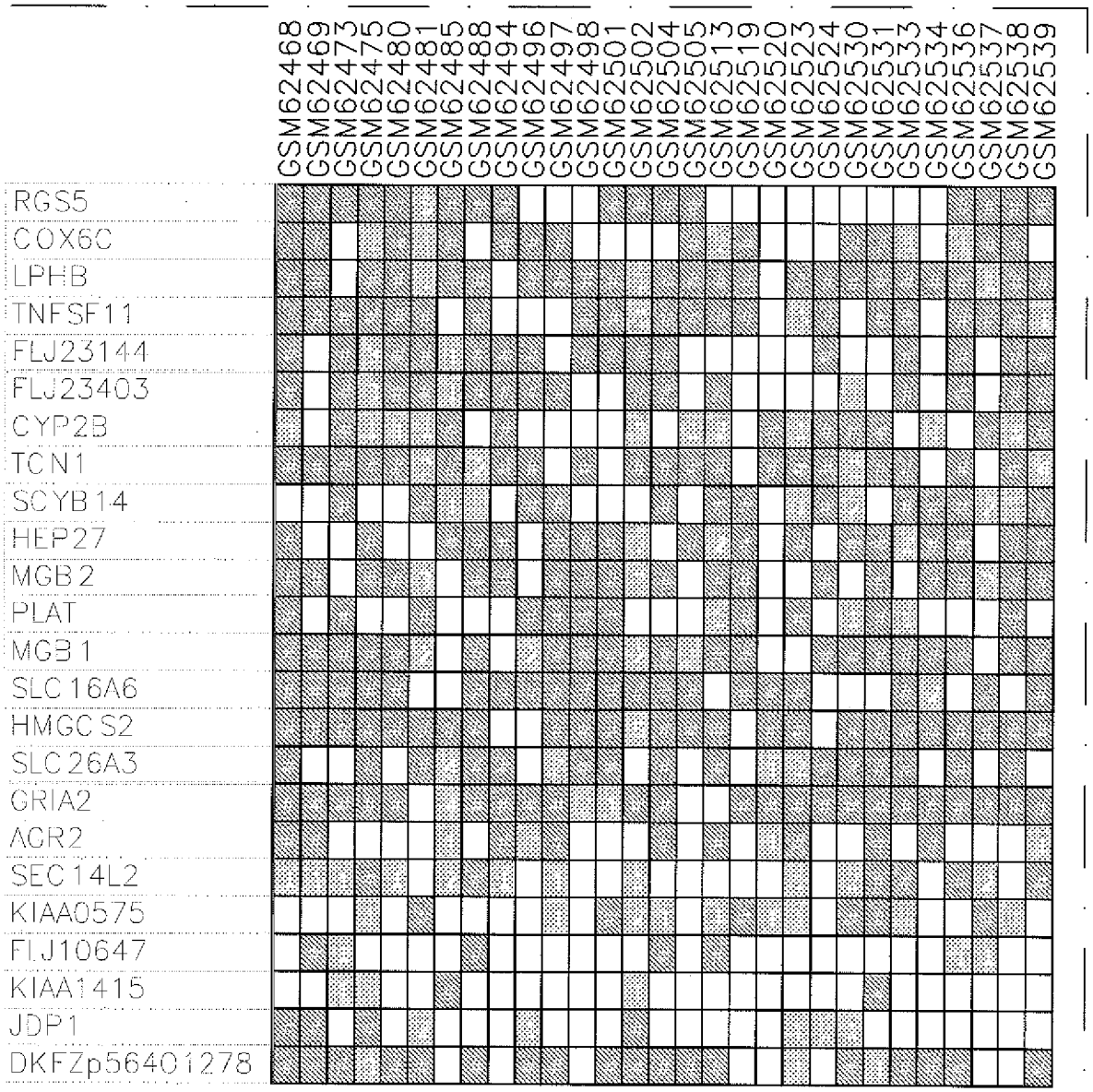
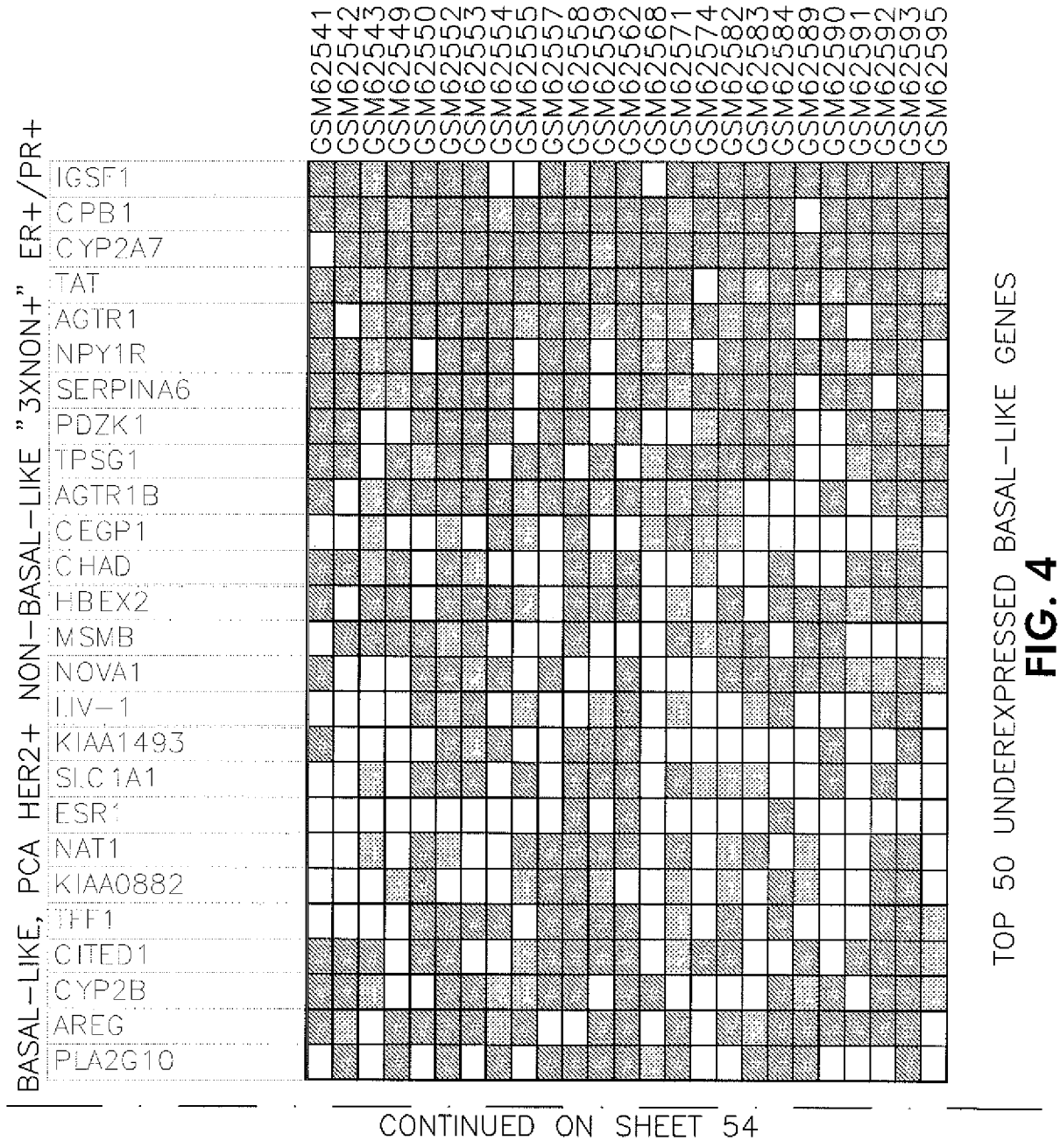


FIG. 4

CONTINUED ON SHEET 53

TOP 50 UNDEREXPRESSED BASAL-LIKE GENES
BASAL-LIKE, PCA HER2+ NON-BASAL-LIKE "3XNON+" ER+/PR+



TOP 50 UNDEREXPRESSED BASAL-LIKE GENES

FIG. 4

CONTINUED ON SHEET 54

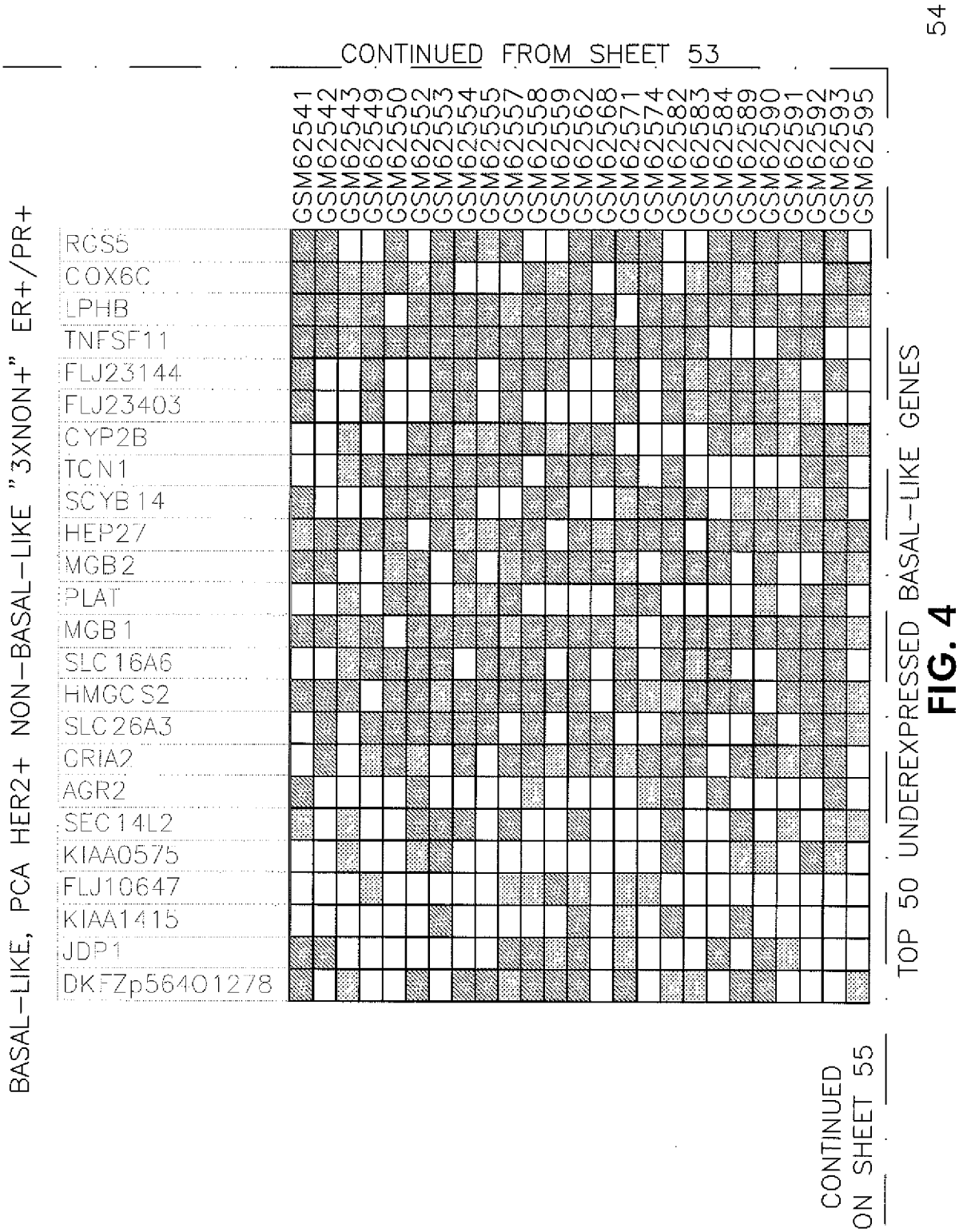
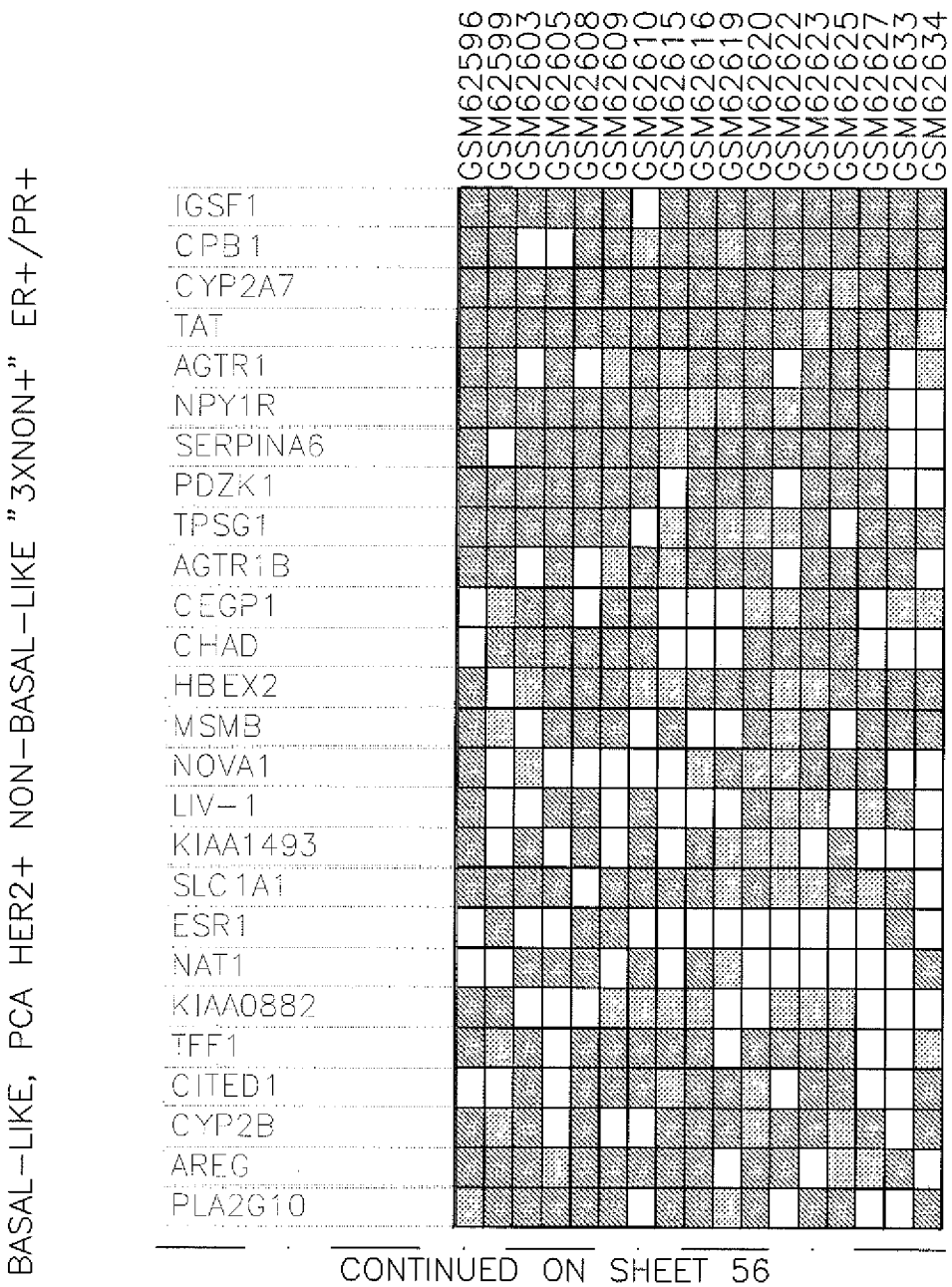

CONTINUED FROM SHEET 53
54
BASAL-LIKE, PCA HER2+ NON-BASAL-LIKE "3XNON+" ER+/PR+
GSM625541
GSM625542
GSM625543
GSM625549
GSM625550
GSM625552
GSM625553
GSM625554
GSM625555
GSM625557
GSM625558
GSM625559
GSM625562
GSM625568
GSM625571
GSM625574
GSM625582
GSM625583
GSM625584
GSM625589
GSM625590
GSM625591
GSM625592
GSM625593
GSM625595
RGS5
COX6C
LPHB
TNFSF11
FLJ23144
FLJ23403
CYP2B
TCN1
SCYB14
HEP27
MGB2
PLAT
MGB1
SLC16A6
HMGCS2
SLC26A3
CRIA2
AGR2
SEC14L2
KIAA0575
FLJ10647
KIAA1415
JDP1
DKFZp564O1278
TOP 50 UNDEREXPRESSED BASAL-LIKE GENES
CONTINUED ON SHEET 55

FIG. 4



TOP 50 UNDEREXPRESSED BASAL-LIKE GENES

FIG. 4

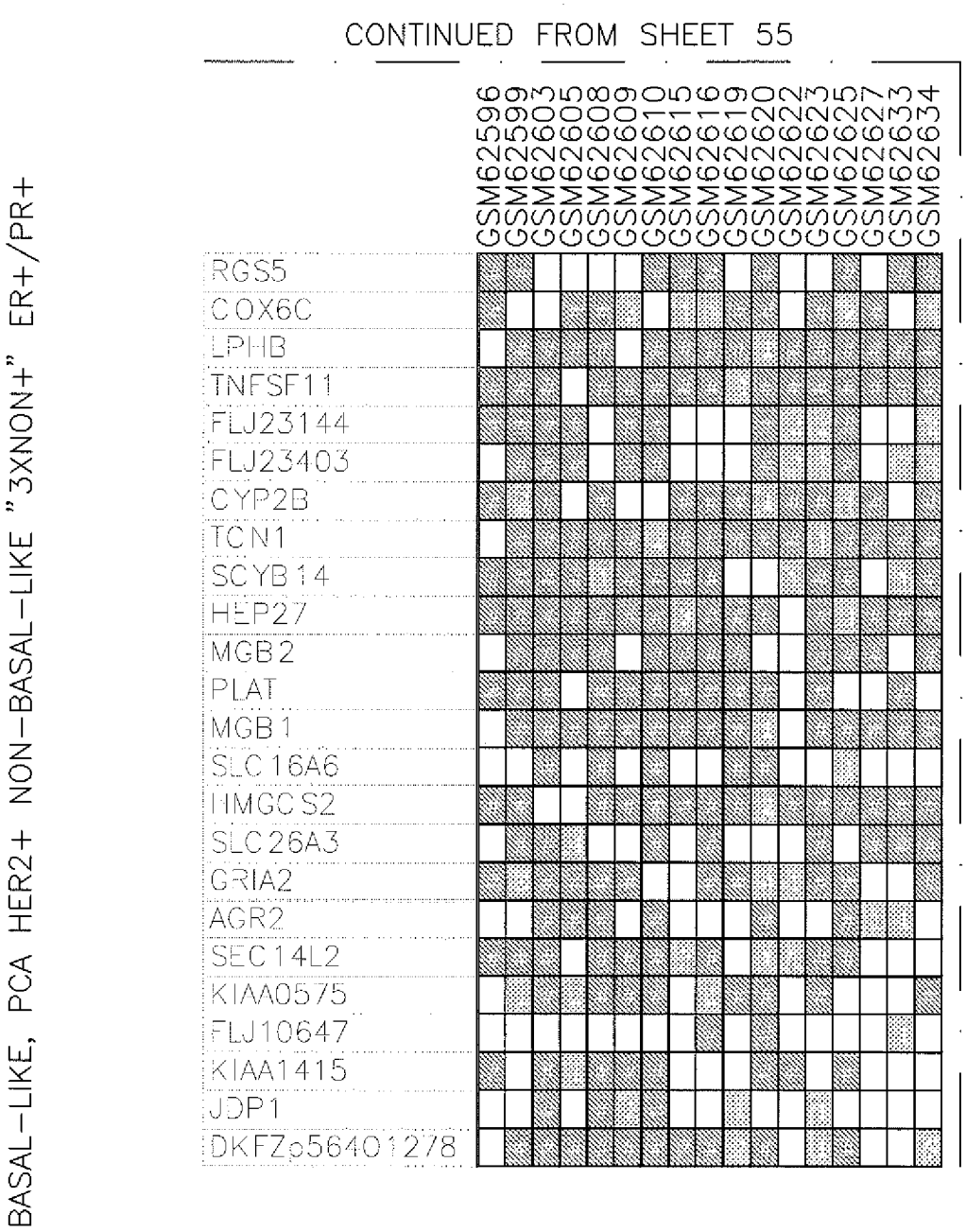
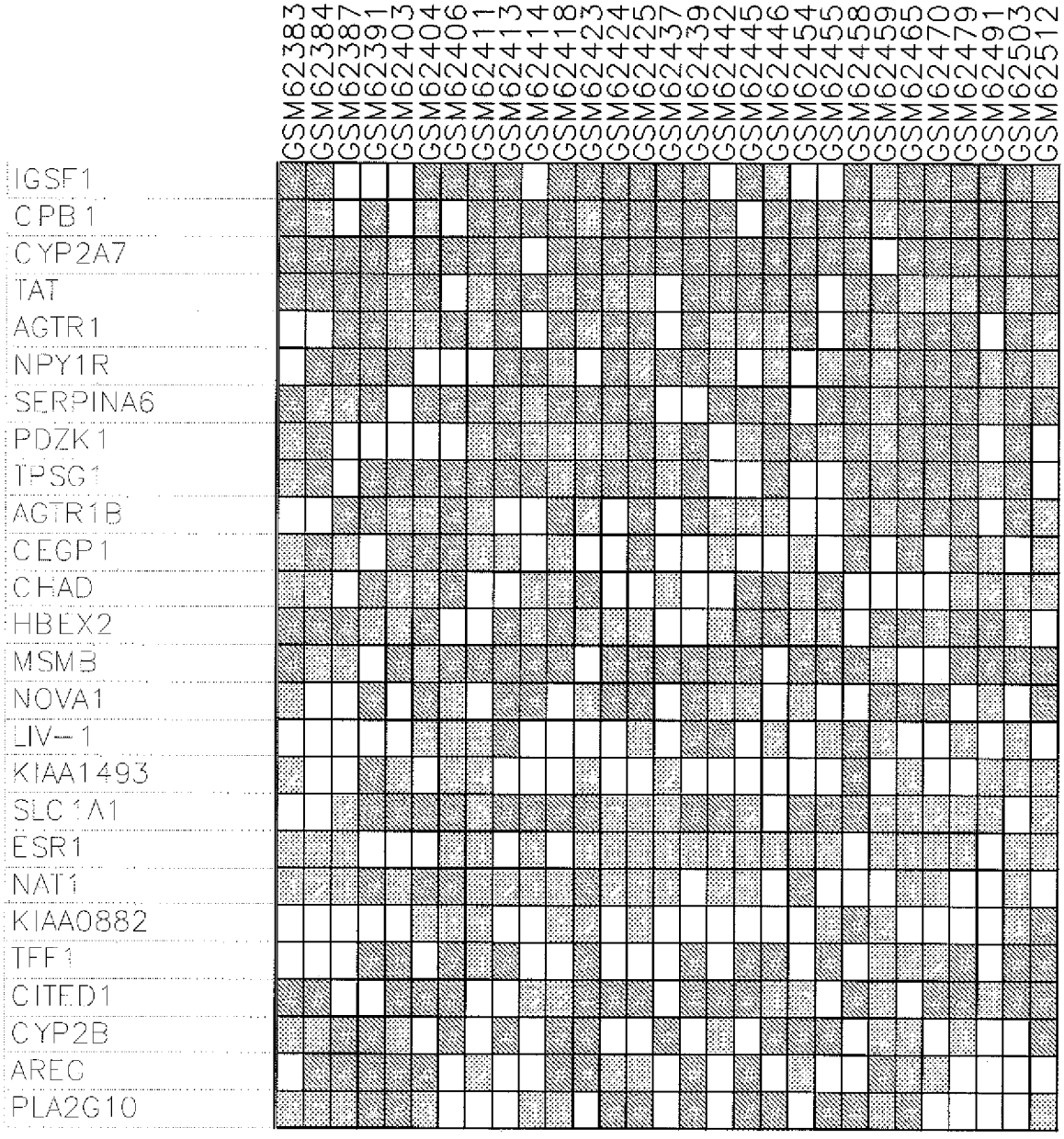

CONTINUED FROM SHEET 55
GSM62596
GSM62599
GSM62603
GSM62605
GSM62608
GSM62609
GSM62610
GSM62615
GSM62616
GSM62619
GSM62620
GSM62622
GSM62623
GSM62625
GSM62627
GSM62633
GSM62634
RGS5
COX6C
LPHB
TNFSF11
FLJ23144
FLJ23403
CYP2B
TCN1
SCYB14
HEP27
MGB2
PLAT
MGB1
SLC16A6
HMGCS2
SLC26A3
GRIA2
AGR2
SEC14L2
KIAA0575
FLJ10647
KIAA1415
JDP1
DKFZp564O1278
CONTINUED ON SHEET 57
TOP 50 UNDEREXPRESSED BASAL-LIKE GENES
BASAL-LIKE, PCA HER2+ NON-BASAL-LIKE "3XNON+" ER+/PR+

FIG. 4



CONTINUED ON SHEET 58

FIG. 4

TOP 50 UNDEREXPRESSED BASAL-LIKE GENES
BASAL-LIKE, PCA HER2+ NON-BASAL-LIKE "3XNON+" ER+/PR+

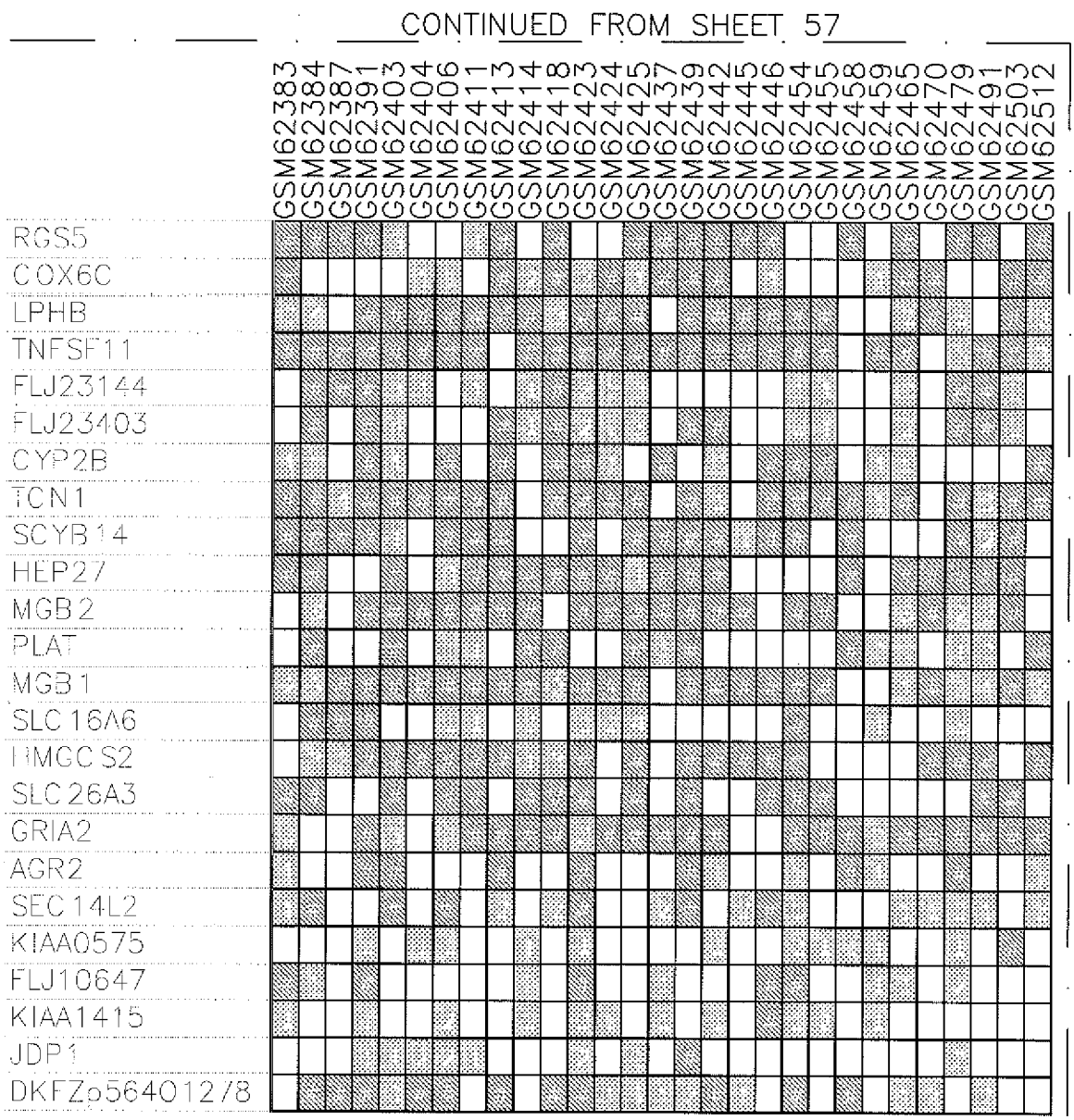
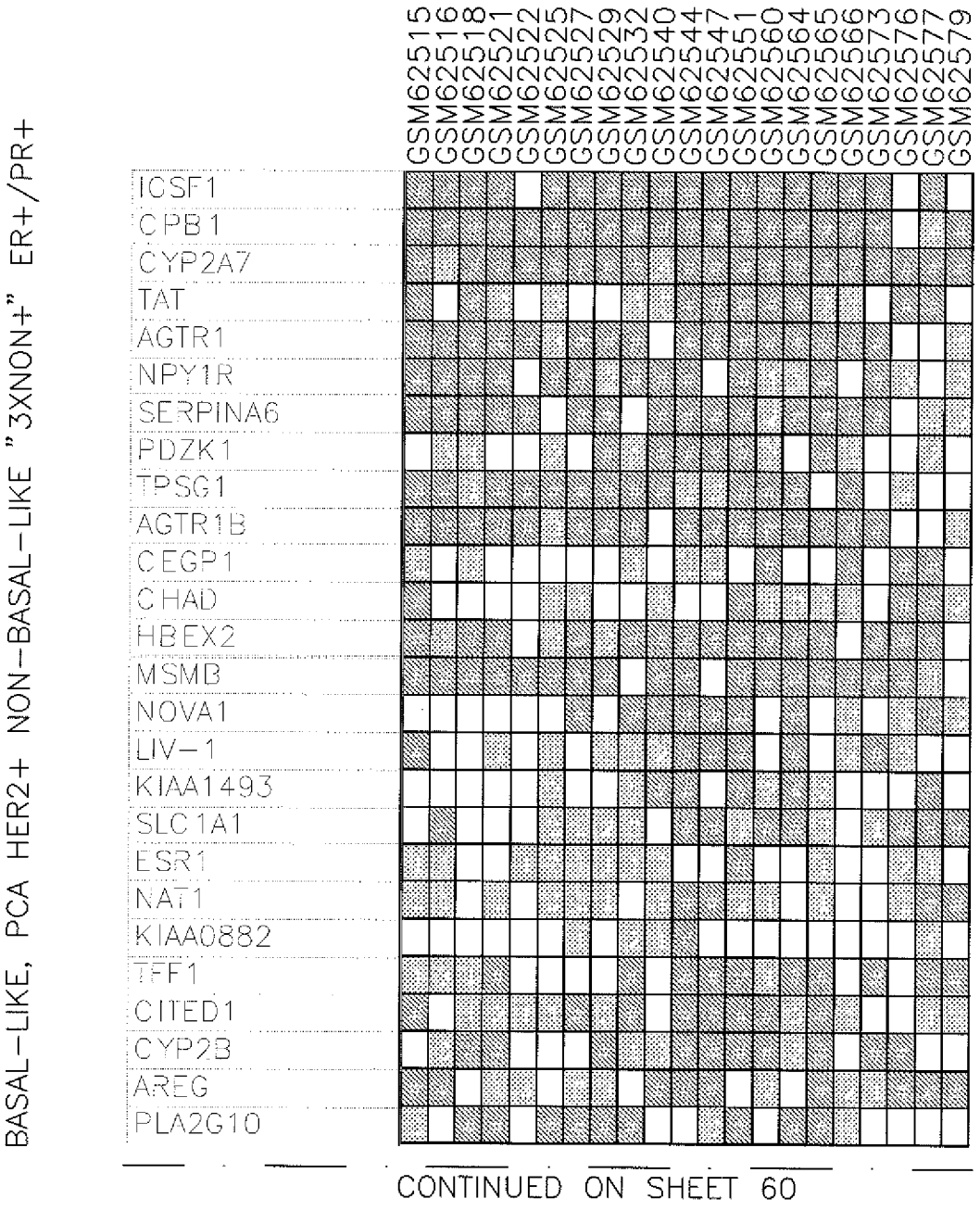


FIG. 4

TOP 50 UNDEREXPRESSED BASAL-LIKE GENES
BASAL-LIKE, PCA HER2+ NON-BASAL-LIKE "3XNON+" ER+/PR+



TOP 50 UNDEREXPRESSED BASAL-LIKE GENES

FIG. 4

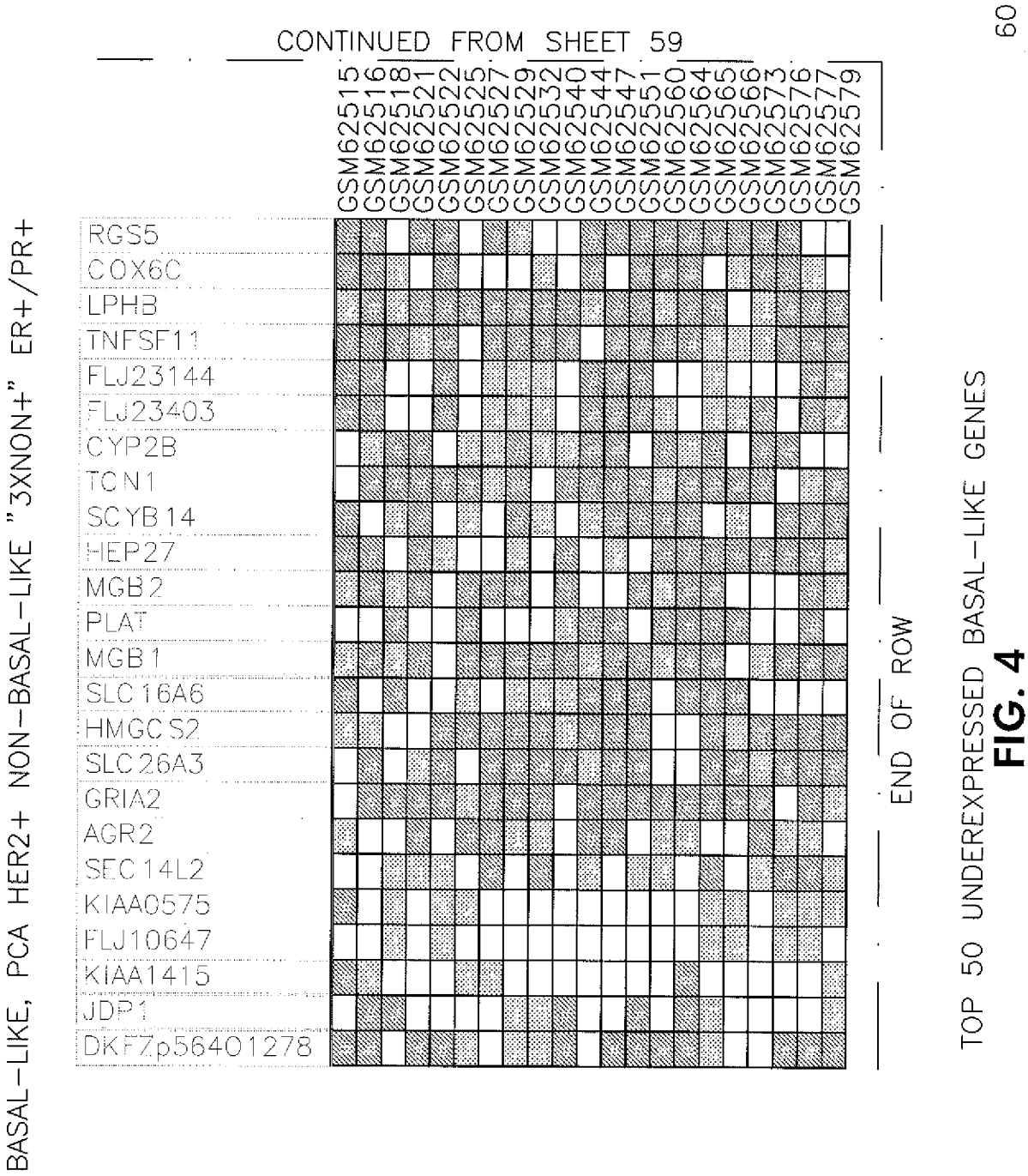

CONTINUED FROM SHEET 59
GSM625515
GSM625516
GSM625518
GSM625521
GSM625522
GSM625525
GSM625527
GSM625529
GSM625532
GSM625540
GSM625544
GSM625547
GSM625551
GSM625560
GSM625564
GSM625565
GSM625566
GSM625573
GSM625576
GSM625577
GSM625579
RGS5
COX6C
LPHB
TNFSF11
FLJ23144
FLJ23403
CYP2B
TCN1
SCYB14
HEP27
MGB2
PLAT
MGB1
SLC16A6
HMGCS2
SLC26A3
GRIA2
AGR2
SEC14L2
KIAA0575
FLJ10647
KIAA1415
JDP1
DKFZp56401278
END OF ROW
BASAL-LIKE, PCA HER2+ NON-BASAL-LIKE "3XNON+" ER+/PR+
TOP 50 UNDEREXPRESSED BASAL-LIKE GENES
60

FIG. 4

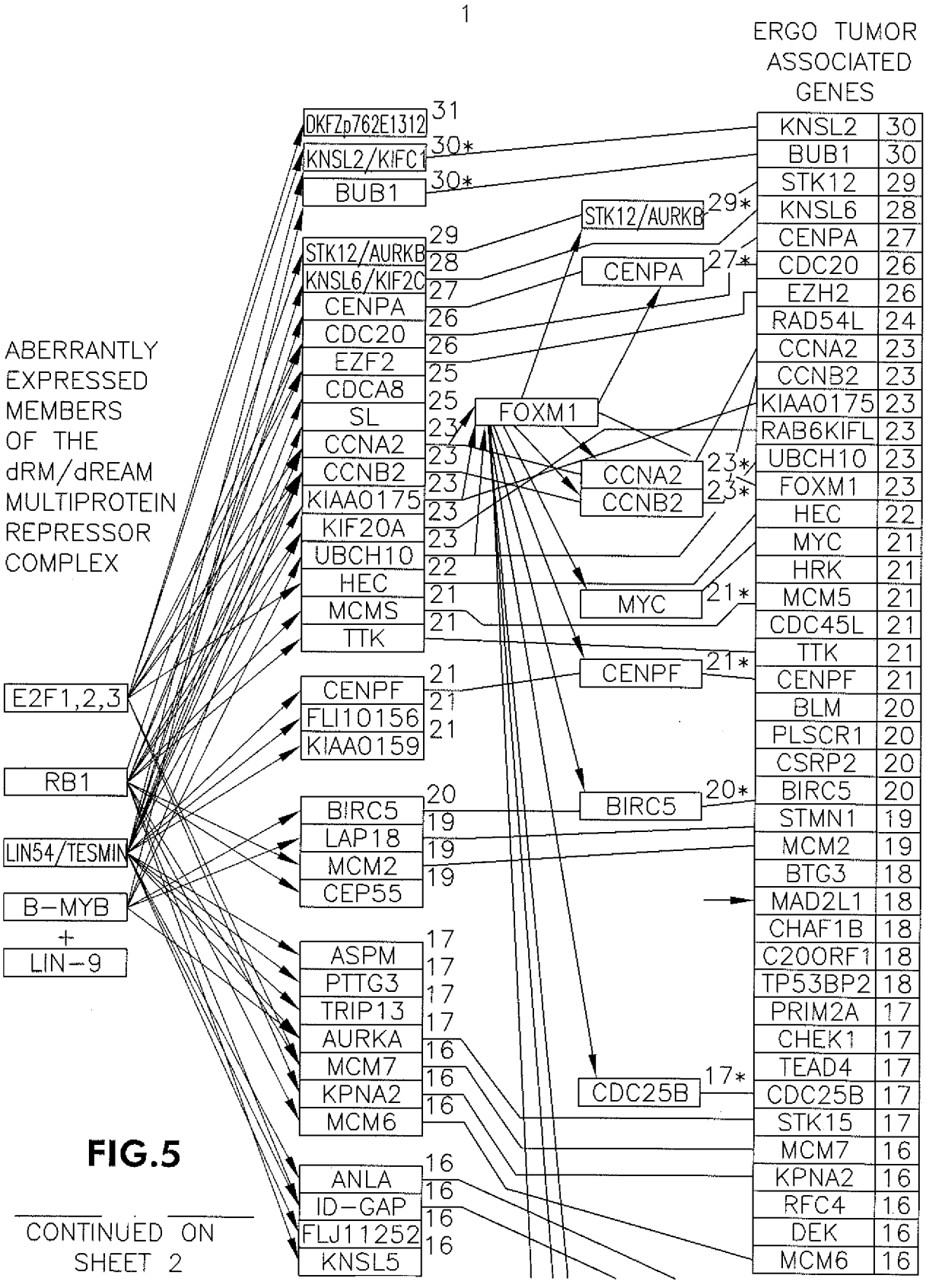


FIG.5

CONTINUED ON SHEET 2

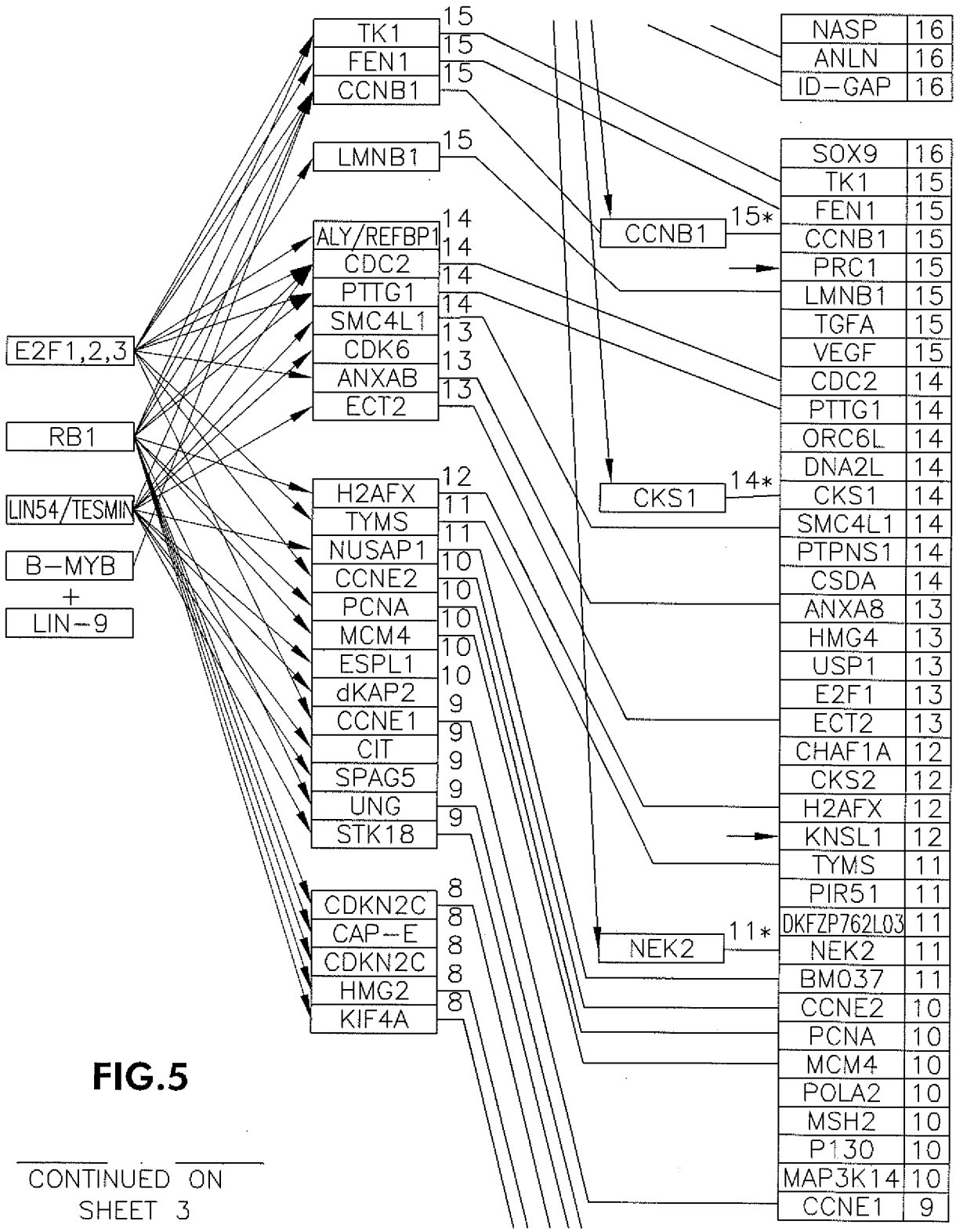


FIG.5

CONTINUED ON SHEET 3

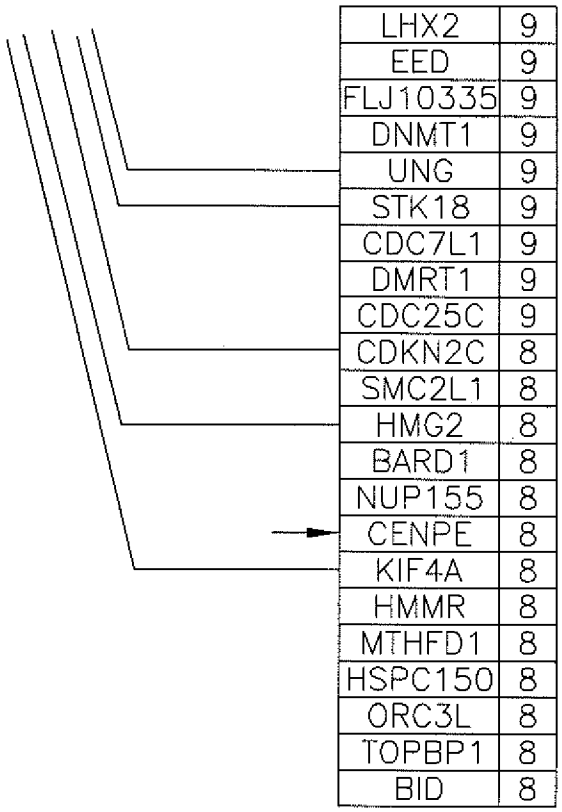

LHX2 9
EED 9
FLJ10335 9
DNMT1 9
UNG 9
STK18 9
CDC7L1 9
DMRT1 9
CDC25C 9
CDKN2C 8
SMC2L1 8
HMG2 8
BARD1 8
NUP155 8
CENPE 8
KIF4A 8
HMMR 8
MTHFD1 8
HSPC150 8
ORC3L 8
TOPBP1 8
BID 8

FIG.5

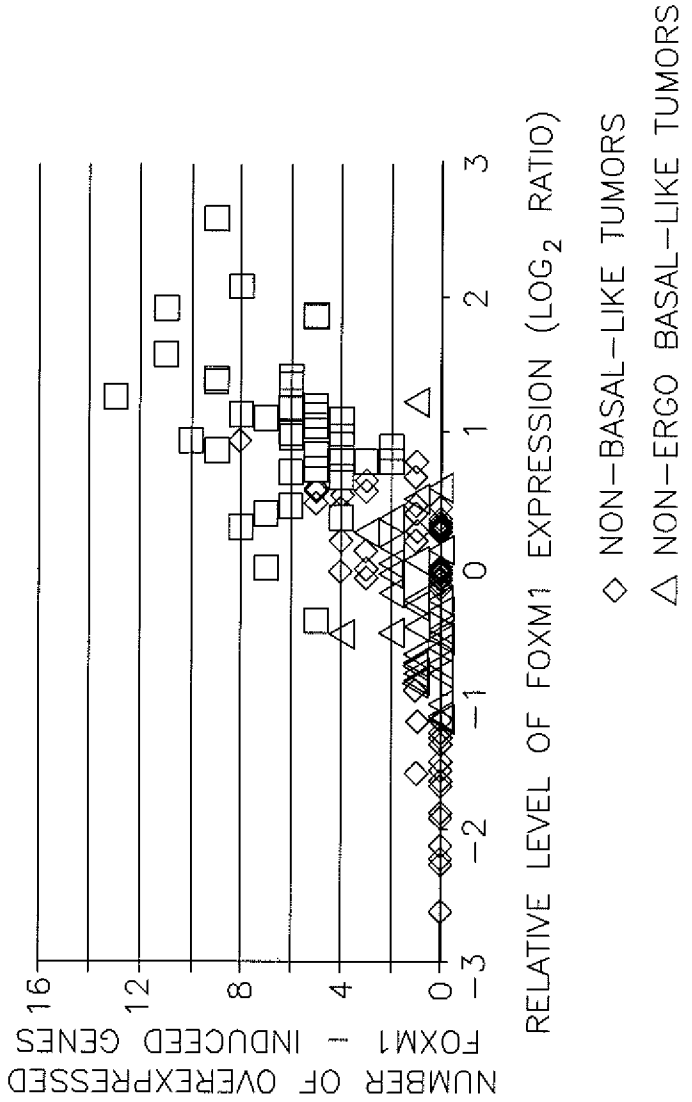

NUMBER OF OVEREXPRESSED FOXM1 - INDUCED GENES
16
12
8
4
0
−3
−2
−1
0
1
2
3
RELATIVE LEVEL OF FOXM1 EXPRESSION (LOG2 RATIO)
◇ NON-BASAL-LIKE TUMORS
△ NON-ERGO BASAL-LIKE TUMORS
□ ERGO TUMORS

FIG.6

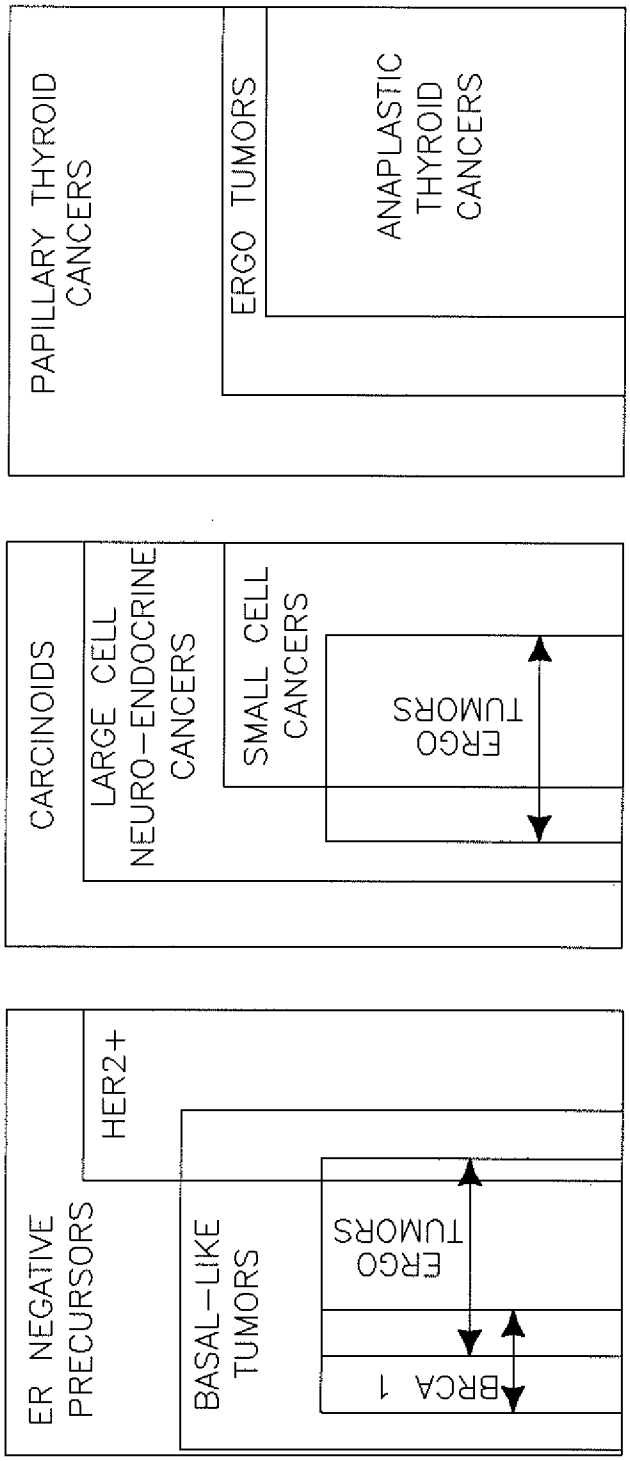
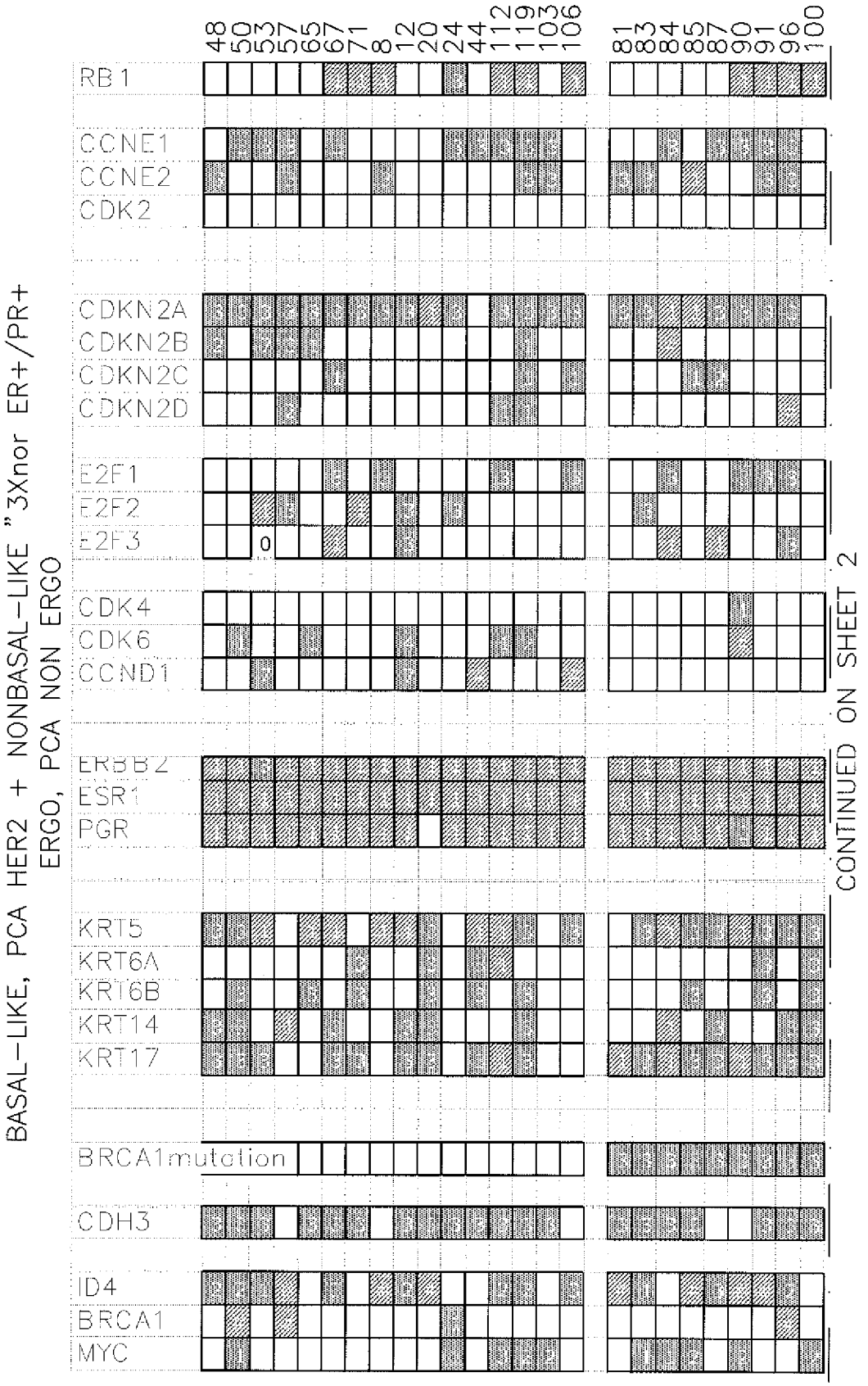

ER NEGATIVE PRECURSORS
HER2+
BASAL-LIKE TUMORS
ERGO TUMORS
BRCA 1
CARCINOIDS
LARGE CELL NEURO-ENDOCRINE CANCERS
SMALL CELL CANCERS
ERGO TUMORS
PAPILLARY THYROID CANCERS
ERGO TUMORS
ANAPLASTIC THYROID CANCERS

FIG.7



SELECTED BIOMARKERS

FIG. 8

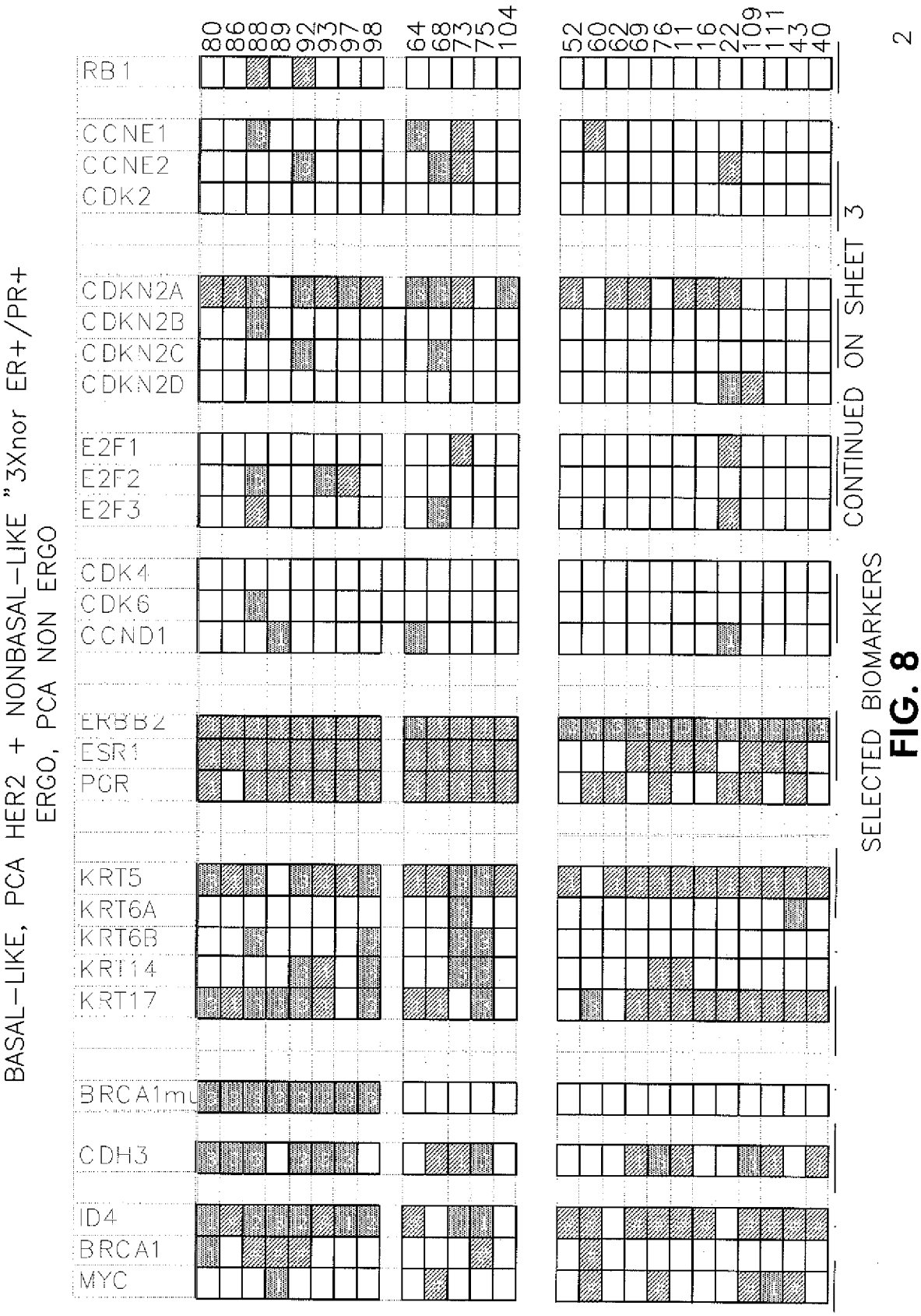
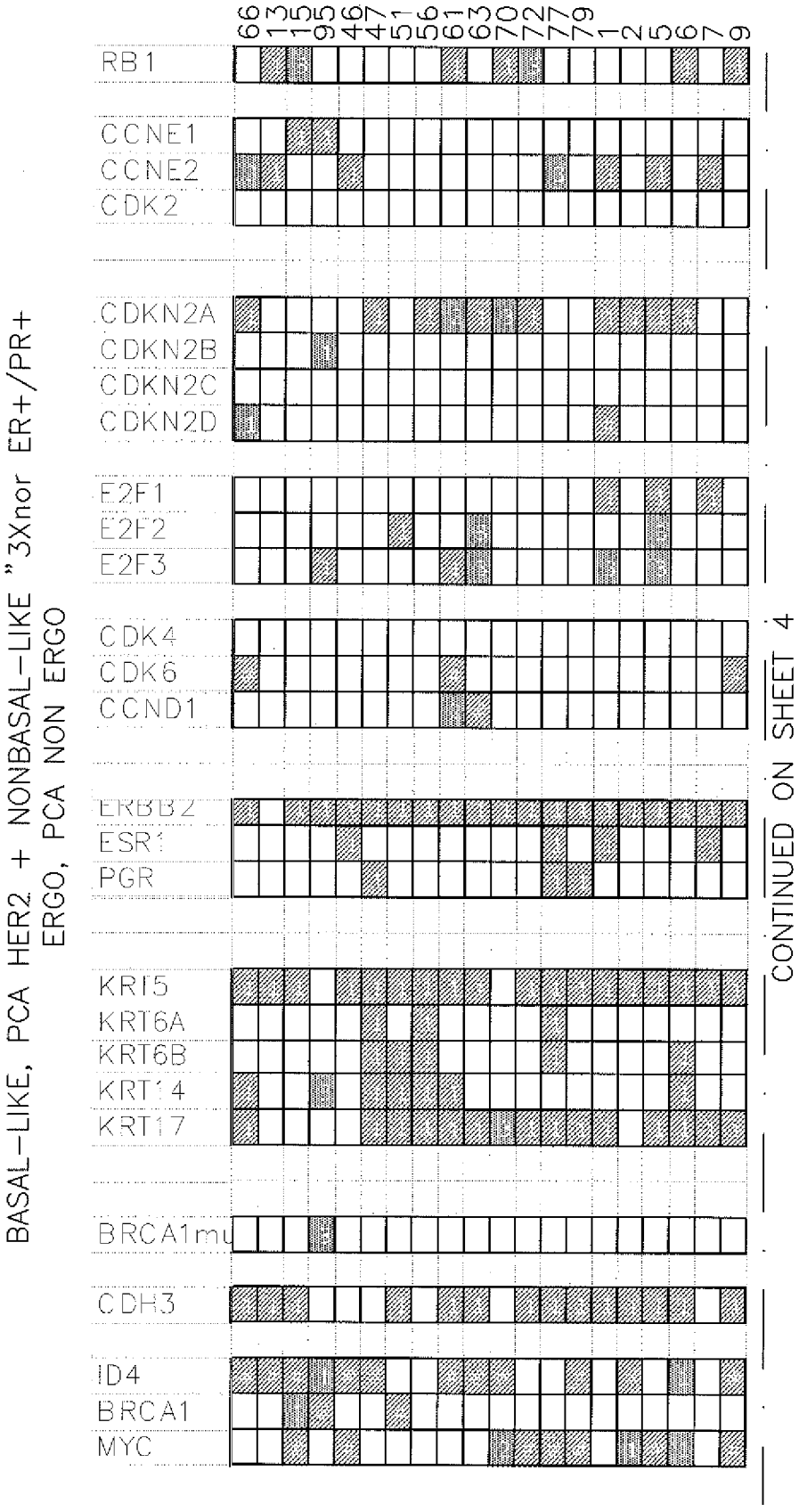
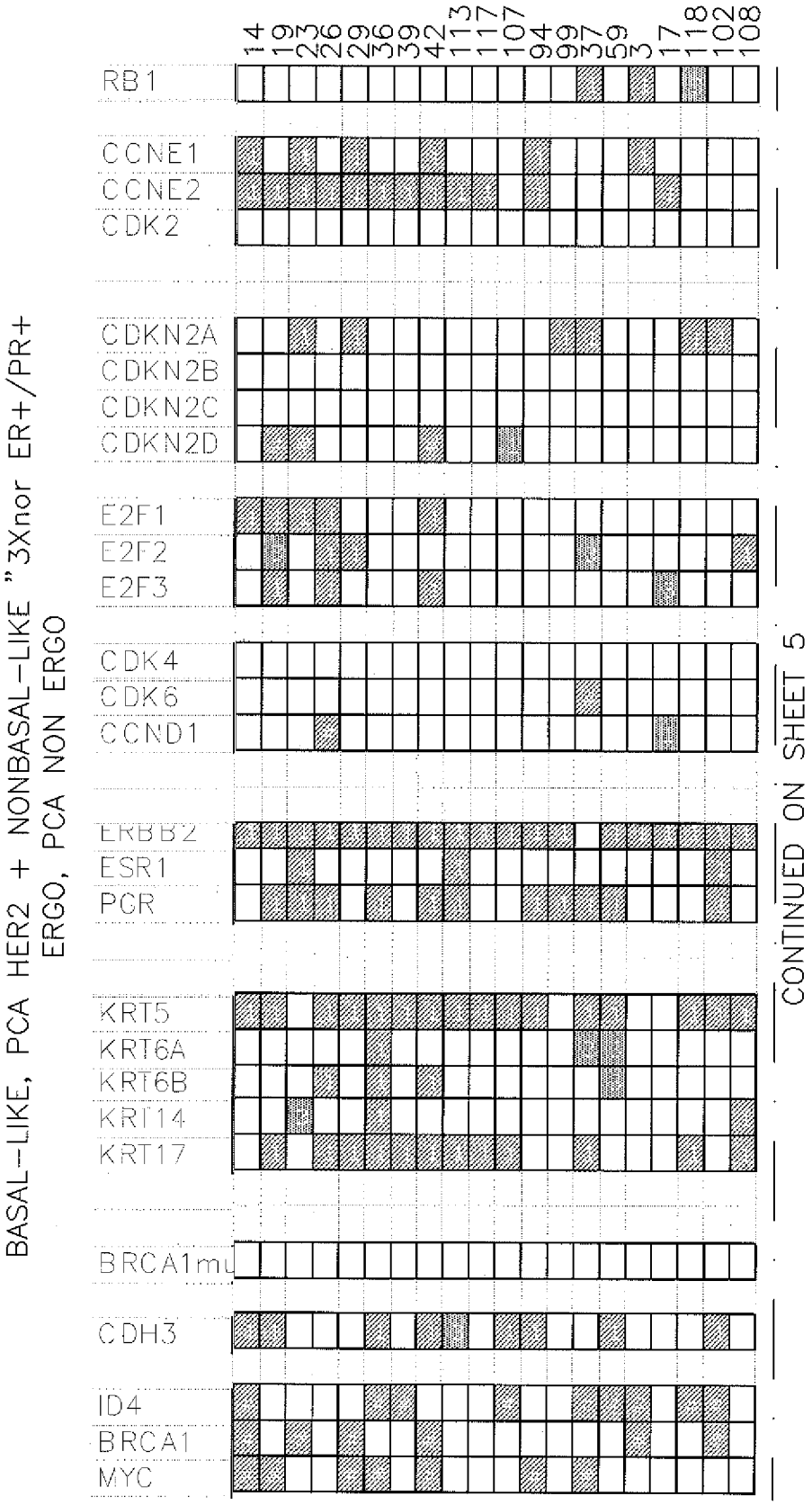

BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+
ERGO, PCA NON ERGO
80 86 88 89 92 93 97 98 64 68 73 75 104 52 60 62 69 76 11 16 22 109 111 43 40
RB1
CCNE1
CCNE2
CDK2
CDKN2A
CDKN2B
CDKN2C
CDKN2D
E2F1
E2F2
E2F3
CDK4
CDK6
CCND1
ERBB2
ESR1
PGR
KRT5
KRT6A
KRT6B
KRT14
KRT17
BRCA1mu
CDH3
ID4
BRCA1
MYC
CONTINUED ON SHEET 3
SELECTED BIOMARKERS
2

FIG. 8



SELECTED BIOMARKERS

FIG. 8



SELECTED BIOMARKERS

FIG. 8

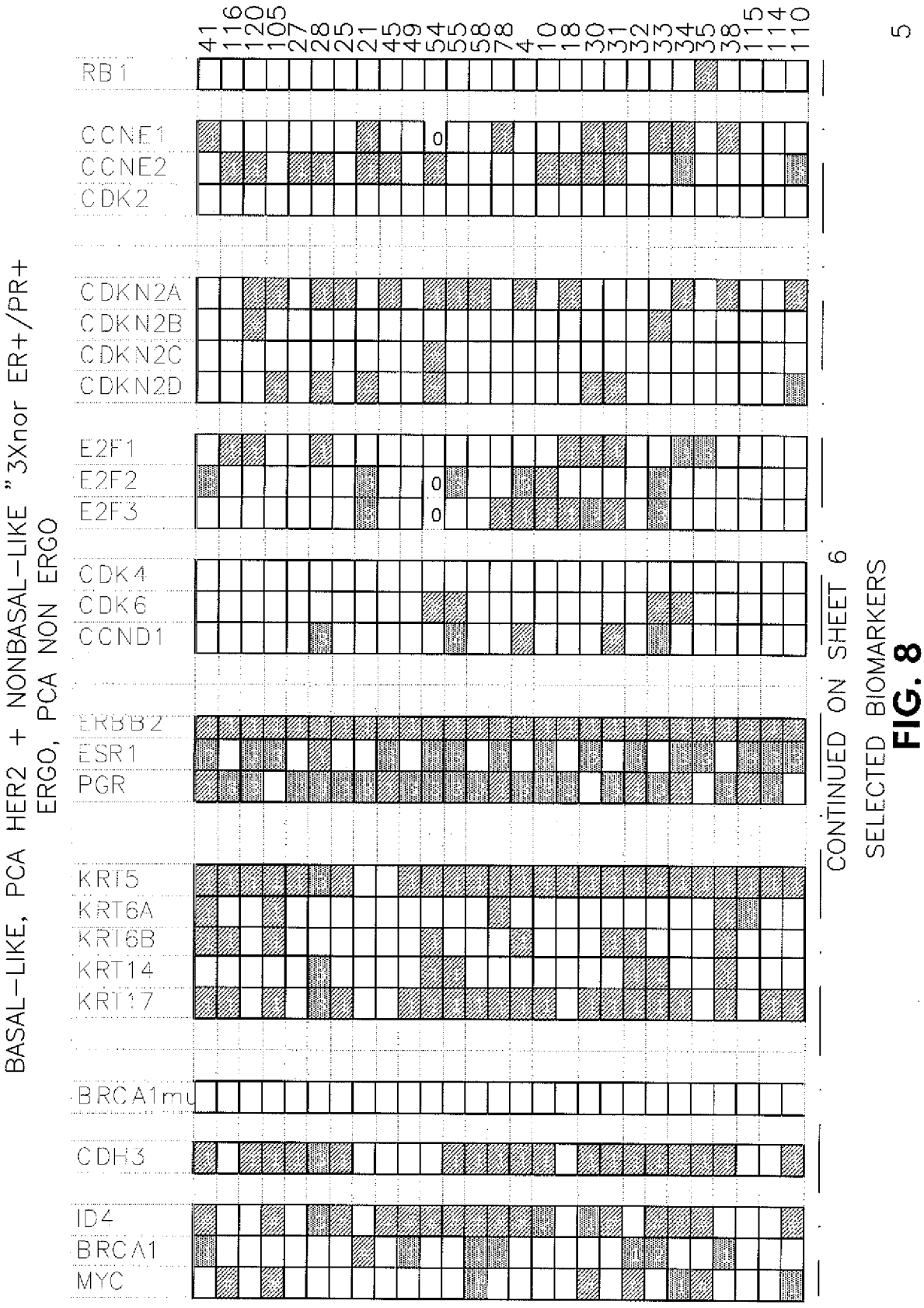
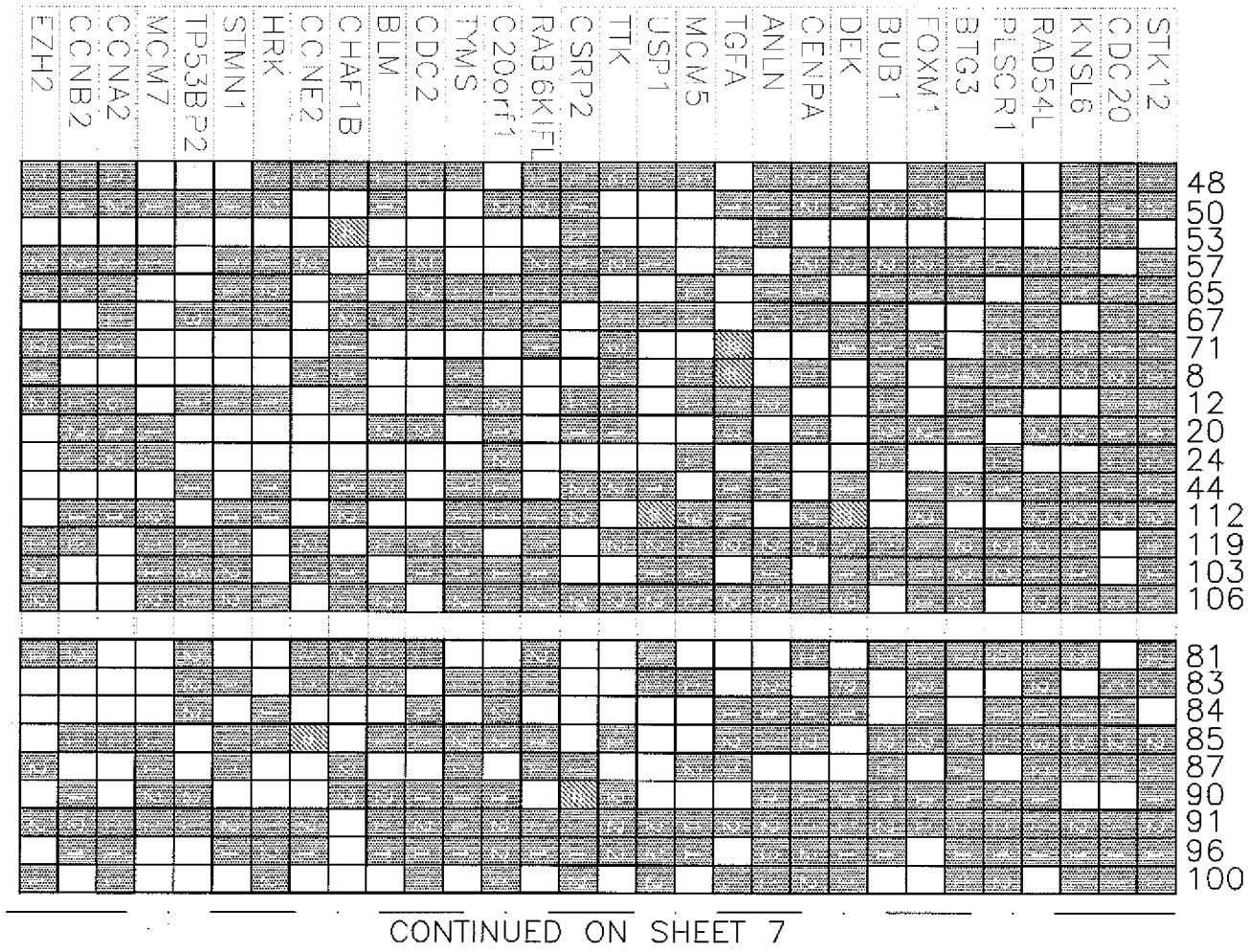
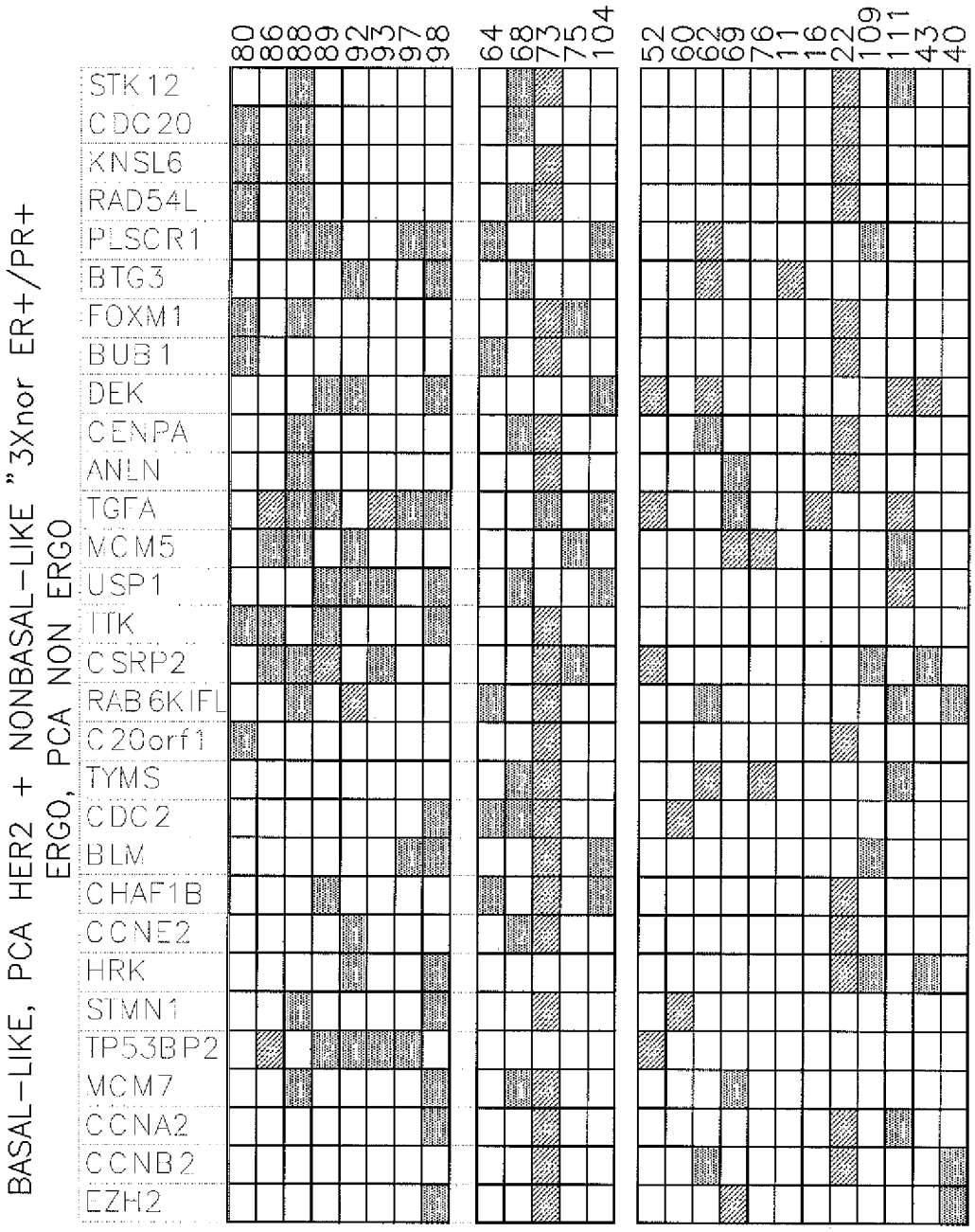

BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+
ERGO, PCA NON ERGO
41 116 120 105 27 28 25 21 45 49 54 55 58 78 4 10 18 30 31 32 33 34 35 38 115 114 110
RB1
CCNE1
CCNE2
CDK2
CDKN2A
CDKN2B
CDKN2C
CDKN2D
E2F1
E2F2
E2F3
CDK4
CDK6
CCND1
ERBB2
ESR1
PGR
KRT5
KRT6A
KRT6B
KRT14
KRT17
BRCA1mu
CDH3
ID4
BRCA1
MYC
CONTINUED ON SHEET 6
SELECTED BIOMARKERS

FIG. 8



TOP 30 OVEREXPRESSED ERGO GENES

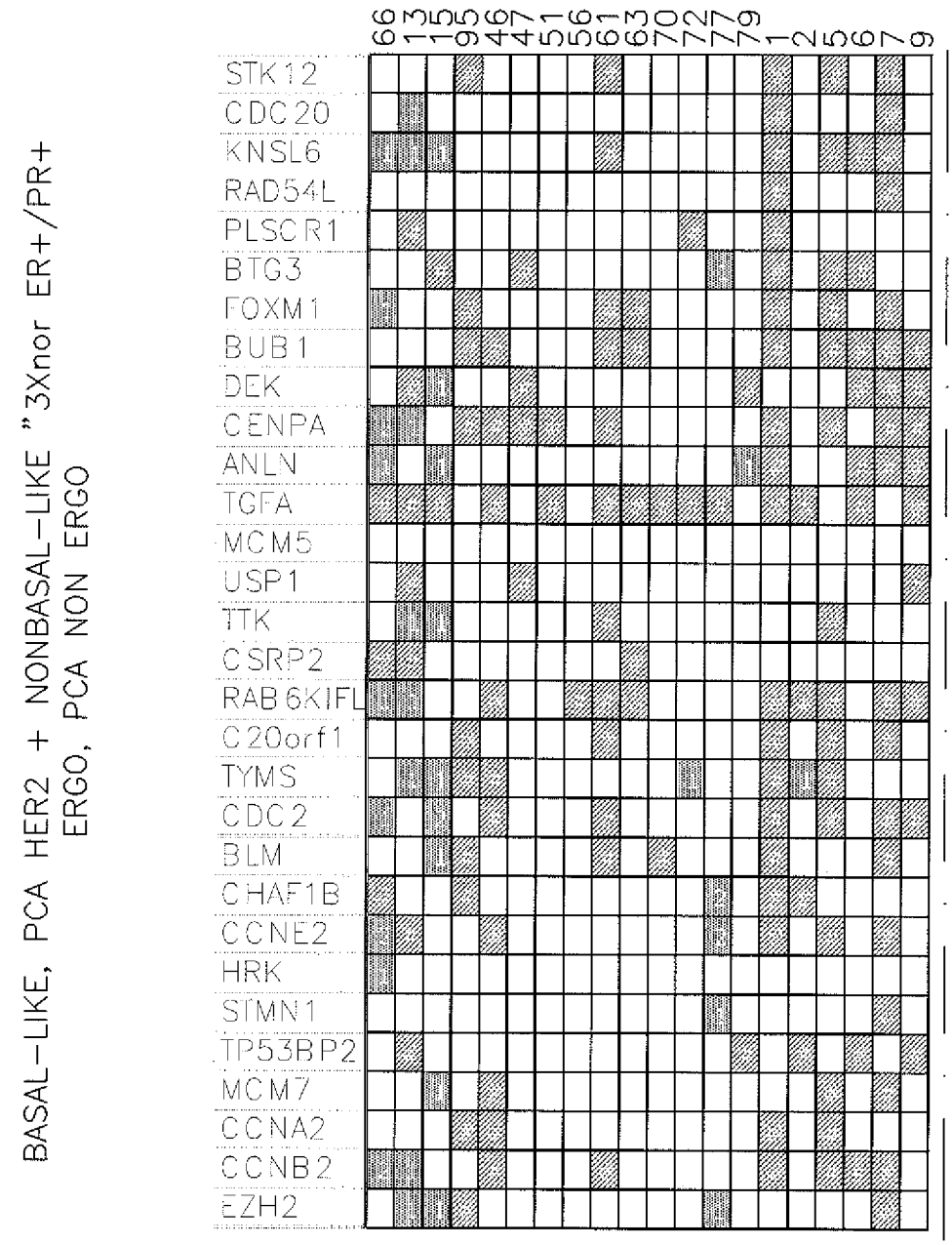
FIG. 8



CONTINUED ON SHEET 8

TOP 30 OVEREXPRESSED ERGO GENES

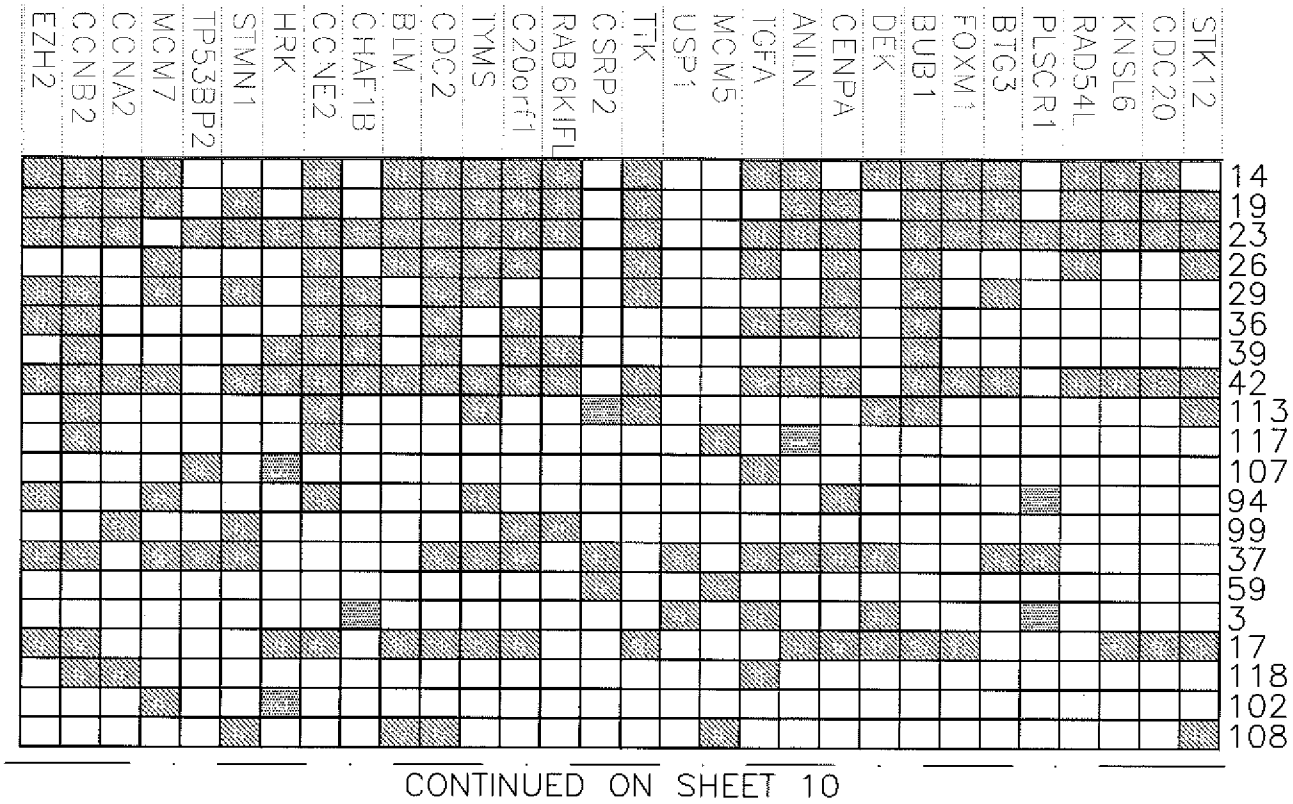
FIG. 8



TOP 30 OVEREXPRESSED ERGO GENES

FIG. 8

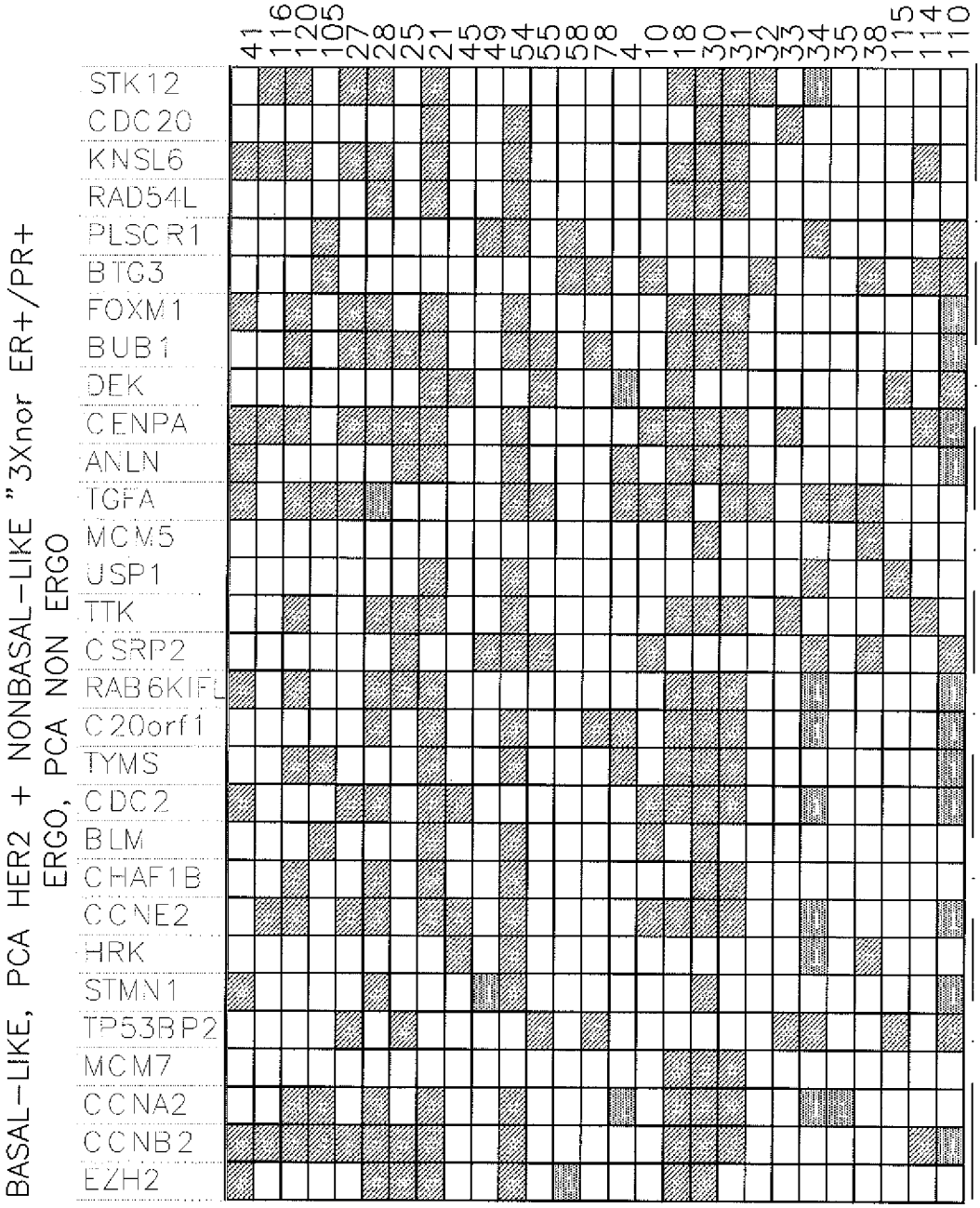
BASAL–LIKE, PCA HER2 + NONBASAL–LIKE "3Xnor ER+/PR+
ERGO, PCA NON ERGO



CONTINUED ON SHEET 10

TOP 30 OVEREXPRESSED ERGO GENES

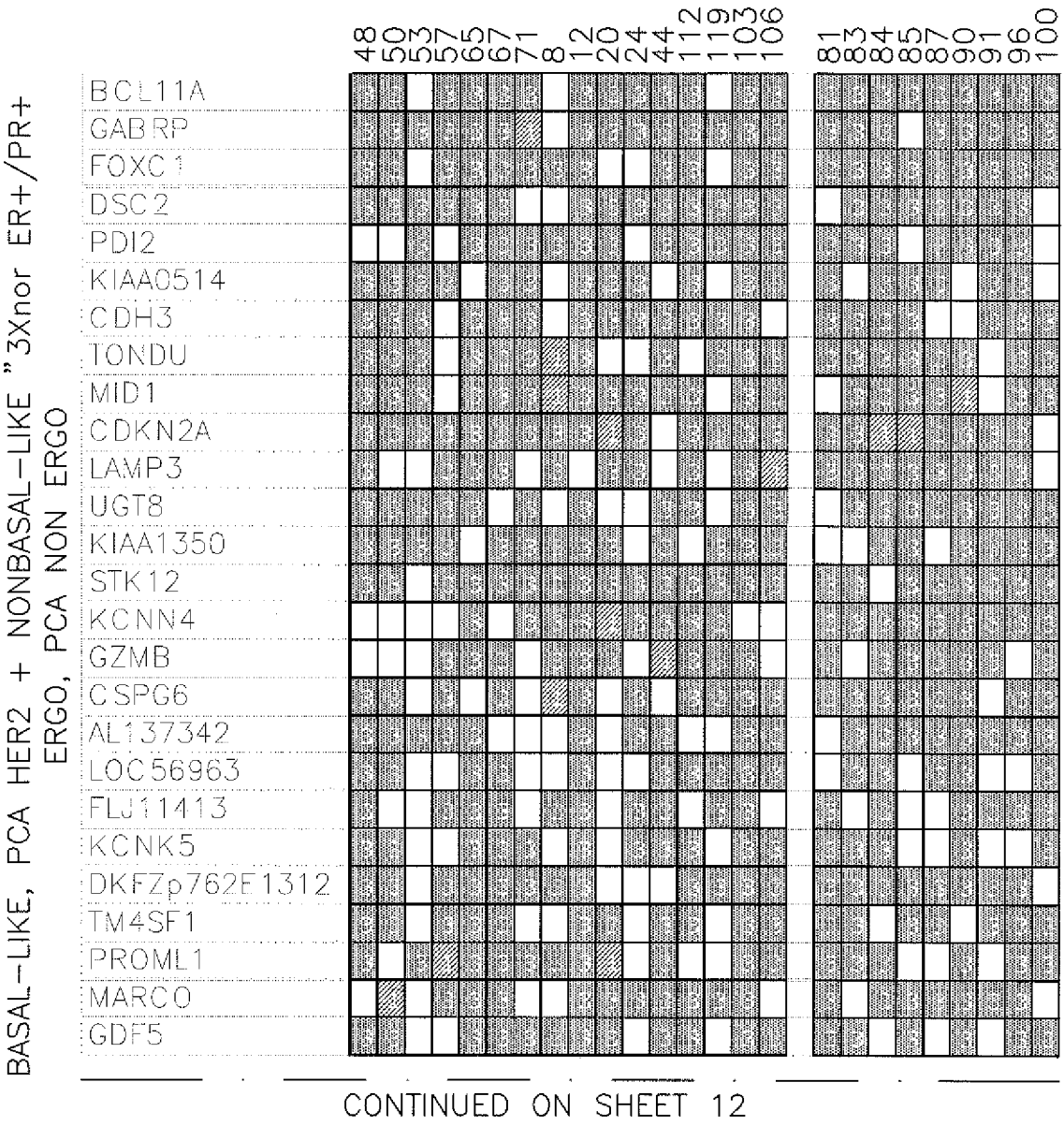
FIG. 8



TOP 30 OVEREXPRESSED ERGO GENES

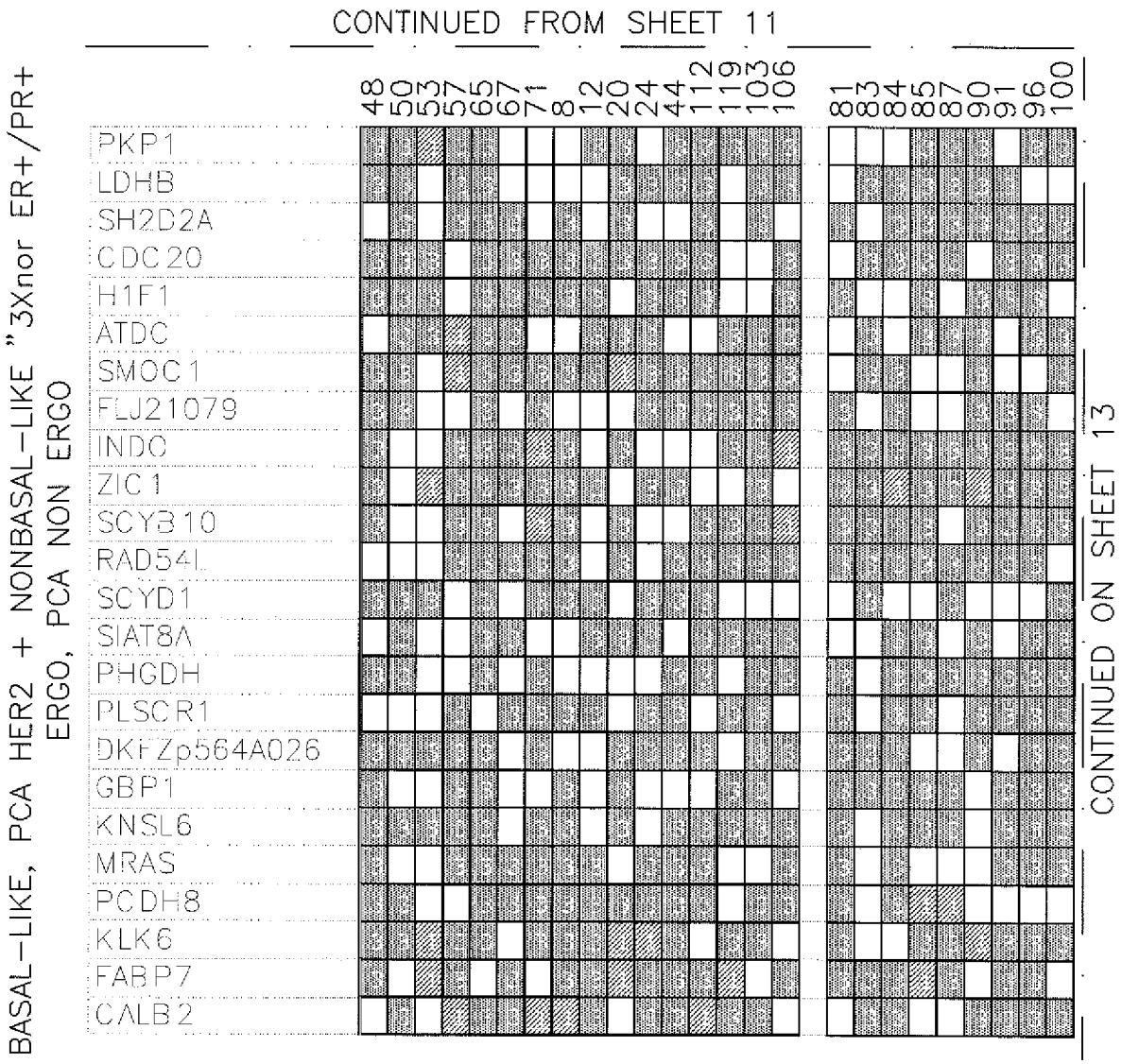
FIG. 8

10



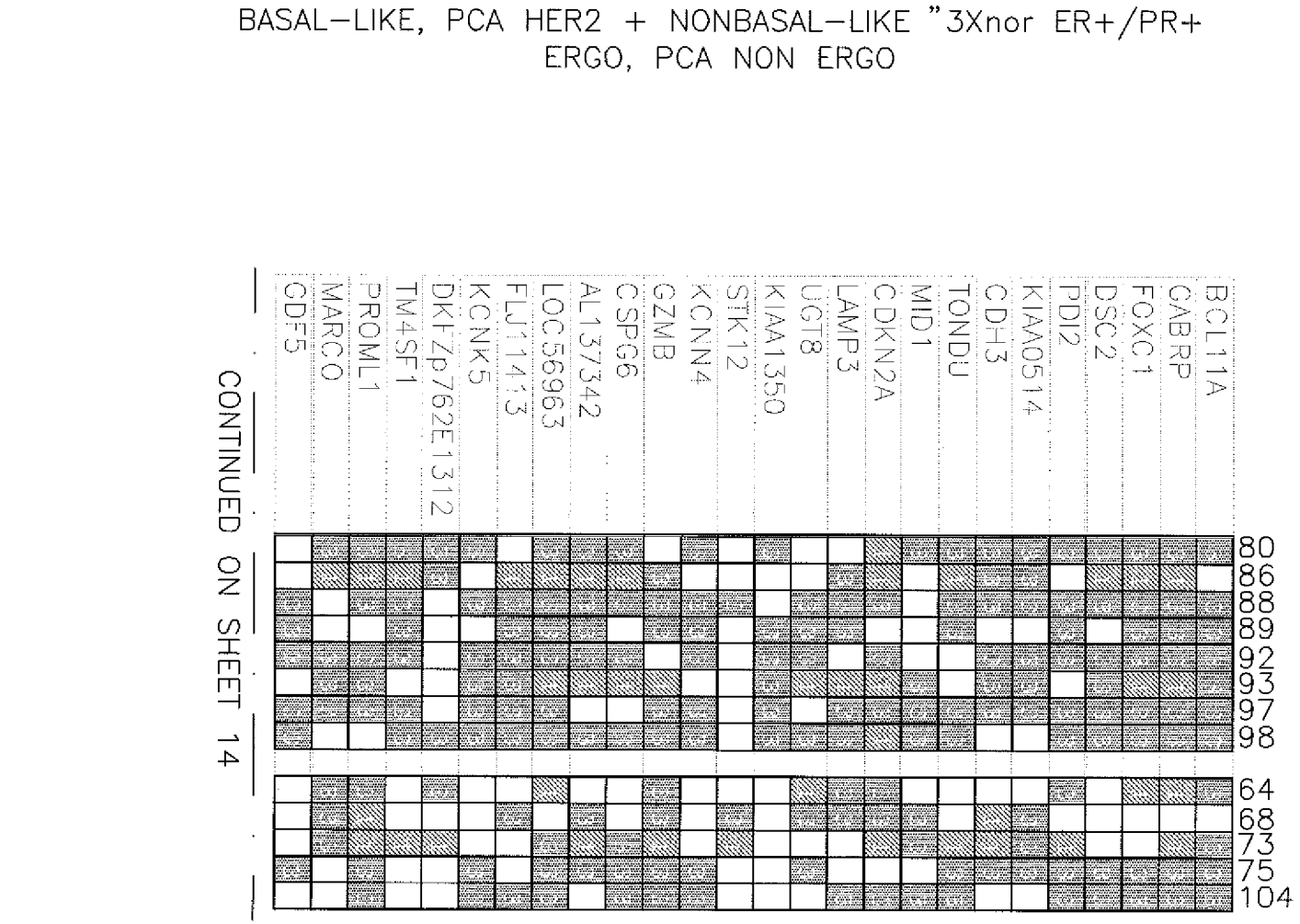
TOP 50 OVEREXPRESSED BASAL-LIKE GENES

FIG. 8



TOP 50 OVEREXPRESSED BASAL-LIKE GENES

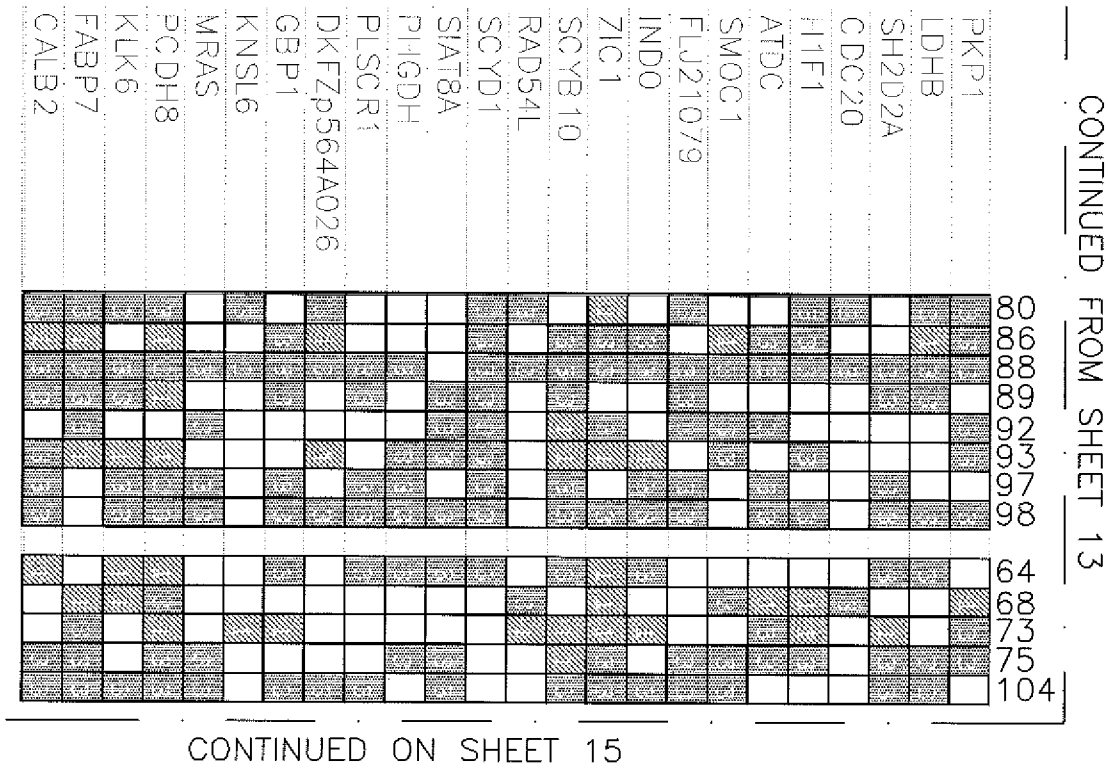
FIG. 8



TOP 50 OVEREXPRESSED BASAL−LIKE GENES

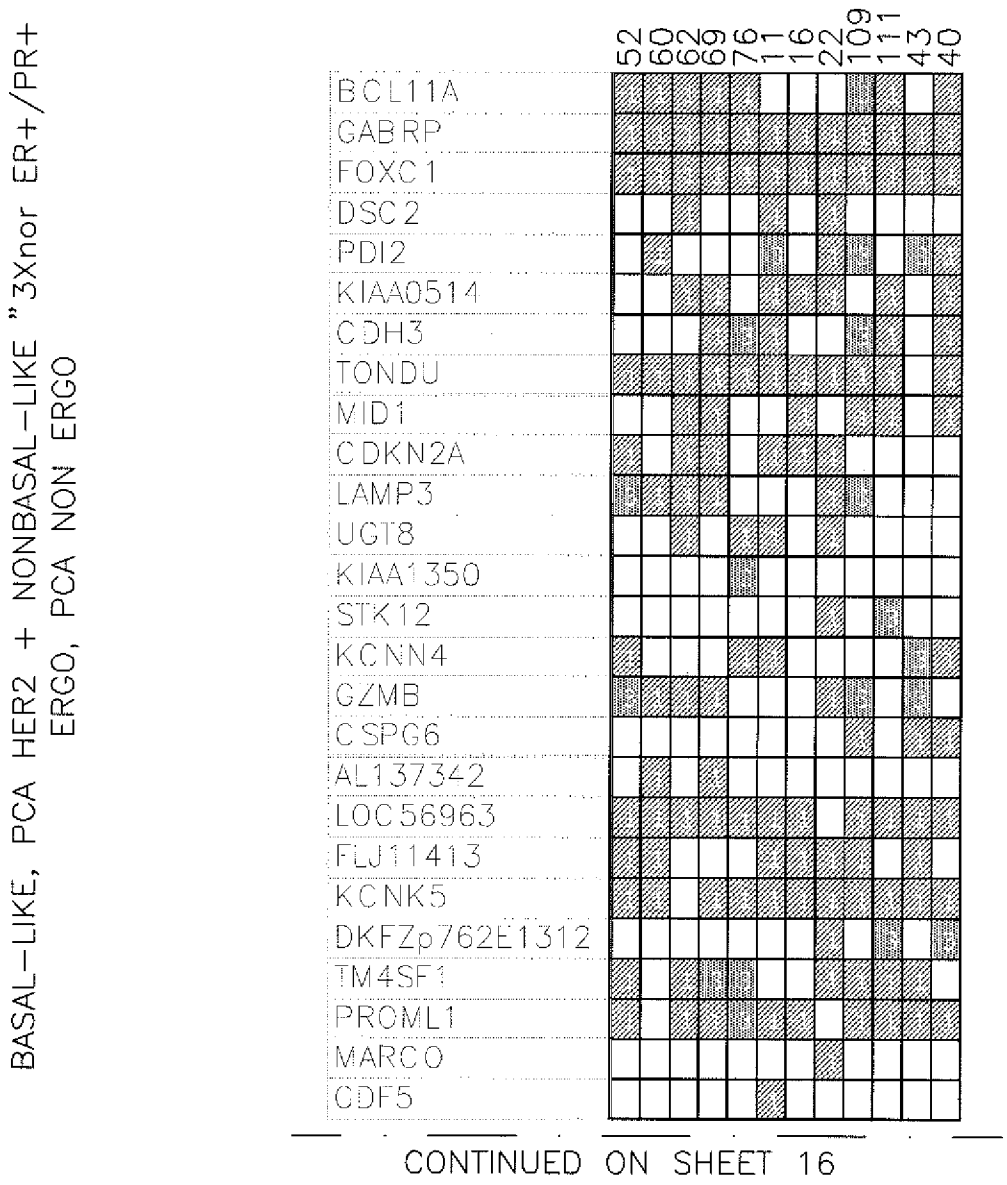
FIG. 8

BASAL–LIKE, PCA HER2 + NONBASAL–LIKE "3Xnor ER+/PR+
ERGO, PCA NON ERGO



TOP 50 OVEREXPRESSED BASAL–LIKE GENES

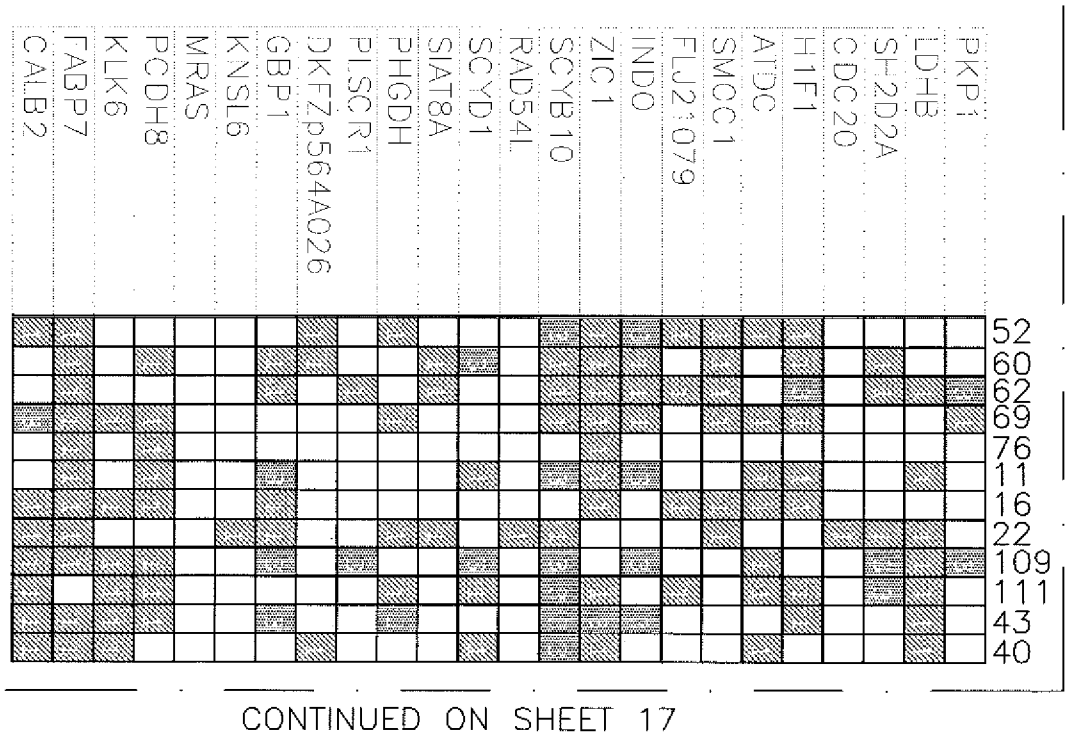
FIG. 8



TOP 50 OVEREXPRESSED BASAL-LIKE GENES

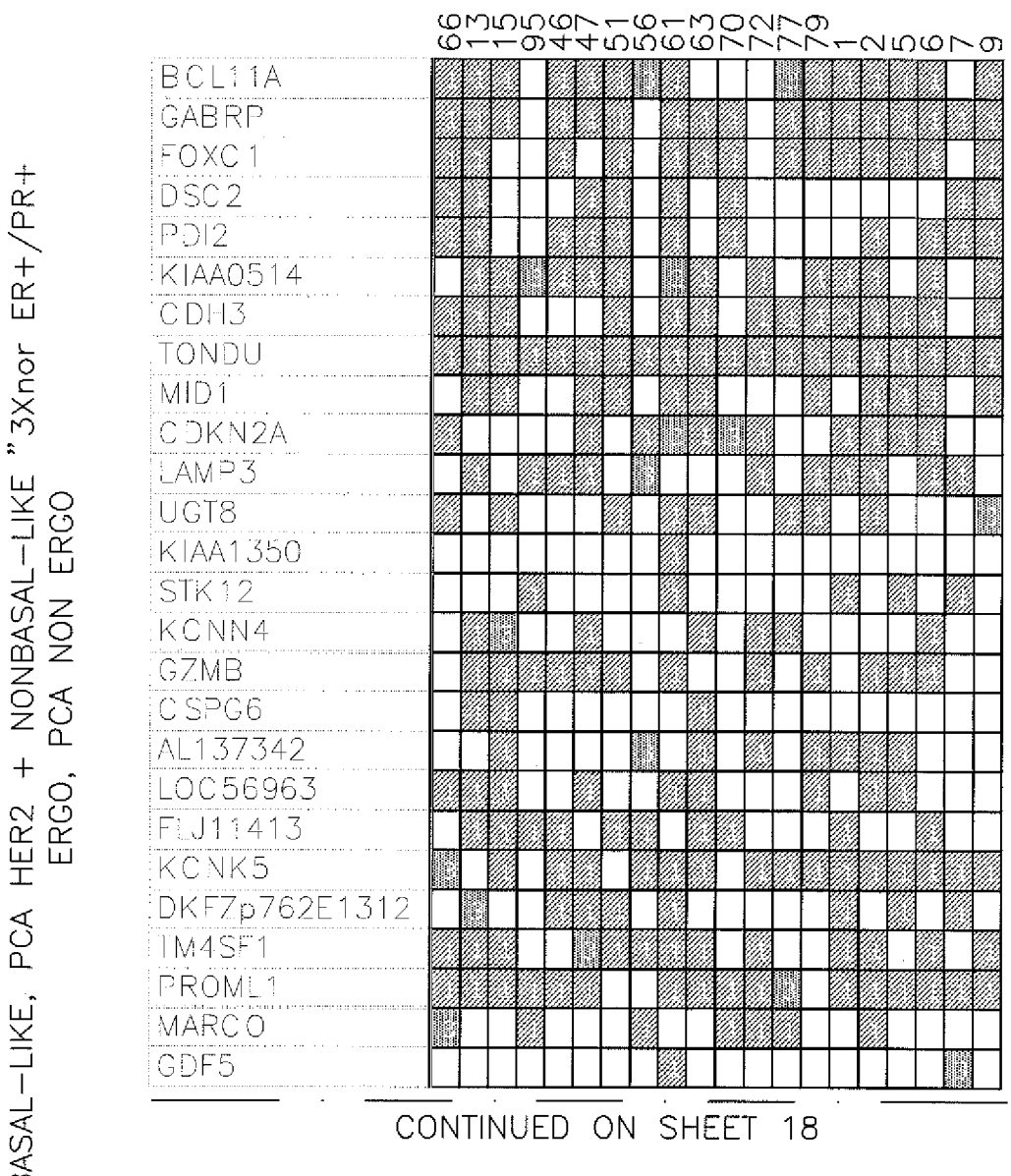
FIG. 8

BASAL–LIKE, PCA HER2 + NONBASAL–LIKE "3Xnor ER+/PR+
ERGO, PCA NON ERGO



TOP 50 OVEREXPRESSED BASAL–LIKE GENES

FIG. 8



TOP 50 OVEREXPRESSED BASAL-LIKE GENES

FIG. 8

CONTINUED FROM SHEET 17
66 13 15 95 46 47 51 56 61 63 70 72 77 79 1 2 5 6 7 9
PKP1
LDHB
SH2D2A
CDC20
H1F1
ATDC
SMOC1
FLJ21079
INDO
ZIC1
SCYB10
RAD54L
SCYD1
SIAT8A
PHGDH
PLSCR1
DKFZp564A026
GBP1
KNSL6
MRAS
PCDH8
KLK6
FABP7
CALB2
CONTINUED ON SHEET 19
BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+ ERGO, PCA NON ERGO
TOP 50 OVEREXPRESSED BASAL-LIKE GENES

FIG. 8

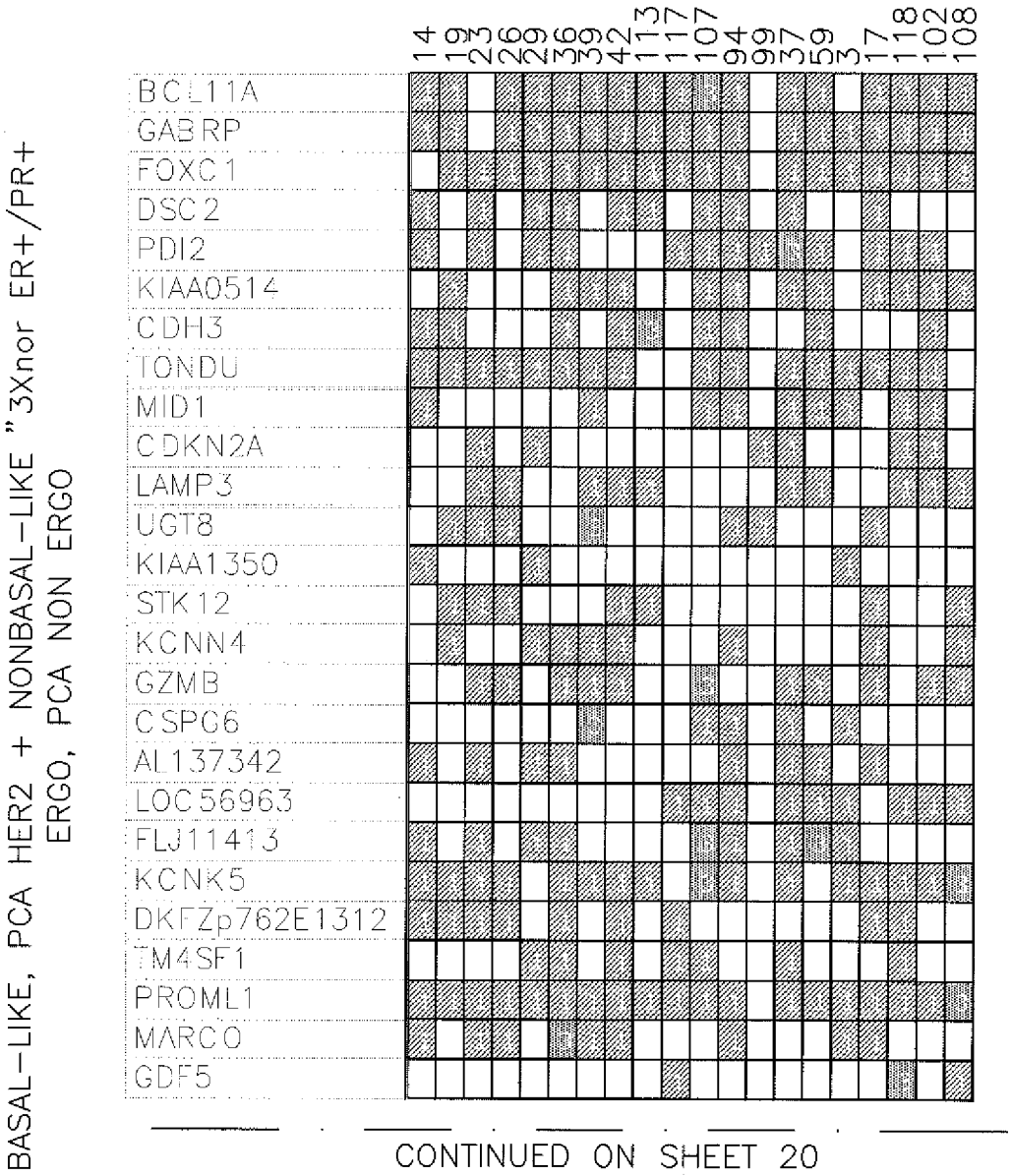
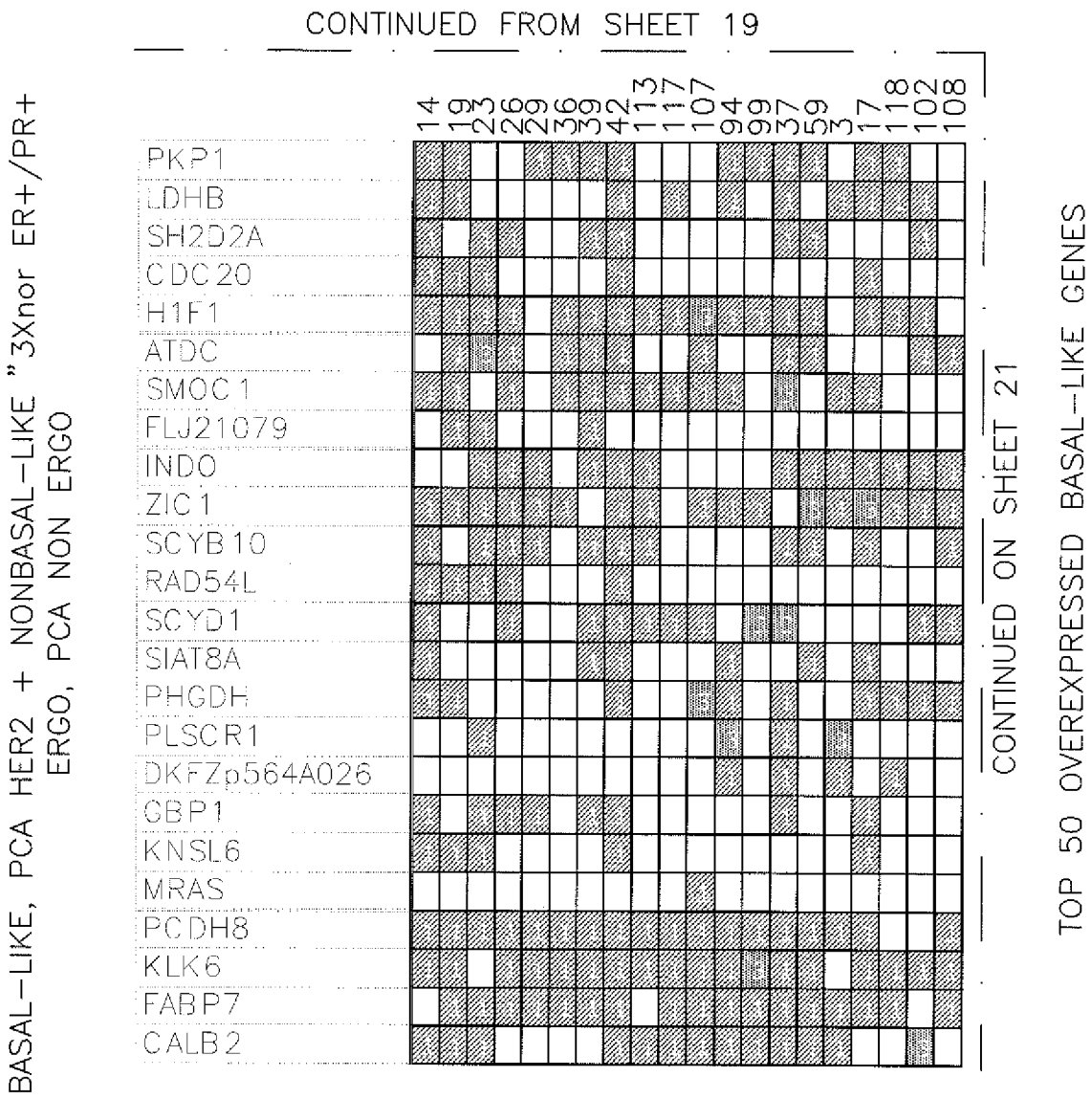

BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+ ERGO, PCA NON ERGO
14 19 23 26 29 36 39 42 113 117 107 94 99 37 59 3 17 118 102 108
BCL11A
GABRP
FOXC1
DSC2
PDI2
KIAA0514
CDH3
TONDU
MID1
CDKN2A
LAMP3
UGT8
KIAA1350
STK12
KCNN4
GZMB
CSPG6
AL137342
LOC56963
FLJ11413
KCNK5
DKFZp762E1312
TM4SF1
PROML1
MARCO
GDF5
TOP 50 OVEREXPRESSED BASAL-LIKE GENES
CONTINUED ON SHEET 20

FIG. 8



TOP 50 OVEREXPRESSED BASAL-LIKE GENES

FIG. 8

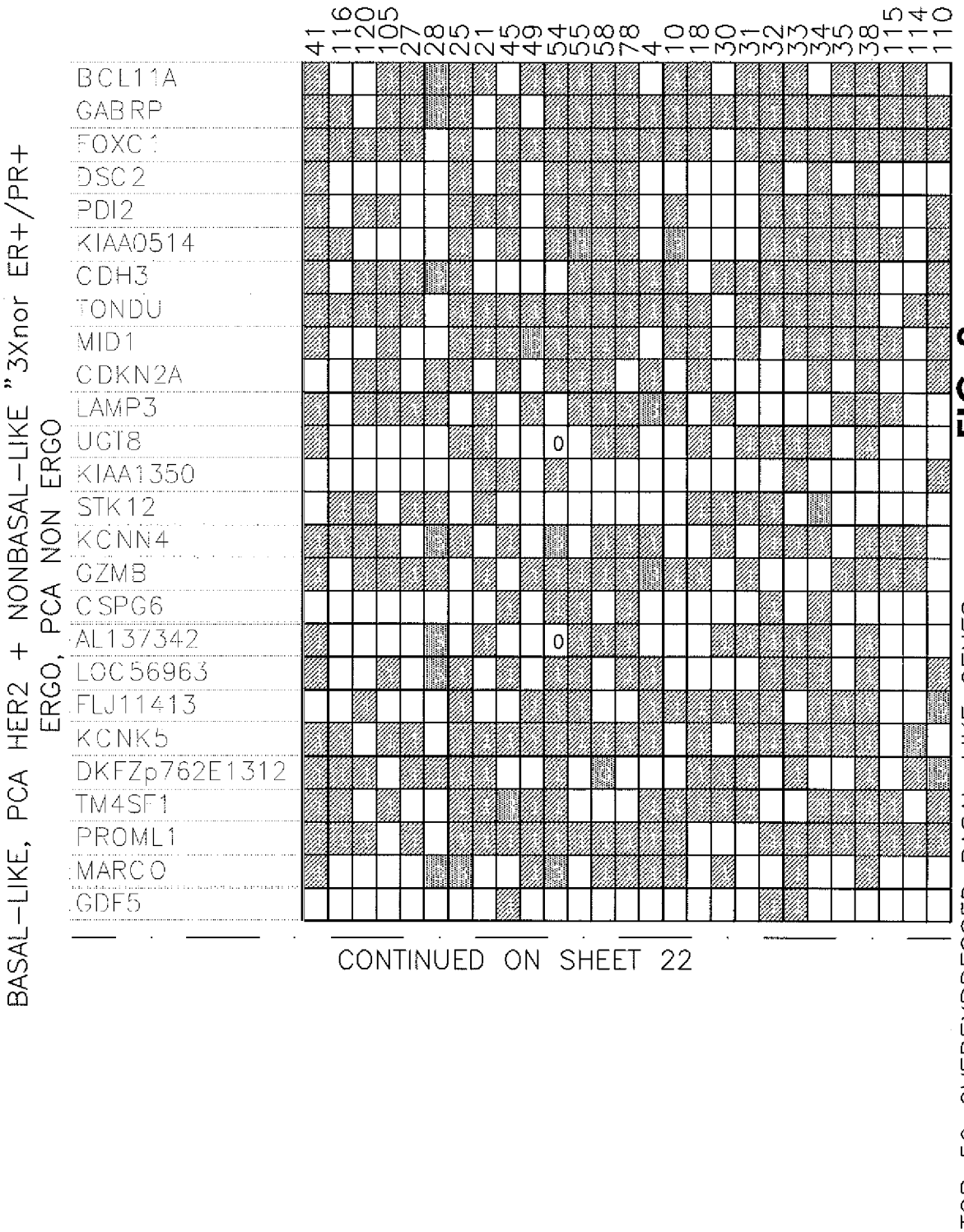

BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+ ERGO, PCA NON ERGO
41 116 120 105 27 28 25 21 45 49 54 55 58 78 4 10 18 30 31 32 33 34 35 38 115 114 110
BCL11A
GABRP
FOXC1
DSC2
PDI2
KIAA0514
CDH3
TONDU
MID1
CDKN2A
LAMP3
UGT8
KIAA1350
STK12
KCNN4
GZMB
CSPG6
AL137342
LOC56963
FLJ11413
KCNK5
DKFZp762E1312
TM4SF1
PROML1
MARCO
GDF5
CONTINUED ON SHEET 22
TOP 50 OVEREXPRESSED BASAL-LIKE GENES

FIG. 8

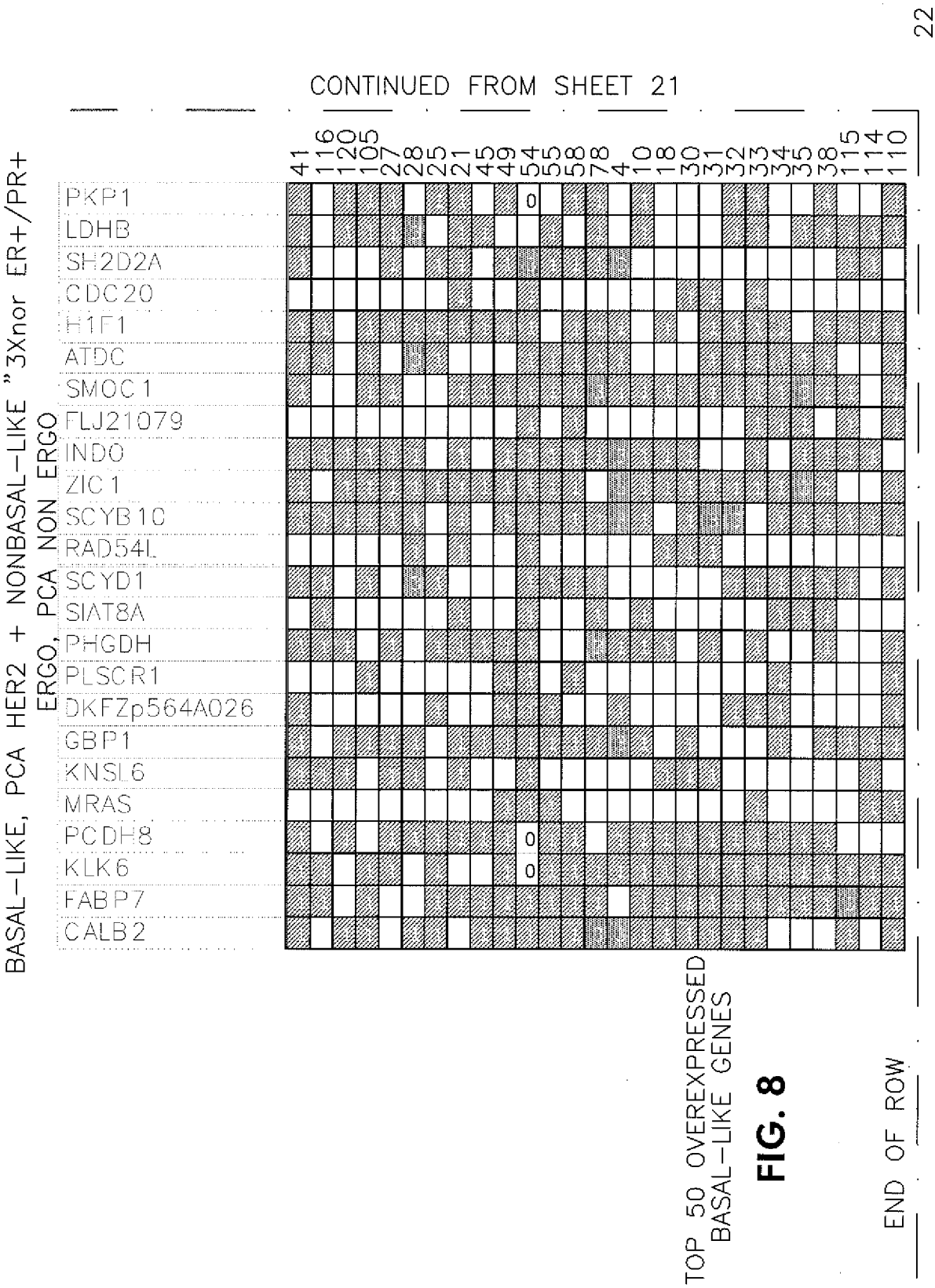
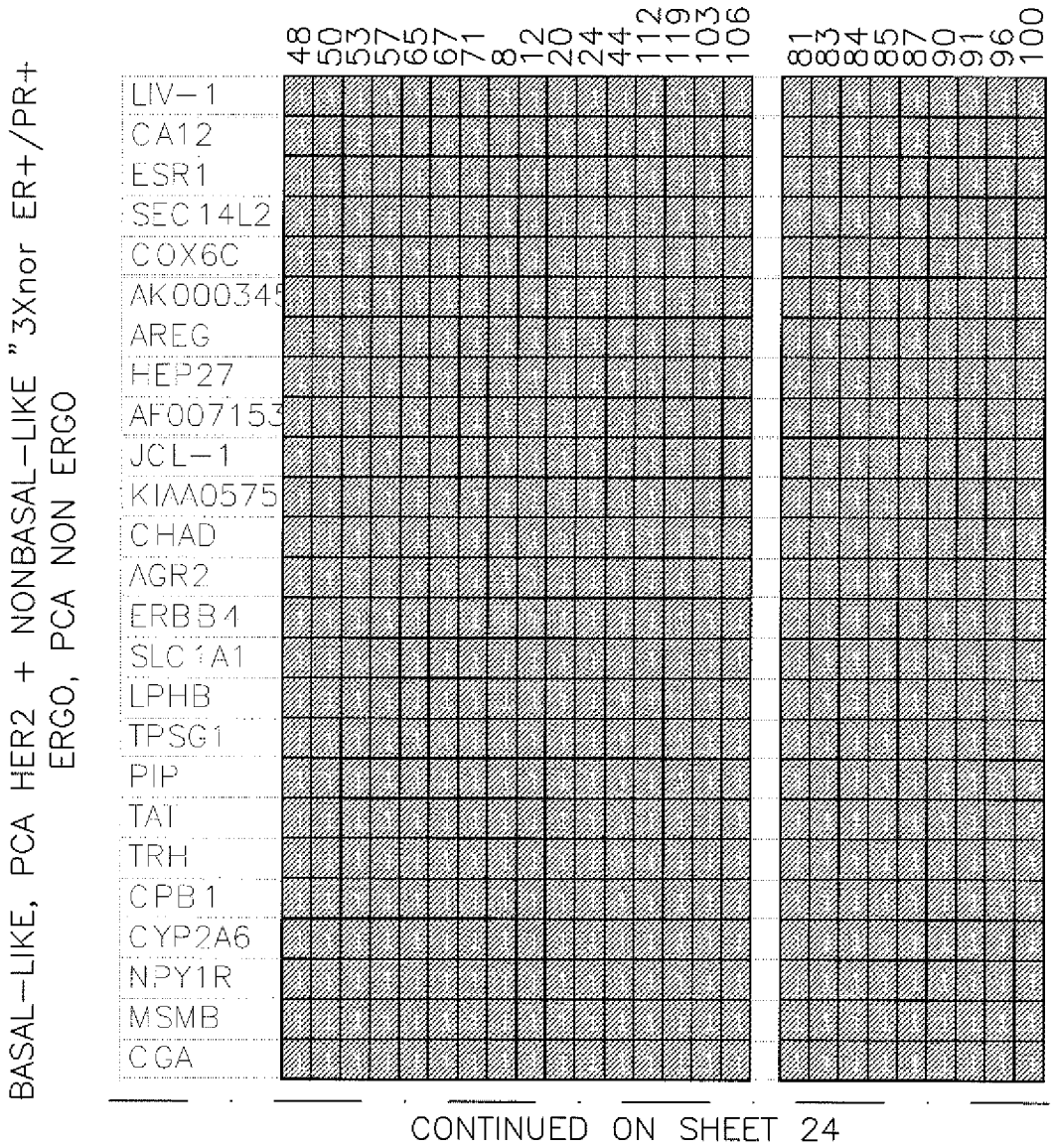

22
CONTINUED FROM SHEET 21
41 116 120 105 27 28 25 21 45 49 54 55 58 78 4 10 18 30 31 32 33 34 35 38 115 114 110
BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+ ERGO, PCA NON ERGO
PKP1
LDHB
SH2D2A
CDC20
H1F1
ATDC
SMOC1
FLJ21079
INDO
ZIC1
SCYB10
RAD54L
SCYD1
SIAT8A
PHGDH
PLSCR1
DKFZp564A026
GBP1
KNSL6
MRAS
PCDH8
KLK6
FABP7
CALB2
0
0
0
TOP 50 OVEREXPRESSED BASAL-LIKE GENES
END OF ROW

FIG. 8



TOP 50 UNDEREXPRESSED BASAL-LIKE GENES

FIG. 8

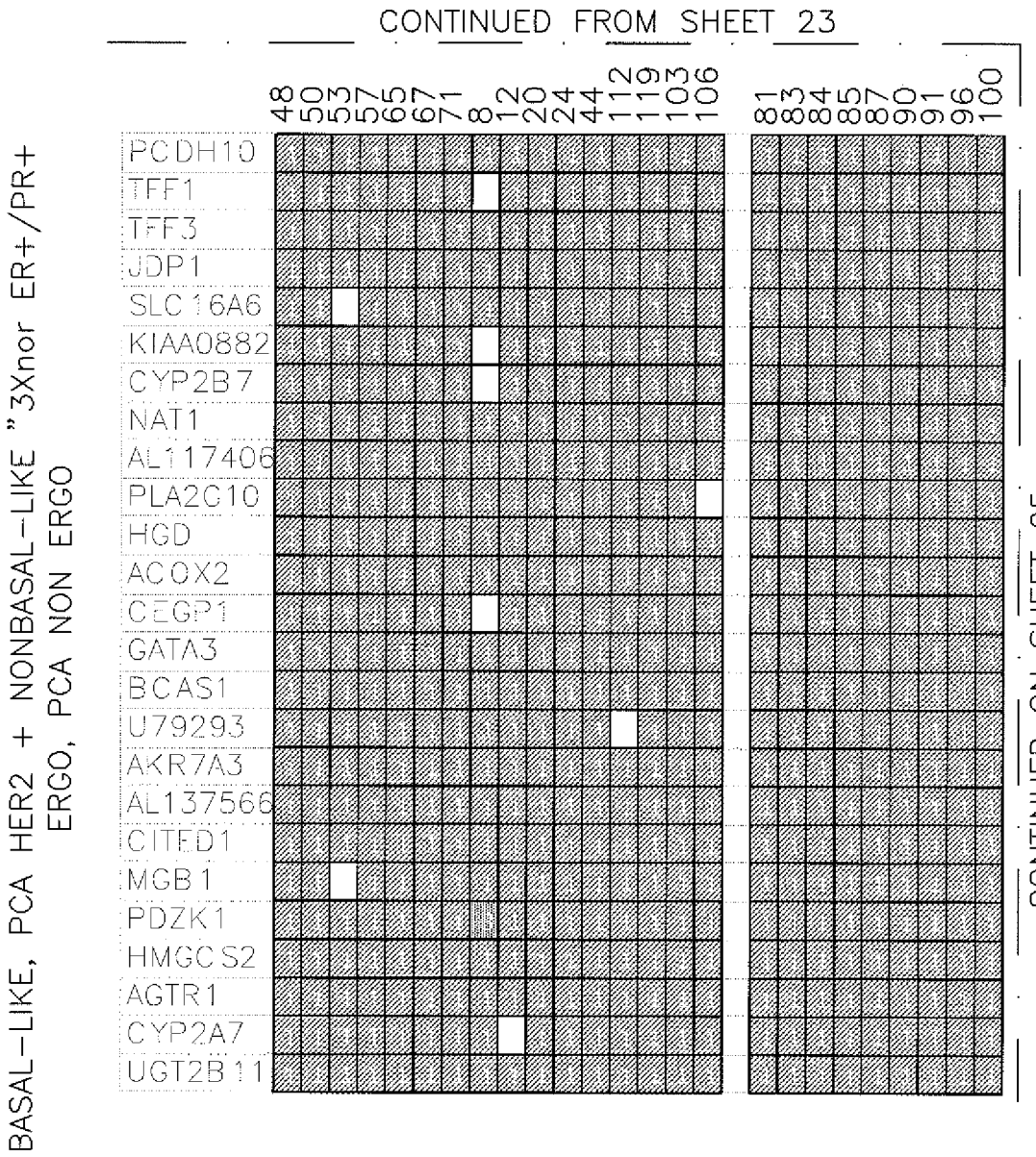
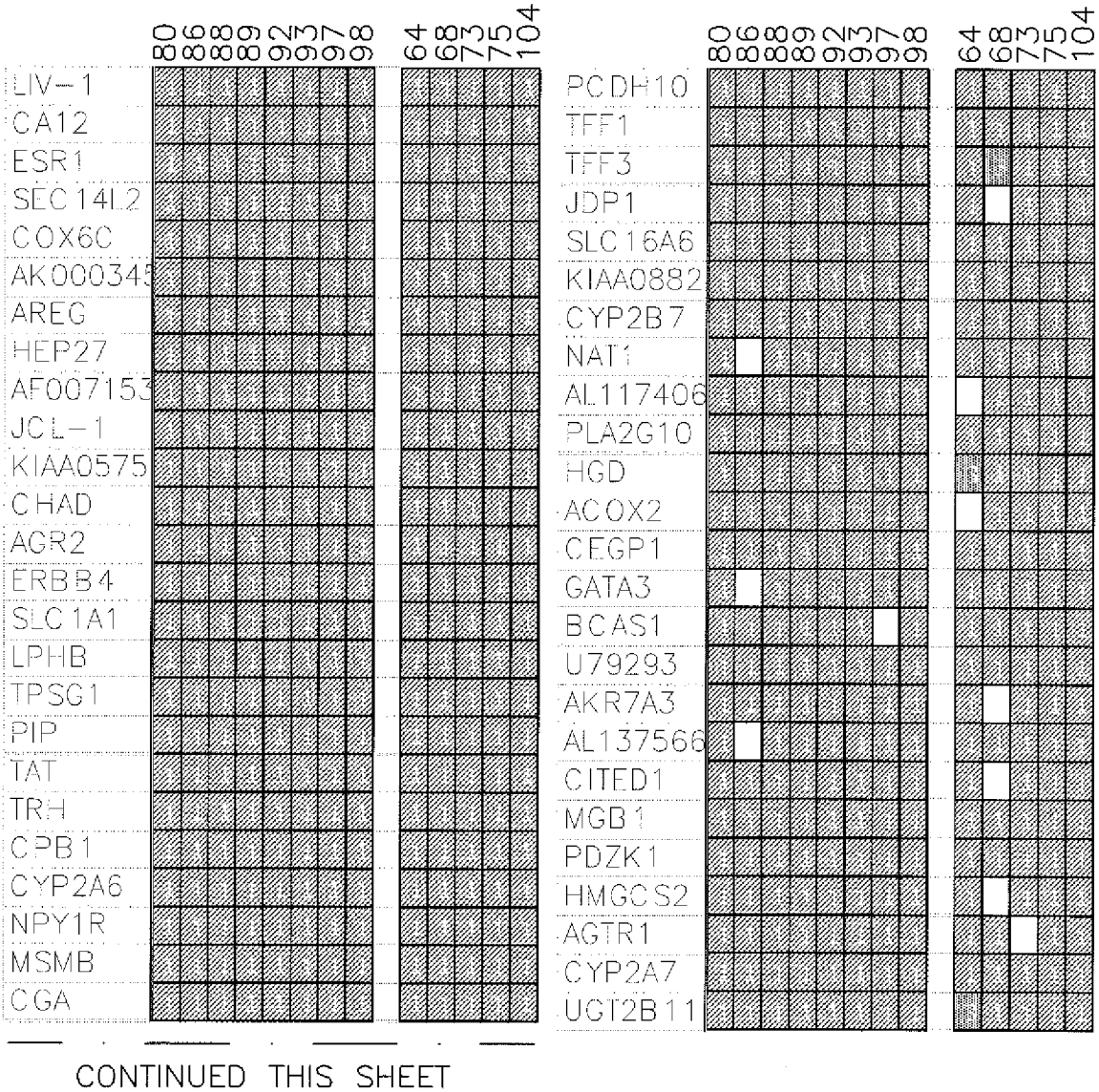

CONTINUED FROM SHEET 23
BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+ ERGO, PCA NON ERGO
48 50 53 57 65 67 71 8 12 20 24 44 112 119 103 106 81 83 84 85 87 90 91 96 100
PCDH10
TFF1
TFF3
JDP1
SLC16A6
KIAA0882
CYP2B7
NAT1
AL117406
PLA2C10
HGD
ACOX2
CEGP1
GATA3
BCAS1
U79293
AKR7A3
AL137566
CITED1
MGB1
PDZK1
HMGCS2
AGTR1
CYP2A7
UGT2B11
CONTINUED ON SHEET 25
TOP 50 UNDEREXPRESSED BASAL-LIKE GENES

FIG. 8

BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+
ERGO, PCA NON ERGO



TOP 50 UNDEREXPRESSED BASAL-LIKE GENES

FIG. 8

TOP 50 UNDEREXPRESSED BASAL-LIKE GENES

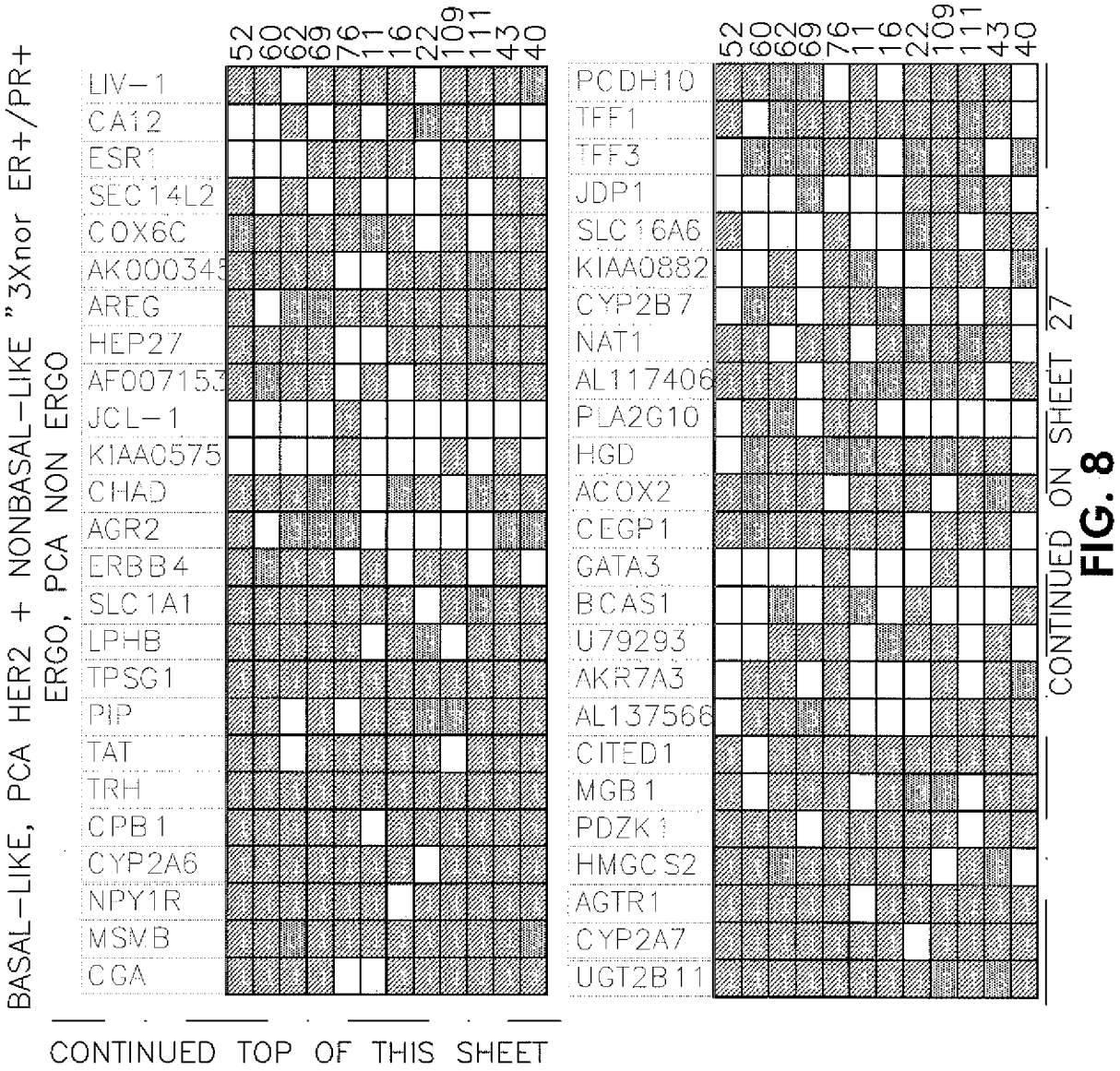


FIG. 8

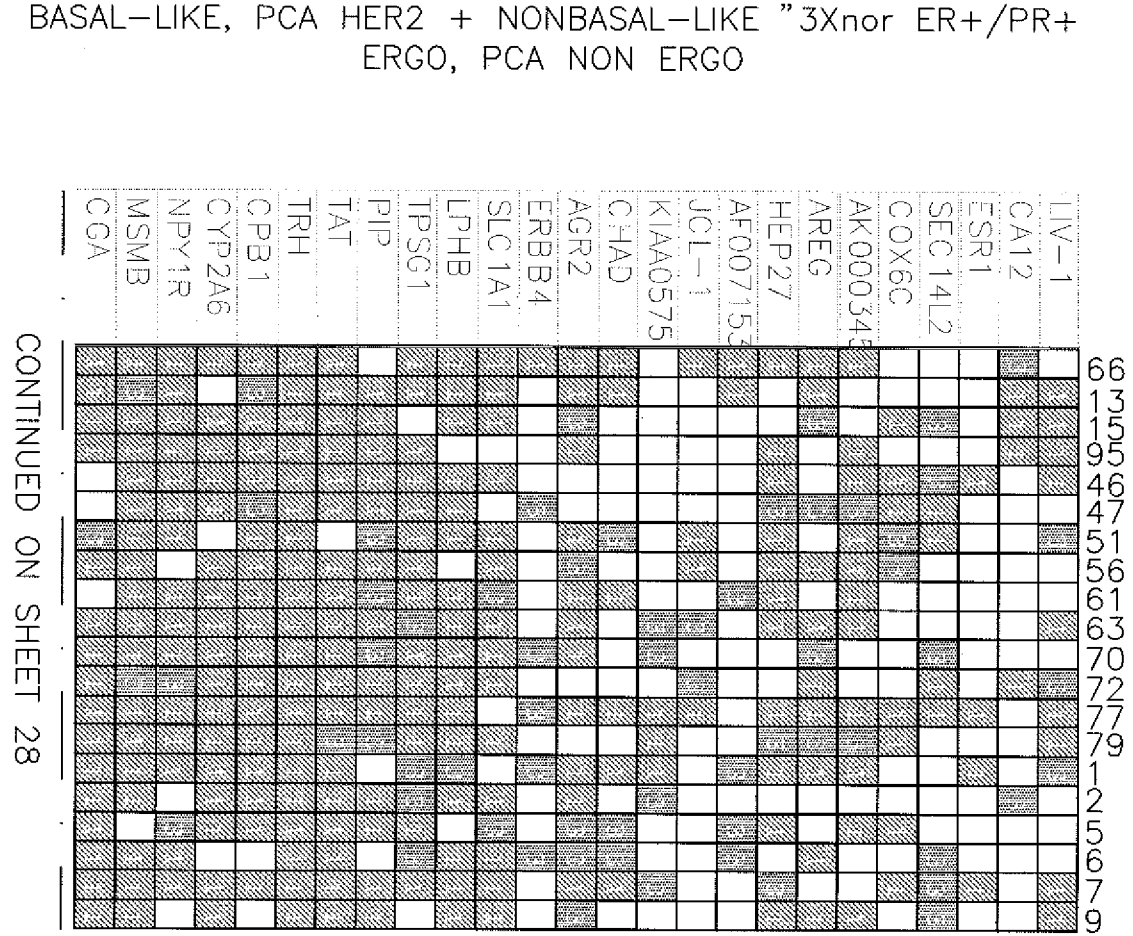
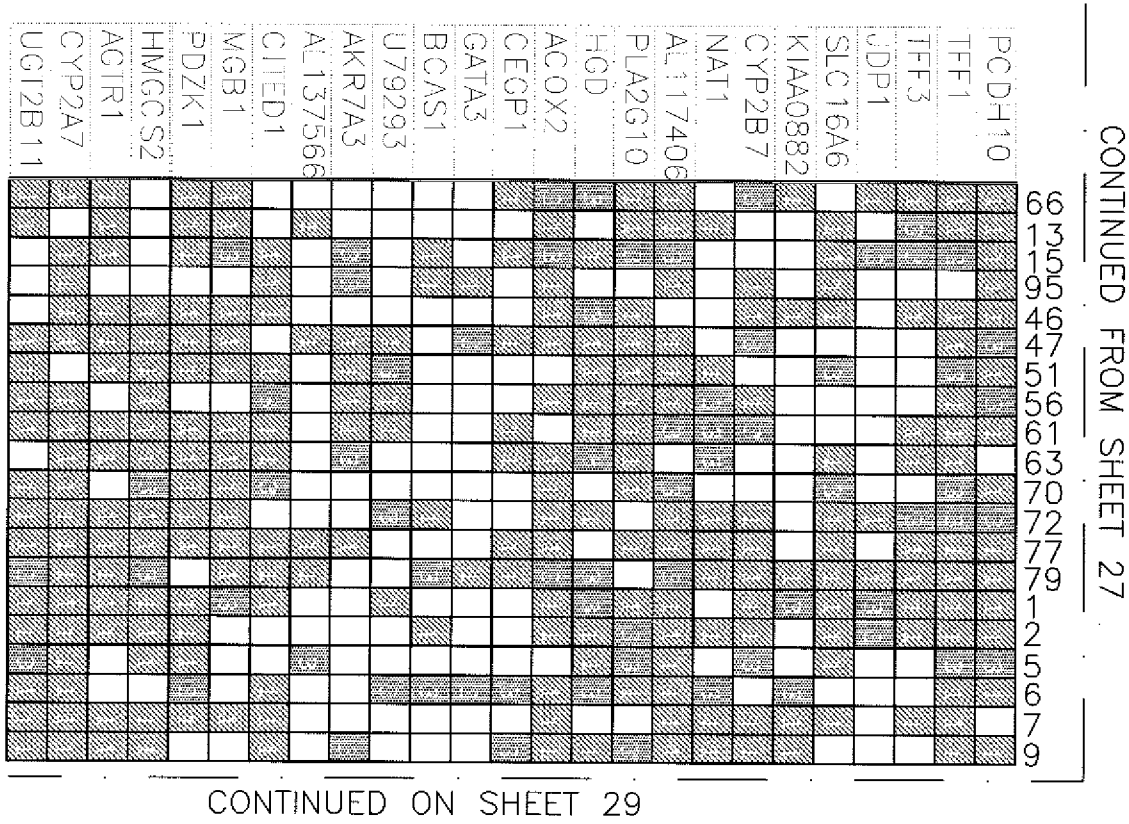

BASAL–LIKE, PCA HER2 + NONBASAL–LIKE "3Xnor ER+/PR+
ERGO, PCA NON ERGO
LIV–1
CA12
ESR1
SEC14L2
COX6C
AK000345
AREG
HEP27
AF007153
JCL–1
KIAA0575
CHAD
AGR2
ERBB4
SLC1A1
LPHB
TPSG1
PIP
TAT
TRH
CPB1
CYP2A6
NPY1R
MSMB
CGA
66
13
15
95
46
47
51
56
61
63
70
72
77
79
1
2
5
6
7
9
CONTINUED ON SHEET 28
TOP 50 UNDEREXPRESSED BASAL–LIKE GENES

FIG. 8

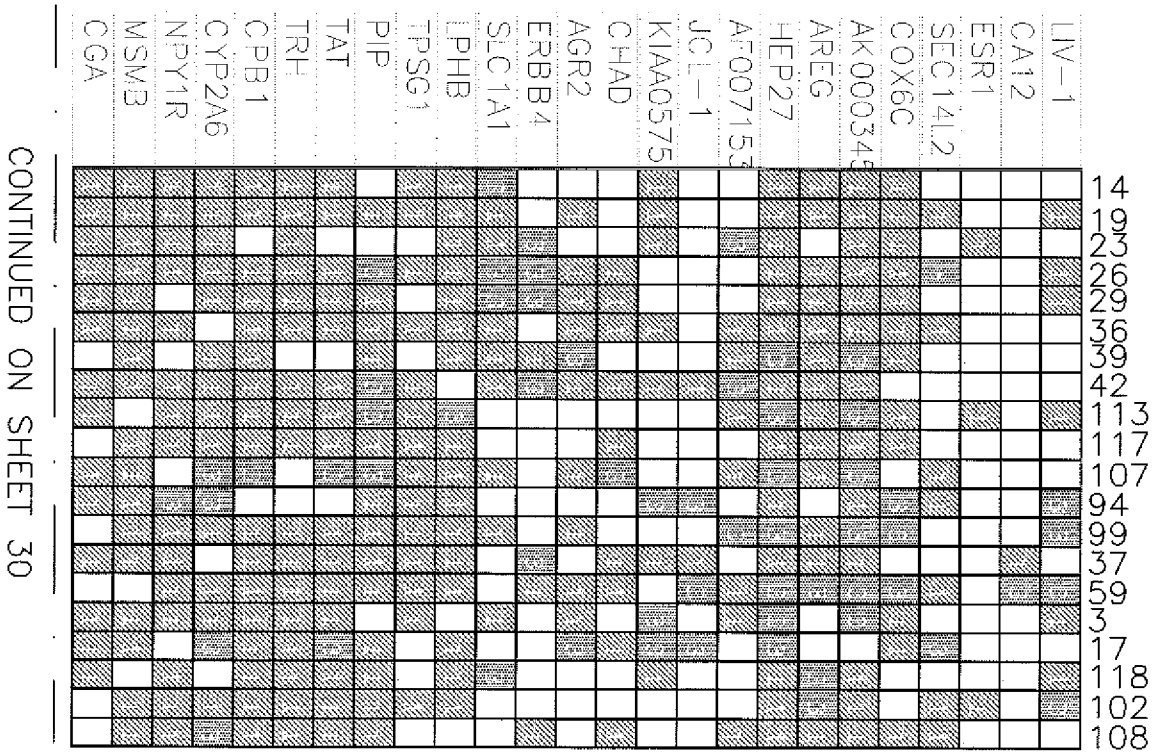
BASAL–LIKE, PCA HER2 + NONBASAL–LIKE "3Xnor ER+/PR+
ERGO, PCA NON ERGO



TOP 50 UNDEREXPRESSED BASAL–LIKE GENES

FIG. 8

BASAL–LIKE, PCA HER2 + NONBASAL–LIKE "3Xnor ER+/PR+
ERGO, PCA NON ERGO



CONTINUED ON SHEET 30

TOP 50 UNDEREXPRESSED BASAL–LIKE GENES

FIG. 8

TOP 50 UNDEREXPRESSED BASAL-LIKE GENES

FIG. 8

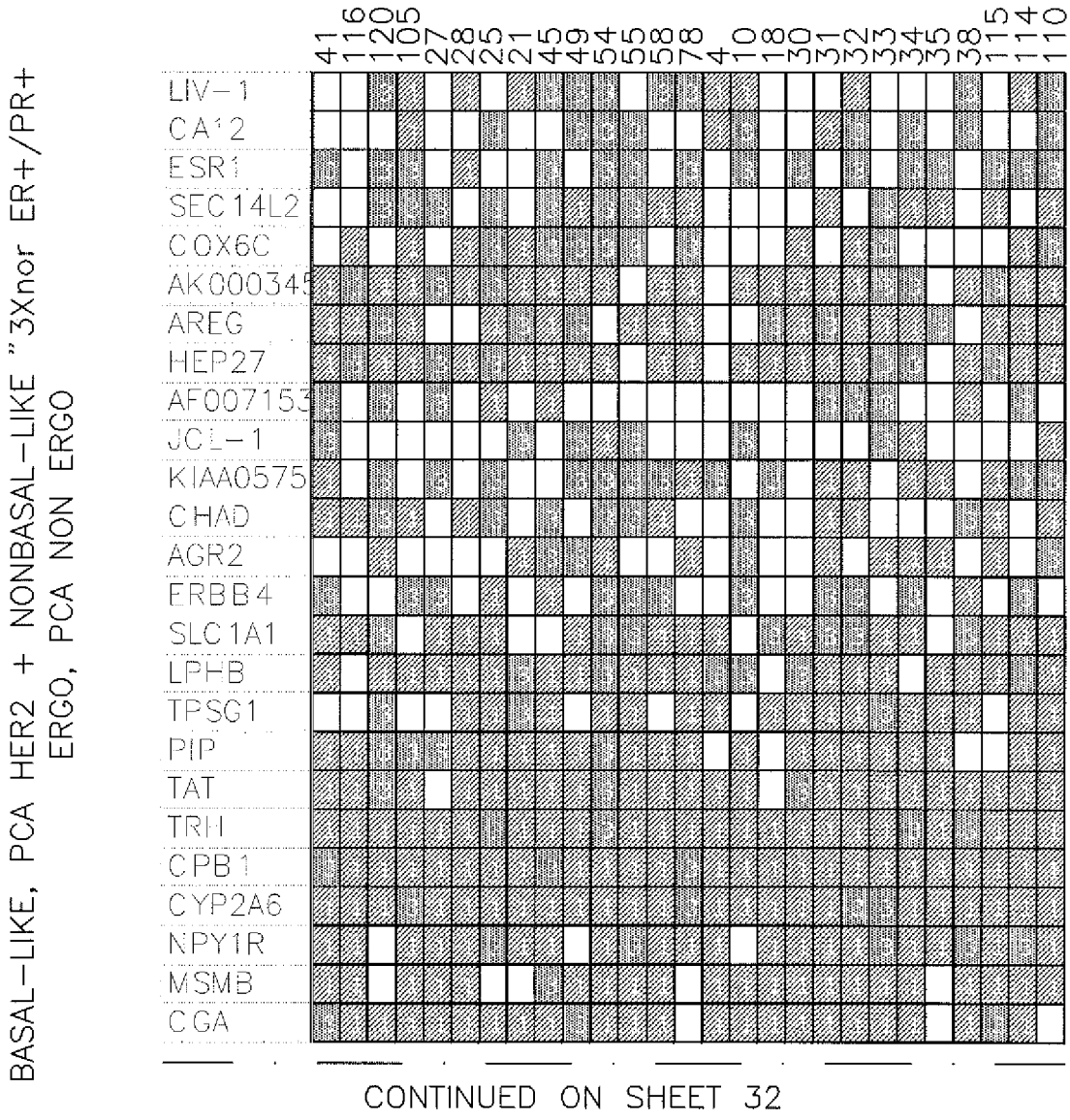

BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+
ERGO, PCA NON ERGO
41 116 120 105 27 28 25 21 45 49 54 55 58 78 4 10 18 30 31 32 33 34 35 38 115 114 110
LIV-1
CA12
ESR1
SEC14L2
COX6C
AK000345
AREG
HEP27
AF007153
JCL-1
KIAA0575
CHAD
AGR2
ERBB4
SLC1A1
LPHB
TPSG1
PIP
TAT
TRH
CPB1
CYP2A6
NPY1R
MSMB
CGA
TOP 50 UNDEREXPRESSED BASAL-LIKE GENES
CONTINUED ON SHEET 32

FIG. 8

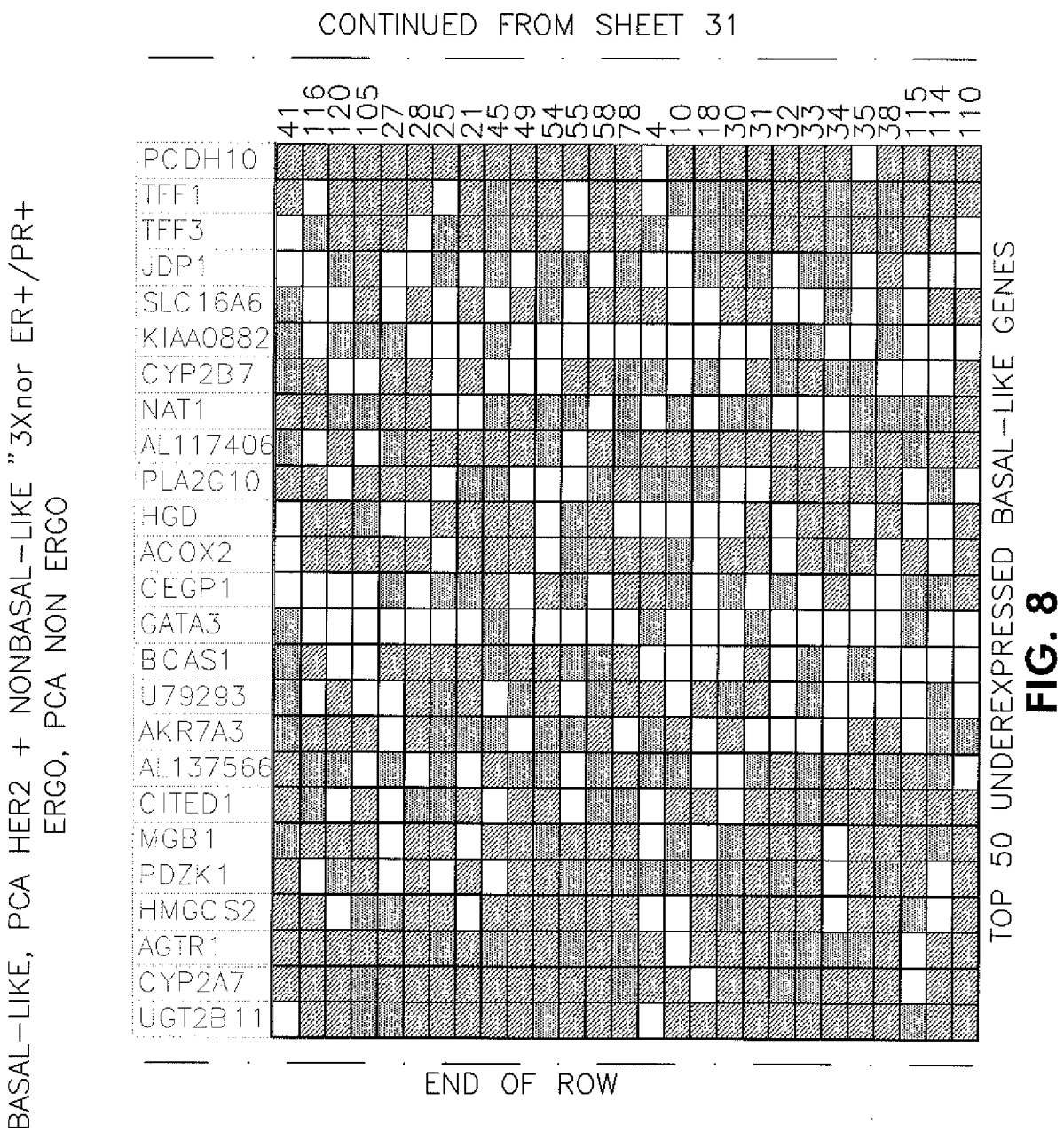

CONTINUED FROM SHEET 31
41 116 120 105 27 28 25 21 45 49 54 55 58 78 4 10 18 30 31 32 33 34 35 38 115 114 110
PCDH10
TFF1
TFF3
JDP1
SLC16A6
KIAA0882
CYP2B7
NAT1
AL117406
PLA2G10
HGD
ACOX2
CEGP1
GATA3
BCAS1
U79293
AKR7A3
AL137566
CITED1
MGB1
PDZK1
HMGCS2
AGTR1
CYP2A7
UGT2B11
END OF ROW
BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+
ERGO, PCA NON ERGO
TOP 50 UNDEREXPRESSED BASAL-LIKE GENES

FIG. 8

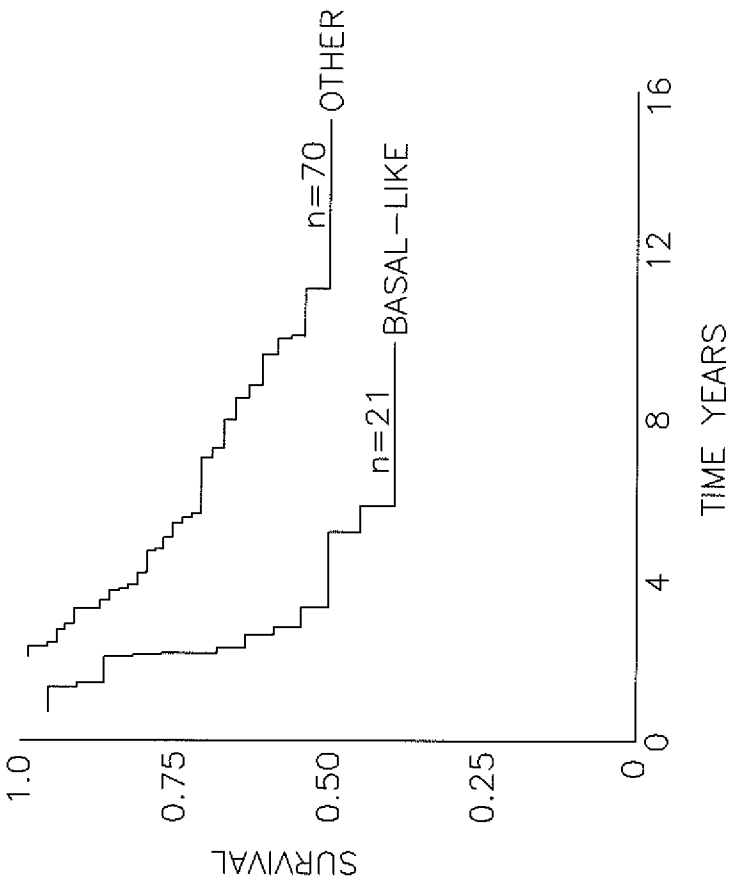

1.0
0.75
0.50
0.25
0
SURVIVAL
0
4
8
12
16
TIME YEARS
n=70
OTHER
n=21
BASAL-LIKE

FIG. 9

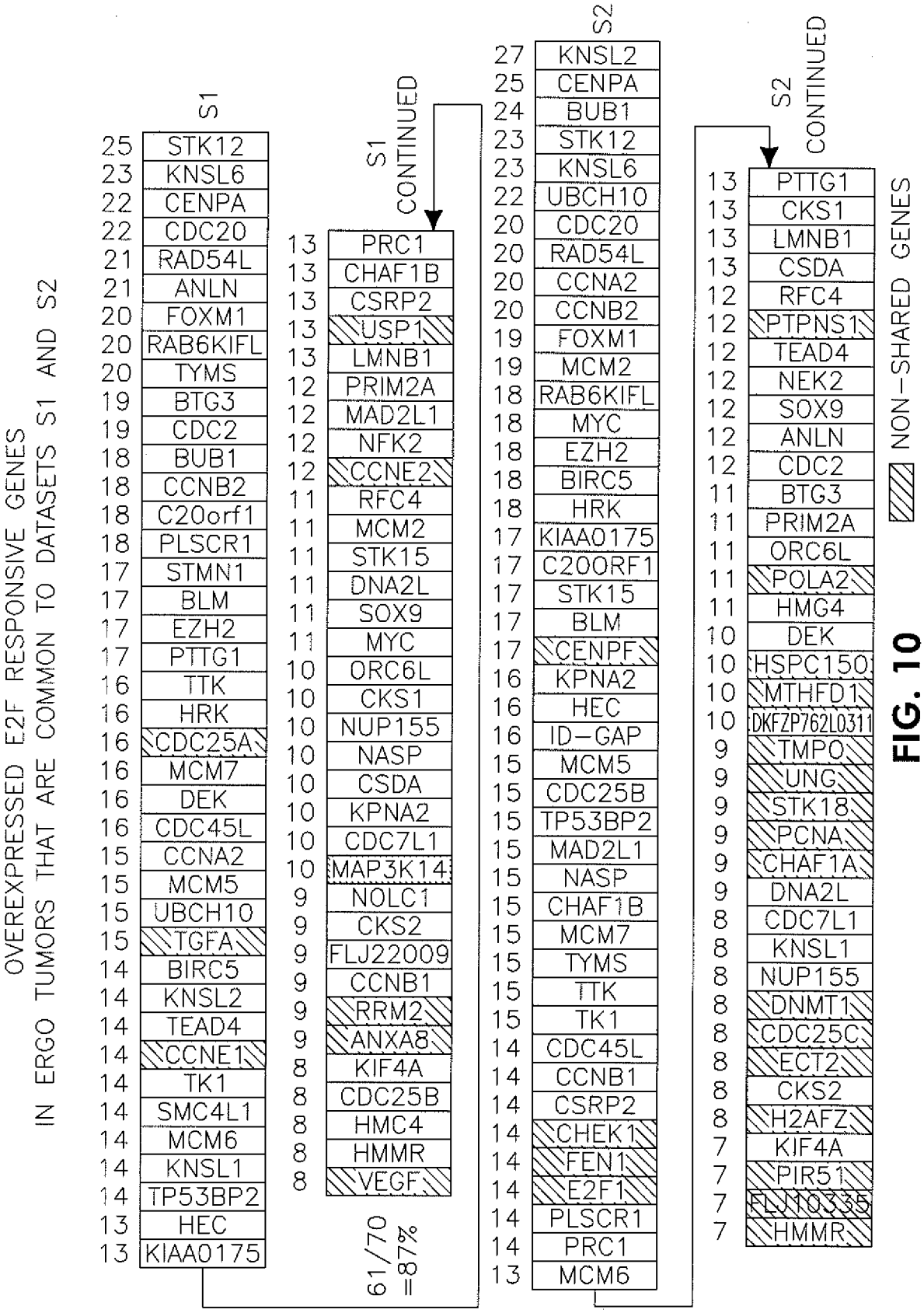
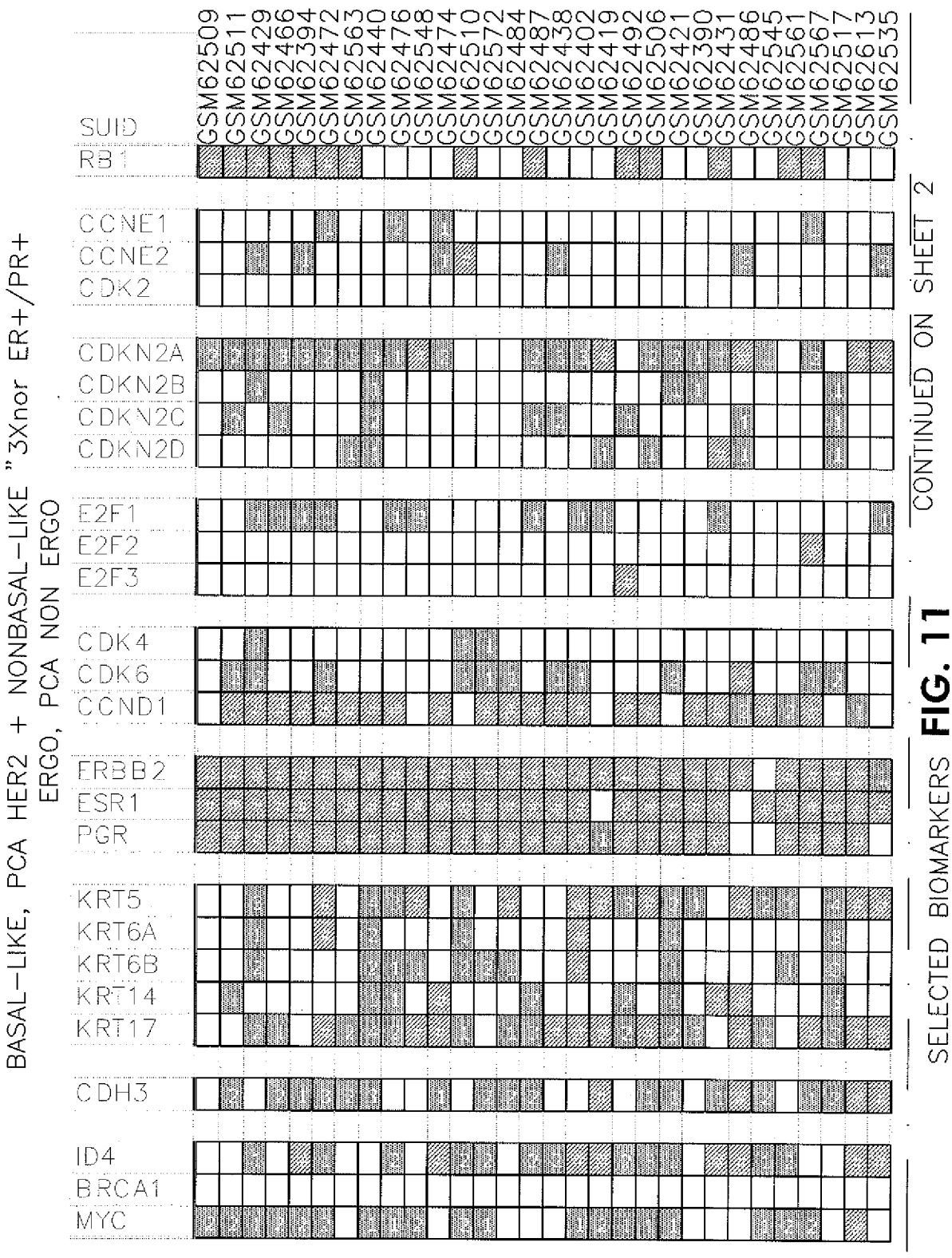

OVEREXPRESSED E2F RESPONSIVE GENES
IN ERGO TUMORS THAT ARE COMMON TO DATASETS S1 AND S2
S1
25 STK12
23 KNSL6
22 CENPA
22 CDC20
21 RAD54L
21 ANLN
20 FOXM1
20 RAB6KIFL
20 TYMS
19 BTG3
19 CDC2
18 BUB1
18 CCNB2
18 C20orf1
18 PLSCR1
17 STMN1
17 BLM
17 EZH2
17 PTTG1
16 TTK
16 HRK
16 CDC25A
16 MCM7
16 DEK
16 CDC45L
15 CCNA2
15 MCM5
15 UBCH10
15 TGFA
14 BIRC5
14 KNSL2
14 TEAD4
14 CCNE1
14 TK1
14 SMC4L1
14 MCM6
14 KNSL1
14 TP53BP2
13 HEC
13 KIAA0175
S1 CONTINUED
13 PRC1
13 CHAF1B
13 CSRP2
13 USP1
13 LMNB1
12 PRIM2A
12 MAD2L1
12 NFK2
12 CCNE2
11 RFC4
11 MCM2
11 STK15
11 DNA2L
11 SOX9
11 MYC
10 ORC6L
10 CKS1
10 NUP155
10 NASP
10 CSDA
10 KPNA2
10 CDC7L1
10 MAP3K14
9 NOLC1
9 CKS2
9 FLJ22009
9 CCNB1
9 RRM2
9 ANXA8
8 KIF4A
8 CDC25B
8 HMC4
8 HMMR
8 VEGF
61/70 =87%
S2
27 KNSL2
25 CENPA
24 BUB1
23 STK12
23 KNSL6
22 UBCH10
20 CDC20
20 RAD54L
20 CCNA2
20 CCNB2
19 FOXM1
19 MCM2
18 RAB6KIFL
18 MYC
18 EZH2
18 BIRC5
18 HRK
17 KIAA0175
17 C20ORF1
17 STK15
17 BLM
17 CENPF
16 KPNA2
16 HEC
16 ID-GAP
15 MCM5
15 CDC25B
15 TP53BP2
15 MAD2L1
15 NASP
15 CHAF1B
15 MCM7
15 TYMS
15 TTK
15 TK1
14 CDC45L
14 CCNB1
14 CSRP2
14 CHEK1
14 FEN1
14 E2F1
14 PLSCR1
14 PRC1
13 MCM6
S2 CONTINUED
13 PTTG1
13 CKS1
13 LMNB1
13 CSDA
12 RFC4
12 PTPNS1
12 TEAD4
12 NEK2
12 SOX9
12 ANLN
12 CDC2
11 BTG3
11 PRIM2A
11 ORC6L
11 POLA2
11 HMG4
10 DEK
10 HSPC150
10 MTHFD1
10 DKFZP762L0311
9 TMPO
9 UNG
9 STK18
9 PCNA
9 CHAF1A
9 DNA2L
8 CDC7L1
8 KNSL1
8 NUP155
8 DNMT1
8 CDC25C
8 ECT2
8 CKS2
8 H2AFZ
7 KIF4A
7 PIR51
7 FLJ10335
7 HMMR
NON-SHARED GENES

FIG. 10



CONTINUED ON SHEET 2

1

SELECTED BIOMARKERS **FIG. 11**

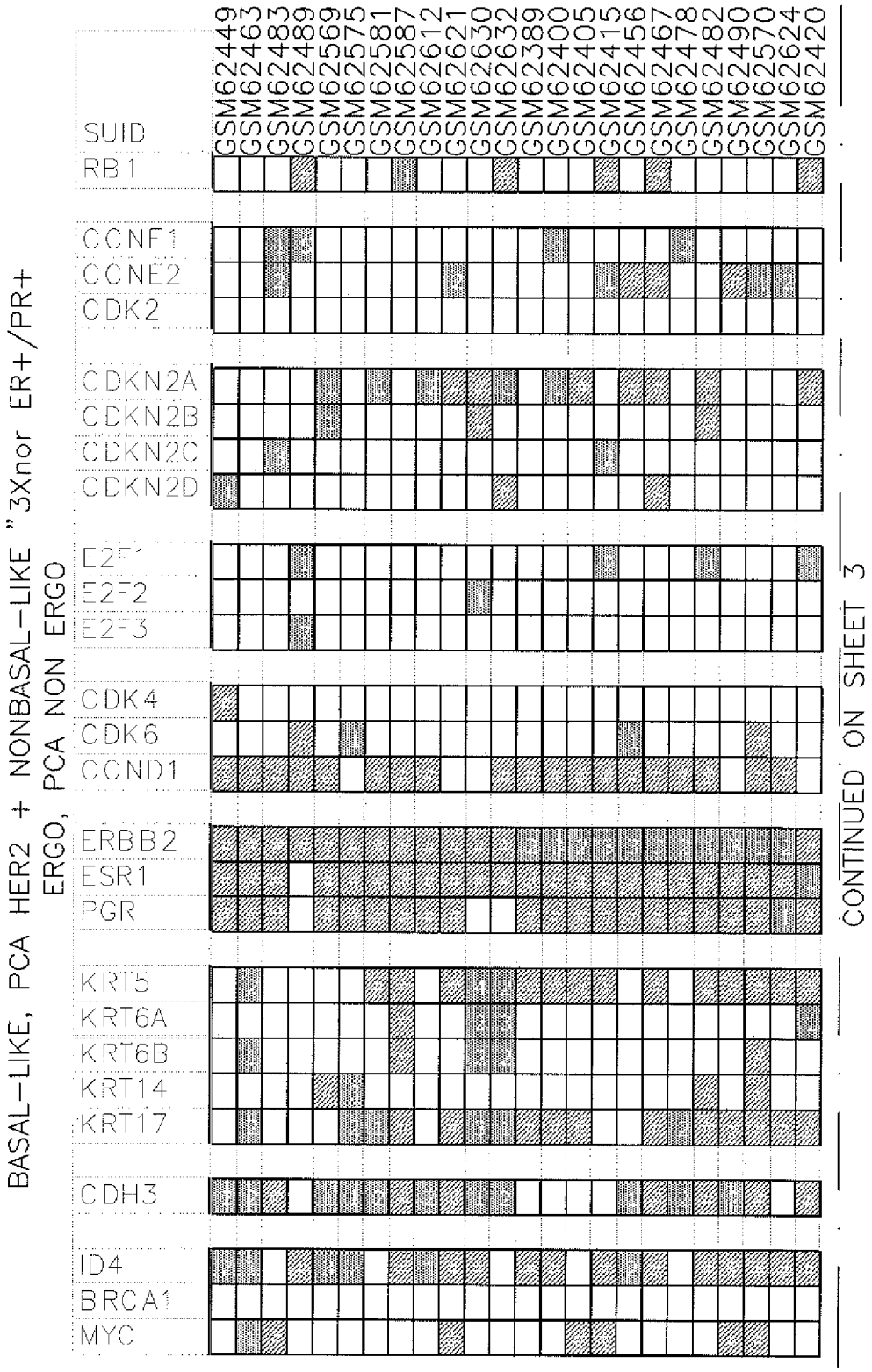
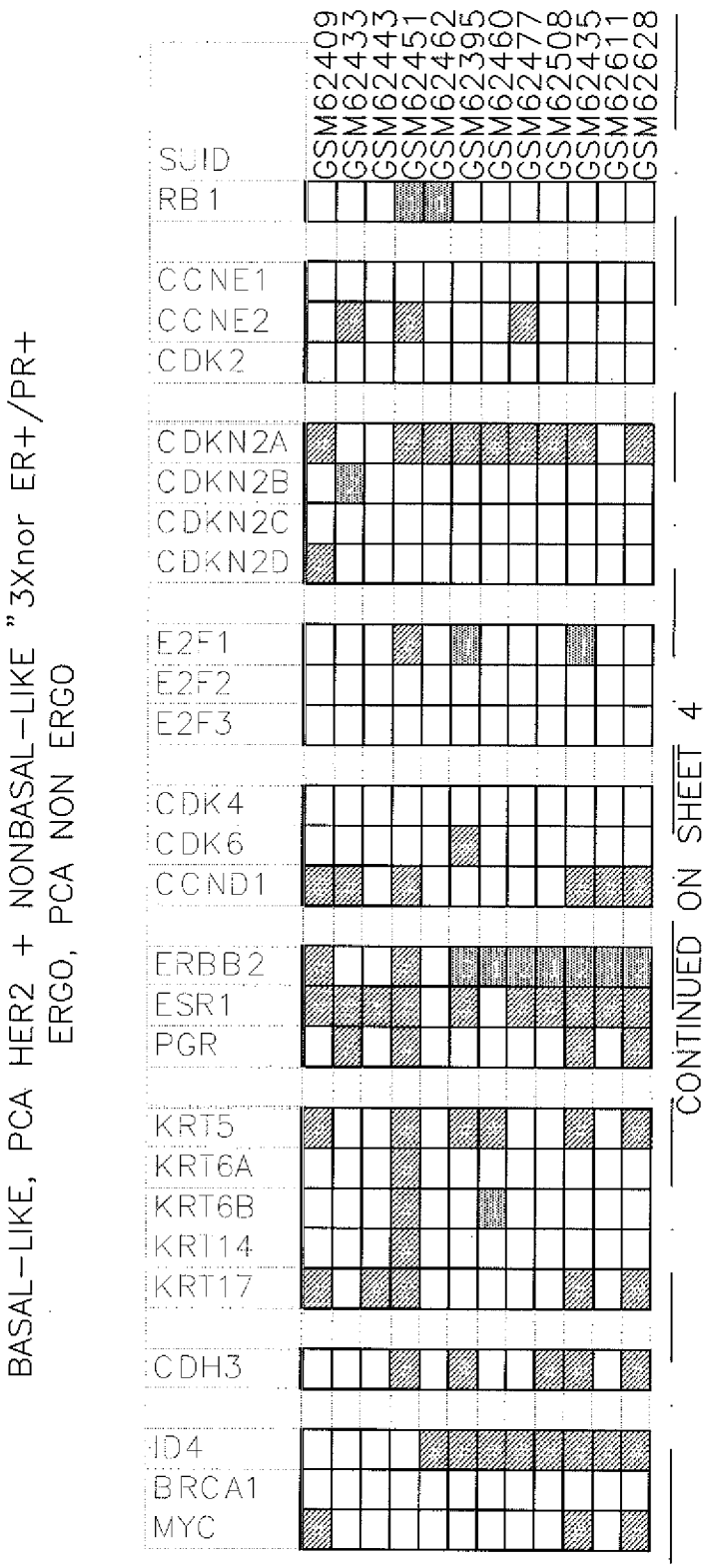

BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+ ERGO, PCA NON ERGO
SUID
RB1
CCNE1
CCNE2
CDK2
CDKN2A
CDKN2B
CDKN2C
CDKN2D
E2F1
E2F2
E2F3
CDK4
CDK6
CCND1
ERBB2
ESR1
PGR
KRT5
KRT6A
KRT6B
KRT14
KRT17
CDH3
ID4
BRCA1
MYC
GSM62449
GSM62463
GSM62483
GSM62489
GSM625569
GSM625575
GSM625581
GSM625587
GSM626612
GSM626621
GSM626630
GSM626632
GSM626389
GSM624400
GSM624405
GSM624415
GSM624456
GSM624467
GSM624478
GSM624482
GSM624490
GSM625570
GSM626624
GSM624420
CONTINUED ON SHEET 3
SELECTED BIOMARKERS

FIG. 11



SELECTED BIOMARKERS

FIG. 11

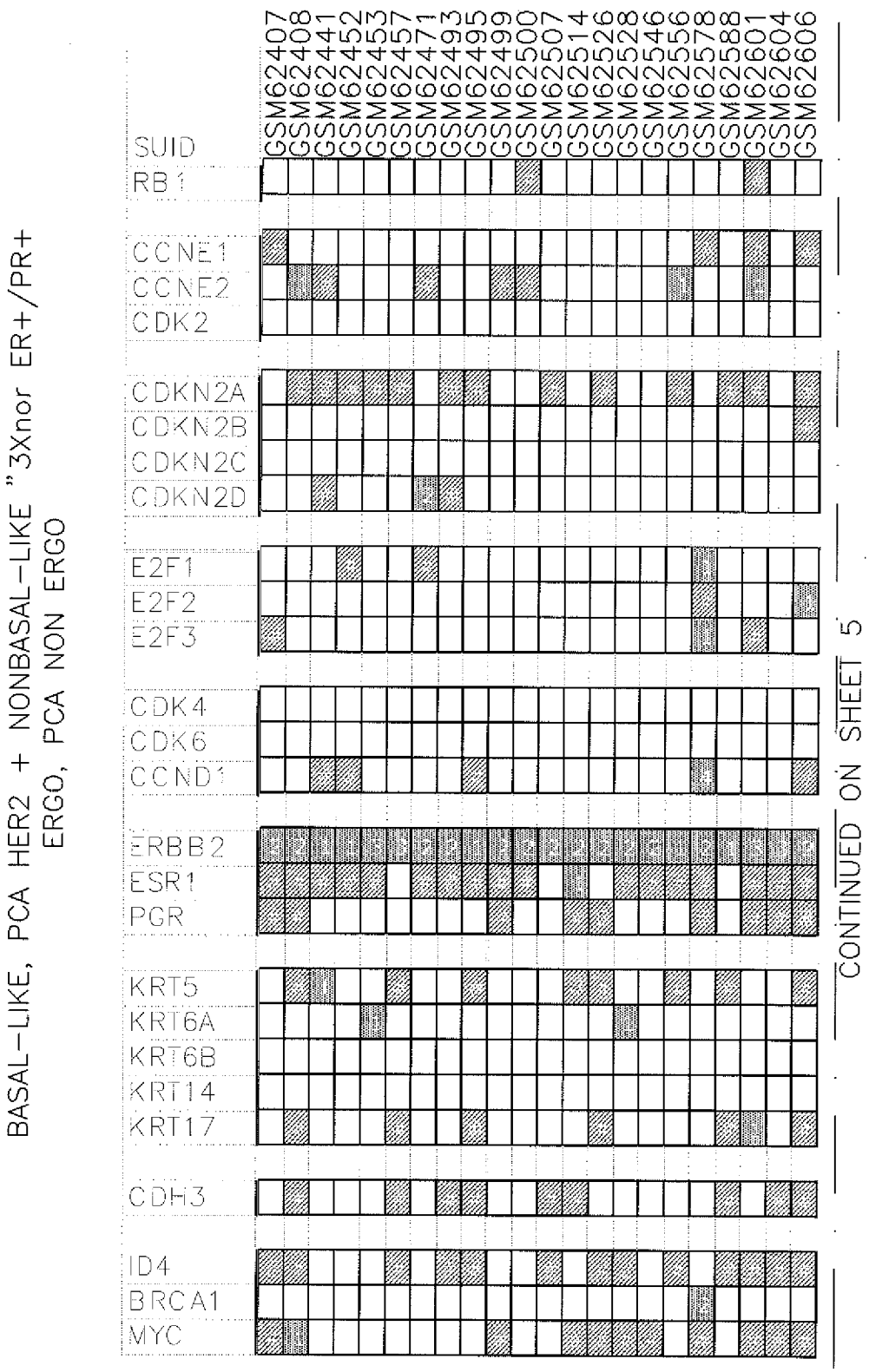

BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+
ERGO, PCA NON ERGO
SUID
RB1
CCNE1
CCNE2
CDK2
CDKN2A
CDKN2B
CDKN2C
CDKN2D
E2F1
E2F2
E2F3
CDK4
CDK6
CCND1
ERBB2
ESR1
PGR
KRT5
KRT6A
KRT6B
KRT14
KRT17
CDH3
ID4
BRCA1
MYC
GSM62407
GSM62408
GSM62441
GSM62452
GSM62453
GSM62457
GSM62471
GSM62493
GSM62495
GSM62499
GSM62500
GSM62507
GSM62514
GSM62526
GSM62528
GSM62546
GSM62556
GSM62578
GSM62588
GSM62601
GSM62604
GSM62606
CONTINUED ON SHEET 5
SELECTED BIOMARKERS

FIG. 11

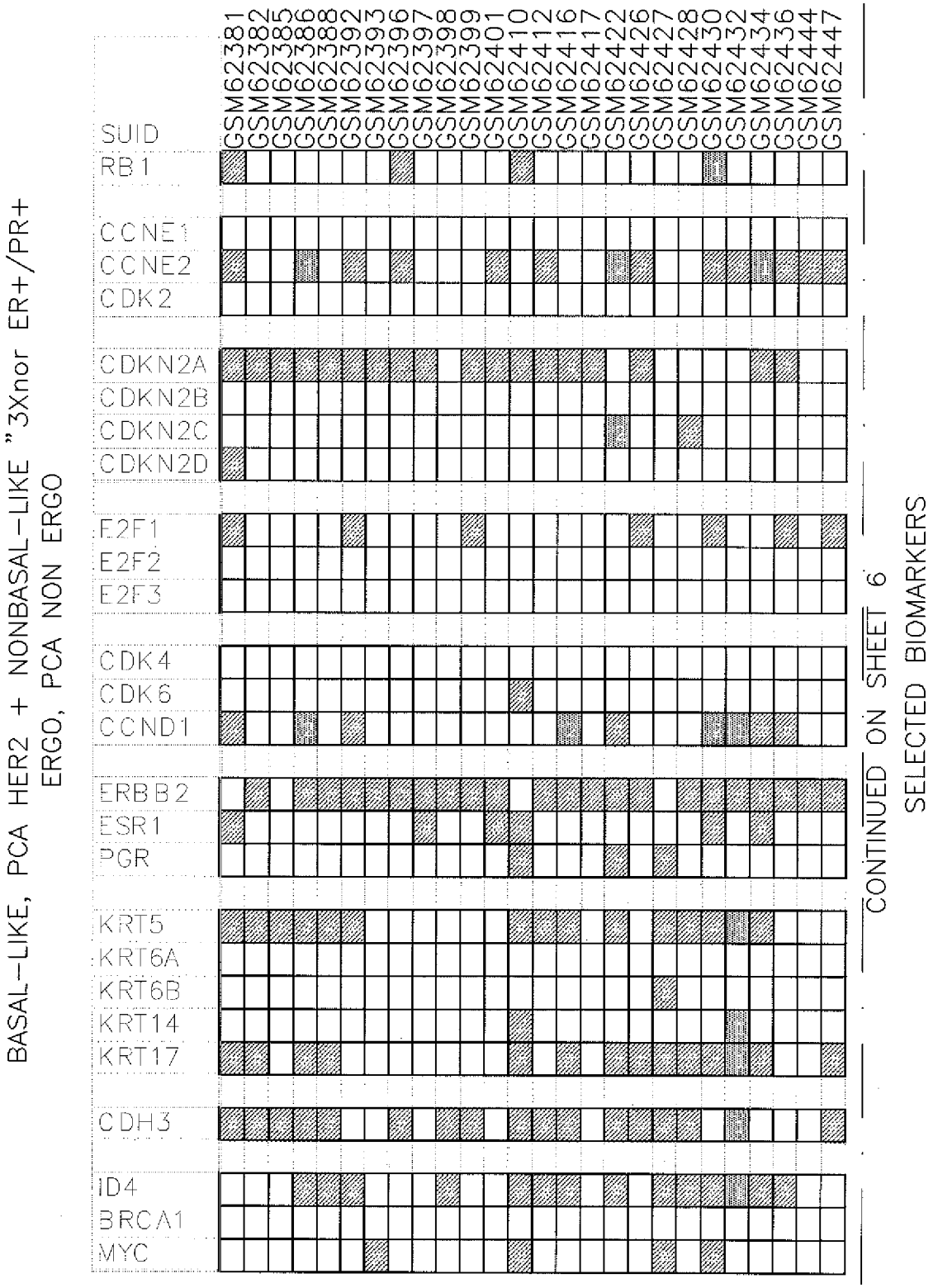
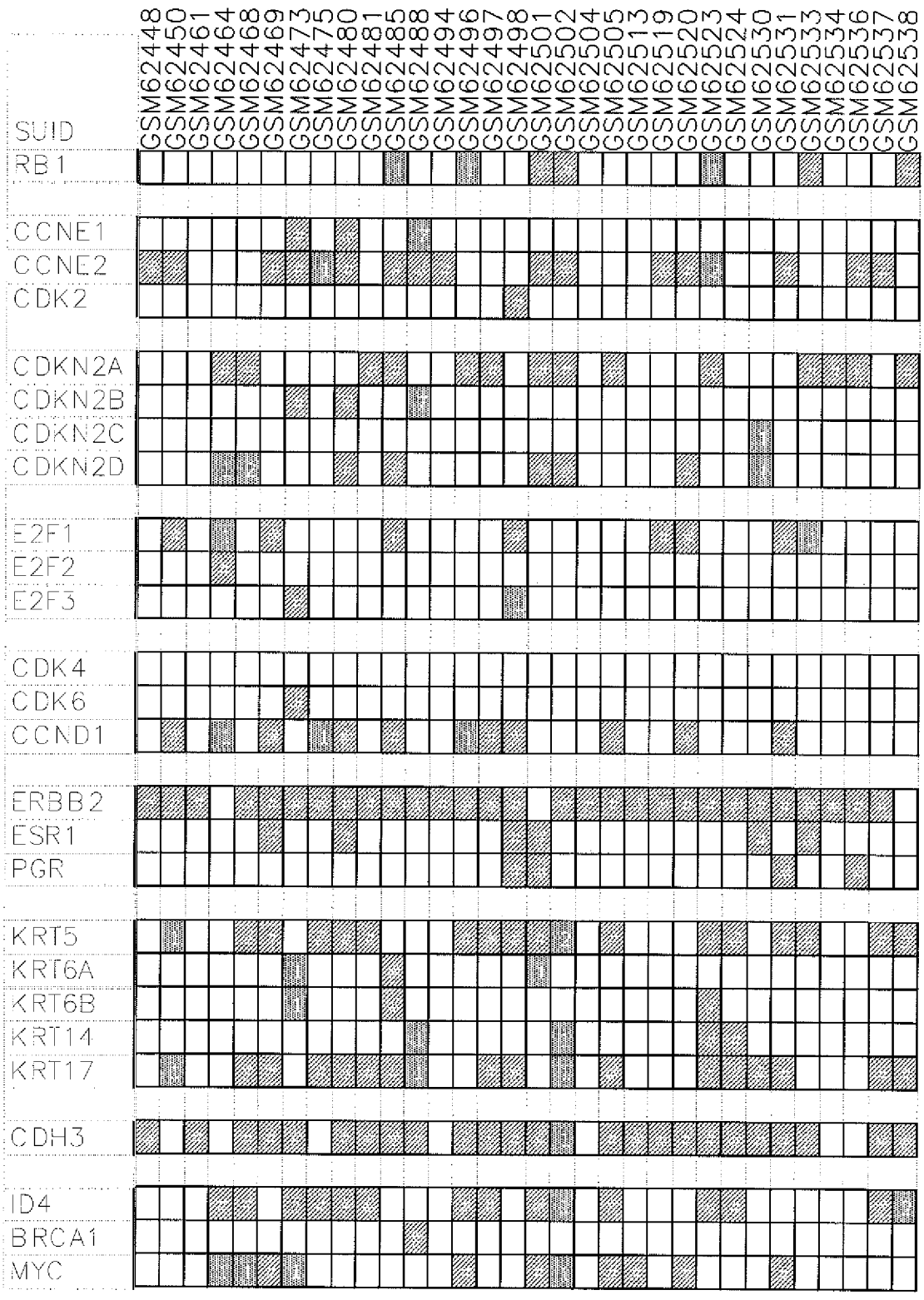

BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+
ERGO, PCA NON ERGO
SUID
RB1
CCNE1
CCNE2
CDK2
CDKN2A
CDKN2B
CDKN2C
CDKN2D
E2F1
E2F2
E2F3
CDK4
CDK6
CCND1
ERBB2
ESR1
PGR
KRT5
KRT6A
KRT6B
KRT14
KRT17
CDH3
ID4
BRCA1
MYC
GSM62381
GSM62382
GSM62385
GSM62386
GSM62388
GSM62392
GSM62393
GSM62396
GSM62397
GSM62398
GSM62399
GSM62401
GSM62410
GSM62412
GSM62416
GSM62417
GSM62422
GSM62426
GSM62427
GSM62428
GSM62430
GSM62432
GSM62434
GSM62436
GSM62444
GSM62447
CONTINUED ON SHEET 6
SELECTED BIOMARKERS

FIG. 11



CONTINUED ON SHEET 7

FIG. 11 SELECTED BIOMARKERS

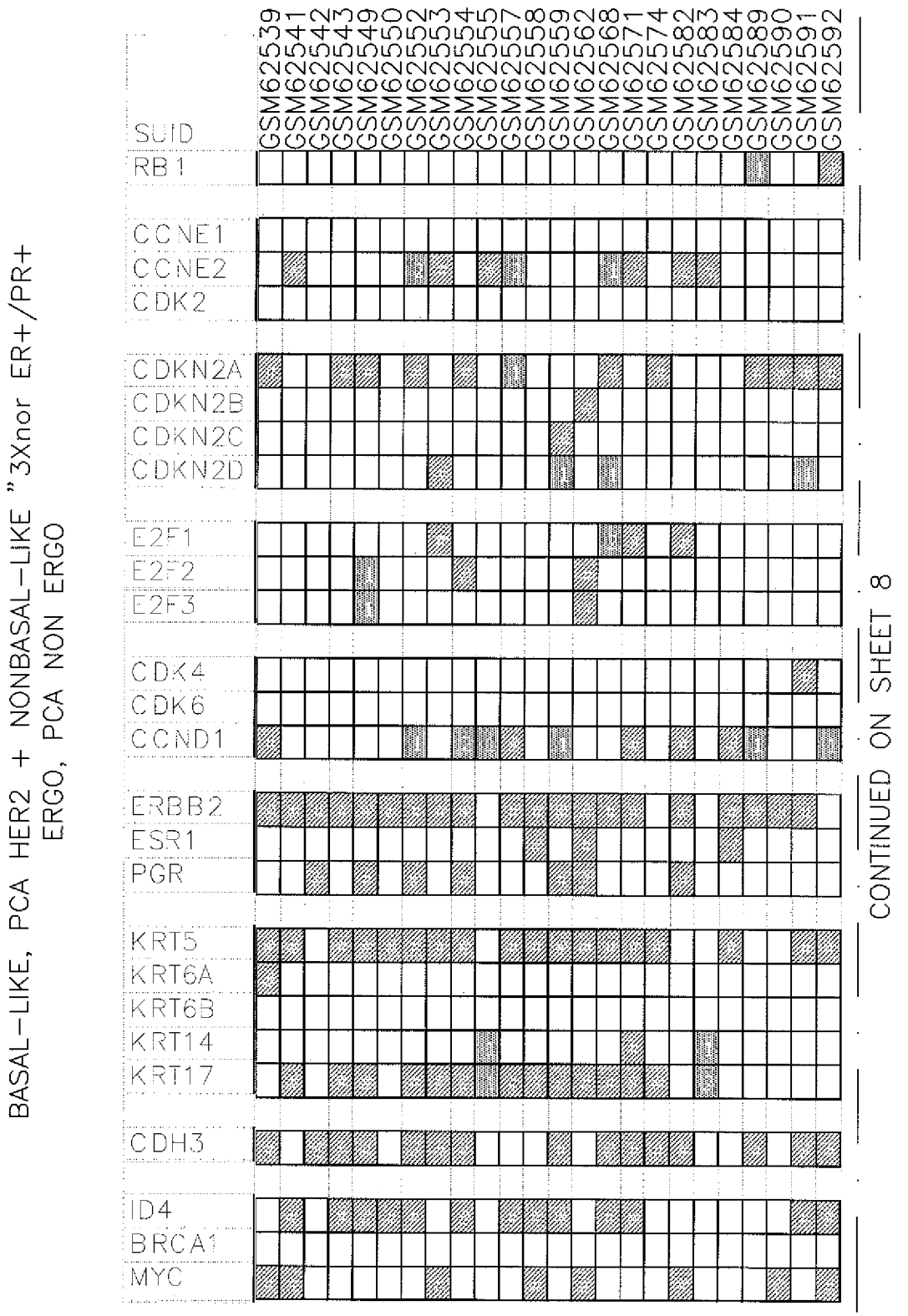
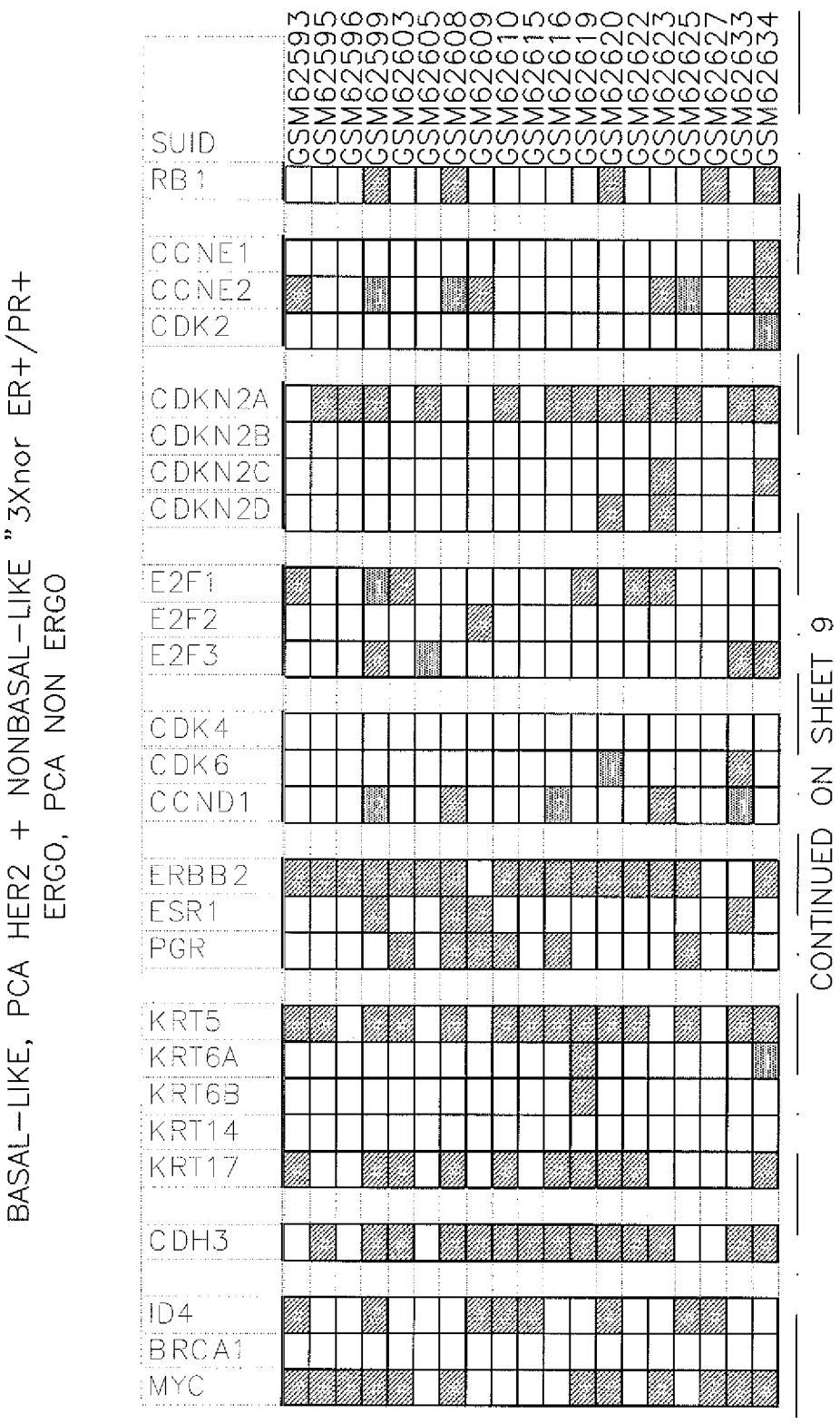
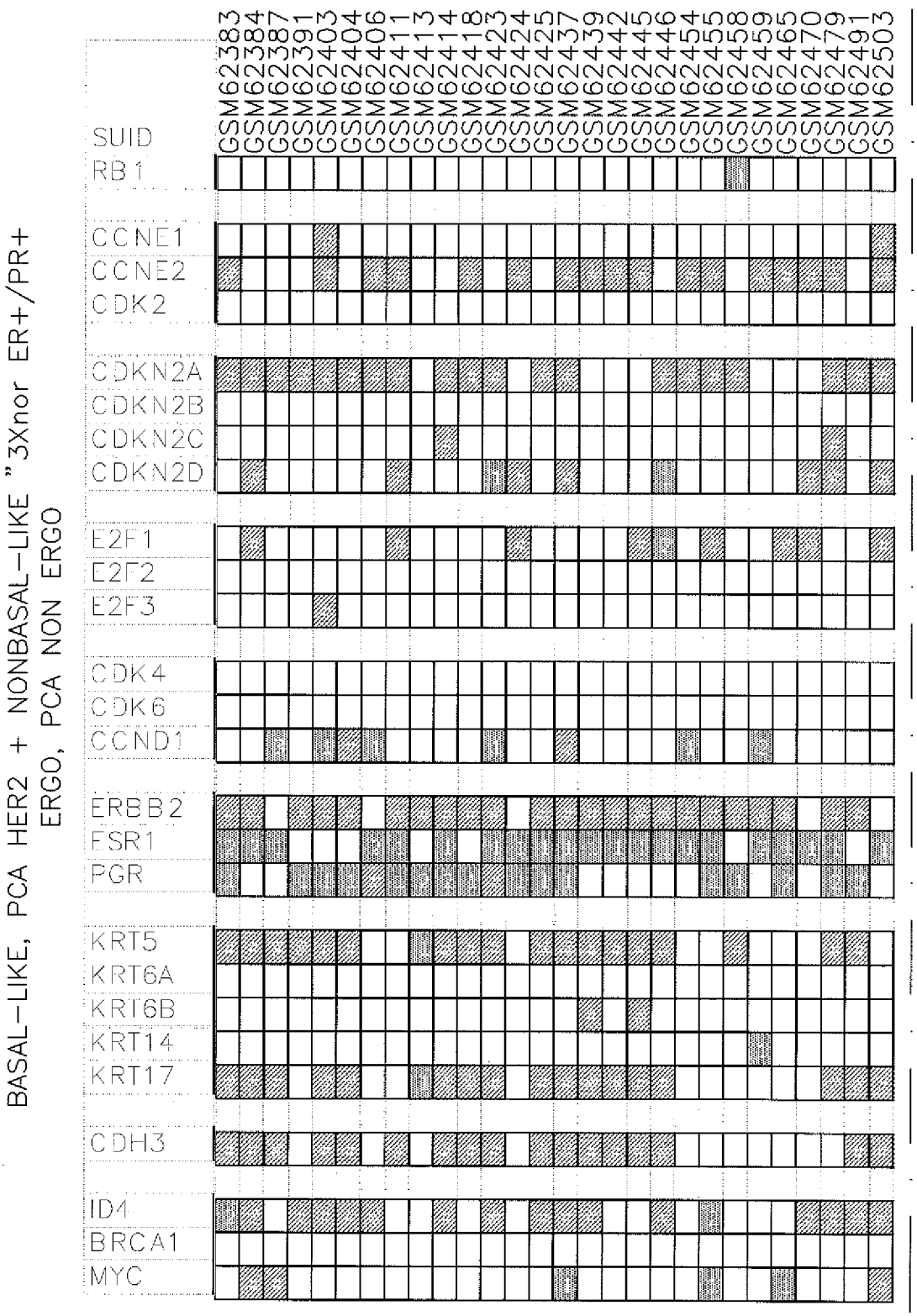

BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+
ERGO, PCA NON ERGO
SUID
GSM625539
GSM625541
GSM625542
GSM625543
GSM625549
GSM625550
GSM625552
GSM625553
GSM625554
GSM625555
GSM625557
GSM625558
GSM625559
GSM625562
GSM625568
GSM625571
GSM625574
GSM625582
GSM625583
GSM625584
GSM625589
GSM625590
GSM625591
GSM625592
RB1
CCNE1
CCNE2
CDK2
CDKN2A
CDKN2B
CDKN2C
CDKN2D
E2F1
E2F2
E2F3
CDK4
CDK6
CCND1
ERBB2
ESR1
PGR
KRT5
KRT6A
KRT6B
KRT14
KRT17
CDH3
ID4
BRCA1
MYC
CONTINUED ON SHEET 8
SELECTED BIOMARKERS

FIG. 11

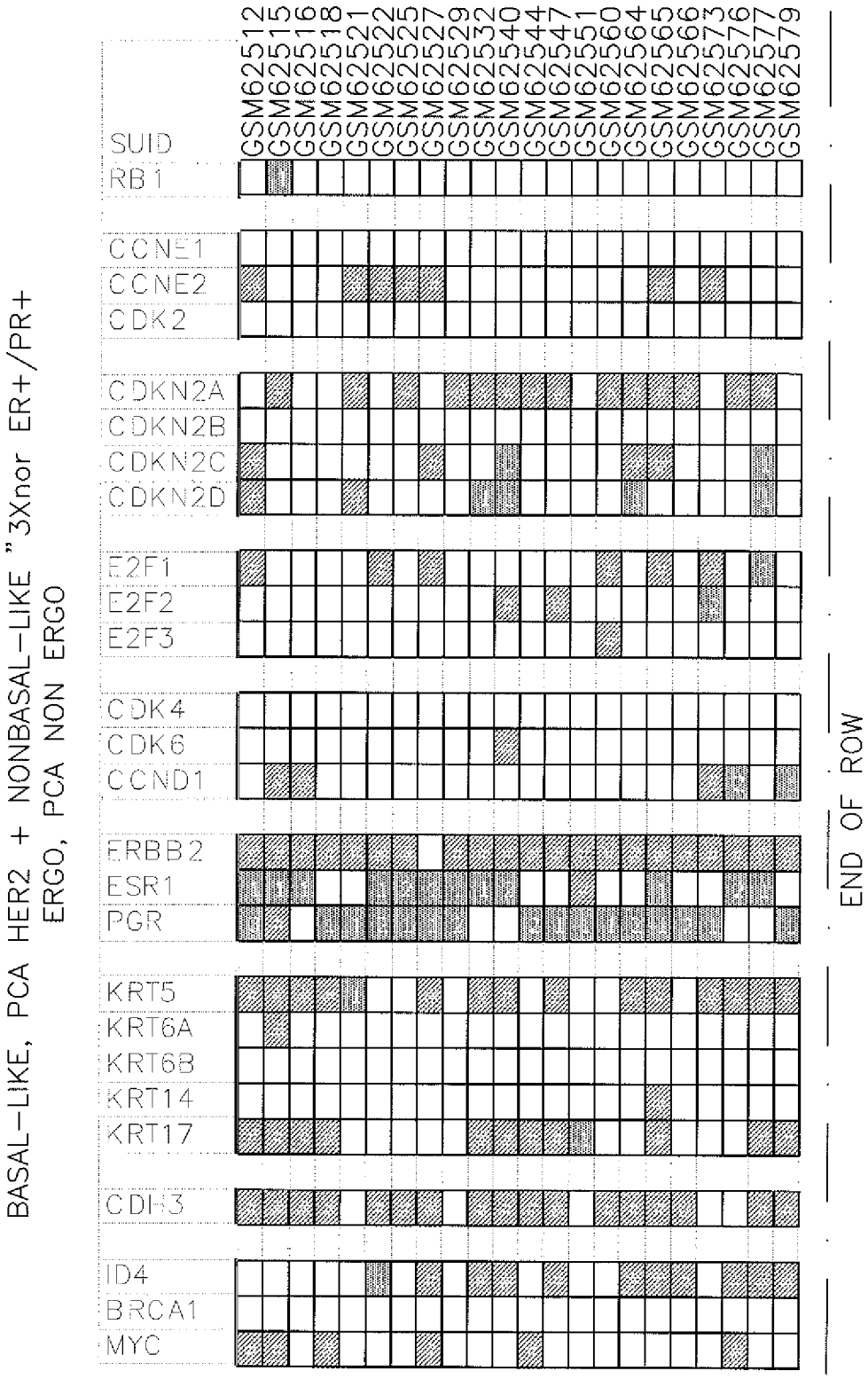


SELECTED BIOMARKERS

FIG. 11

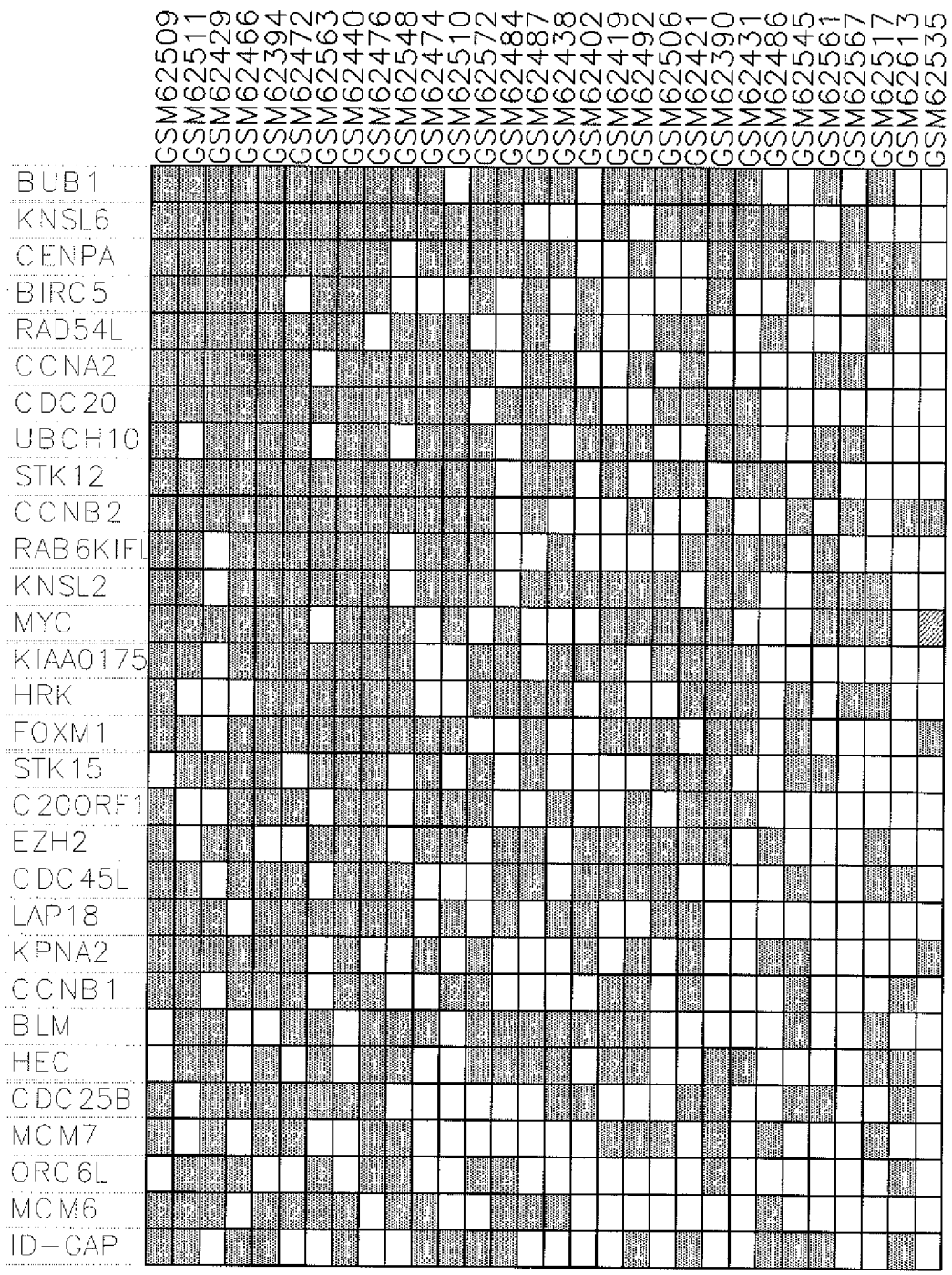


SELECTED BIOMARKERS **FIG. 11**



SELECTED BIOMARKERS

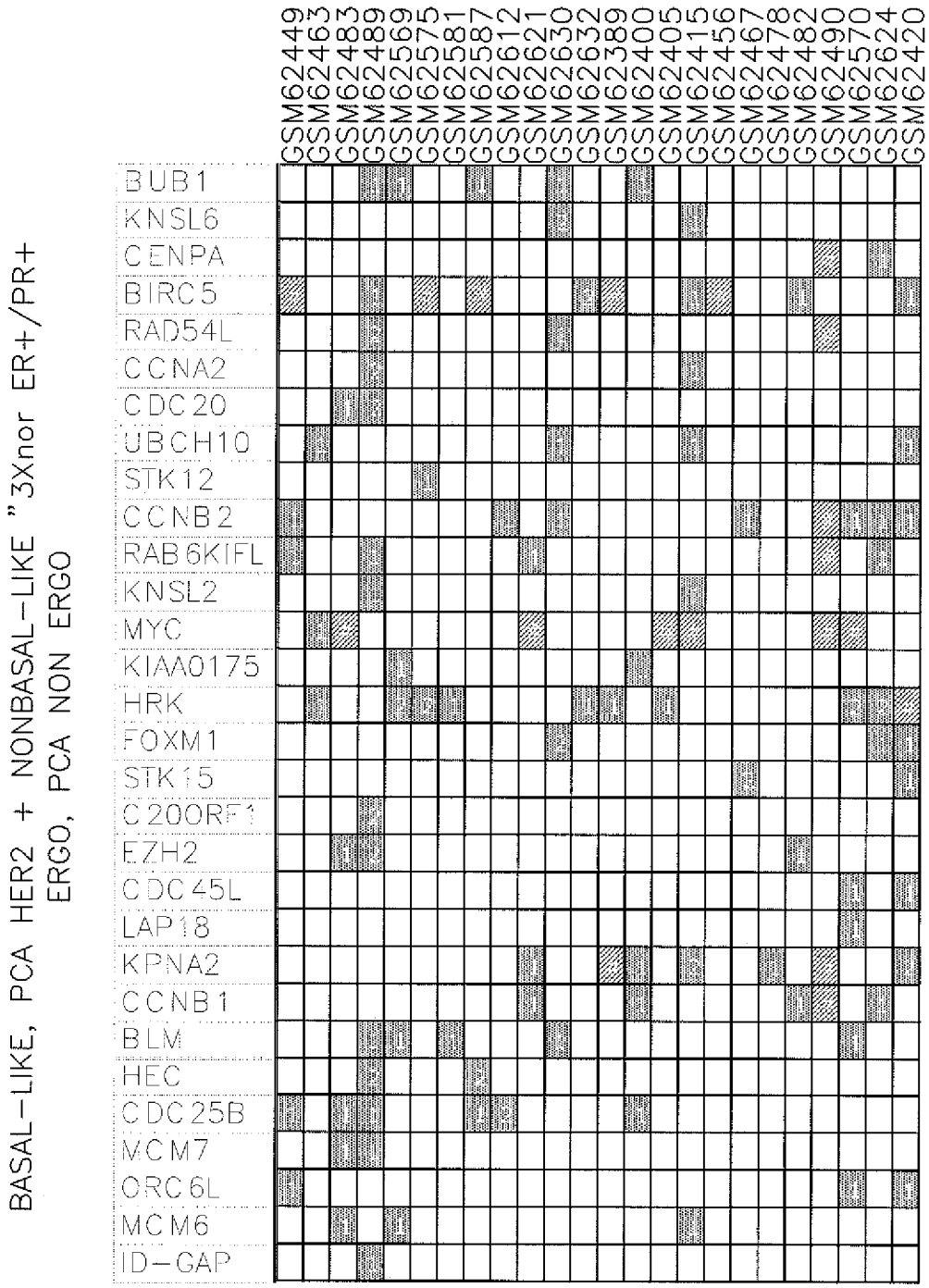
FIG. 11



BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+ ERGO, PCA NON ERGO

TOP 30 OVEREXPRESSED ERGO GENES **FIG. 11**

CONTINUED ON SHEET 12

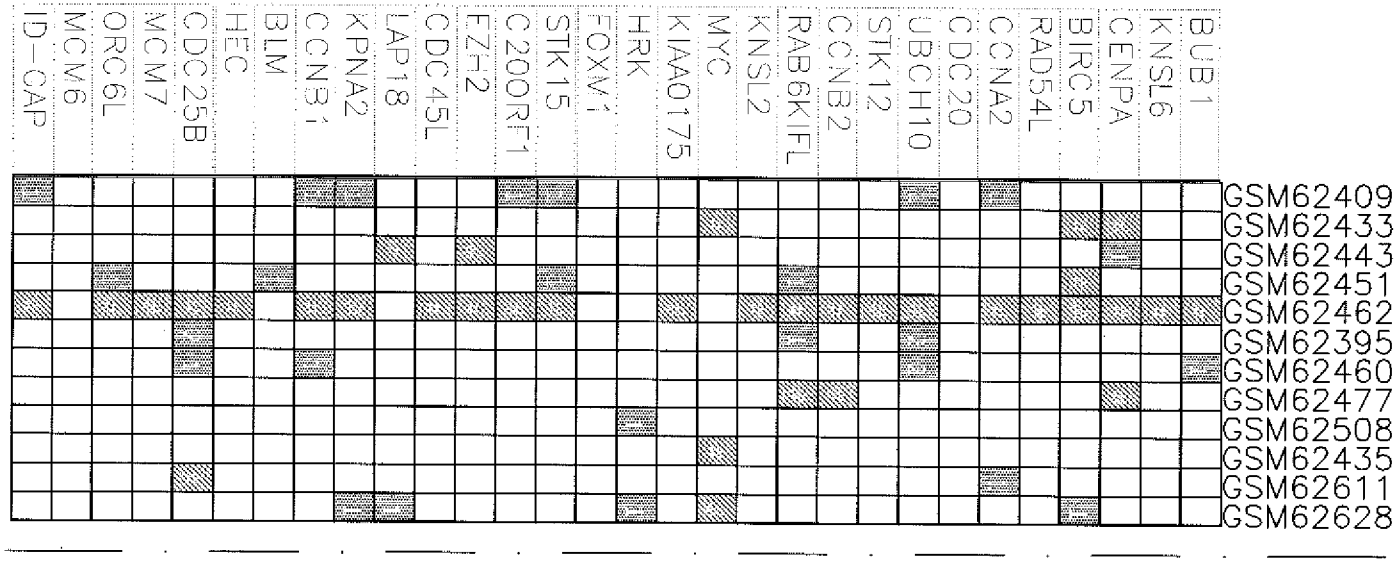


CONTINUED ON SHEET 13

TOP 30 OVEREXPRESSED ERGO GENES

FIG. 11

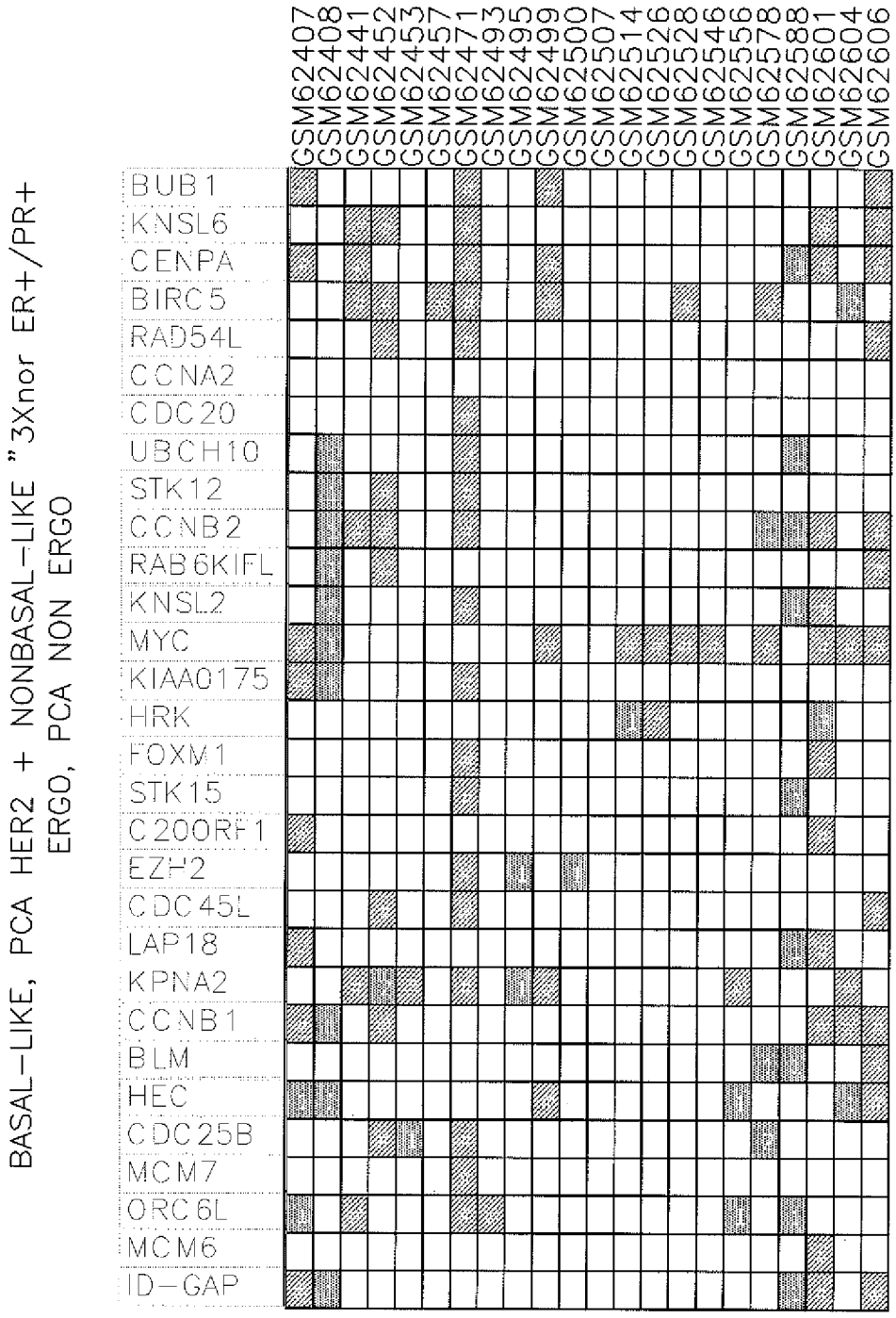
BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+
ERGO, PCA NON ERGO



CONTINUED ON SHEET 14

TOP 30 OVEREXPRESSED ERGO GENES

FIG. 11



TOP 30 OVEREXPRESSED ERGO GENES

FIG. 11

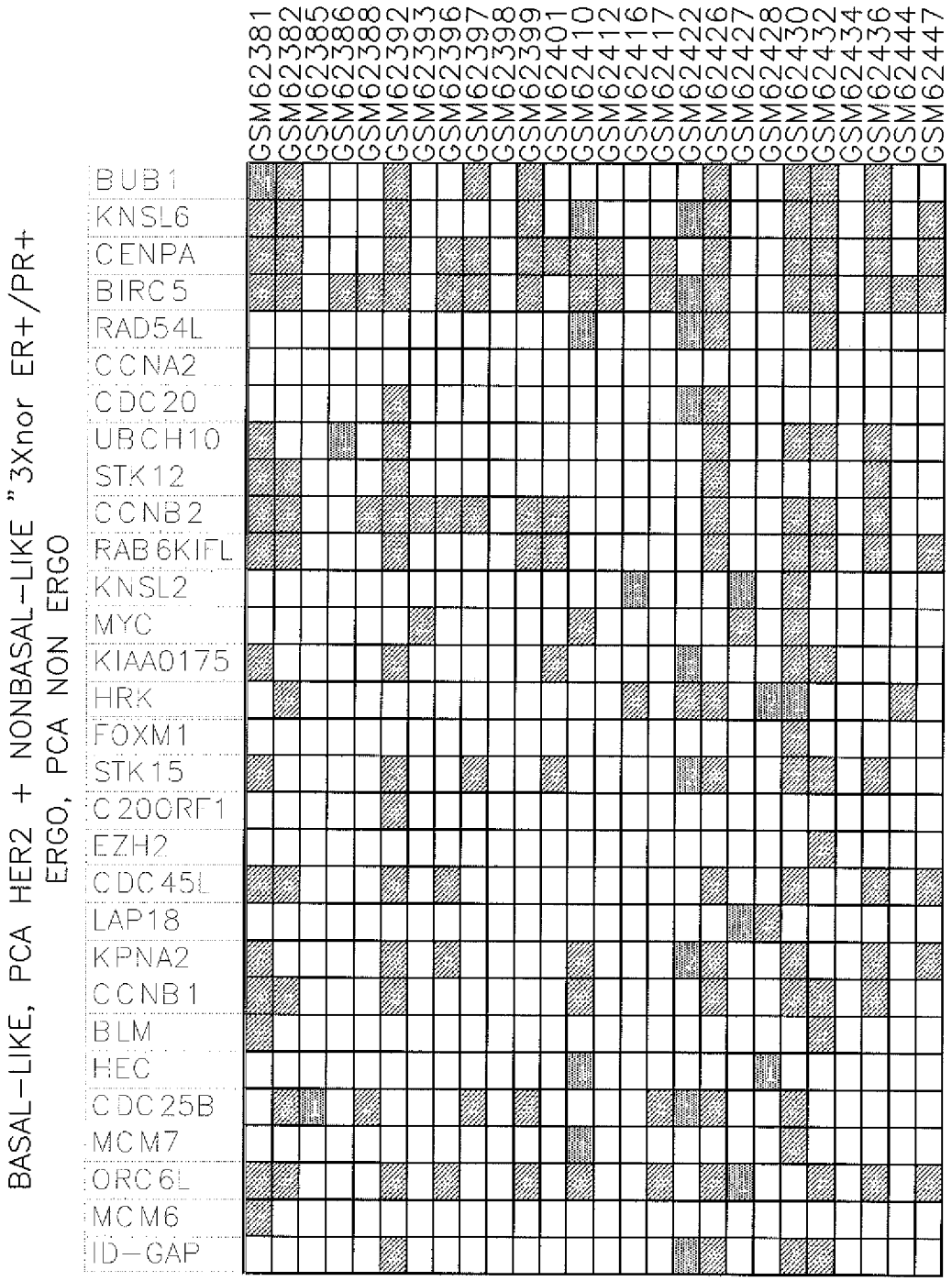
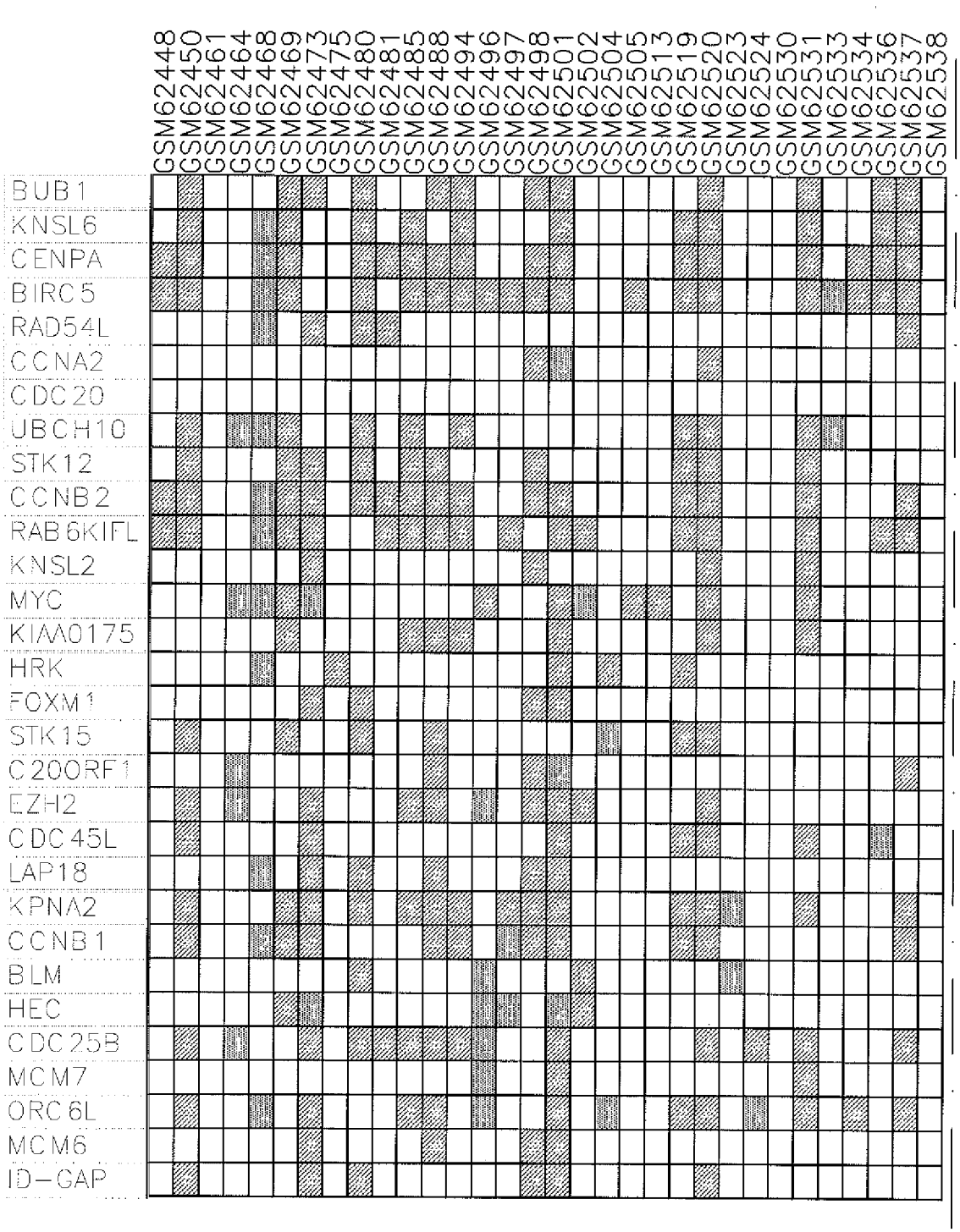

BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+
ERGO, PCA NON ERGO
GSM62381
GSM62382
GSM62385
GSM62386
GSM62388
GSM62392
GSM62393
GSM62396
GSM62397
GSM62398
GSM62399
GSM62401
GSM62410
GSM62412
GSM62416
GSM62417
GSM62422
GSM62426
GSM62427
GSM62428
GSM62430
GSM62432
GSM62434
GSM62436
GSM62444
GSM62447
BUB1
KNSL6
CENPA
BIRC5
RAD54L
CCNA2
CDC20
UBCH10
STK12
CCNB2
RAB6KIFL
KNSL2
MYC
KIAA0175
HRK
FOXM1
STK15
C20ORF1
EZH2
CDC45L
LAP18
KPNA2
CCNB1
BLM
HEC
CDC25B
MCM7
ORC6L
MCM6
ID-GAP
CONTINUED ON SHEET 16
TOP 30 OVEREXPRESSED ERGO GENES

FIG. 11



TOP 30 OVEREXPRESSED ERGO GENES **FIG. 11**

CONTINUED ON SHEET 17

BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+
ERGO, PCA NON ERGO

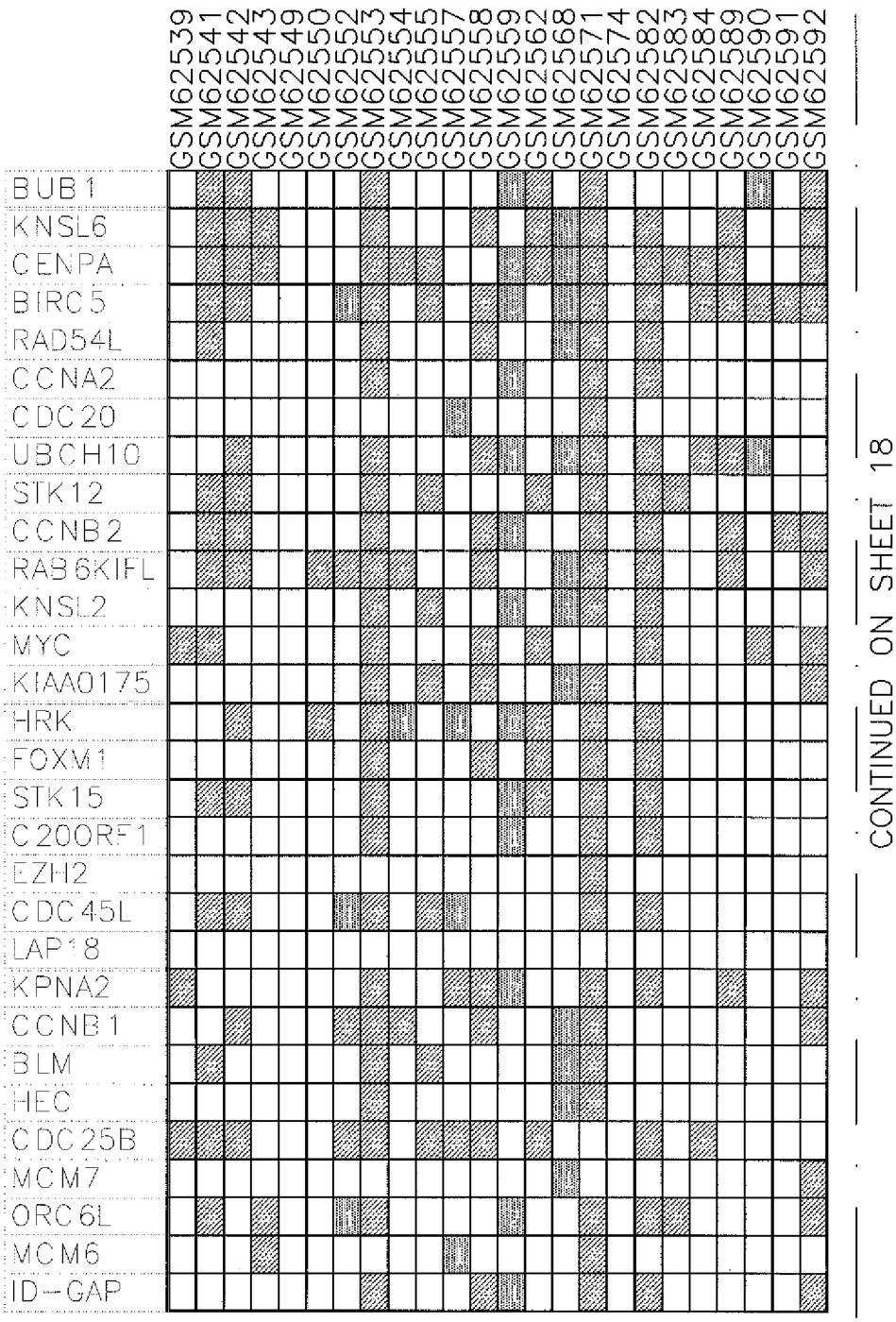
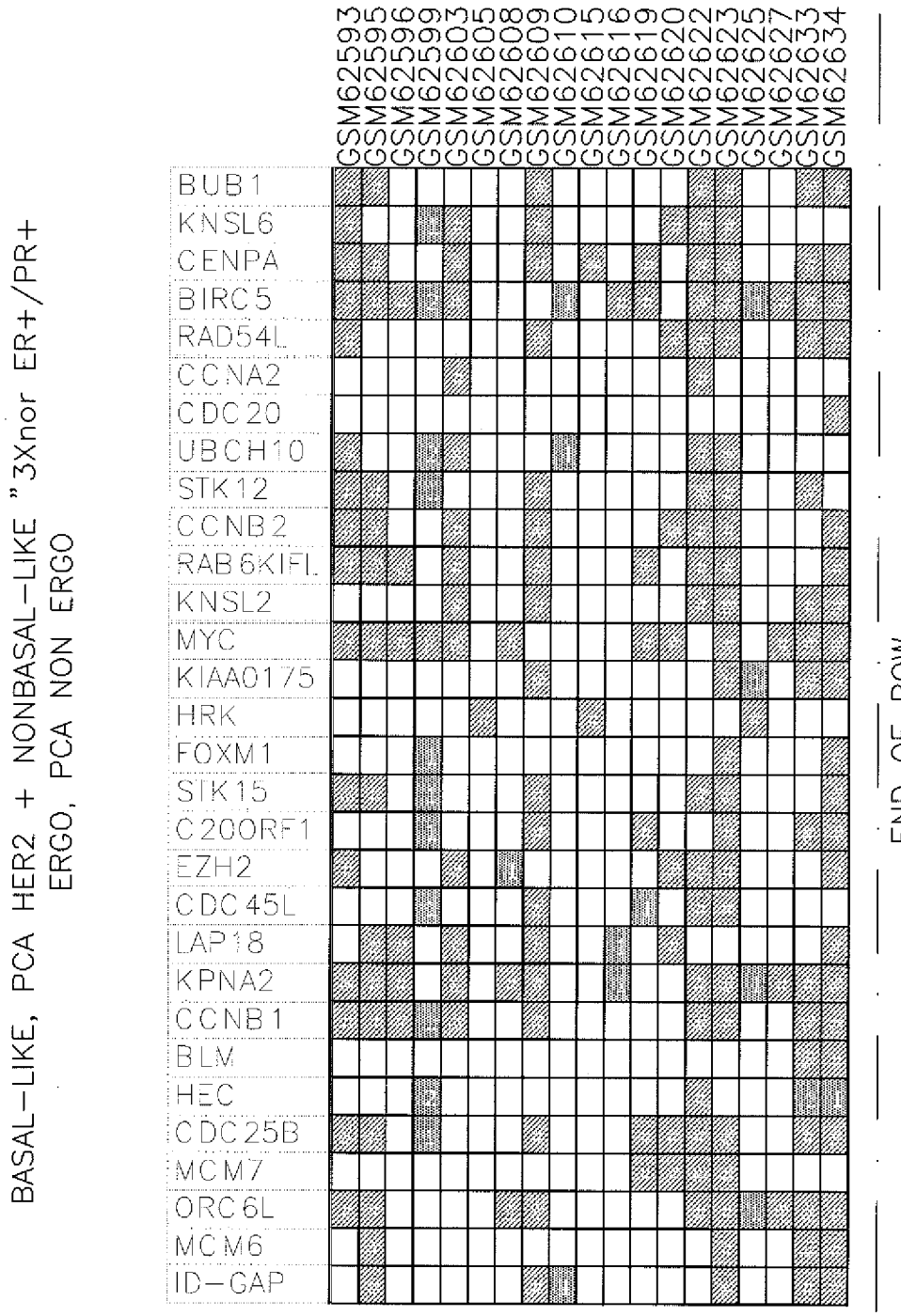


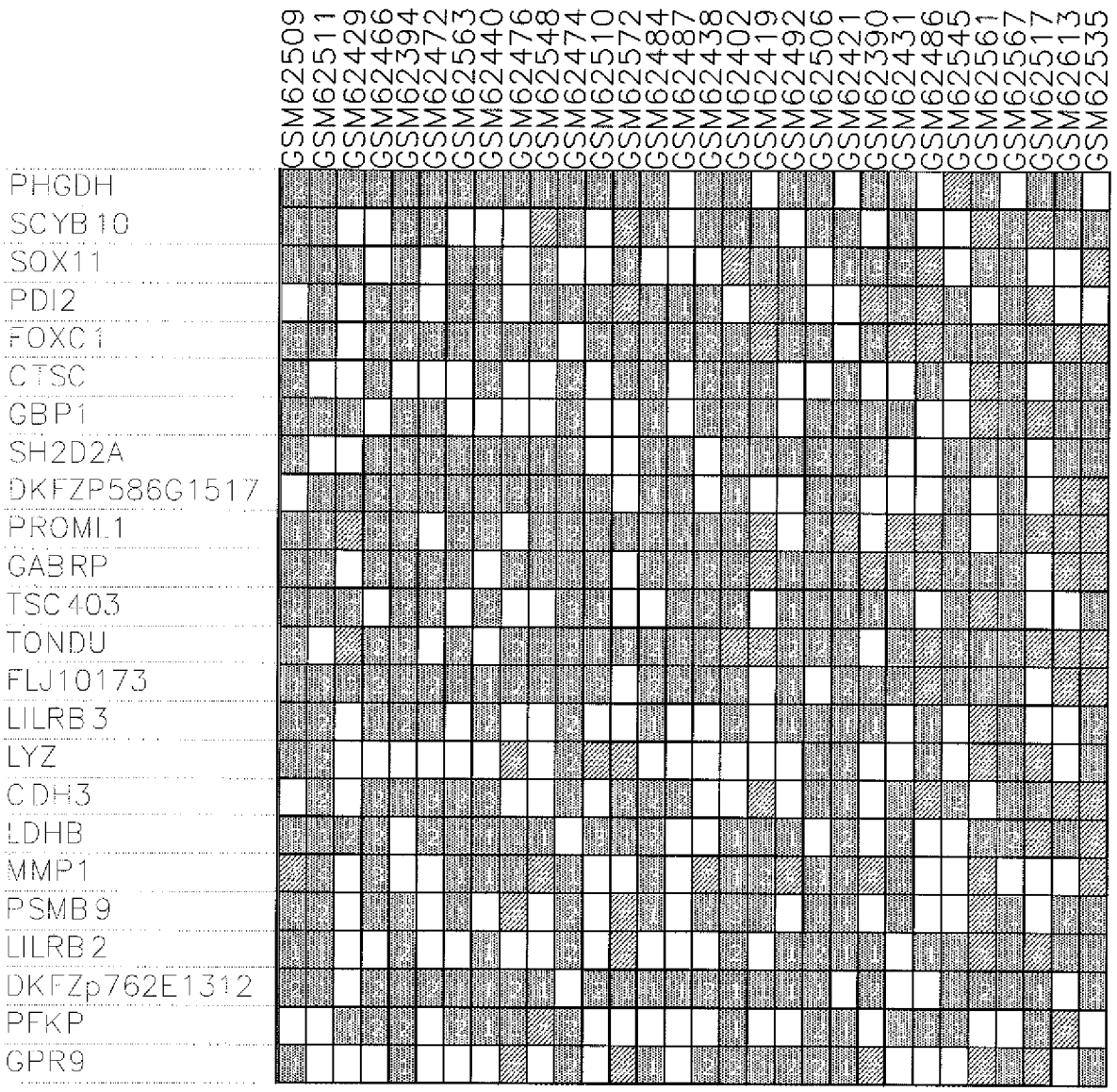
FIG. 11

TOP 30 OVEREXPRESSED ERGO GENES



TOP 30 OVEREXPRESSED ERGO GENES

FIG. 11



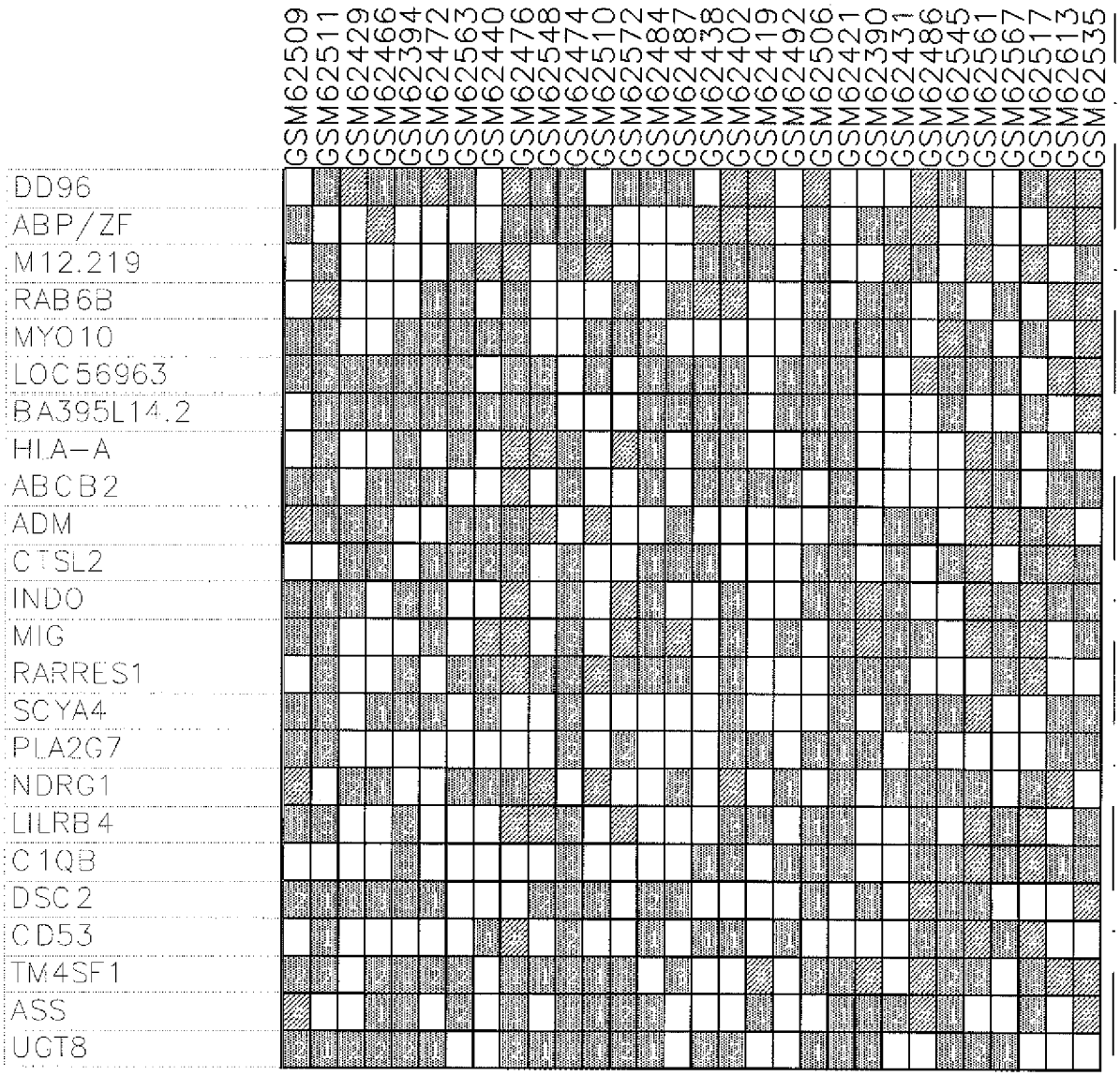
CONTINUED ON SHEET 20

BASAL−LIKE, PCA HER2 + NONBASAL−LIKE "3Xnor ER+/PR+
ERGO, PCA NON ERGO

TOP 50
OVEREXPRESSED
BASAL−LIKE GENES

FIG. 11

CONTINUED FROM SHEET 19



BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+
ERGO, PCA NON ERGO

TOP 50
OVEREXPRESSED
BASAL-LIKE GENES

FIG. 11

CONTINUED ON SHEET 21

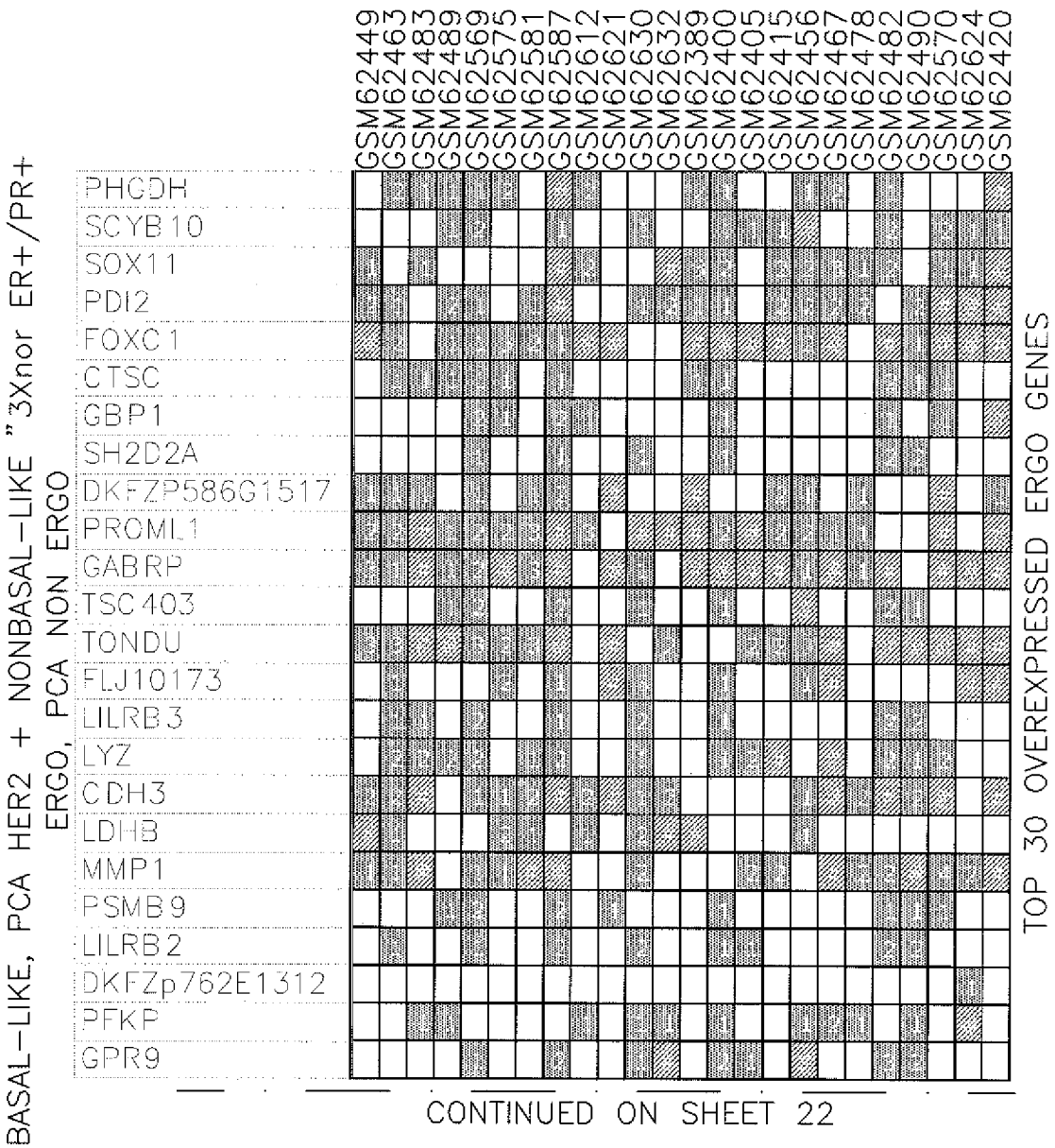

BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+ ERGO, PCA NON ERGO
GSM62449
GSM62463
GSM62483
GSM62489
GSM625569
GSM625575
GSM625581
GSM625587
GSM626612
GSM626621
GSM626630
GSM626632
GSM626389
GSM624400
GSM624405
GSM624415
GSM624456
GSM624467
GSM624478
GSM624482
GSM624490
GSM625570
GSM62624
GSM62420
PHGDH
SCYB10
SOX11
PDI2
FOXC1
CTSC
GBP1
SH2D2A
DKFZP586G1517
PROML1
GABRP
TSC403
TONDU
FLJ10173
LILRB3
LYZ
CDH3
LDHB
MMP1
PSMB9
LILRB2
DKFZp762E1312
PFKP
GPR9
TOP 30 OVEREXPRESSED ERGO GENES
CONTINUED ON SHEET 22

FIG. 11

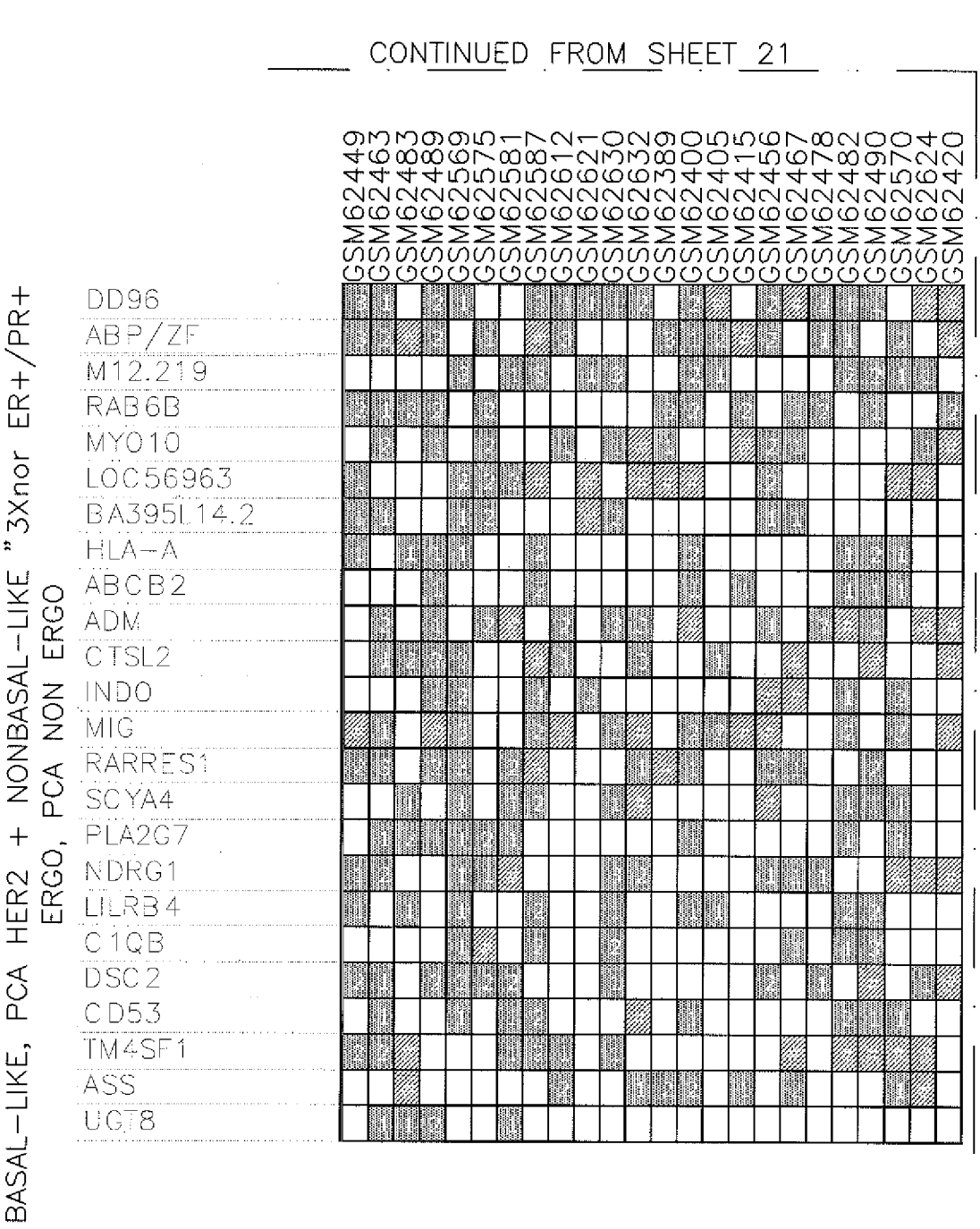
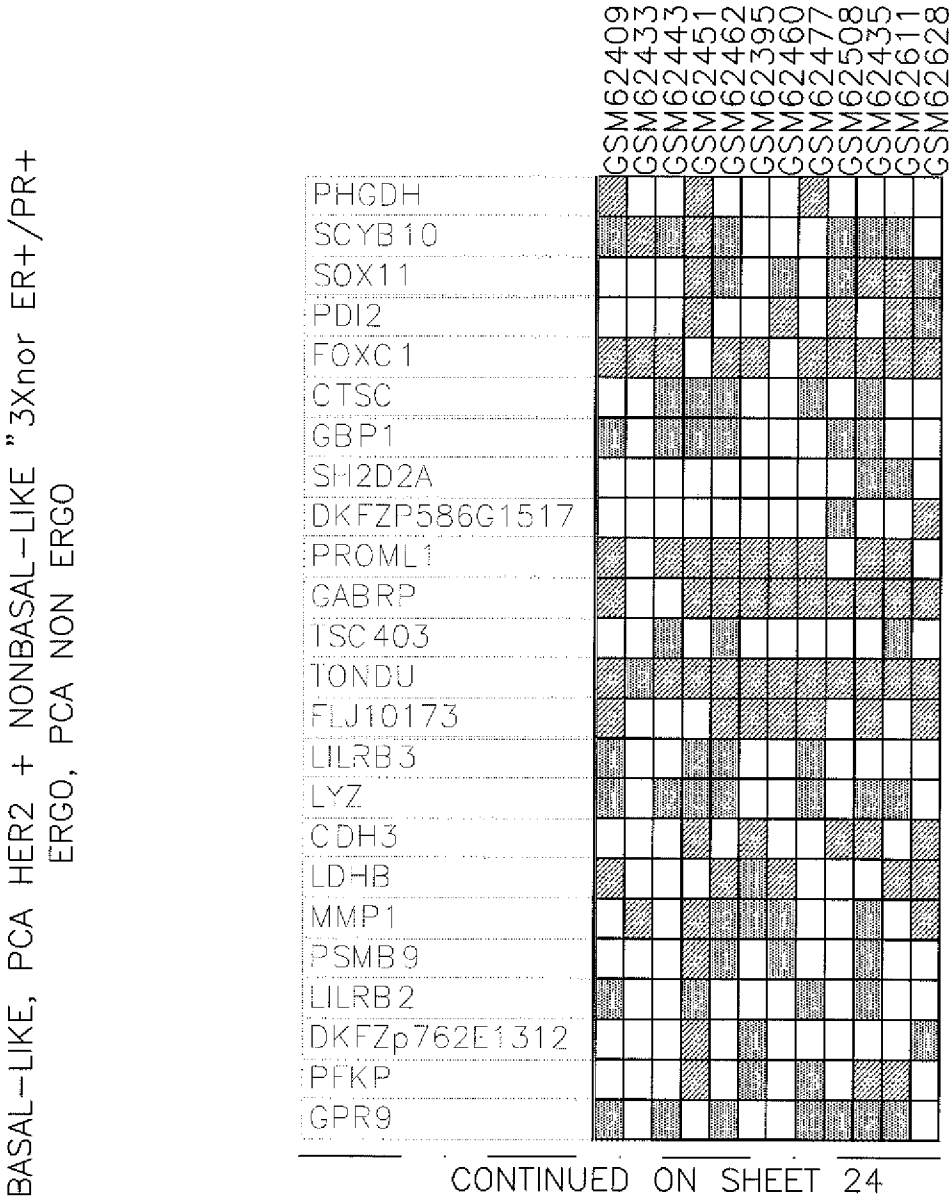
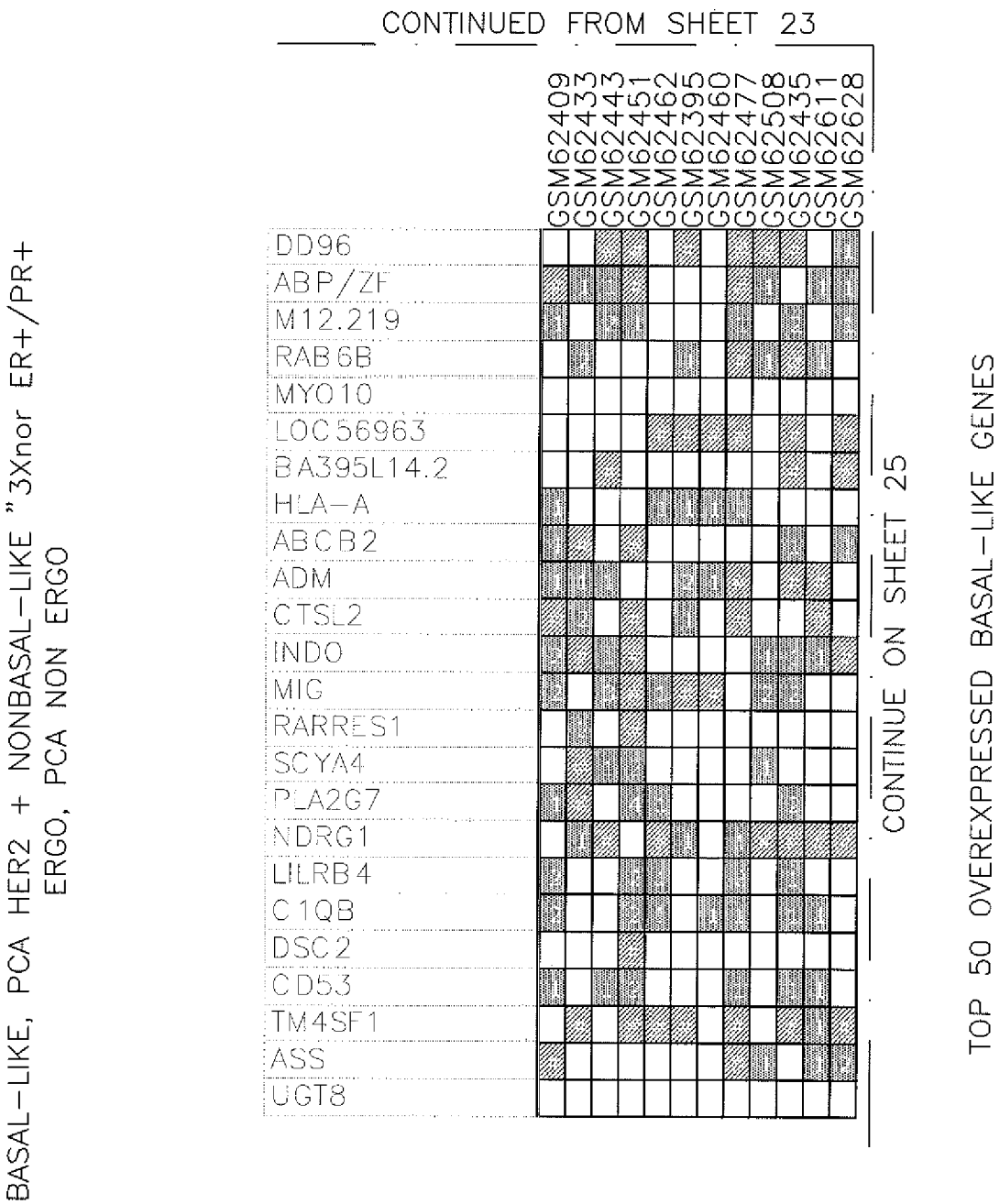

CONTINUED FROM SHEET 21
GSM62449
GSM62463
GSM62483
GSM62489
GSM625569
GSM625575
GSM625581
GSM625587
GSM626612
GSM626621
GSM626630
GSM626632
GSM623389
GSM62400
GSM62405
GSM62415
GSM624556
GSM624567
GSM624578
GSM624582
GSM624590
GSM625570
GSM626624
GSM62420
DD96
ABP/ZF
M12.219
RAB6B
MYO10
LOC56963
BA395L14.2
HLA-A
ABCB2
ADM
CTSL2
INDO
MIG
RARRES1
SCYA4
PLA2G7
NDRG1
LILRB4
C1QB
DSC2
CD53
TM4SF1
ASS
UGT8
BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+ ERGO, PCA NON ERGO
CONTINUE ON SHEET 23
TOP 50 OVEREXPRESSED BASAL-LIKE GENES

FIG. 11



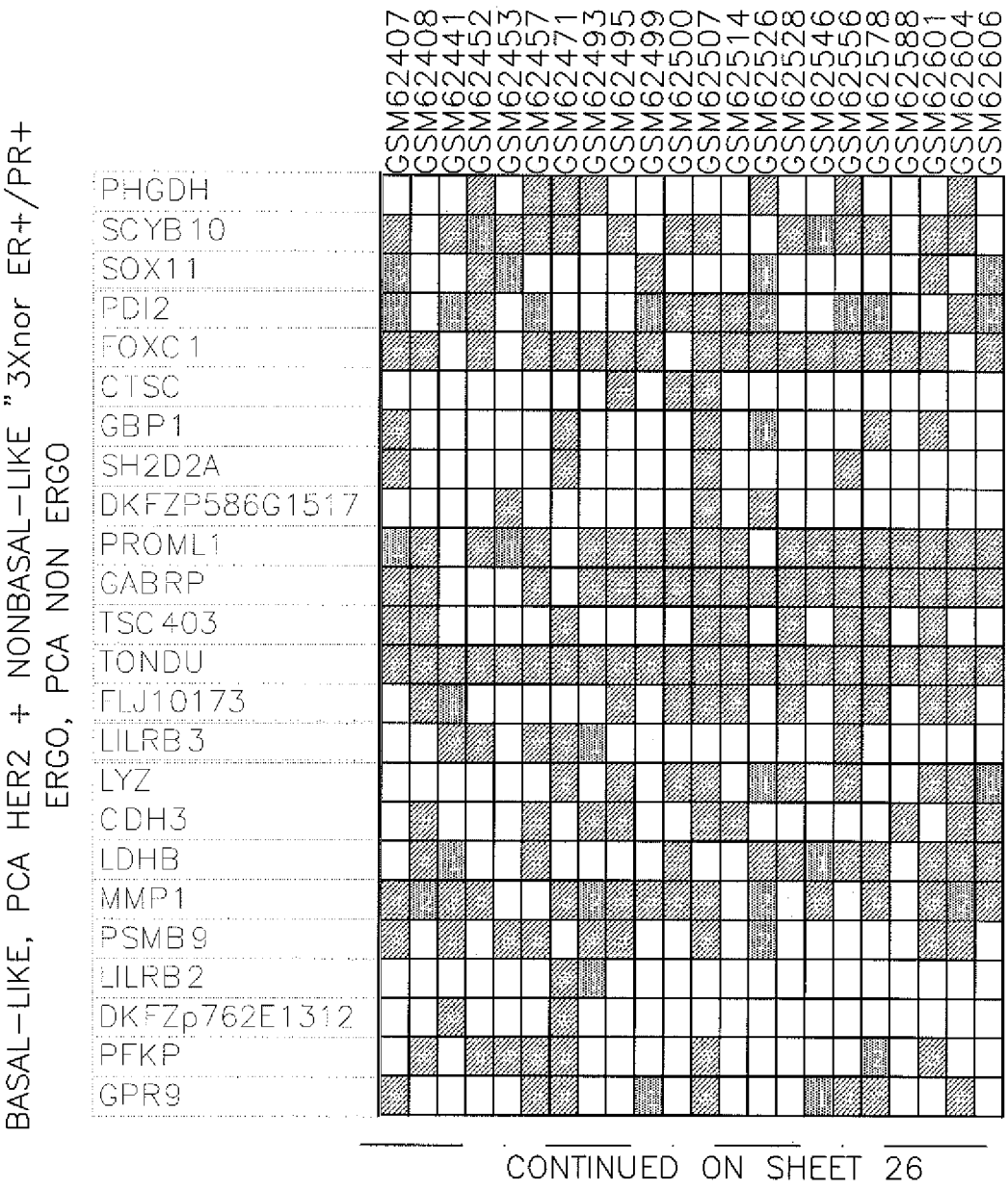
TOP 50 OVEREXPRESSED BASAL-LIKE GENES

FIG. 11



TOP 50 OVEREXPRESSED BASAL-LIKE GENES

FIG. 11



TOP 50 OVEREXPRESSED BASAL-LIKE GENES

FIG. 11

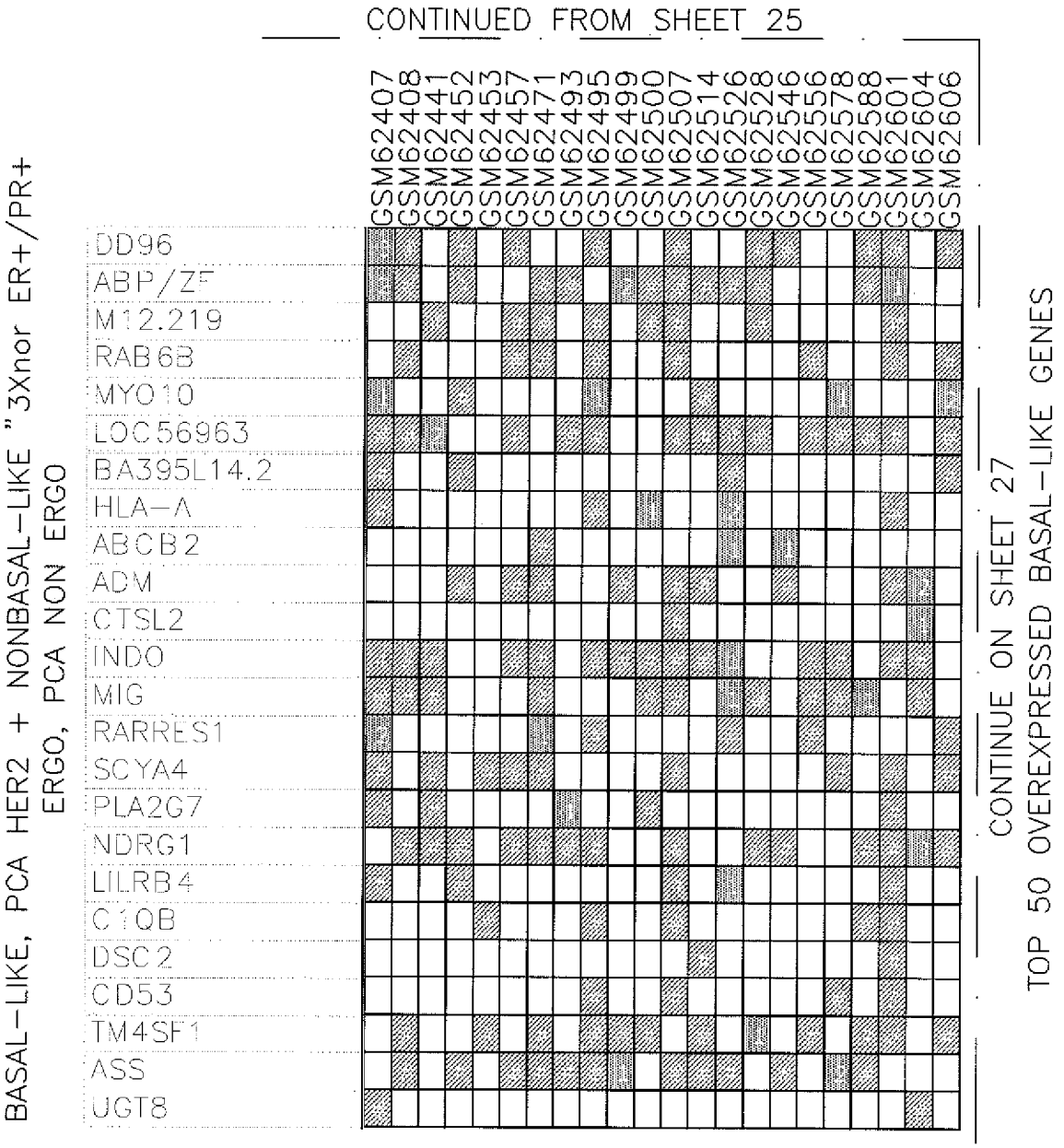
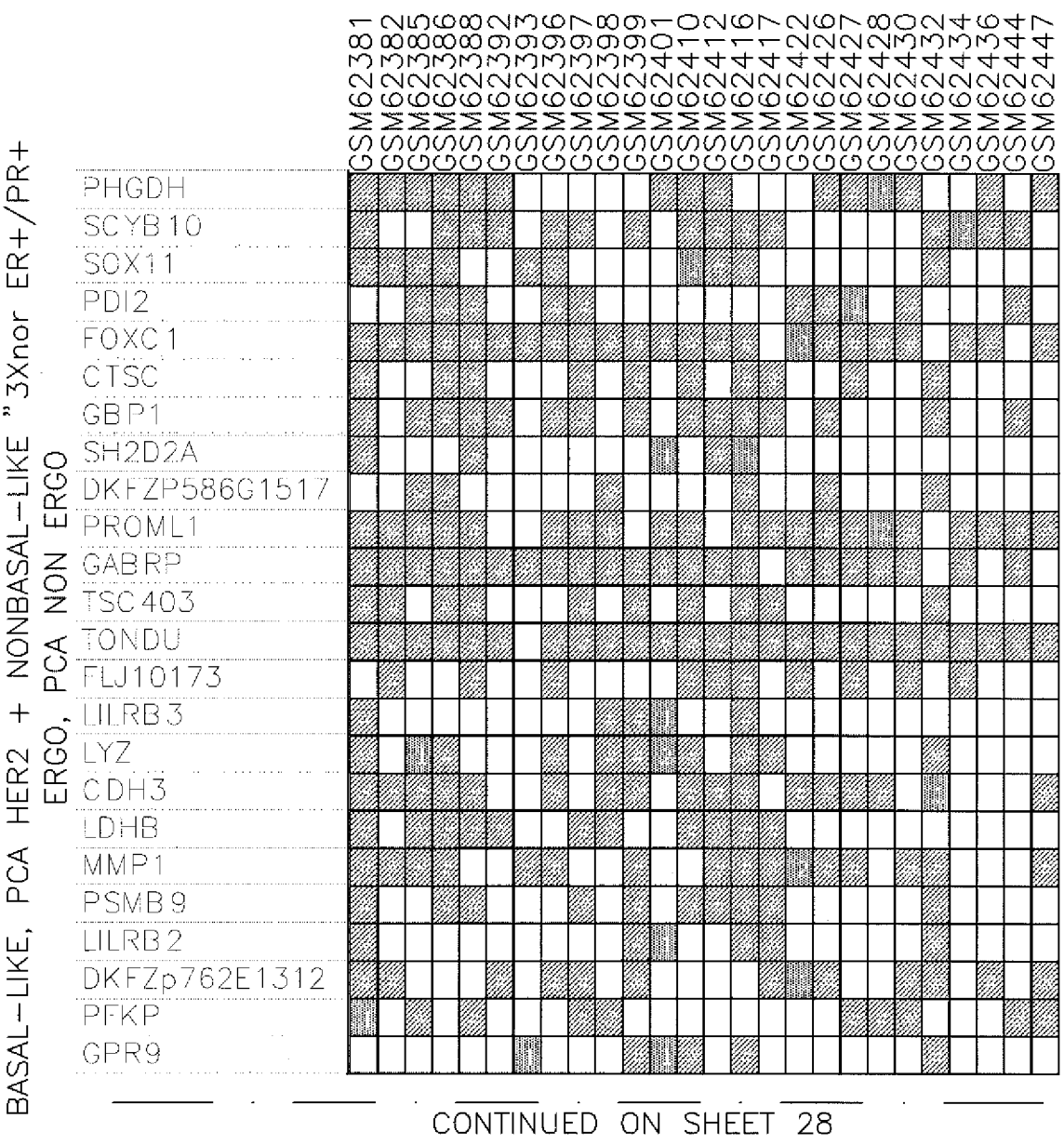

CONTINUED FROM SHEET 25
BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+ ERGO, PCA NON ERGO
GSM62407
GSM62408
GSM62441
GSM62452
GSM62453
GSM62457
GSM62471
GSM62493
GSM62495
GSM62499
GSM62500
GSM62507
GSM62514
GSM62526
GSM62528
GSM62546
GSM62556
GSM62578
GSM62588
GSM62601
GSM62604
GSM62606
DD96
ABP/Z
M12.219
RAB6B
MYO10
LOC56963
BA395L14.2
HLA-A
ABCB2
ADM
CTSL2
INDO
MIG
RARRES1
SCYA4
PLA2G7
NDRG1
LILRB4
C1QB
DSC2
CD53
TM4SF1
ASS
UGT8
CONTINUE ON SHEET 27
TOP 50 OVEREXPRESSED BASAL-LIKE GENES

FIG. 11


GSM62381
GSM62382
GSM62385
GSM62386
GSM62388
GSM62392
GSM62393
GSM62396
GSM62397
GSM62398
GSM62399
GSM62401
GSM62410
GSM62412
GSM62416
GSM62417
GSM62422
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GSM62427
GSM62428
GSM62430
GSM62432
GSM62434
GSM62436
GSM62444
GSM62447
PHGDH
SCYB10
SOX11
PDI2
FOXC1
CTSC
GBP1
SH2D2A
DKFZP586G1517
PROML1
GABRP
TSC403
TONDU
FLJ10173
LILRB3
LYZ
CDH3
LDHB
MMP1
PSMB9
LILRB2
DKFZp762E1312
PFKP
GPR9
BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+ ERGO, PCA NON ERGO
TOP 50 OVEREXPRESSED BASAL-LIKE GENES
CONTINUED ON SHEET 28

FIG. 11

CONTINUED FROM SHEET 27
GSM62381
GSM62382
GSM62385
GSM62386
GSM62388
GSM62392
GSM62393
GSM62396
GSM62397
GSM62398
GSM62399
GSM62401
GSM62410
GSM62412
GSM62416
GSM62417
GSM62422
GSM62426
GSM62427
GSM62428
GSM62430
GSM62432
GSM62434
GSM62436
GSM62444
GSM62447
BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+ ERGO, PCA NON ERGO
DD96
ABP/ZF
M12.219
RAB6B
MYO10
LOC56963
BA395L14.2
HLA-A
ABCB2
ADM
CTSL2
INDO
MIG
RARRES1
SCYA4
PLA2G7
NDRG1
LILRB4
C1QB
DSC2
CD53
TM4SF1
ASS
UGT8
CONTINUE ON SHEET 29
TOP 50 OVEREXPRESSED BASAL-LIKE GENES

FIG. 11

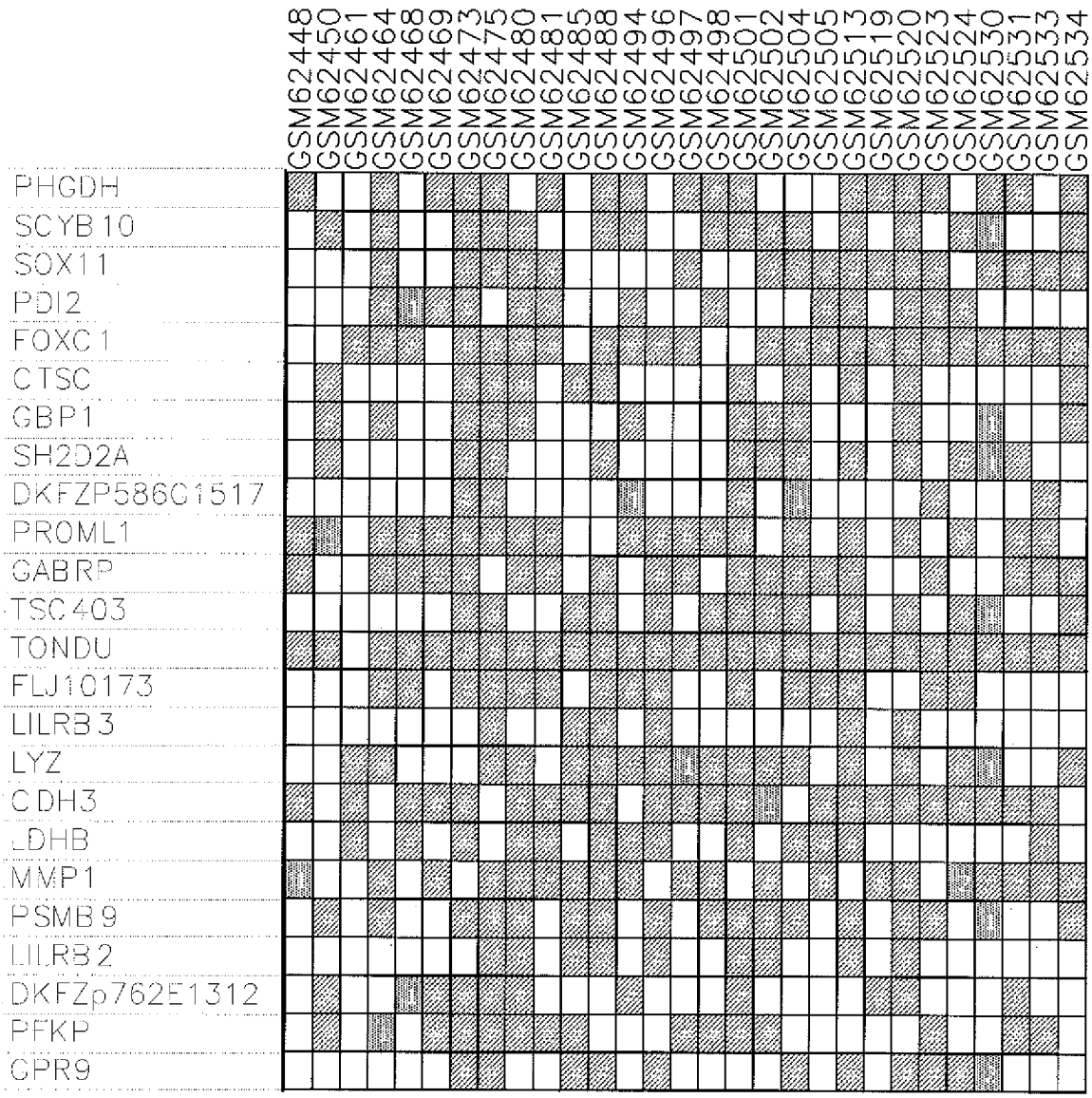


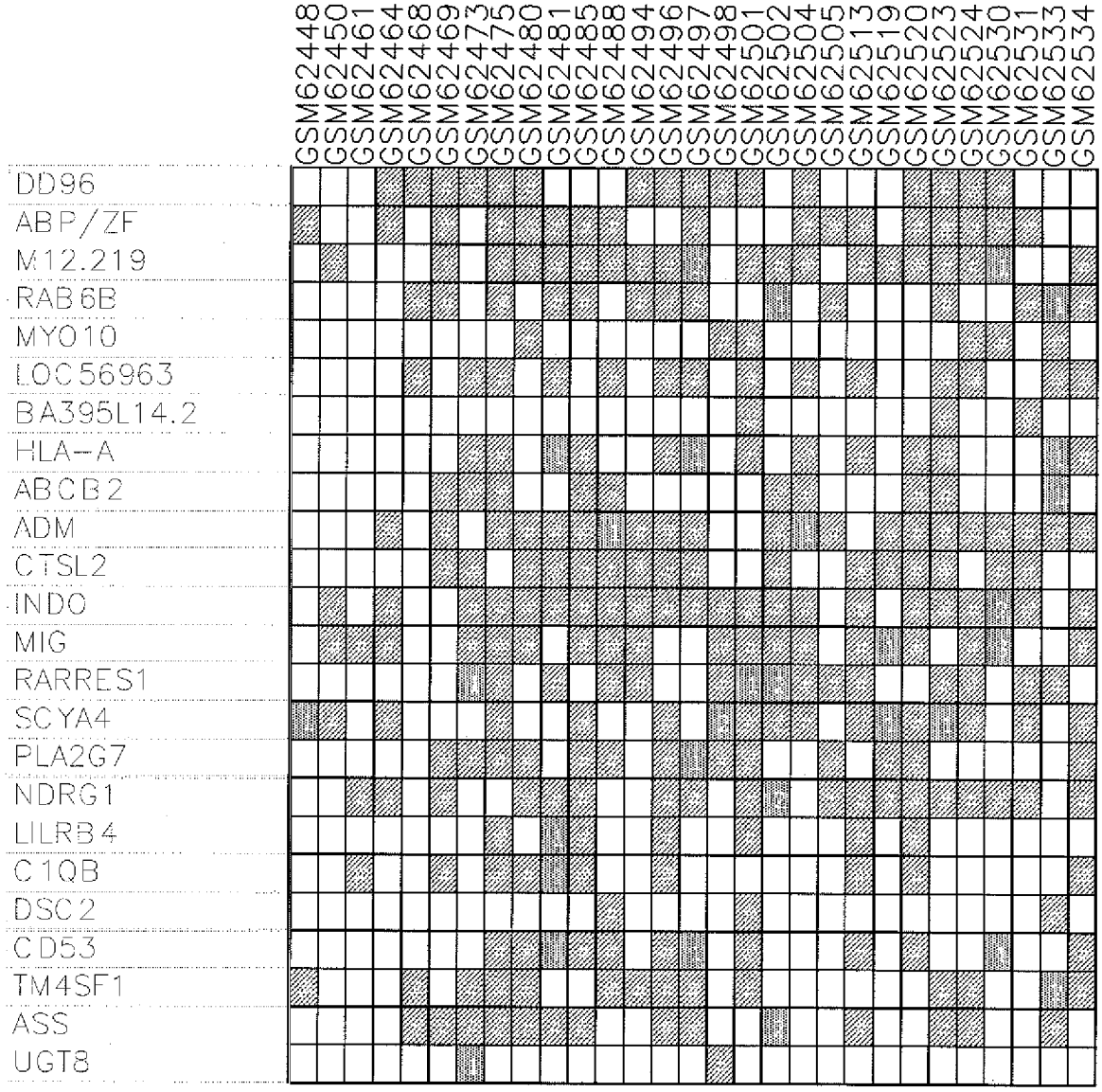
FIG. 11

CONTINUED ON SHEET 30

BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+ ERGO, PCA NON ERGO

TOP 50
OVEREXPRESSED
BASAL-LIKE GENES

CONTINUED FROM SHEET 29

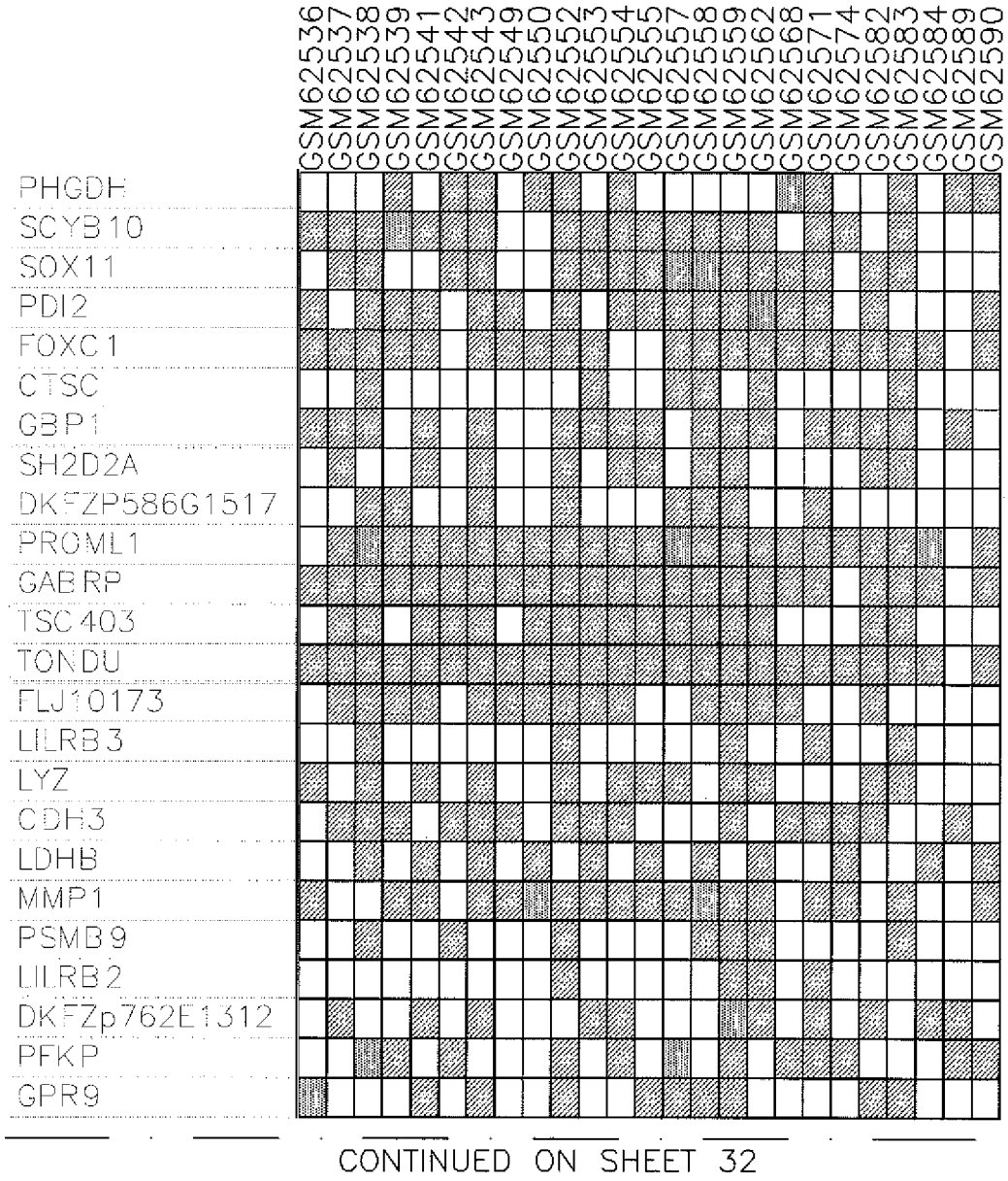


BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+ ERGO, PCA NON ERGO

TOP 50
OVEREXPRESSED
BASAL-LIKE GENES

FIG. 11

CONTINUE ON SHEET 31



CONTINUED ON SHEET 32

FIG. 11

BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+ ERGO, PCA NON ERGO

TOP 50
OVEREXPRESSED
BASAL-LIKE GENES

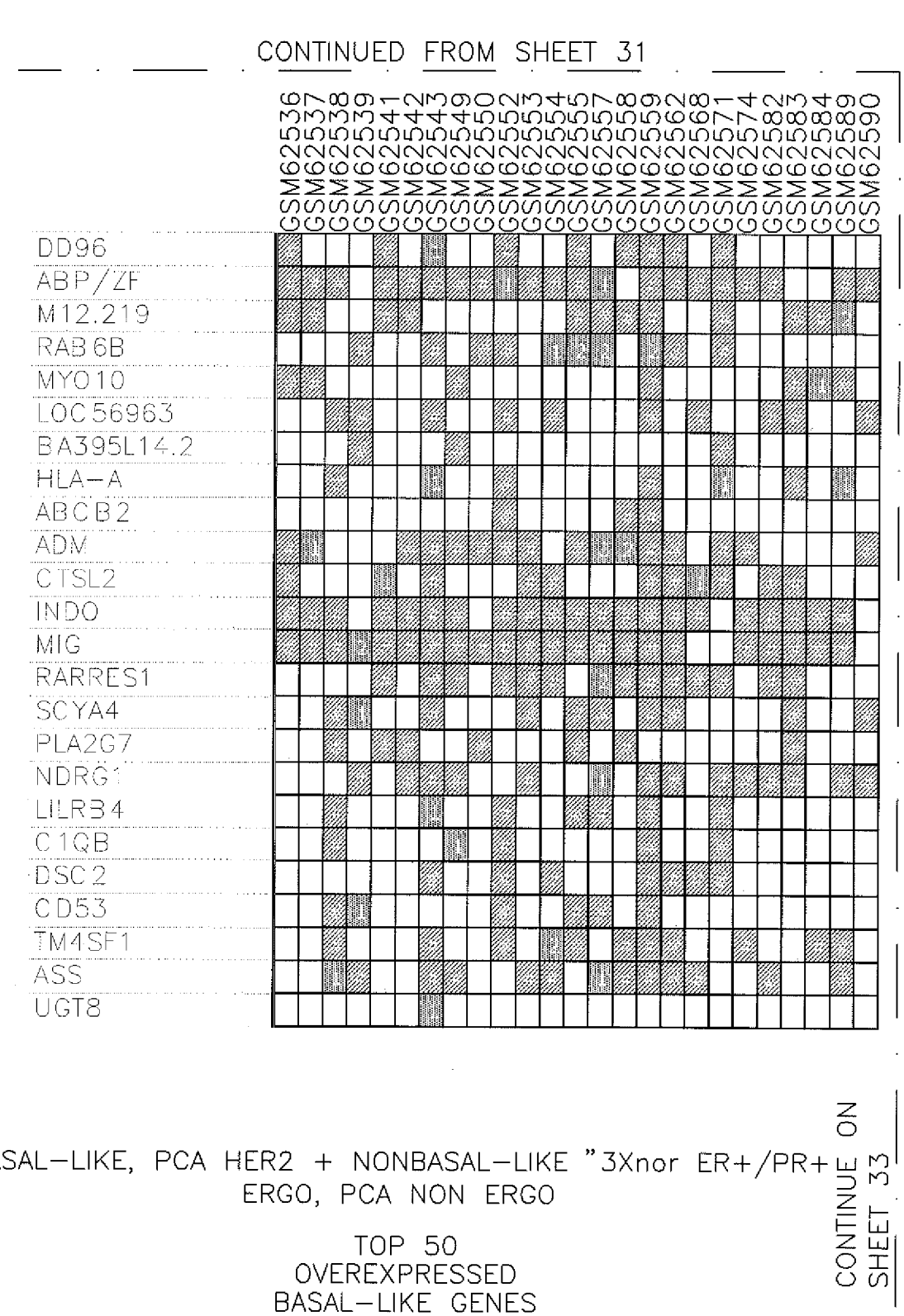

32
CONTINUED FROM SHEET 31
GSM625536
GSM625537
GSM625538
GSM625539
GSM625541
GSM625542
GSM625543
GSM625549
GSM625550
GSM625552
GSM625553
GSM625554
GSM625555
GSM625557
GSM625558
GSM625559
GSM625562
GSM625568
GSM625571
GSM625574
GSM625582
GSM625583
GSM625584
GSM625589
GSM625590
DD96
ABP/ZF
M12.219
RAB6B
MYO10
LOC56963
BA395L14.2
HLA-A
ABCB2
ADM
CTSL2
INDO
MIG
RARRES1
SCYA4
PLA2G7
NDRG1
LILRB4
C1QB
DSC2
CD53
TM4SF1
ASS
UGT8
BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+
ERGO, PCA NON ERGO
TOP 50
OVEREXPRESSED
BASAL-LIKE GENES
CONTINUE ON
SHEET 33

FIG. 11

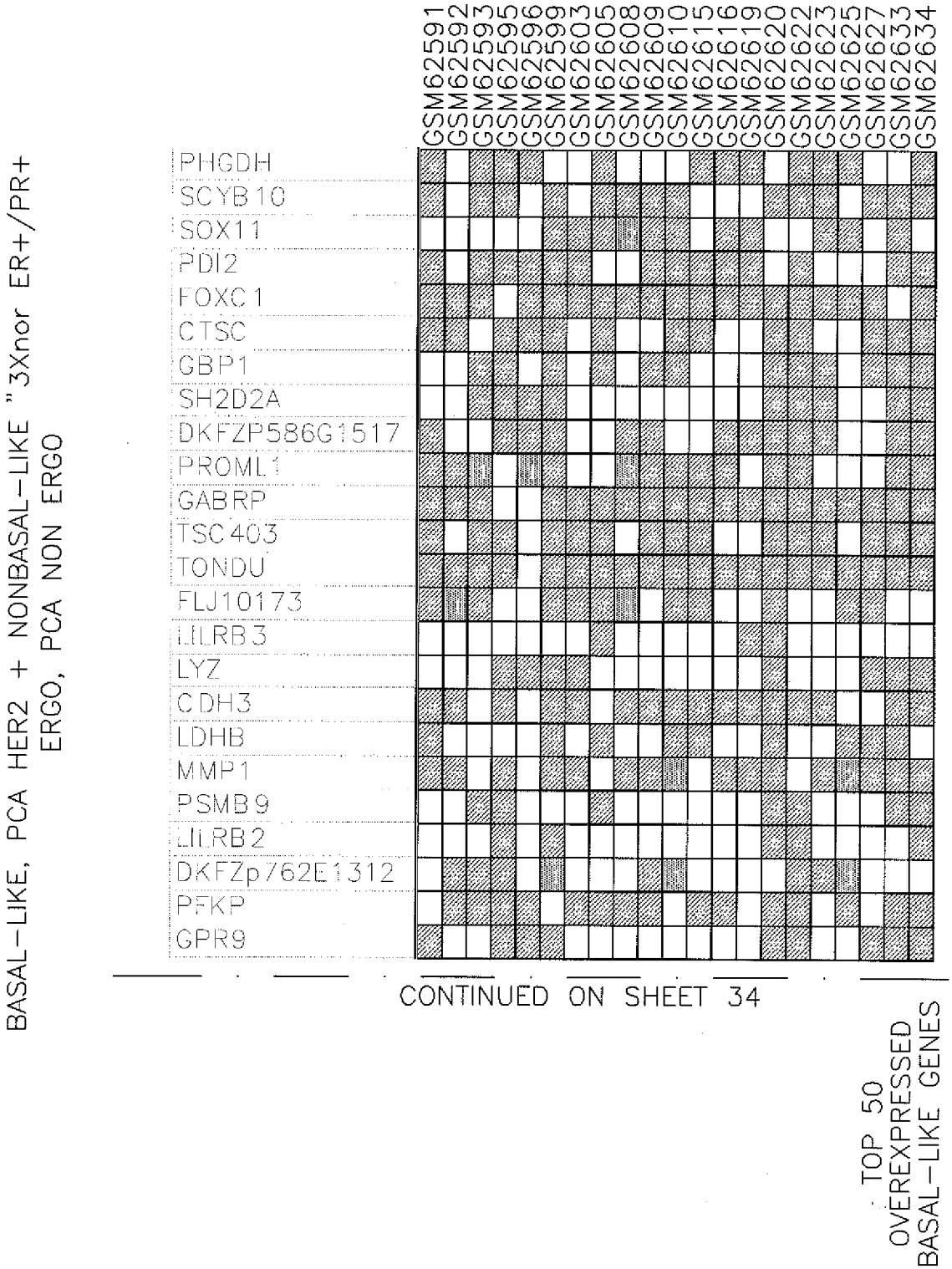

BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+
ERGO, PCA NON ERGO
GSM62591
GSM62592
GSM62593
GSM62595
GSM62596
GSM62599
GSM62603
GSM62605
GSM62608
GSM62609
GSM62610
GSM62615
GSM62616
GSM62619
GSM62620
GSM62622
GSM62623
GSM62625
GSM62627
GSM62633
GSM62634
PHGDH
SCYB10
SOX11
PDI2
FOXC1
CTSC
GBP1
SH2D2A
DKFZP586G1517
PROML1
GABRP
TSC403
TONDU
FLJ10173
LILRB3
LYZ
CDH3
LDHB
MMP1
PSMB9
LILRB2
DKFZp762E1312
PFKP
GPR9
CONTINUED ON SHEET 34
TOP 50
OVEREXPRESSED
BASAL-LIKE GENES

FIG. 11

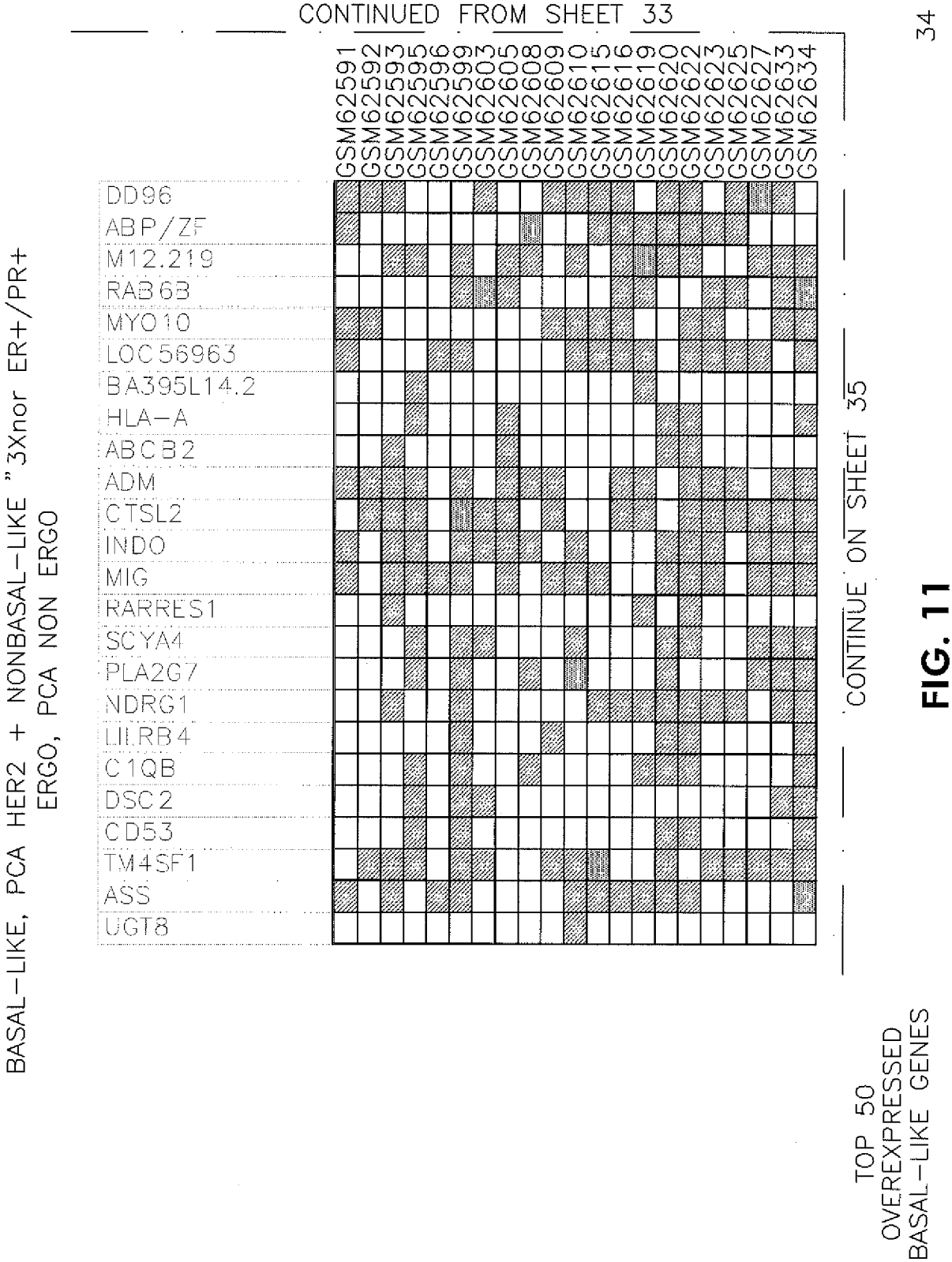
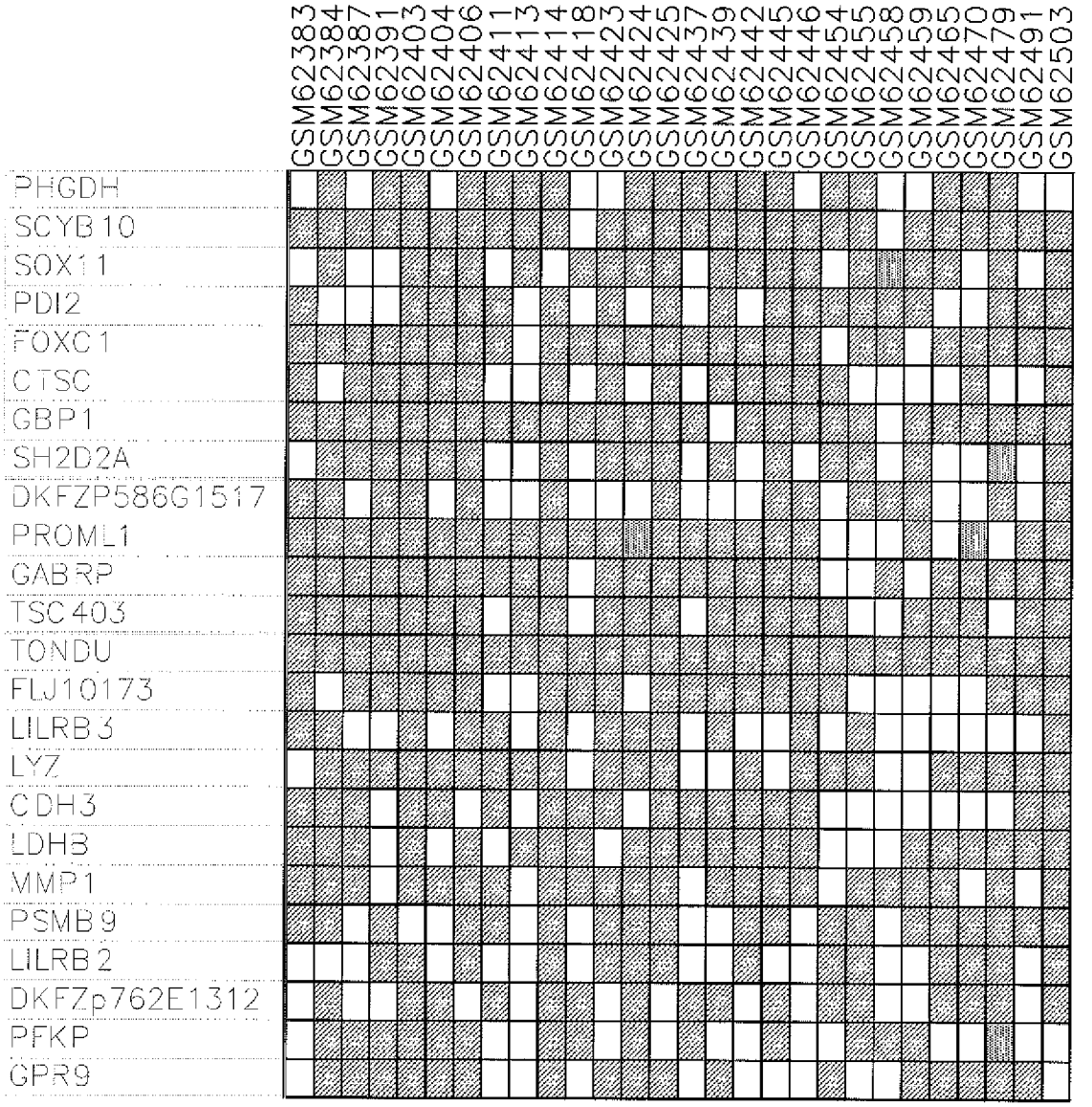

CONTINUED FROM SHEET 33
CONTINUE ON SHEET 35
34
BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+
ERGO, PCA NON ERGO
TOP 50
OVEREXPRESSED
BASAL-LIKE GENES
GSM62591
GSM62592
GSM62593
GSM62595
GSM62596
GSM62599
GSM62603
GSM62605
GSM62608
GSM62609
GSM62610
GSM62615
GSM62616
GSM62619
GSM62620
GSM62622
GSM62623
GSM62625
GSM62627
GSM62633
GSM62634
DD96
ABP/ZF
M12.219
RAB6B
MYO10
LOC56963
BA395L14.2
HLA-A
ABCB2
ADM
CTSL2
INDO
MIG
RARRES1
SCYA4
PLA2G7
NDRG1
LILRB4
C1QB
DSC2
CD53
TM4SF1
ASS
UGT8

FIG. 11

35



CONTINUED ON SHEET 36

FIG. 11

BASAL–LIKE, PCA HER2 + NONBASAL–LIKE "3Xnor ER+/PR+ ERGO, PCA NON ERGO

TOP 50
OVEREXPRESSED
BASAL–LIKE GENES

CONTINUED FROM SHEET 35

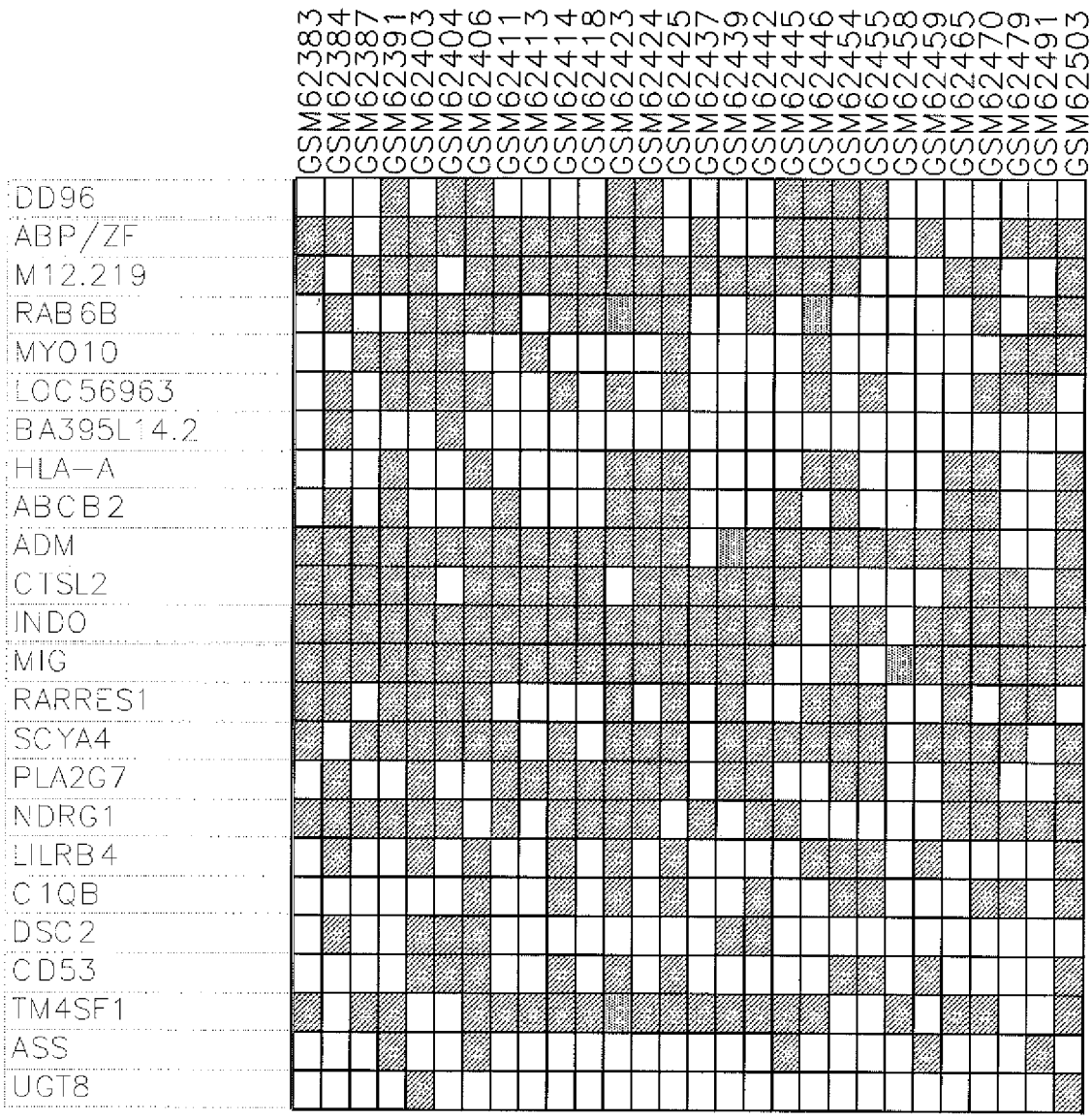
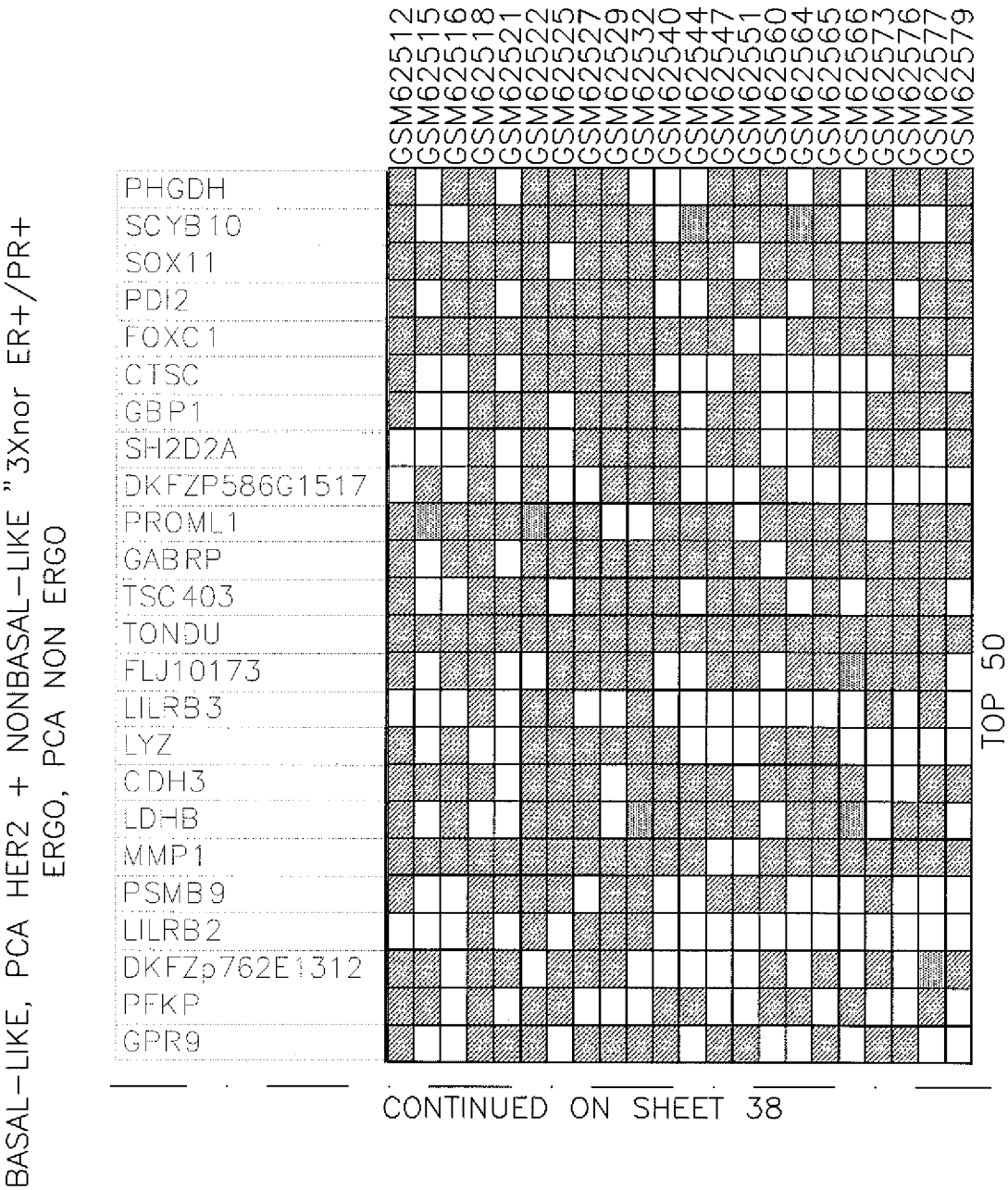


FIG. 11

BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+ ERGO, PCA NON ERGO

TOP 50
OVEREXPRESSED
BASAL-LIKE GENES

CONTINUE ON SHEET 37


BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+
ERGO, PCA NON ERGO
GSM625512
GSM625515
GSM625516
GSM625518
GSM625521
GSM625522
GSM625525
GSM625527
GSM625529
GSM625532
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GSM625566
GSM625573
GSM625576
GSM625577
GSM625579
PHGDH
SCYB10
SOX11
PDI2
FOXC1
CTSC
GBP1
SH2D2A
DKFZP586G1517
PROML1
GABRP
TSC403
TONDU
FLJ10173
LILRB3
LYZ
CDH3
LDHB
MMP1
PSMB9
LILRB2
DKFZp762E1312
PFKP
GPR9
TOP 50
OVEREXPRESSED
BASAL-LIKE GENES
CONTINUED ON SHEET 38

FIG. 11

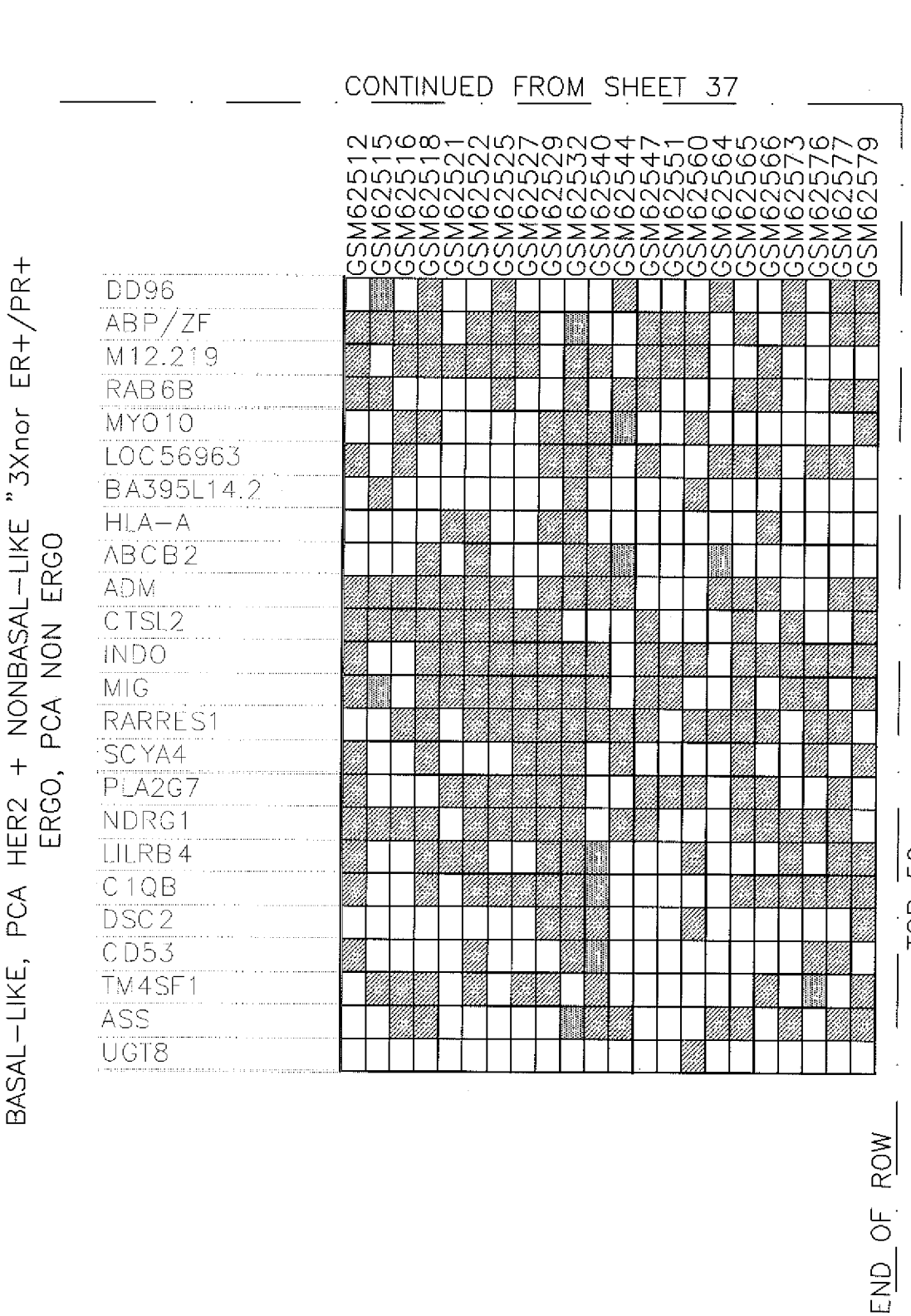
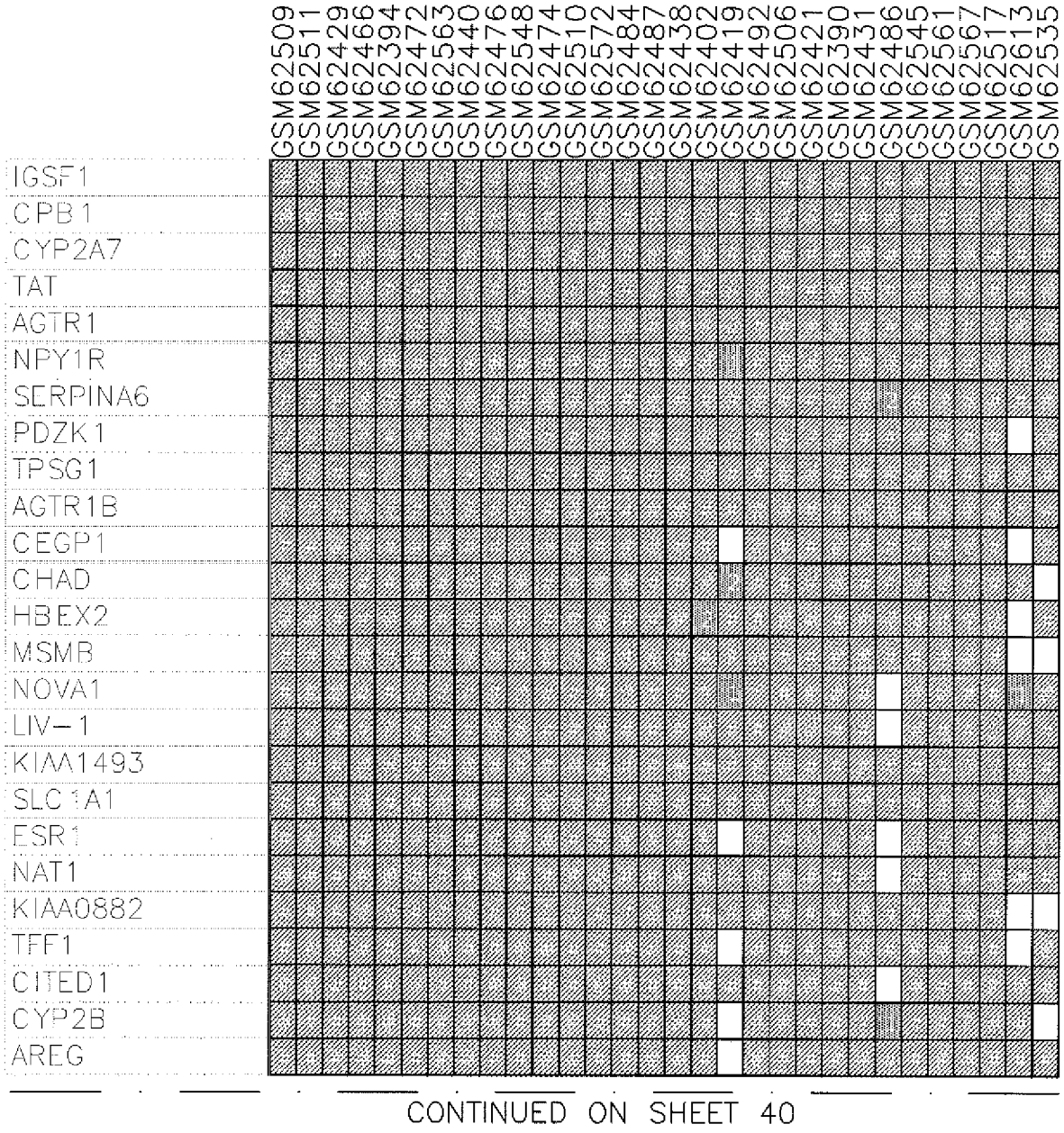

CONTINUED FROM SHEET 37
BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+ ERGO, PCA NON ERGO
GSM62512
GSM62515
GSM62516
GSM62518
GSM62521
GSM62522
GSM62525
GSM62527
GSM62529
GSM62532
GSM62540
GSM62544
GSM62547
GSM62551
GSM62560
GSM62564
GSM62565
GSM62566
GSM62573
GSM62576
GSM62577
GSM62579
DD96
ABP/ZF
M12.219
RAB6B
MYO10
LOC56963
BA395L14.2
HLA-A
ABCB2
ADM
CTSL2
INDO
MIG
RARRES1
SCYA4
PLA2G7
NDRG1
LILRB4
C1QB
DSC2
CD53
TM4SF1
ASS
UGT8
END OF ROW
TOP 50 OVEREXPRESSED BASAL-LIKE GENES

FIG. 11



CONTINUED ON SHEET 40

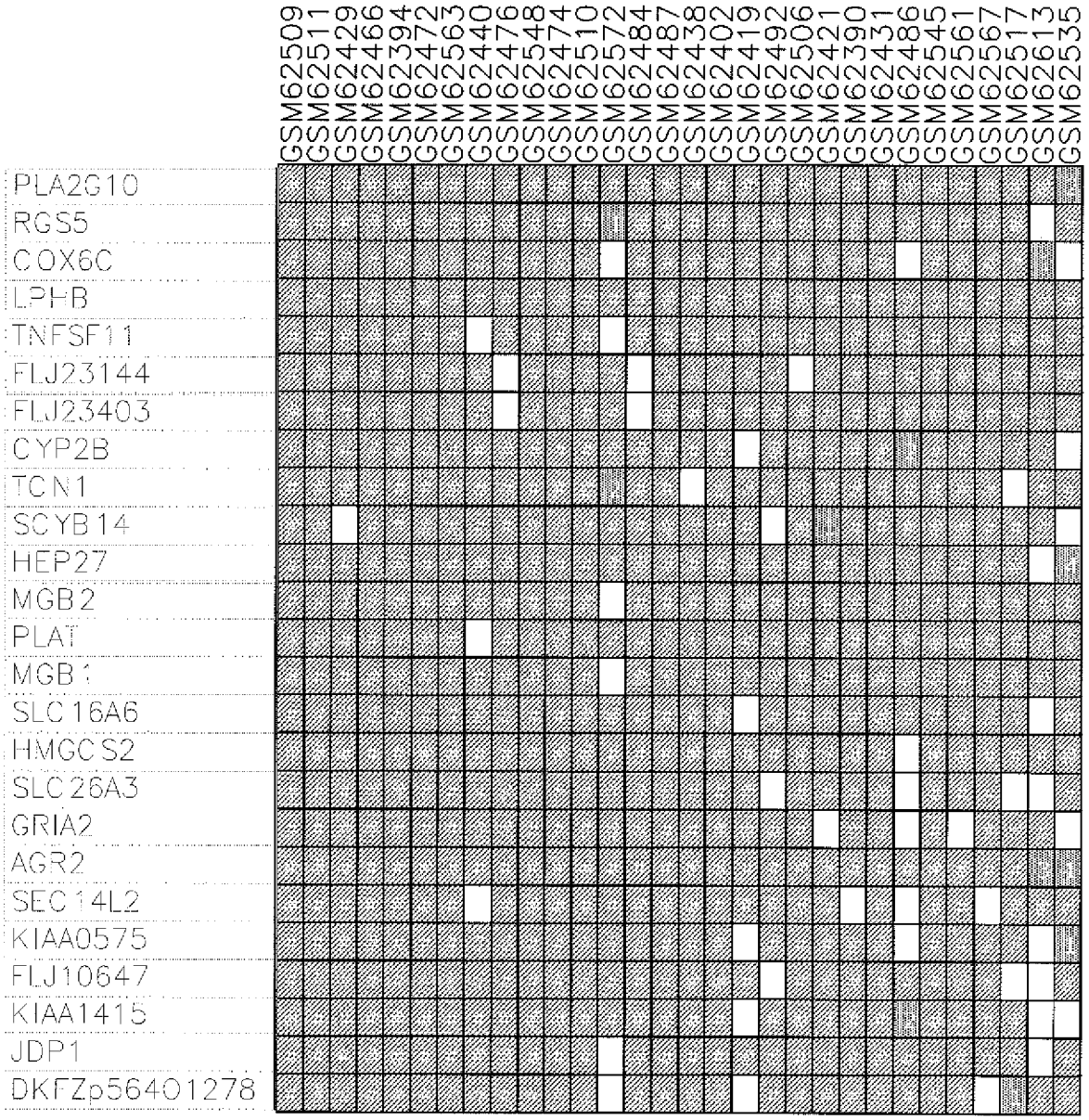
FIG. 11

BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+ ERGO, PCA NON ERGO

TOP 50
UNDEREXPRESSED
BASAL-LIKE GENES

40

CONTINUED FROM SHEET 40



BASAL–LIKE, PCA HER2 + NONBASAL–LIKE "3Xnor ER+/PR+ ERGO, PCA NON ERGO

TOP 50 UNDEREXPRESSED BASAL–LIKE GENES

FIG. 11

CONTINUED ON SHEET 41

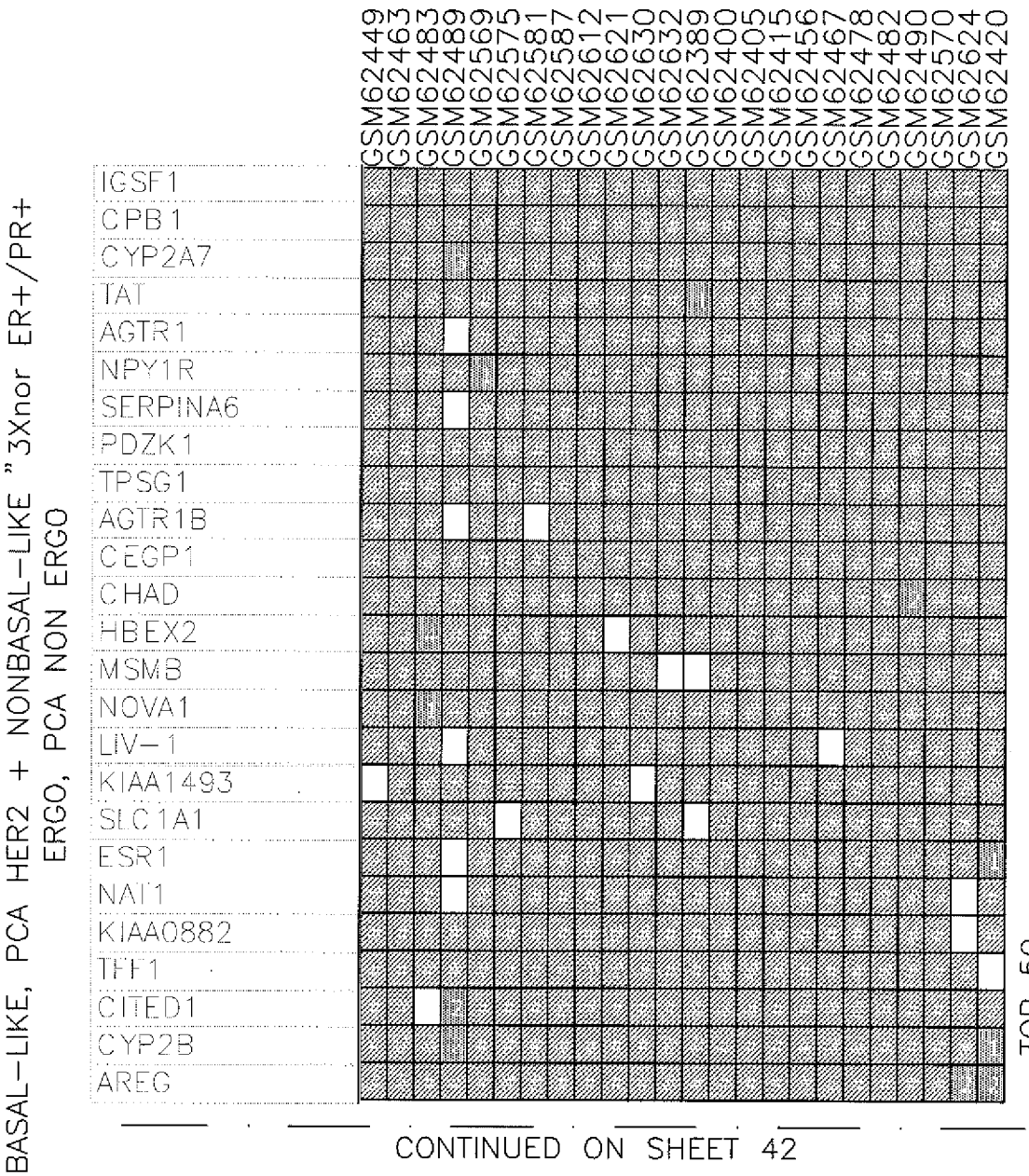

BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+ ERGO, PCA NON ERGO
GSM62449
GSM62463
GSM62483
GSM62489
GSM62569
GSM62575
GSM62581
GSM62587
GSM62612
GSM62621
GSM62630
GSM62632
GSM62389
GSM62400
GSM62405
GSM62415
GSM62456
GSM62467
GSM62478
GSM62482
GSM62490
GSM62570
GSM62624
GSM62420
IGSF1
CPB1
CYP2A7
TAT
AGTR1
NPY1R
SERPINA6
PDZK1
TPSG1
AGTR1B
CEGP1
CHAD
HBEX2
MSMB
NOVA1
LIV-1
KIAA1493
SLC1A1
ESR1
NAT1
KIAA0882
TFF1
CITED1
CYP2B
AREG
CONTINUED ON SHEET 42
TOP 50 UNDEREXPRESSED BASAL-LIKE GENES

FIG. 11

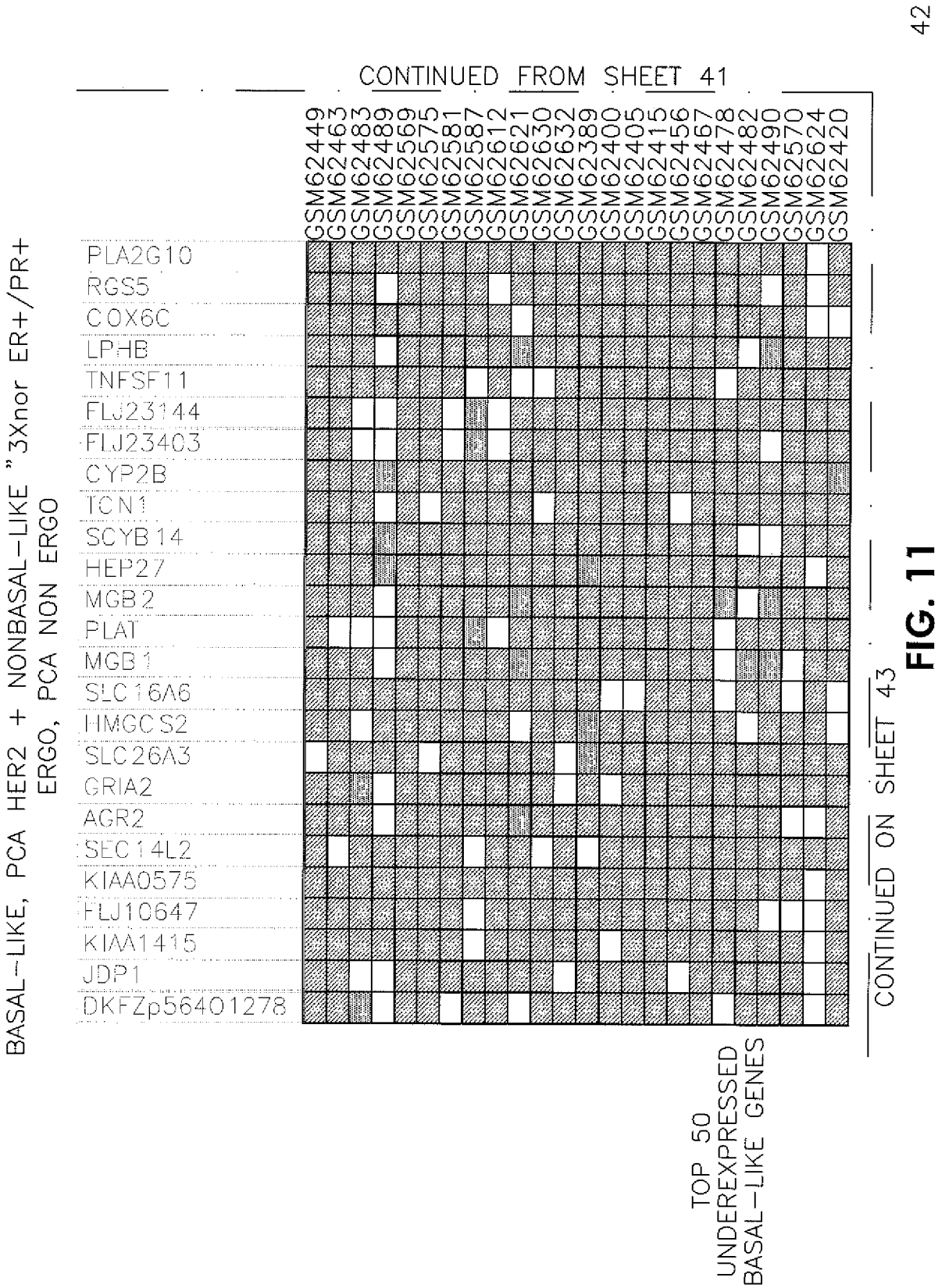
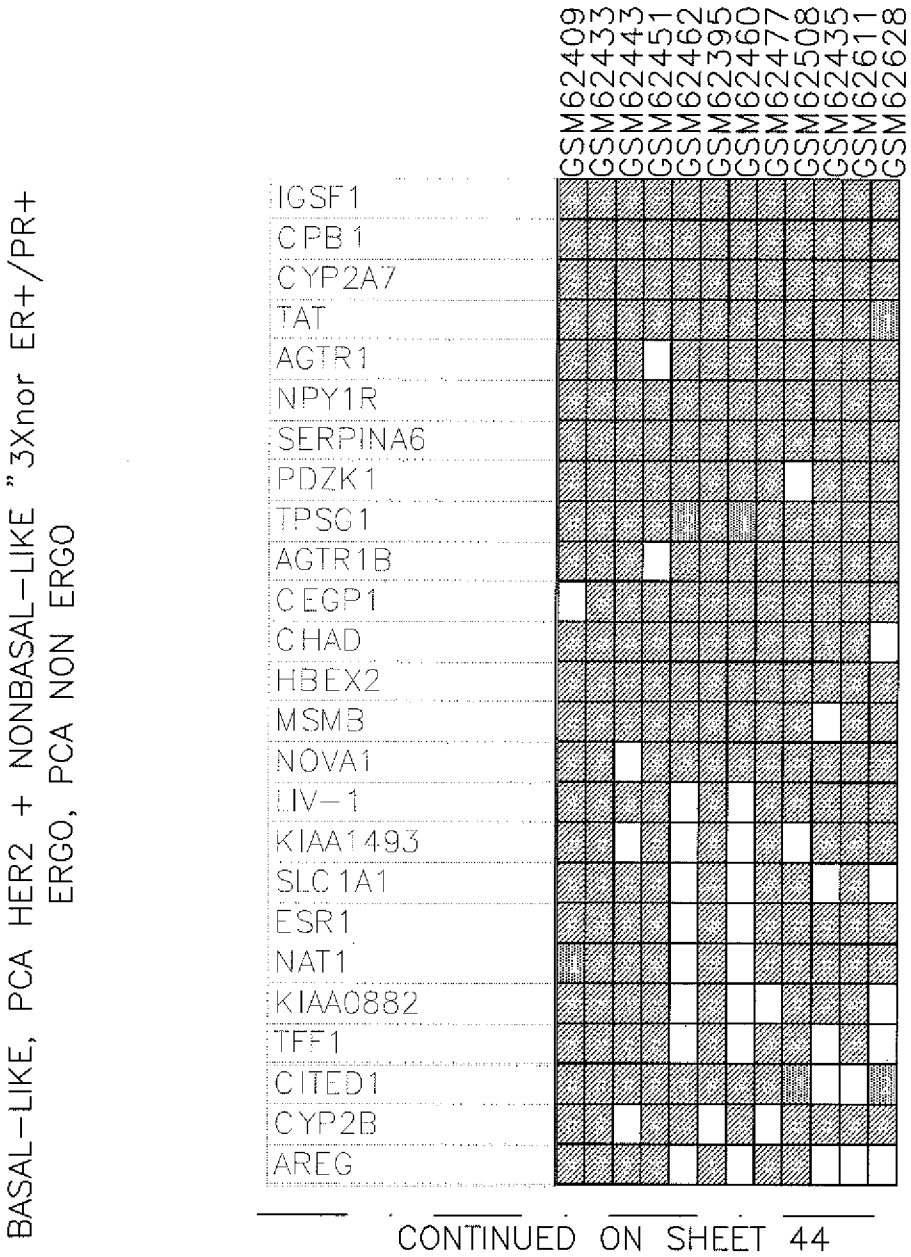

42
CONTINUED FROM SHEET 41
GSM62449
GSM62463
GSM62483
GSM62489
GSM62569
GSM62575
GSM62581
GSM62587
GSM62612
GSM62621
GSM62630
GSM62632
GSM62389
GSM62400
GSM62405
GSM62415
GSM62456
GSM62467
GSM62478
GSM62482
GSM62490
GSM62570
GSM62624
GSM62420
BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+ ERGO, PCA NON ERGO
PLA2G10
RGS5
COX6C
LPHB
TNFSF11
FLJ23144
FLJ23403
CYP2B
TCN1
SCYB14
HEP27
MGB2
PLAT
MGB1
SLC16A6
HMGCS2
SLC26A3
GRIA2
AGR2
SEC14L2
KIAA0575
FLJ10647
KIAA1415
JDP1
DKFZp56401278
TOP 50 UNDEREXPRESSED BASAL-LIKE GENES
CONTINUED ON SHEET 43

FIG. 11



TOP 50
UNDEREXPRESSED
BASAL-LIKE GENES

FIG. 11

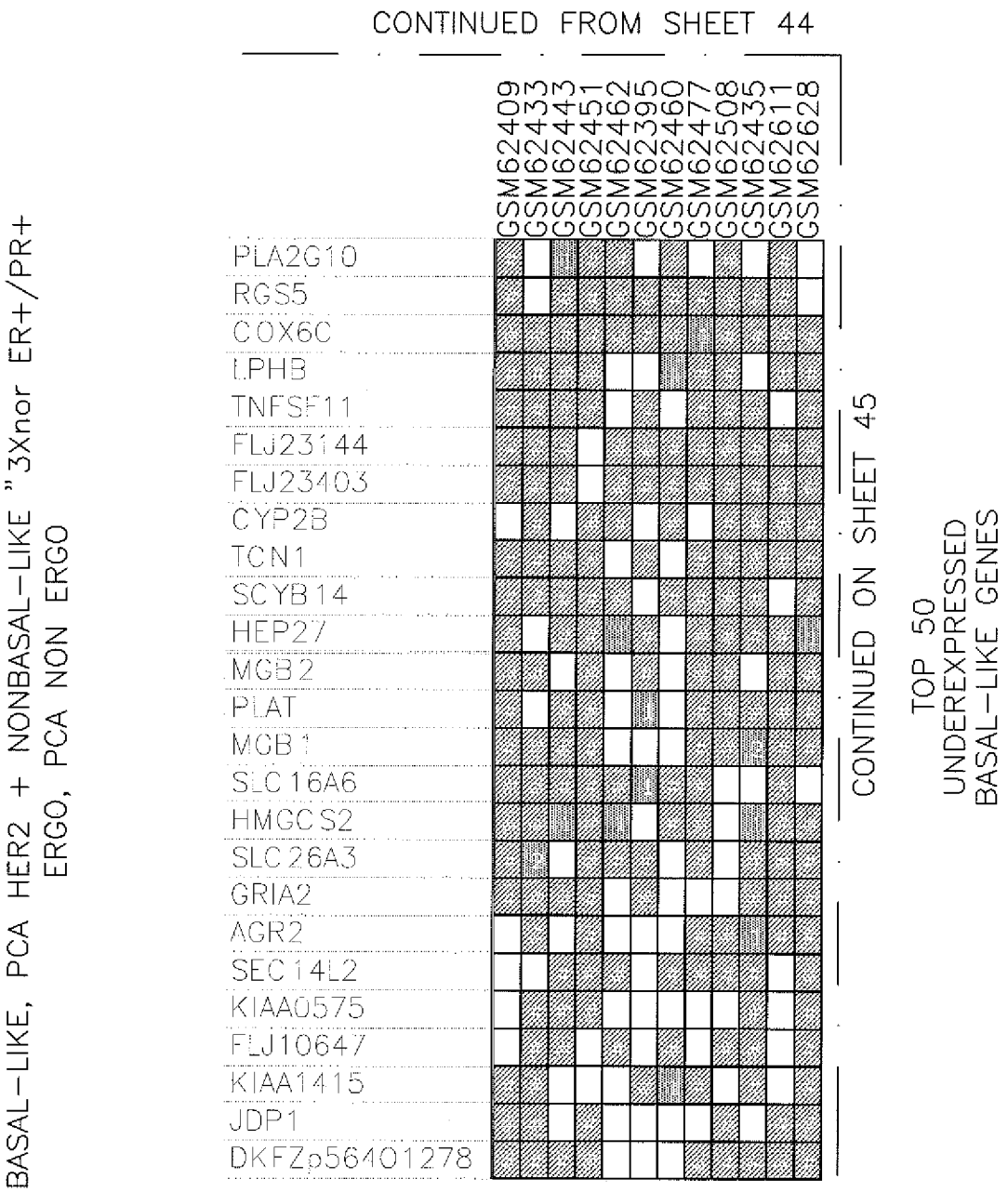

CONTINUED FROM SHEET 44
GSM62409
GSM62433
GSM62443
GSM62451
GSM62462
GSM62395
GSM62460
GSM62477
GSM62508
GSM62435
GSM62611
GSM62628
PLA2G10
RGS5
COX6C
LPHB
TNFSF11
FLJ23144
FLJ23403
CYP2B
TCN1
SCYB14
HEP27
MGB2
PLAT
MGB1
SLC16A6
HMGCS2
SLC26A3
GRIA2
AGR2
SEC14L2
KIAA0575
FLJ10647
KIAA1415
JDP1
DKFZp56401278
CONTINUED ON SHEET 45
TOP 50
UNDEREXPRESSED
BASAL-LIKE GENES
BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+
ERGO, PCA NON ERGO

FIG. 11

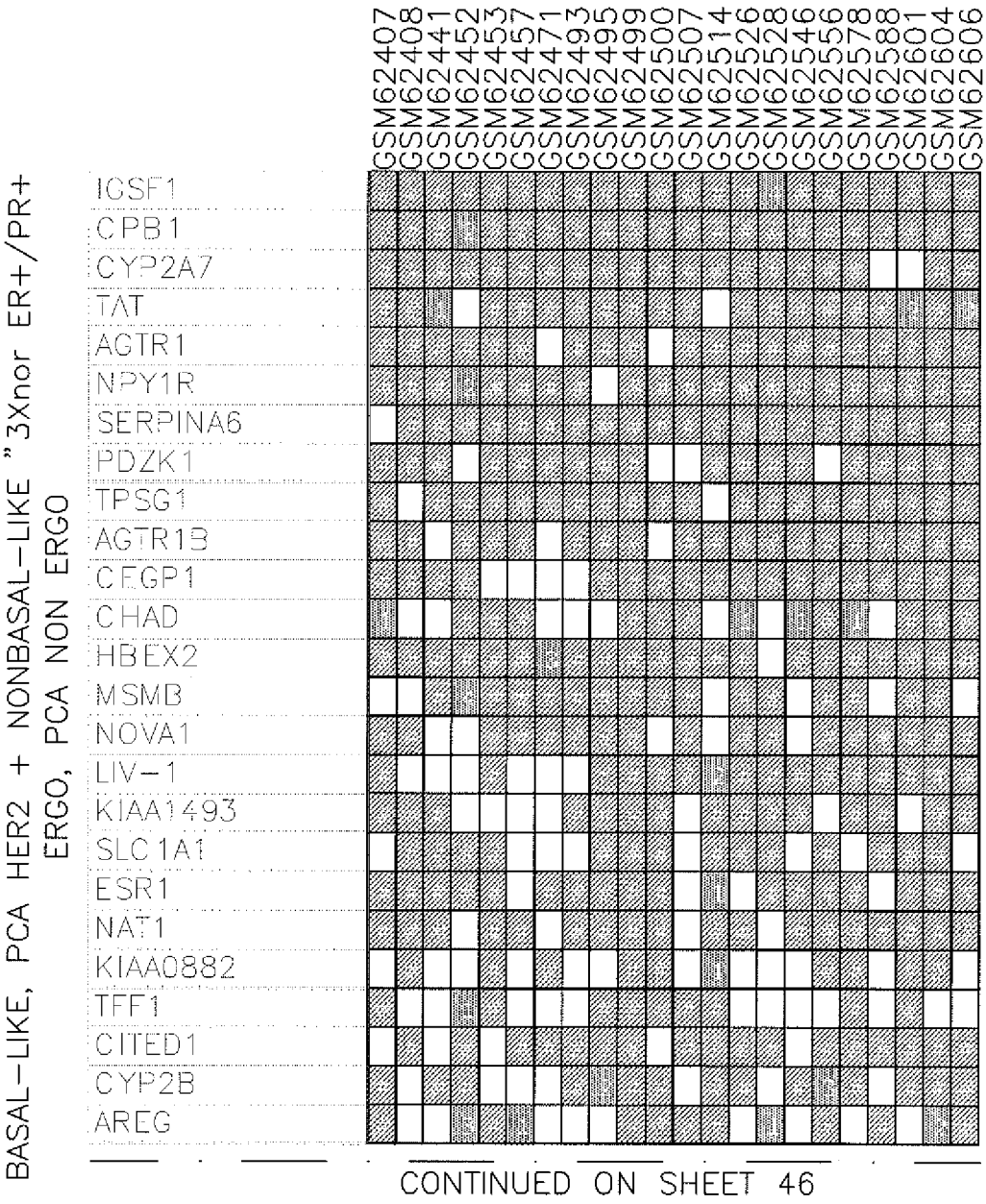

BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+ ERGO, PCA NON ERGO
GSM62407
GSM62408
GSM62441
GSM62452
GSM62453
GSM62457
GSM62471
GSM62493
GSM62495
GSM62499
GSM62500
GSM62507
GSM62514
GSM62526
GSM62528
GSM62546
GSM62556
GSM62578
GSM62588
GSM62601
GSM62604
GSM62606
IGSF1
CPB1
CYP2A7
TAT
AGTR1
NPY1R
SERPINA6
PDZK1
TPSG1
AGTR1B
CEGP1
CHAD
HBEX2
MSMB
NOVA1
LIV-1
KIAA1493
SLC1A1
ESR1
NAT1
KIAA0882
TFF1
CITED1
CYP2B
AREG
TOP 50 UNDEREXPRESSED BASAL-LIKE GENES
CONTINUED ON SHEET 46

FIG. 11

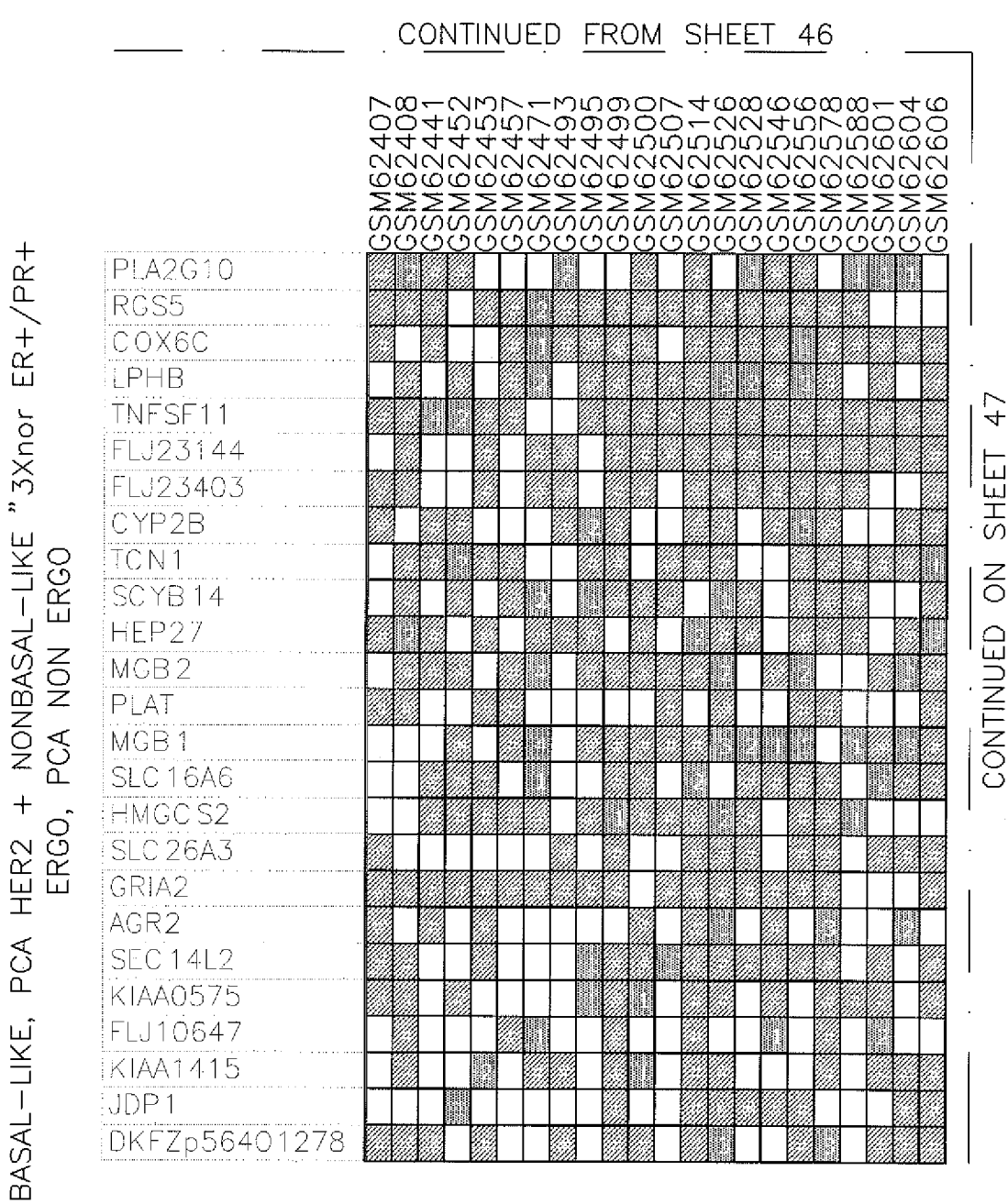

CONTINUED FROM SHEET 46
BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+ ERGO, PCA NON ERGO
GSM62407
GSM62408
GSM62441
GSM62452
GSM62453
GSM62457
GSM62471
GSM62493
GSM62495
GSM62499
GSM62500
GSM62507
GSM62514
GSM62526
GSM62528
GSM62546
GSM62556
GSM62578
GSM62588
GSM62601
GSM62604
GSM62606
PLA2G10
RGS5
COX6C
LPHB
TNFSF11
FLJ23144
FLJ23403
CYP2B
TCN1
SCYB14
HEP27
MGB2
PLAT
MGB1
SLC16A6
HMGCS2
SLC26A3
GRIA2
AGR2
SEC14L2
KIAA0575
FLJ10647
KIAA1415
JDP1
DKFZp56401278
CONTINUED ON SHEET 47
TOP 50
UNDEREXPRESSED
BASAL-LIKE GENES

FIG. 11

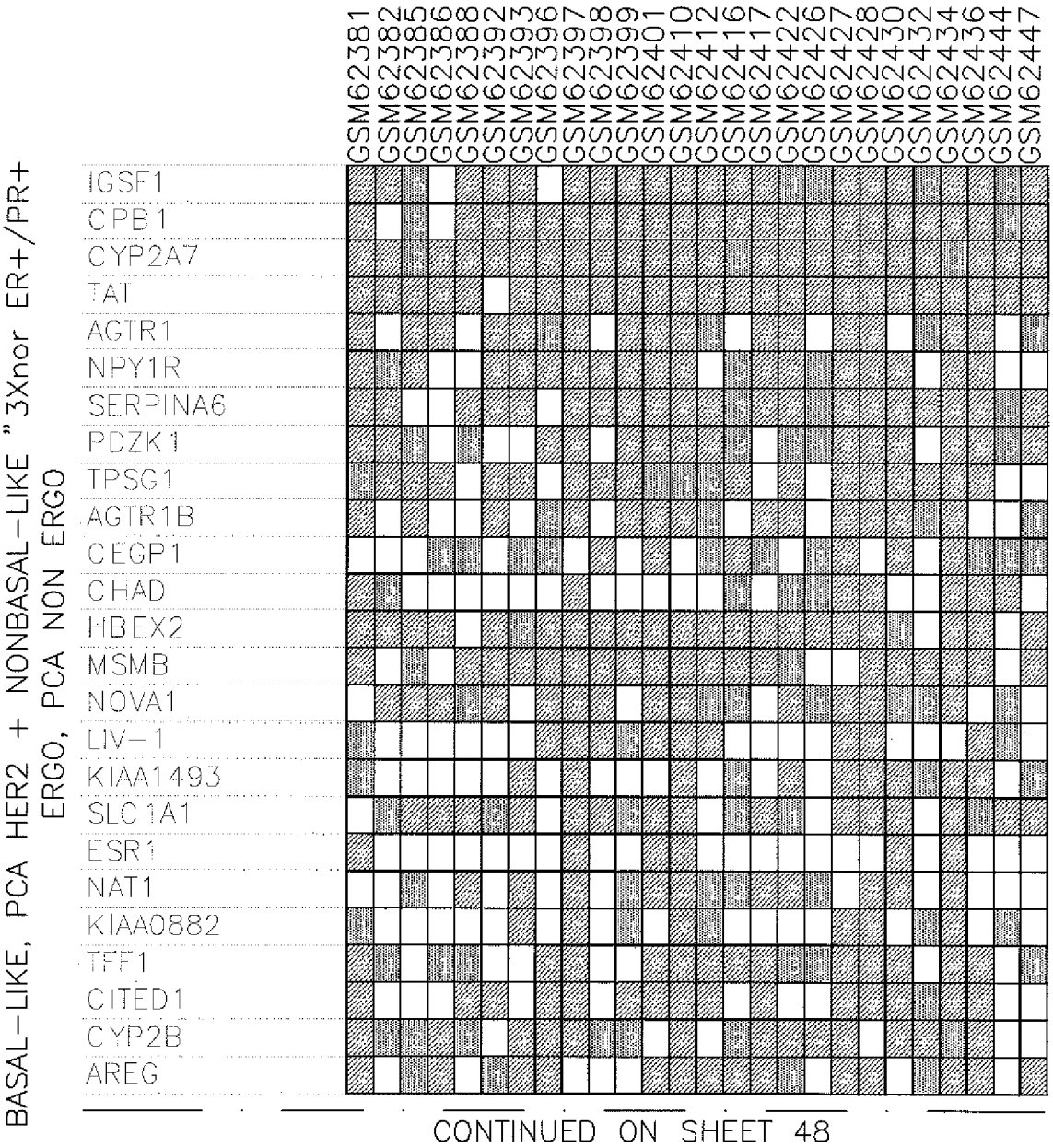
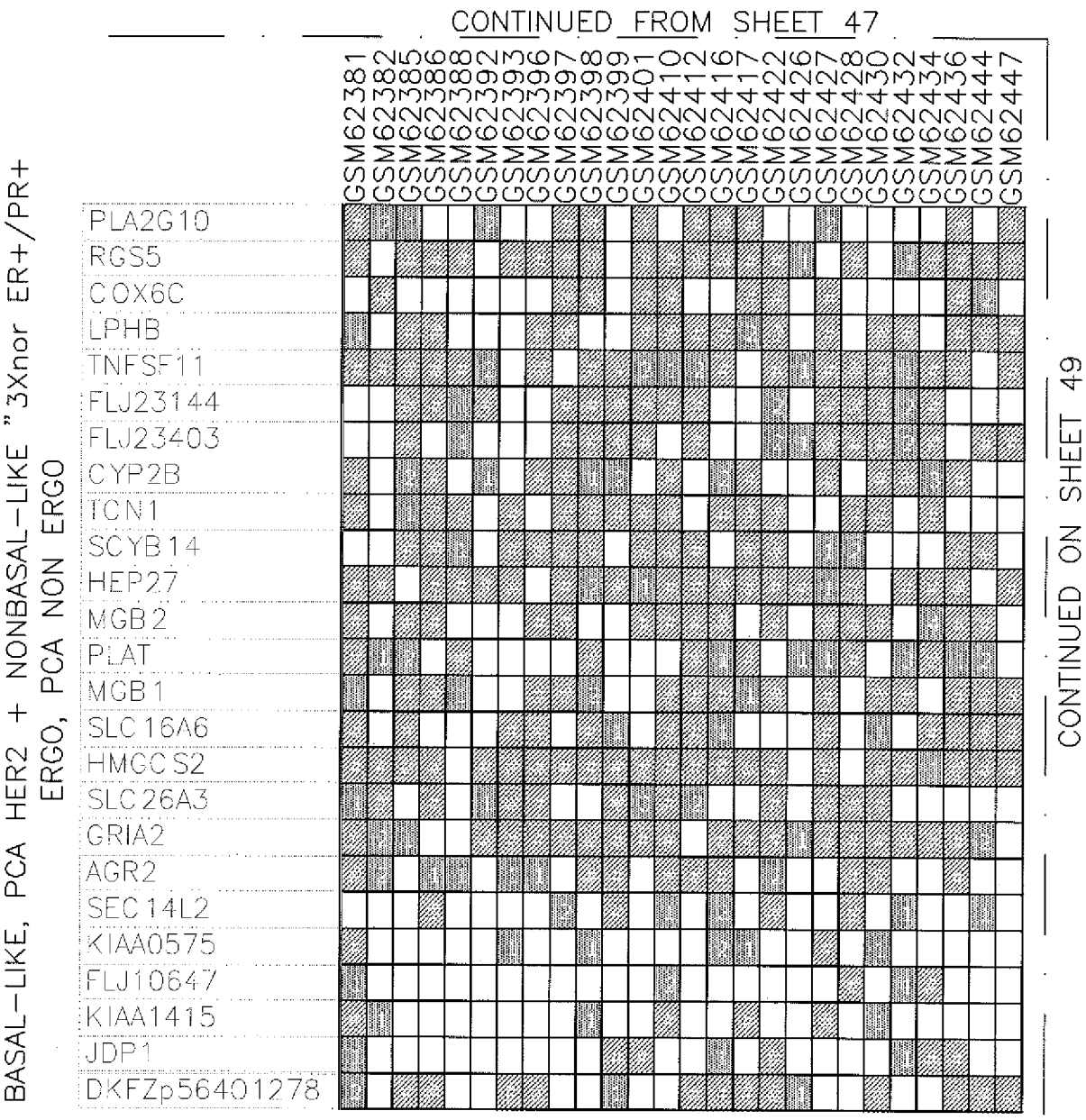


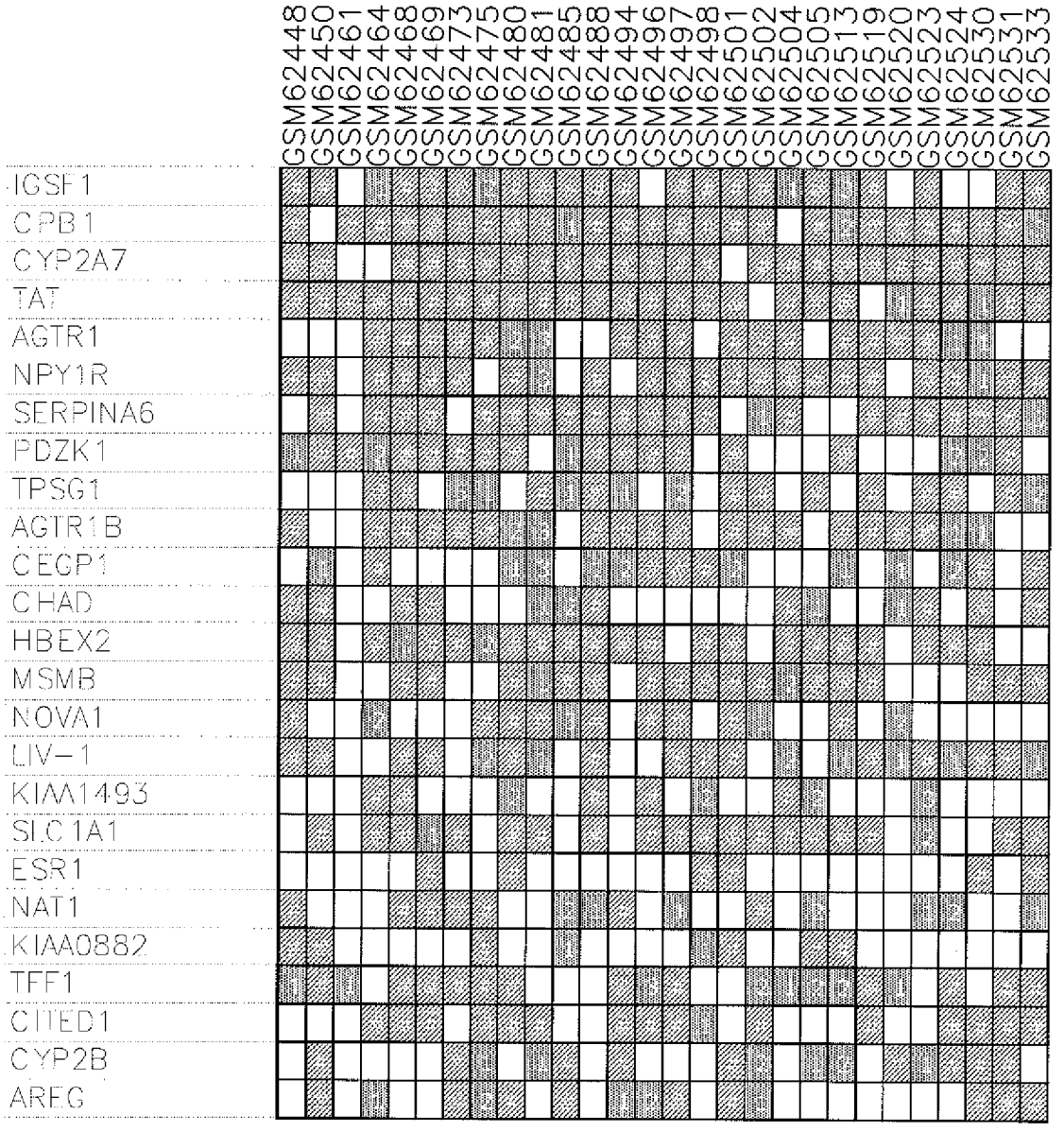
FIG. 11

TOP 50
UNDEREXPRESSED
BASAL-LIKE GENES



TOP 50
UNDEREXPRESSED
BASAL-LIKE GENES

FIG. 11



CONTINUED ON SHEET 50

FIG. 11

BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+ ERGO, PCA NON ERGO

TOP 50
UNDEREXPRESSED
BASAL-LIKE GENES

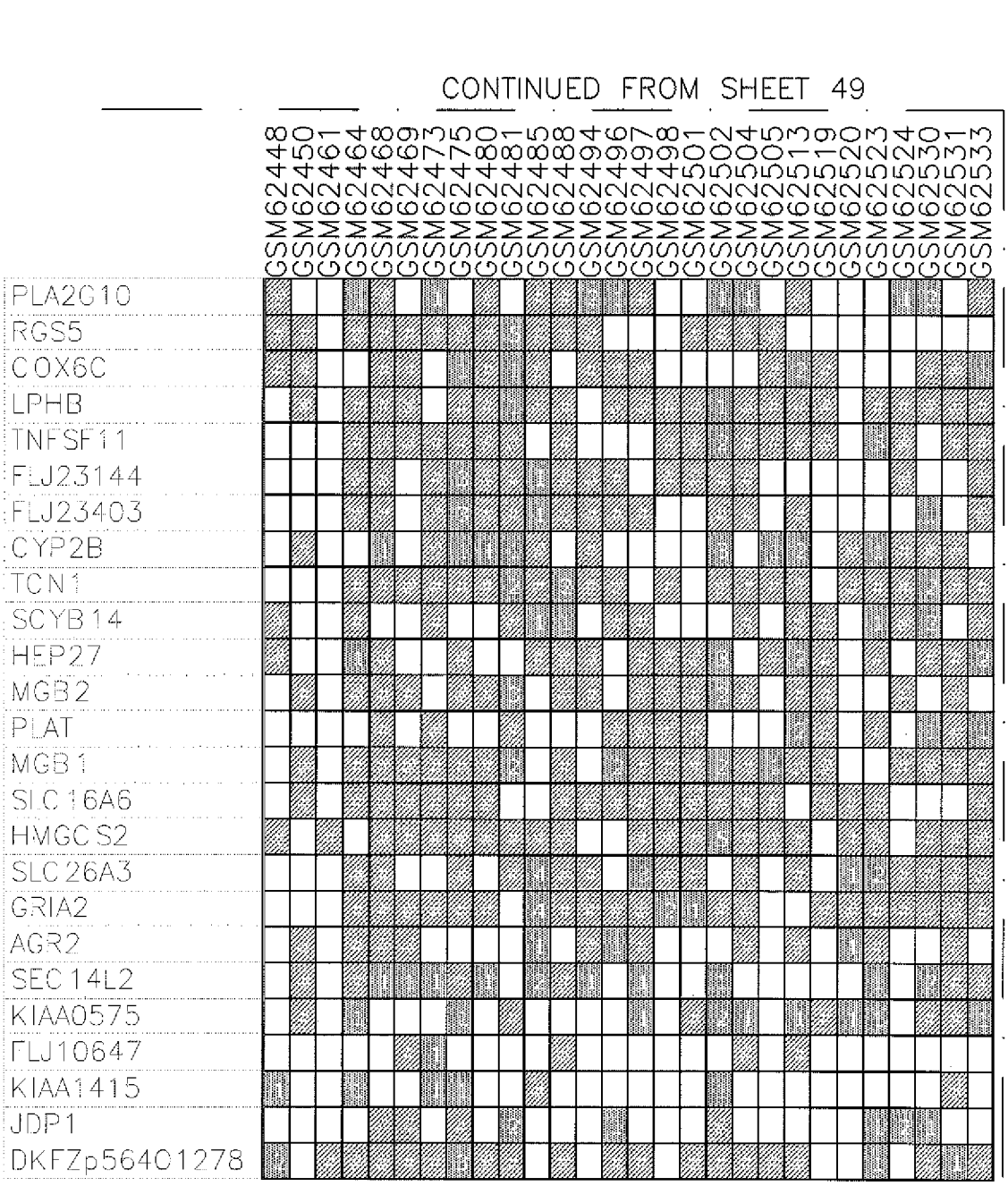


FIG. 11

BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+
ERGO, PCA NON ERGO

TOP 50
UNDEREXPRESSED
BASAL-LIKE GENES

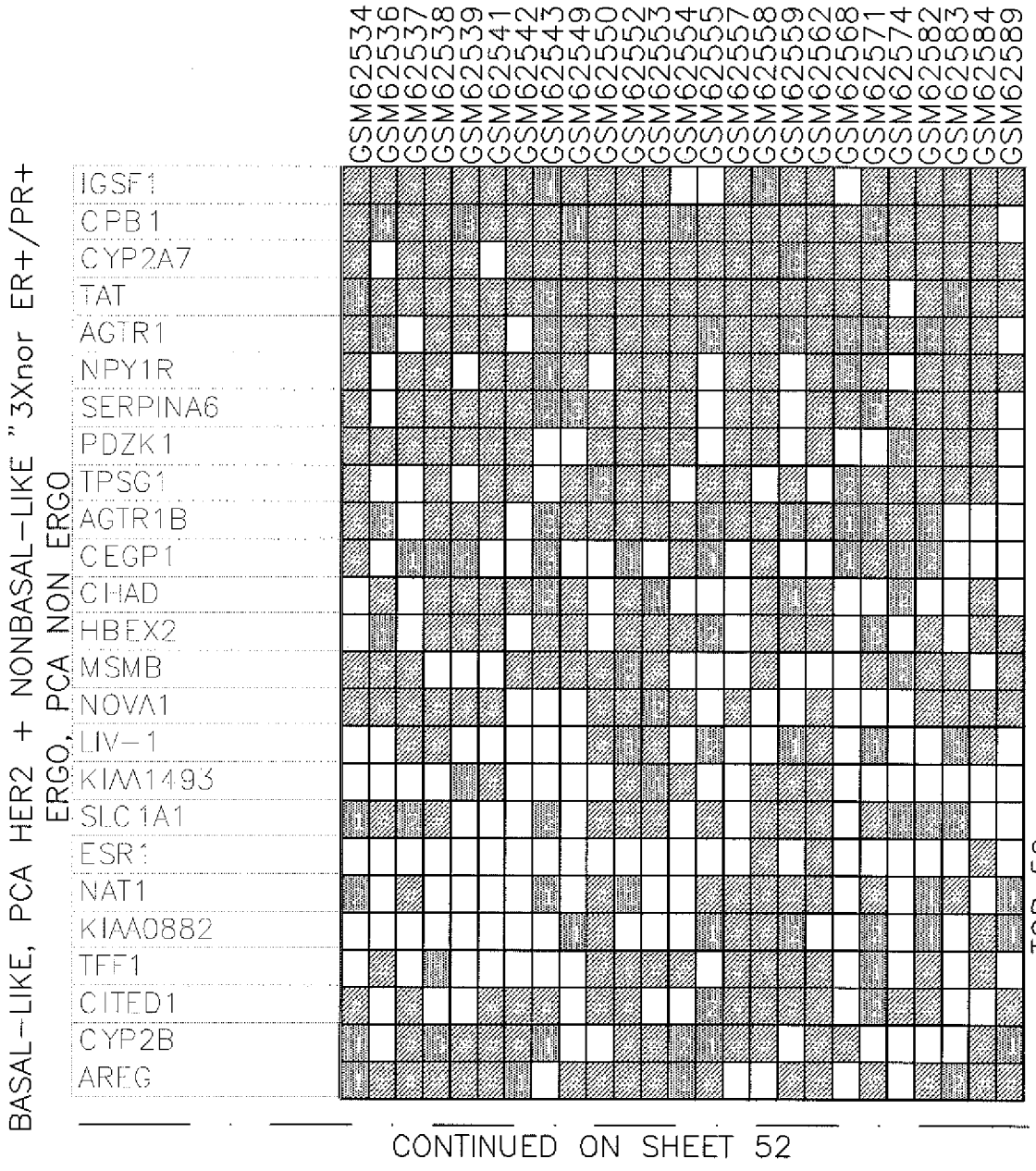

GSM62534
GSM62536
GSM62537
GSM62538
GSM62539
GSM62541
GSM62542
GSM62543
GSM62549
GSM62550
GSM62552
GSM62553
GSM62554
GSM62555
GSM62557
GSM62558
GSM62559
GSM62562
GSM62568
GSM62571
GSM62574
GSM62582
GSM62583
GSM62584
GSM62589
IGSF1
CPB1
CYP2A7
TAT
AGTR1
NPY1R
SERPINA6
PDZK1
TPSG1
AGTR1B
CEGP1
CHAD
HBEX2
MSMB
NOVA1
LIV-1
KIAA1493
SLC1A1
ESR1
NAT1
KIAA0882
TFF1
CITED1
CYP2B
AREG
BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+ ERGO, PCA NON ERGO
TOP 50 UNDEREXPRESSED BASAL-LIKE GENES
CONTINUED ON SHEET 52

FIG. 11

52

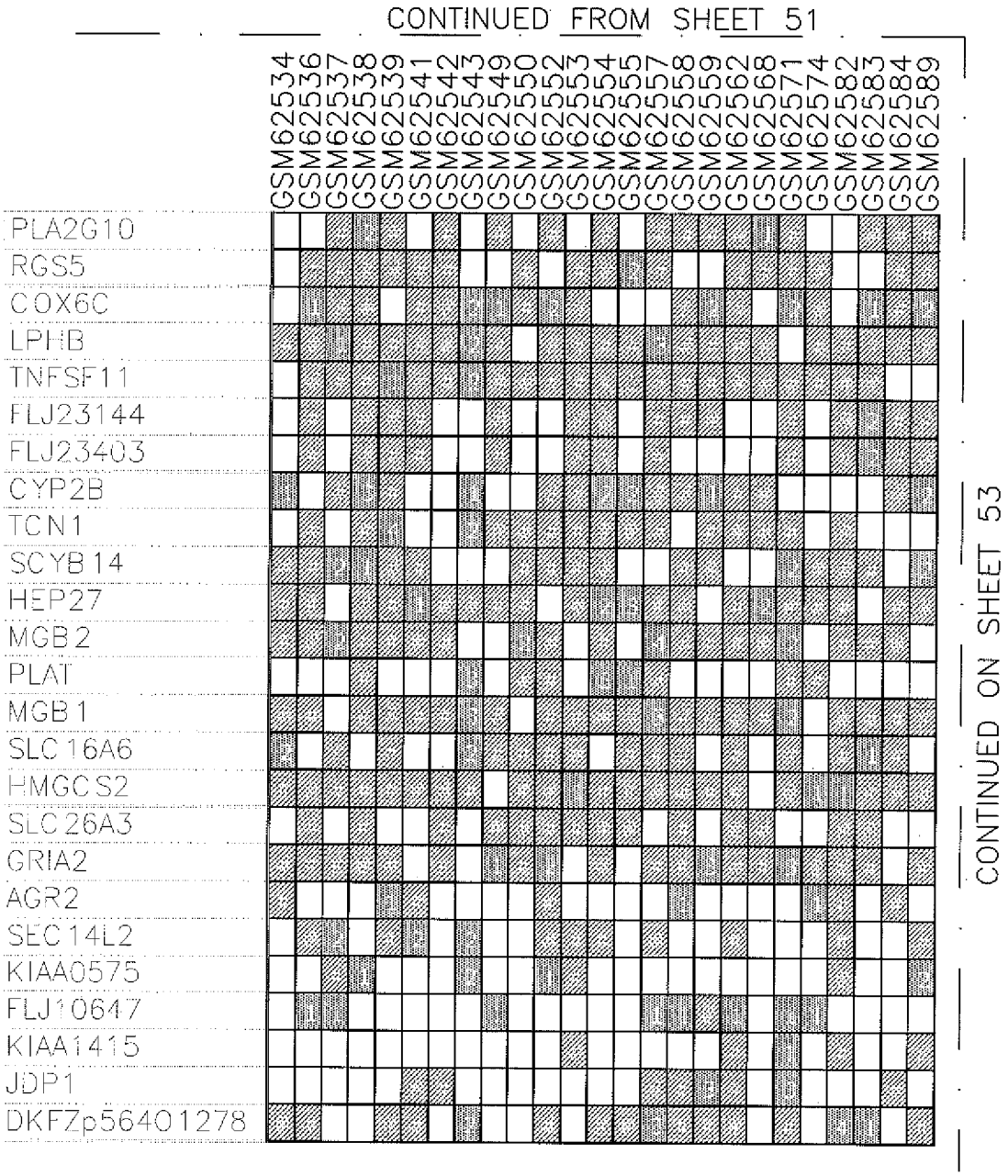


FIG. 11

BASAL–LIKE, PCA HER2 + NONBASAL–LIKE "3Xnor ER+/PR+ ERGO, PCA NON ERGO

TOP 50
UNDEREXPRESSED
BASAL–LIKE GENES

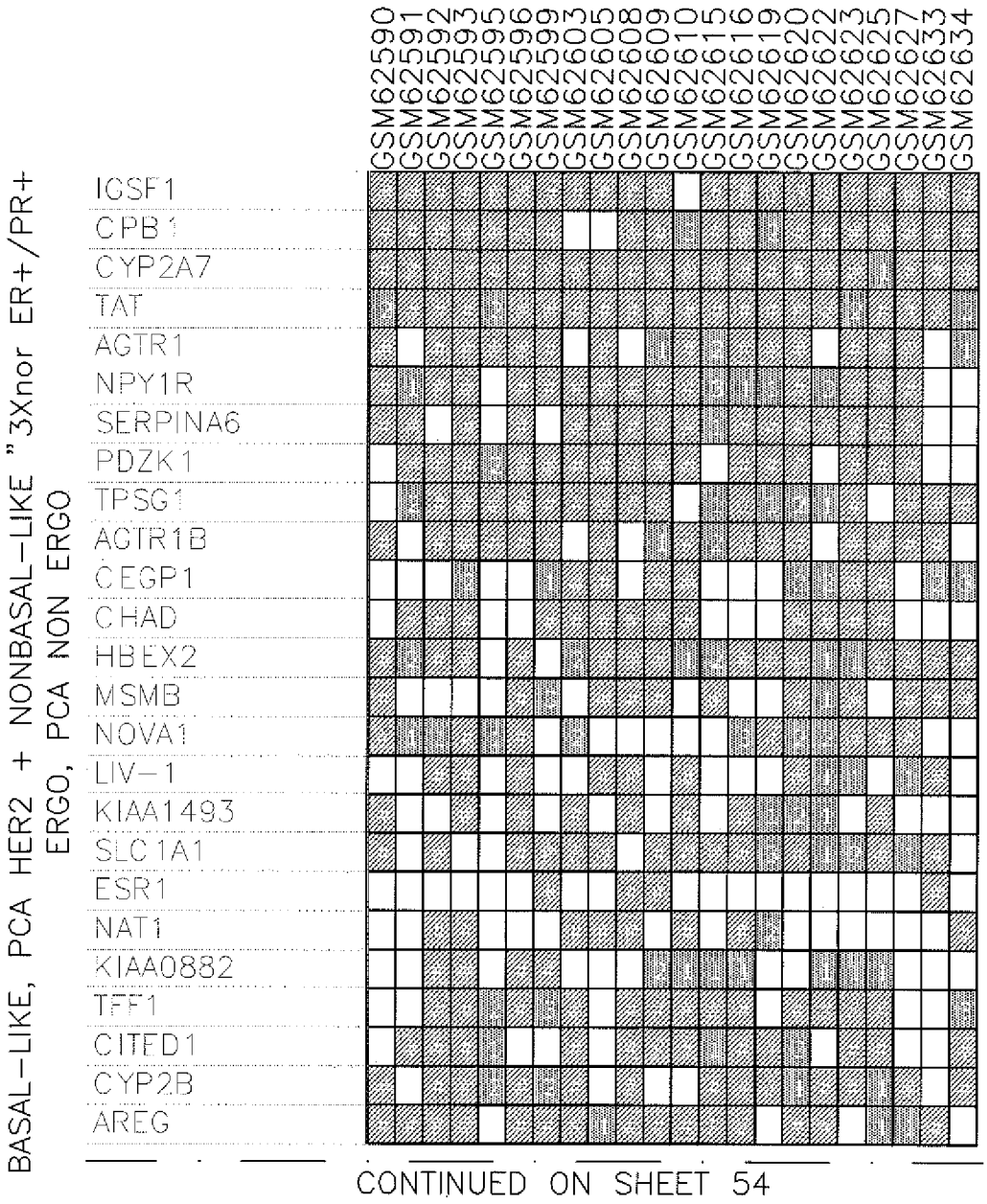

GSM625590
GSM625591
GSM625592
GSM625593
GSM625595
GSM625596
GSM625599
GSM626003
GSM626005
GSM626008
GSM626009
GSM626610
GSM626615
GSM626616
GSM626619
GSM626620
GSM626622
GSM626623
GSM626625
GSM626627
GSM626633
GSM626634
IGSF1
CPB1
CYP2A7
TAT
AGTR1
NPY1R
SERPINA6
PDZK1
TPSG1
ACTR1B
CEGP1
CHAD
HBEX2
MSMB
NOVA1
LIV-1
KIAA1493
SLC1A1
ESR1
NAT1
KIAA0882
TFF1
CITED1
CYP2B
AREG
BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+ ERGO, PCA NON ERGO
TOP 50 UNDEREXPRESSED BASAL-LIKE GENES
CONTINUED ON SHEET 54

FIG. 11

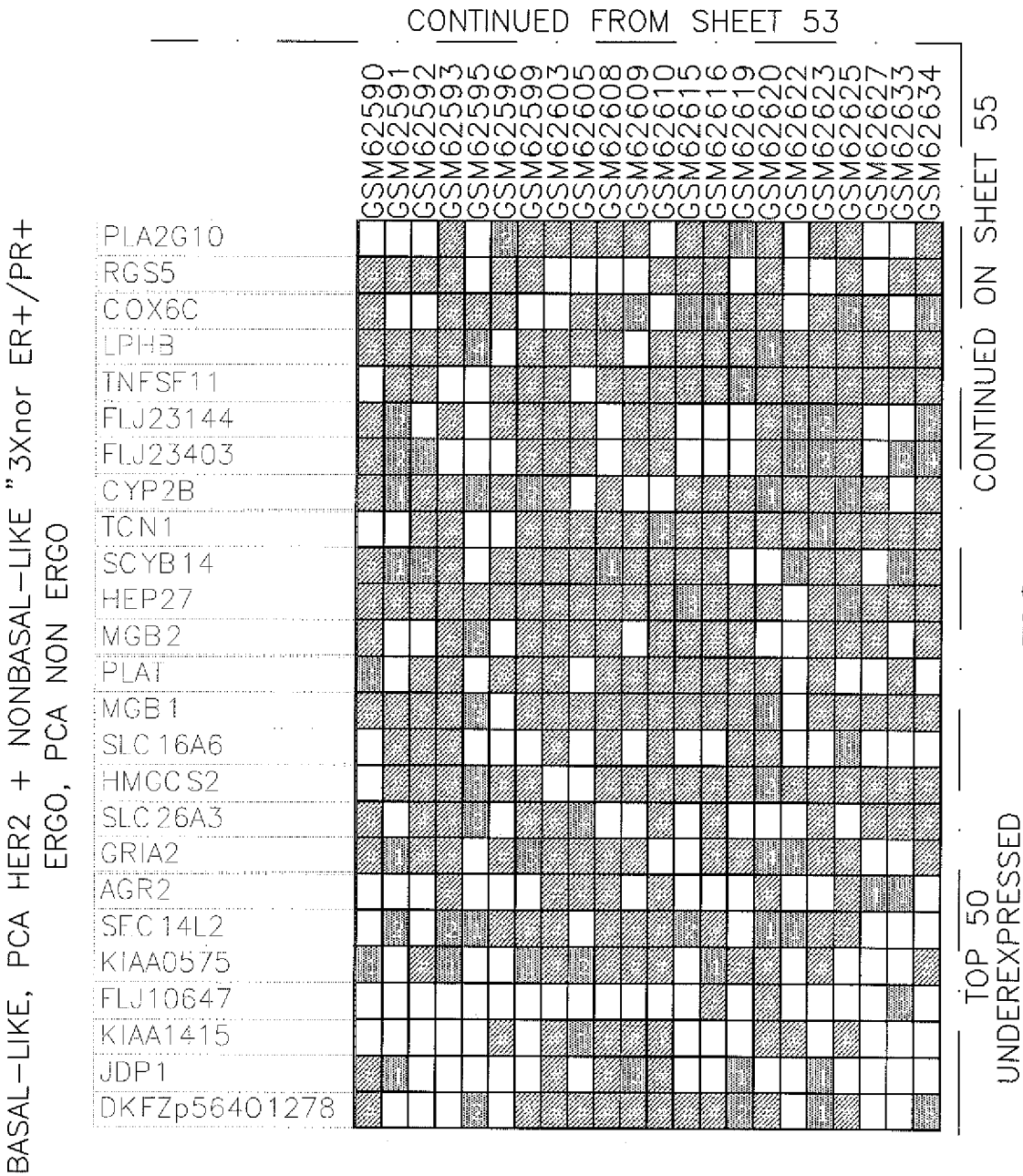
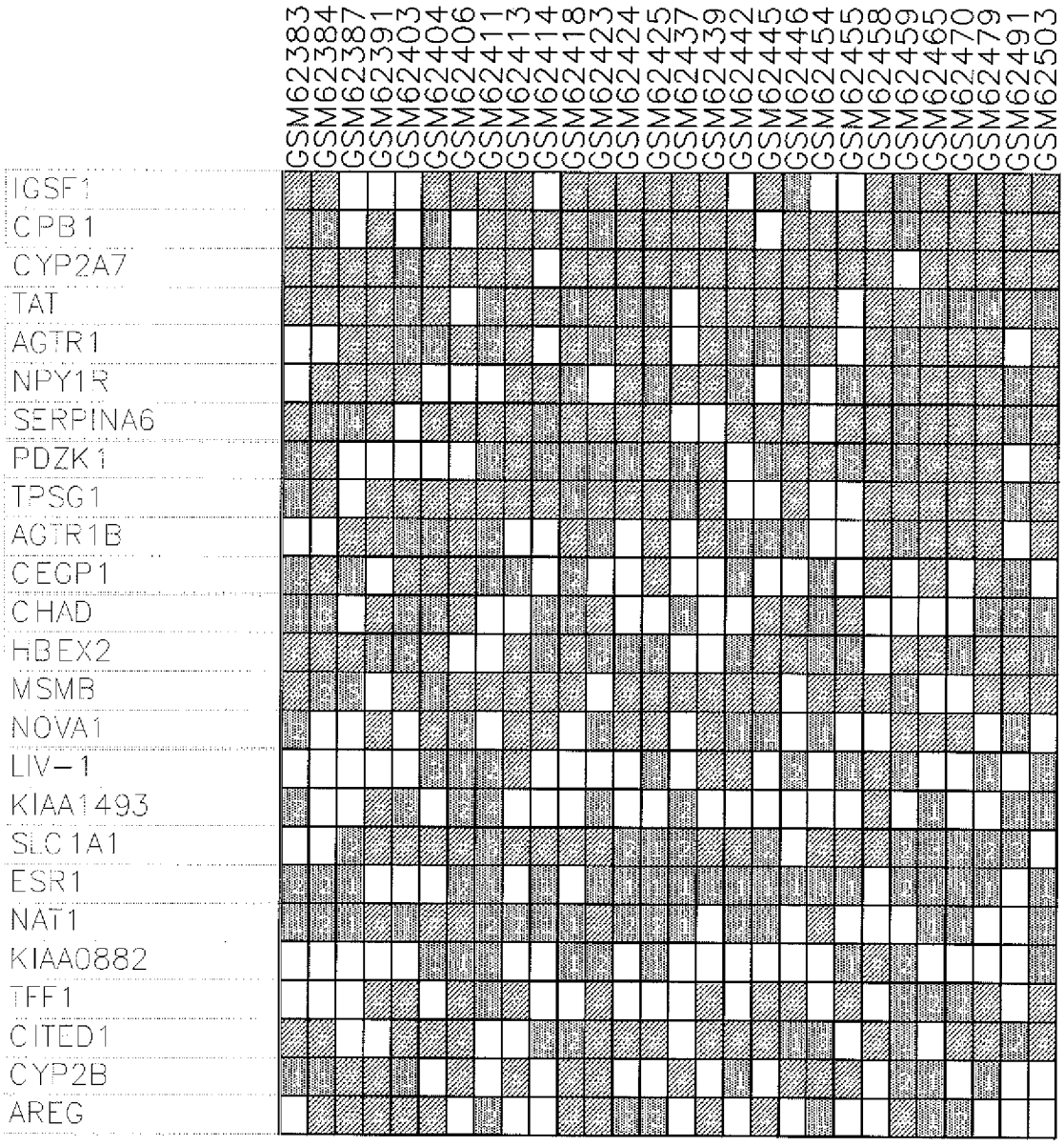

CONTINUED FROM SHEET 53
GSM62590
GSM62591
GSM62592
GSM62593
GSM62595
GSM62596
GSM62599
GSM62603
GSM62605
GSM62608
GSM62609
GSM62610
GSM62615
GSM62616
GSM62619
GSM62620
GSM62622
GSM62623
GSM62625
GSM62627
GSM62633
GSM62634
PLA2G10
RGS5
COX6C
LPHB
TNFSF11
FLJ23144
FLJ23403
CYP2B
TCN1
SCYB14
HEP27
MGB2
PLAT
MGB1
SLC16A6
HMGCS2
SLC26A3
GRIA2
AGR2
SFC14L2
KIAA0575
FLJ10647
KIAA1415
JDP1
DKFZp56401278
CONTINUED ON SHEET 55
TOP 50 UNDEREXPRESSED BASAL-LIKE GENES
BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+ ERGO, PCA NON ERGO

FIG. 11

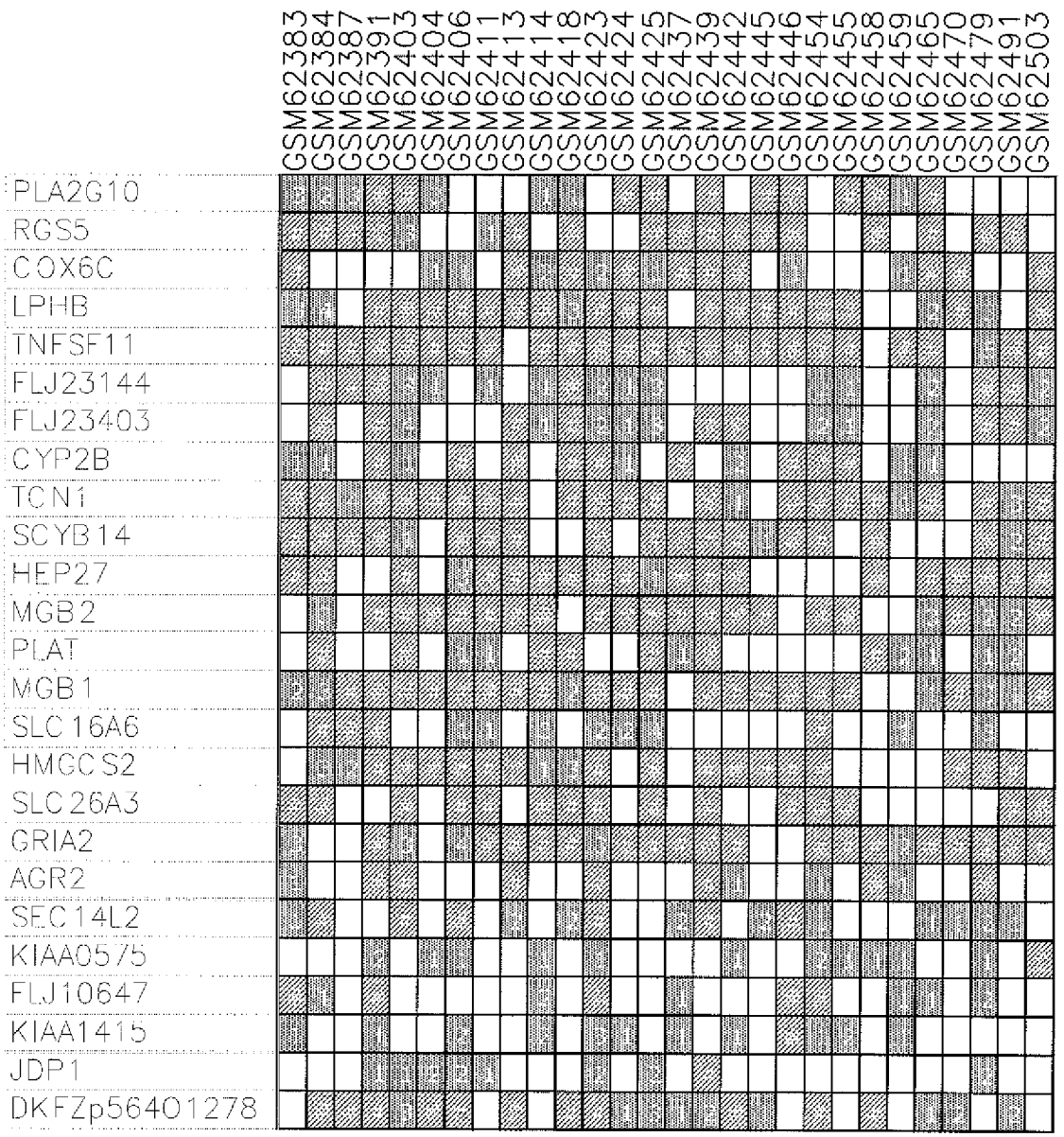


CONTINUED ON SHEET 56

FIG. 11

BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+
ERGO, PCA NON ERGO
TOP 50
UNDEREXPRESSED
BASAL-LIKE GENES

CONTINUED FROM SHEET 55



CONTINUED ON SHEET 57

FIG. 11

BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+
ERGO, PCA NON ERGO
TOP 50
UNDEREXPRESSED
BASAL-LIKE GENES

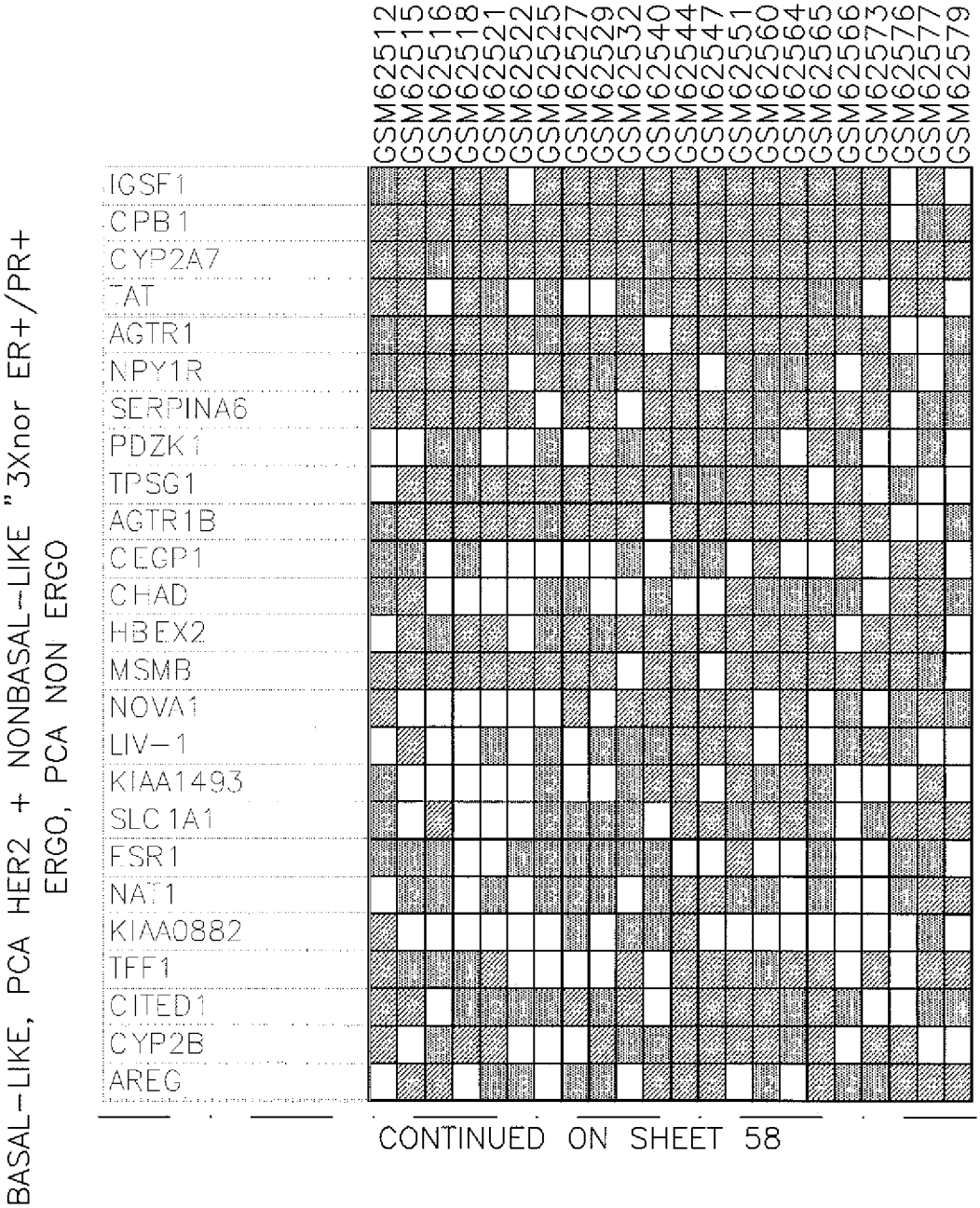
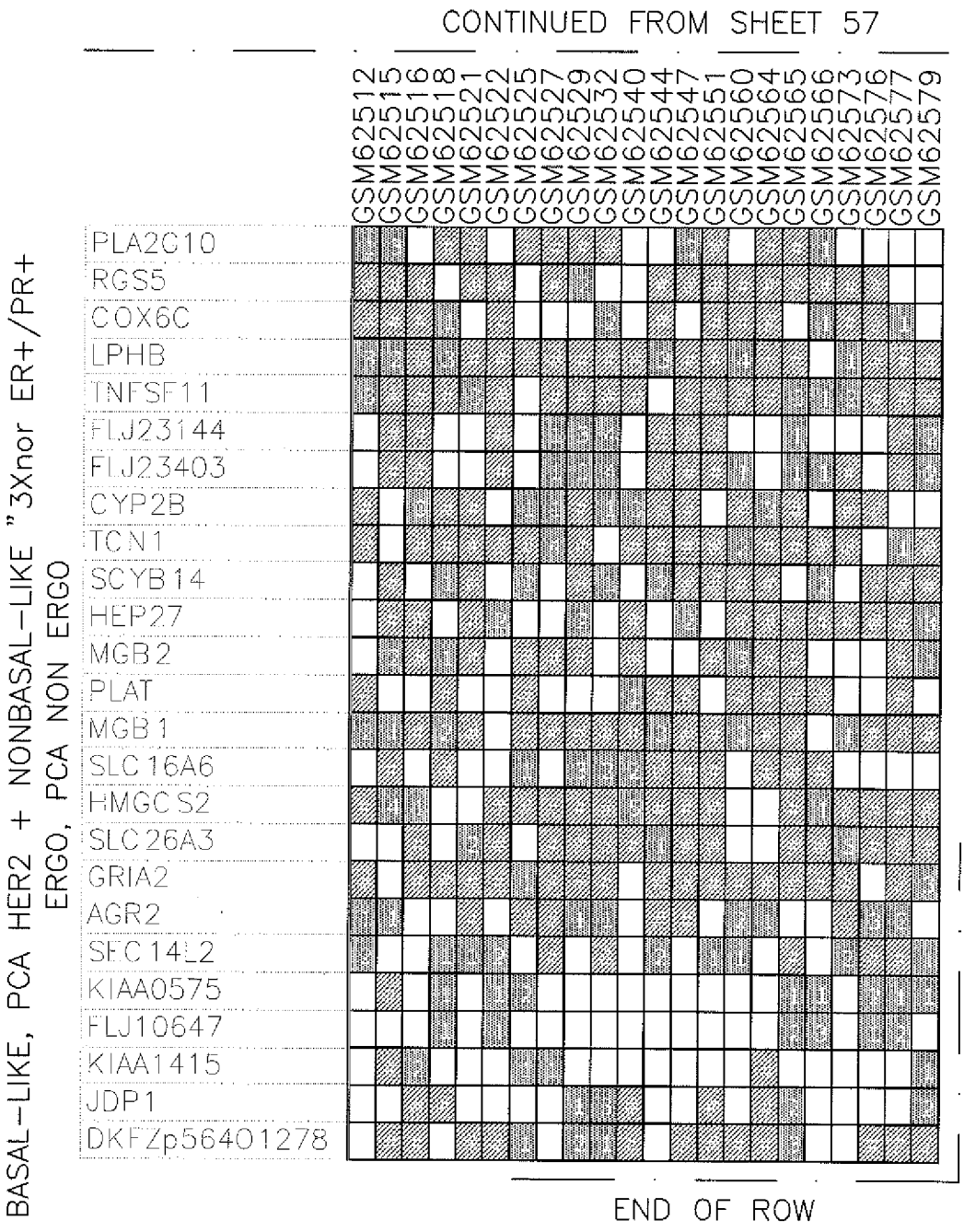

BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+
ERGO, PCA NON ERGO
GSM62512
GSM62515
GSM62516
GSM62518
GSM62521
GSM62522
GSM62525
GSM62527
GSM62529
GSM62532
GSM62540
GSM62544
GSM62547
GSM62551
GSM62560
GSM62564
GSM62565
GSM62566
GSM62573
GSM62576
GSM62577
GSM62579
IGSF1
CPB1
CYP2A7
TAT
AGTR1
NPY1R
SERPINA6
PDZK1
TPSG1
AGTR1B
CEGP1
CHAD
HBEX2
MSMB
NOVA1
LIV-1
KIAA1493
SLC1A1
ESR1
NAT1
KIAA0882
TFF1
CITED1
CYP2B
AREG
TOP 50
UNDEREXPRESSED
BASAL-LIKE GENES
CONTINUED ON SHEET 58

FIG. 11


CONTINUED FROM SHEET 57
GSM625512
GSM625515
GSM625516
GSM625518
GSM625521
GSM625522
GSM625525
GSM625527
GSM625529
GSM625532
GSM625540
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GSM625579
PLA2C10
RGS5
COX6C
LPHB
TNFSF11
FLJ23144
FLJ23403
CYP2B
TCN1
SCYB14
HEP27
MGB2
PLAT
MGB1
SLC16A6
HMGCS2
SLC26A3
GRIA2
AGR2
SEC14L2
KIAA0575
FLJ10647
KIAA1415
JDP1
DKFZp564O1278
BASAL-LIKE, PCA HER2 + NONBASAL-LIKE "3Xnor ER+/PR+ ERGO, PCA NON ERGO
TOP 50 UNDEREXPRESSED BASAL-LIKE GENES
END OF ROW

FIG. 11

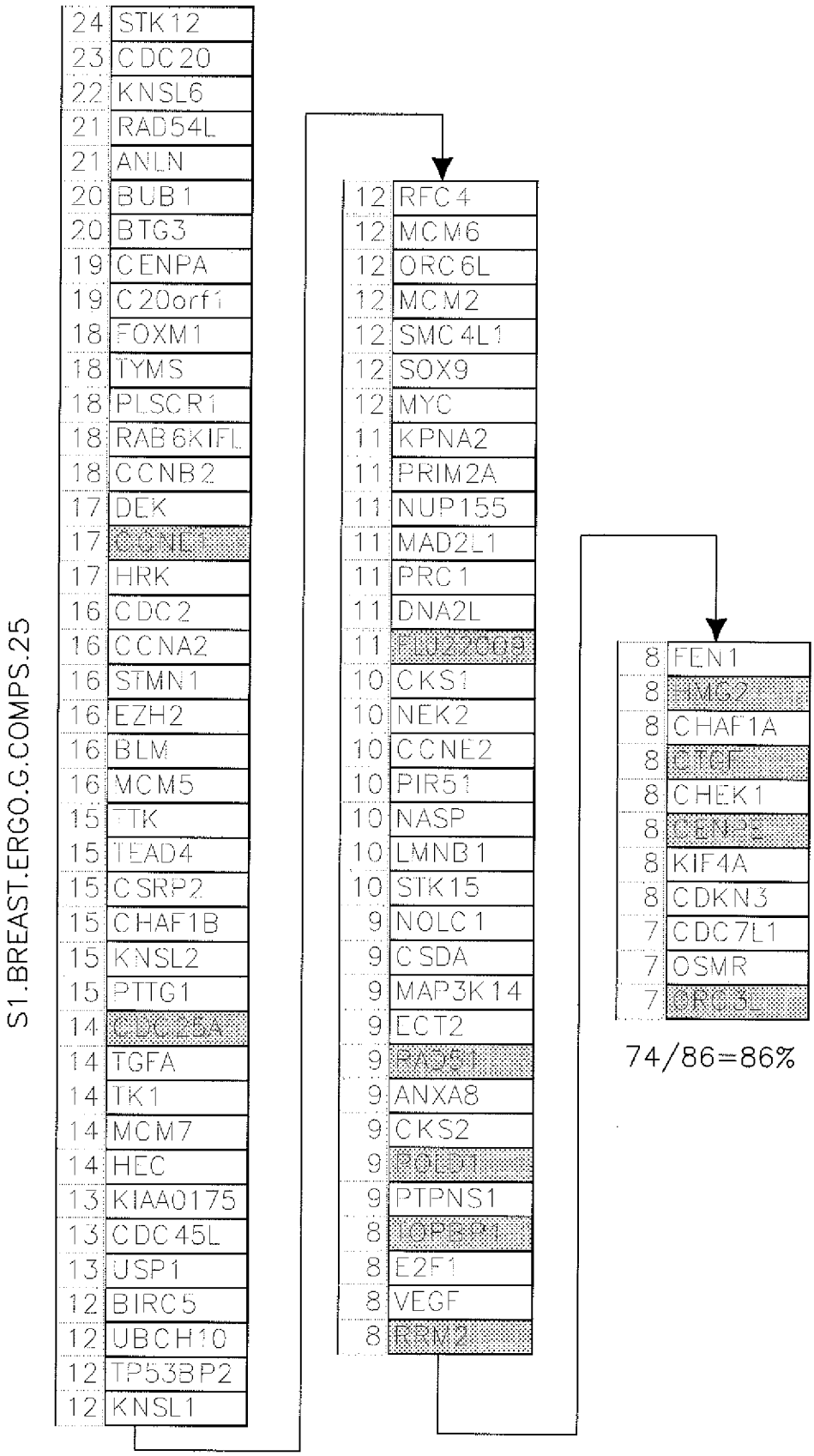

S1.BREAST.ERGO.G.COMPS.25
24 STK12
23 CDC20
22 KNSL6
21 RAD54L
21 ANLN
20 BUB1
20 BTG3
19 CENPA
19 C20orf1
18 FOXM1
18 TYMS
18 PLSCR1
18 RAB6KIFL
18 CCNB2
17 DEK
17 [illegible]
17 HRK
16 CDC2
16 CCNA2
16 STMN1
16 EZH2
16 BLM
16 MCM5
15 TTK
15 TEAD4
15 CSRP2
15 CHAF1B
15 KNSL2
15 PTTG1
14 [illegible]
14 TGFA
14 TK1
14 MCM7
14 HEC
13 KIAA0175
13 CDC45L
13 USP1
12 BIRC5
12 UBCH10
12 TP53BP2
12 KNSL1
12 RFC4
12 MCM6
12 ORC6L
12 MCM2
12 SMC4L1
12 SOX9
12 MYC
11 KPNA2
11 PRIM2A
11 NUP155
11 MAD2L1
11 PRC1
11 DNA2L
11 [illegible]
10 CKS1
10 NEK2
10 CCNE2
10 PIR51
10 NASP
10 LMNB1
10 STK15
9 NOLC1
9 CSDA
9 MAP3K14
9 ECT2
9 [illegible]
9 ANXA8
9 CKS2
9 [illegible]
9 PTPNS1
8 [illegible]
8 E2F1
8 VEGF
8 [illegible]
8 FEN1
8 [illegible]
8 CHAF1A
8 [illegible]
8 CHEK1
8 [illegible]
8 KIF4A
8 CDKN3
7 CDC7L1
7 OSMR
7 [illegible]
74/86=86%

FIG. 12

S2.ERGO.COMPS.25
CENPA 24
BUB1 23
KNSL2 22
KNSL6 21
STK12 21
CDC20 20
CCNB2 20
FOXM1 19
MYC 19
UBCH10 18
KIAA0175 18
EZH2 18
CCNA2 18
HRK 18
CDC45L 17
RAD54L 17
RAB6KIFL 17
HEC 16
BLM 16
BIRC5 16
MAD2L1 16
MCM5 16
CSRP2 16
STK15 15
[illegible] 15
[illegible] 15
KPNA2 15
MCM2 15
LAP18/STMN1 15
TTK 14
C20ORF1 14
[illegible] 14
CHEK1 14
TP53BP2 14
MCM6 13
TEAD4 13
SOX9 13
PRC1 12
MCM7 12
CKS1 12
[illegible] 12
LMNB1 12
NASP 12
PRIM2A 12
CHAF1B 12
PLSCR1 12
VEGF 12
CSDA 12
PTTG1 11
E2F1 11
FEN1 11
TK1 11
RFC4 11
BTG3 11
PTPNS1 11
ORC6L 10
CHAF1A 10
CDC2 10
[illegible] 10
ANLN 10
ANXA8 10
TGFA 10
[illegible] 9
NEK2 9
ECT2 9
KNSL1 9
CAP-C/SMC4L1 9
[illegible] 9
[illegible] 9
P130/NOLC1 9
DEK 9
[illegible] 8
[illegible] 8
CDC7L1 8
DNA2L 8
[illegible] 8
DNMT1 8
[illegible] 8
MCM4 8
[illegible] 8
[illegible] 8
USP1 8
MAP3K14 8
[illegible] 7
[illegible] 7
TYMS 7
PIR51 7
[illegible] 7
[illegible] 7
[illegible] 7
[illegible] 7
CCNE2 6
KIF4A 6
[illegible] 6
[illegible] 6
NUP155 6
[illegible] 6
[illegible] 6
[illegible] 6
OSMR 6
[illegible] 6

FIG. 12 2

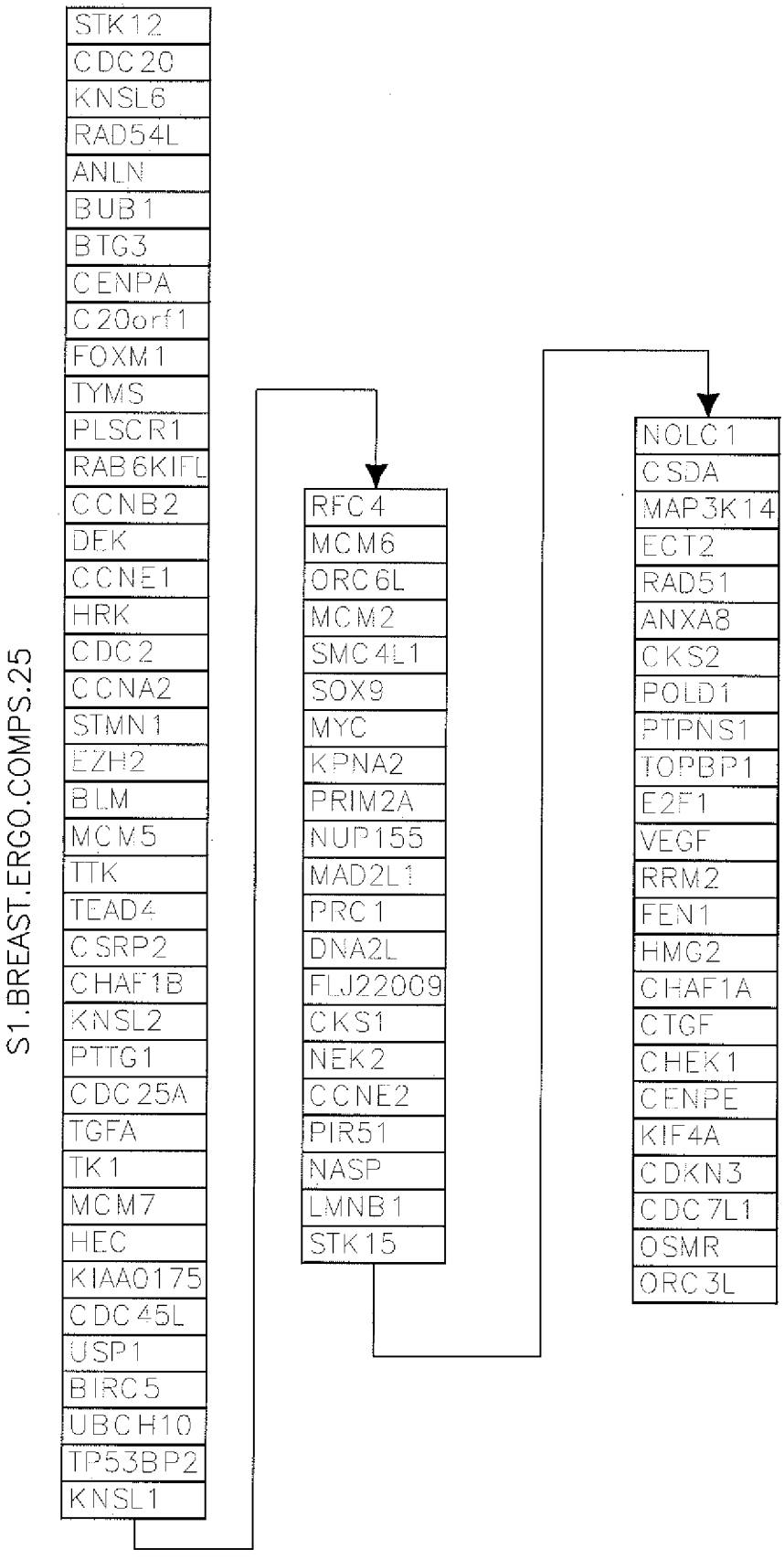

S1.BREAST.ERGO.COMPS.25
STK12
CDC20
KNSL6
RAD54L
ANLN
BUB1
BTG3
CENPA
C20orf1
FOXM1
TYMS
PLSCR1
RAB6KIFL
CCNB2
DEK
CCNE1
HRK
CDC2
CCNA2
STMN1
EZH2
BLM
MCM5
TTK
TEAD4
CSRP2
CHAF1B
KNSL2
PTTG1
CDC25A
TGFA
TK1
MCM7
HEC
KIAA0175
CDC45L
USP1
BIRC5
UBCH10
TP53BP2
KNSL1
RFC4
MCM6
ORC6L
MCM2
SMC4L1
SOX9
MYC
KPNA2
PRIM2A
NUP155
MAD2L1
PRC1
DNA2L
FLJ22009
CKS1
NEK2
CCNE2
PIR51
NASP
LMNB1
STK15
NOLC1
CSDA
MAP3K14
ECT2
RAD51
ANXA8
CKS2
POLD1
PTPNS1
TOPBP1
E2F1
VEGF
RRM2
FEN1
HMG2
CHAF1A
CTGF
CHEK1
CENPE
KIF4A
CDKN3
CDC7L1
OSMR
ORC3L

FIG. 13

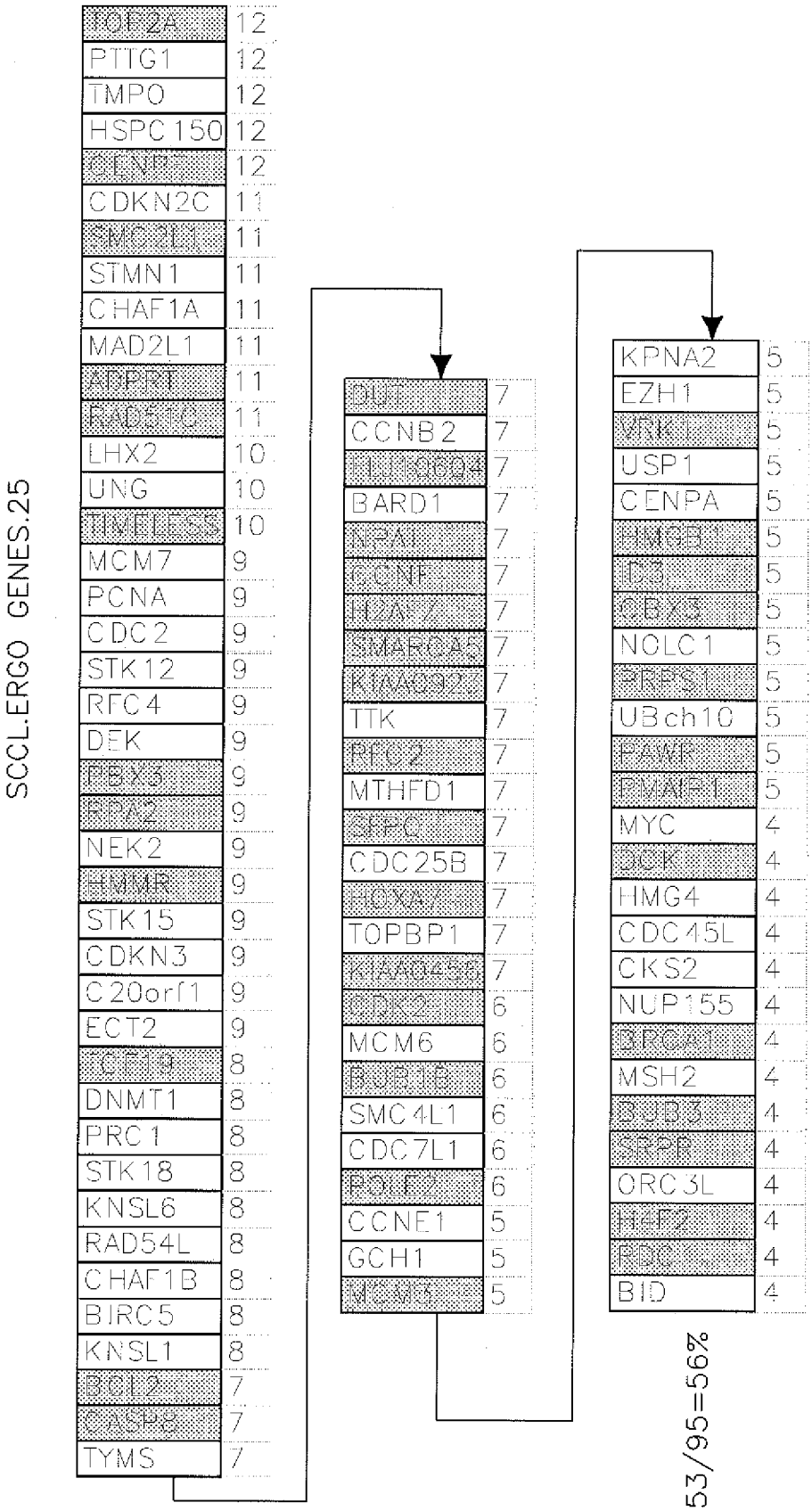

SCCL.ERGO GENES.25
TOP2A 12
PTTG1 12
TMPO 12
HSPC150 12
CENPF 12
CDKN2C 11
SMC2L1 11
STMN1 11
CHAF1A 11
MAD2L1 11
ADPRT 11
RAD51C 11
LHX2 10
UNG 10
TIMELESS 10
MCM7 9
PCNA 9
CDC2 9
STK12 9
RFC4 9
DEK 9
PBX3 9
RPA2 9
NEK2 9
HMMR 9
STK15 9
CDKN3 9
C20orf1 9
ECT2 9
CCT4 8
DNMT1 8
PRC1 8
STK18 8
KNSL6 8
RAD54L 8
CHAF1B 8
BIRC5 8
KNSL1 8
BCL2 7
CASP8 7
TYMS 7
DUT 7
CCNB2 7
FLJ39080 7
BARD1 7
NPAT 7
CCNF 7
HDAC7 7
SMARCA5 7
KIAA0922 7
TTK 7
RFC2 7
MTHFD1 7
SFPQ 7
CDC25B 7
HOXA7 7
TOPBP1 7
KIAA0458 7
CDK2 6
MCM6 6
BUB1B 6
SMC4L1 6
CDC7L1 6
RCL 6
CCNE1 5
GCH1 5
MCM5 5
KPNA2 5
EZH1 5
VRK1 5
USP1 5
CENPA 5
HMGB1 5
ID3 5
CBX3 5
NOLC1 5
SRPS1 5
UBch10 5
PAWR 5
PMAIP1 5
MYC 4
SCK 4
HMG4 4
CDC45L 4
CKS2 4
NUP155 4
BPGAP1 4
MSH2 4
BUB3 4
SRPR 4
ORC3L 4
HIF2 4
FDC 4
BID 4
53/95=56%

FIG. 13

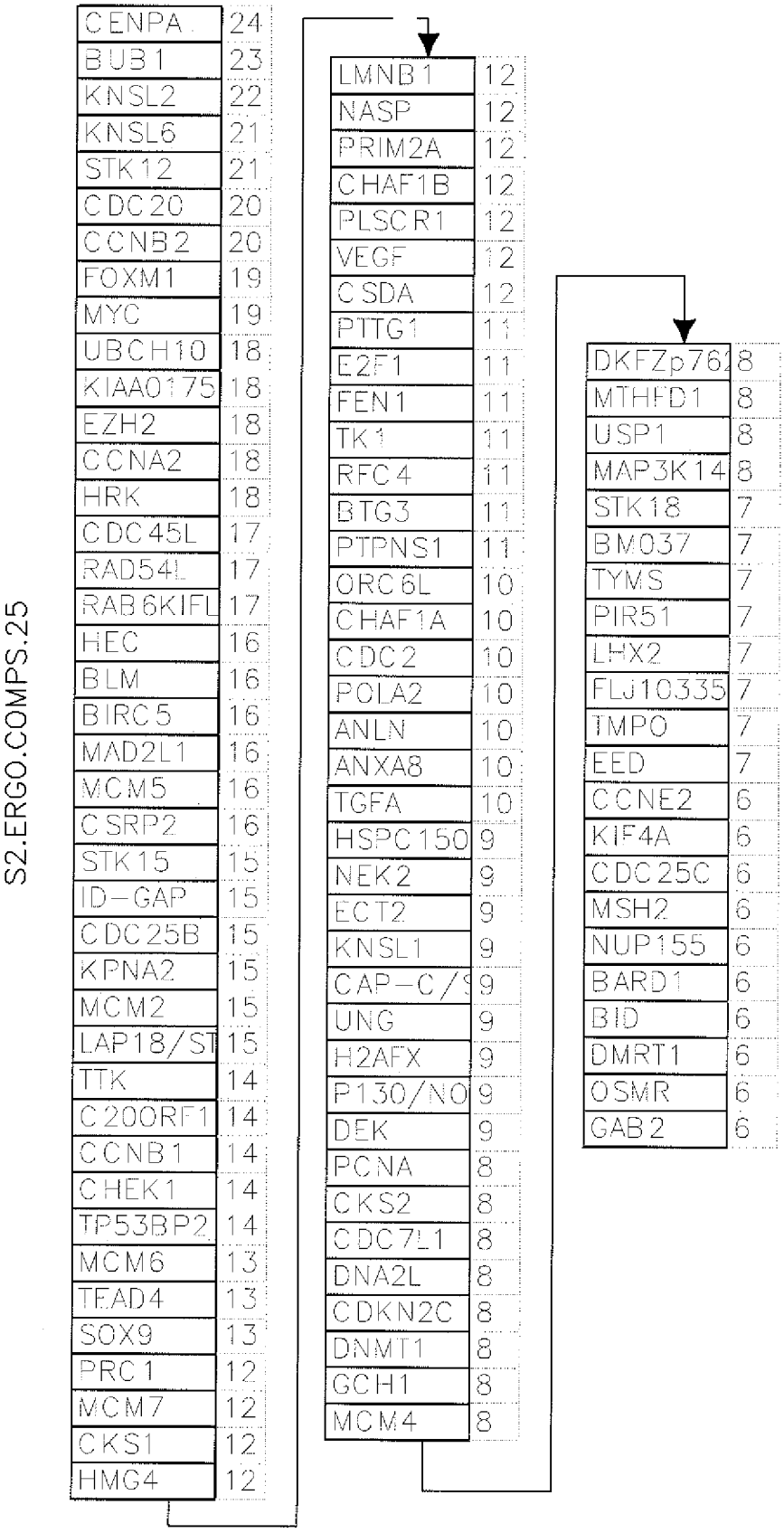

S2.ERGO.COMPS.25
CENPA 24
BUB1 23
KNSL2 22
KNSL6 21
STK12 21
CDC20 20
CCNB2 20
FOXM1 19
MYC 19
UBCH10 18
KIAA0175 18
EZH2 18
CCNA2 18
HRK 18
CDC45L 17
RAD54L 17
RAB6KIFL 17
HEC 16
BLM 16
BIRC5 16
MAD2L1 16
MCM5 16
CSRP2 16
STK15 15
ID-GAP 15
CDC25B 15
KPNA2 15
MCM2 15
LAP18/ST 15
TTK 14
C20ORF1 14
CCNB1 14
CHEK1 14
TP53BP2 14
MCM6 13
TEAD4 13
SOX9 13
PRC1 12
MCM7 12
CKS1 12
HMG4 12
LMNB1 12
NASP 12
PRIM2A 12
CHAF1B 12
PLSCR1 12
VEGF 12
CSDA 12
PTTG1 11
E2F1 11
FEN1 11
TK1 11
RFC4 11
BTG3 11
PTPNS1 11
ORC6L 10
CHAF1A 10
CDC2 10
POLA2 10
ANLN 10
ANXA8 10
TGFA 10
HSPC150 9
NEK2 9
ECT2 9
KNSL1 9
CAP-C/ 9
UNG 9
H2AFX 9
P130/NO 9
DEK 9
PCNA 8
CKS2 8
CDC7L1 8
DNA2L 8
CDKN2C 8
DNMT1 8
GCH1 8
MCM4 8
DKFZp762 8
MTHFD1 8
USP1 8
MAP3K14 8
STK18 7
BM037 7
TYMS 7
PIR51 7
LHX2 7
FLJ10335 7
TMPO 7
EED 7
CCNE2 6
KIF4A 6
CDC25C 6
MSH2 6
NUP155 6
BARD1 6
BID 6
DMRT1 6
OSMR 6
GAB2 6

FIG. 13

3

PCA ERGO TUMOR LARGE CELL
NEUROENDOCRINE TUMOR CARCINOIDS

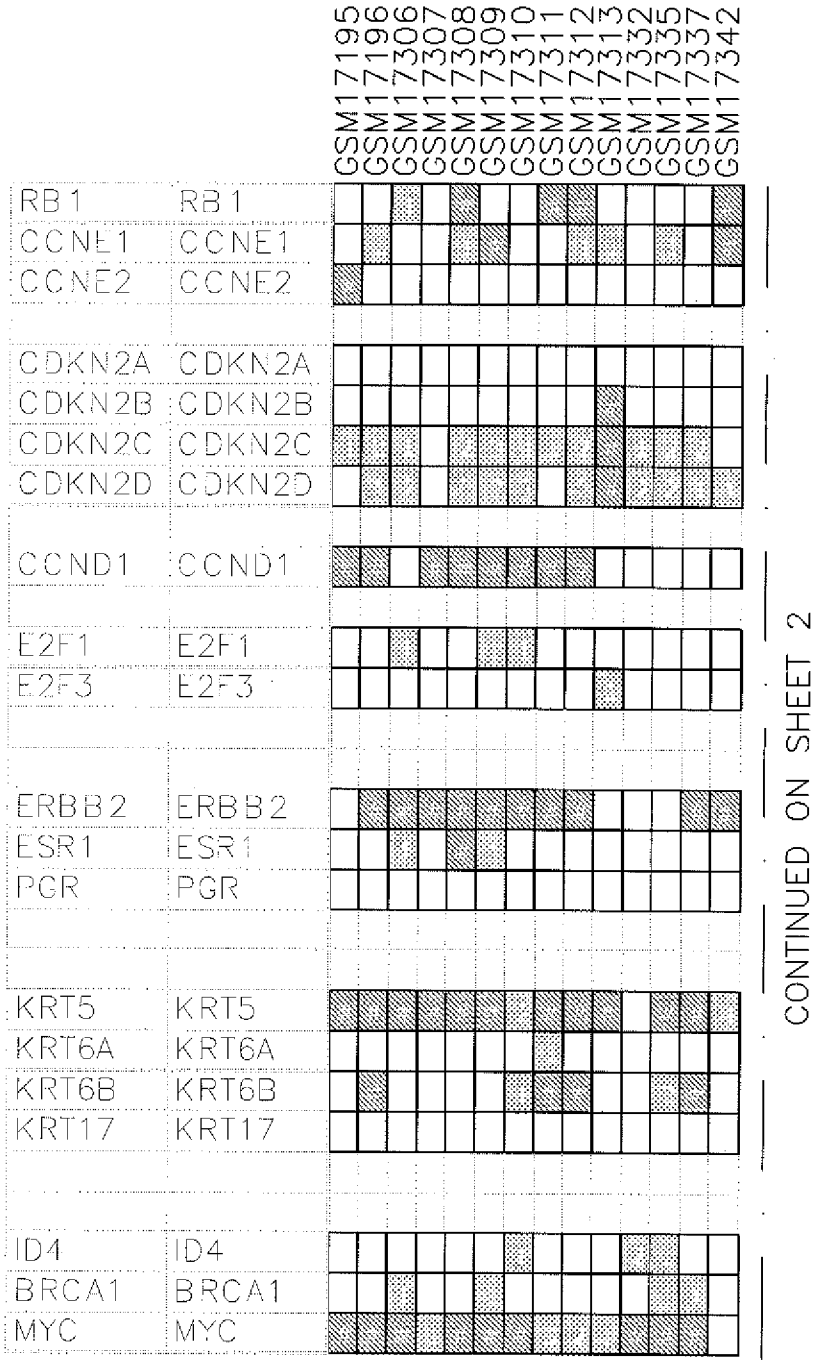


FIG. 14

PCA ERGO TUMOR LARGE CELL
NEUROENDOCRINE TUMOR CARCINOIDS

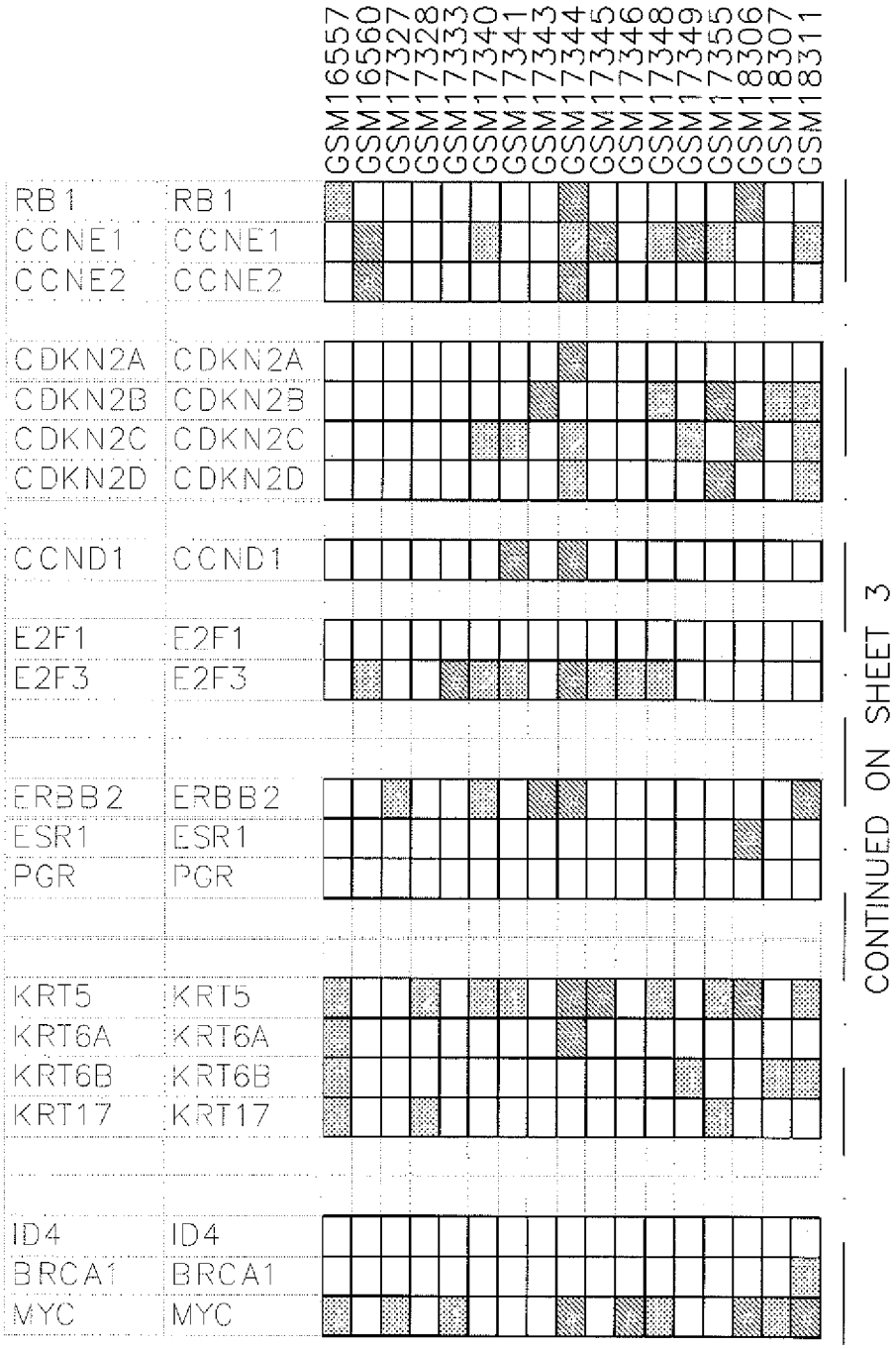


FIG. 14

PCA ERGO TUMOR LARGE CELL
NEUROENDOCRINE TUMOR CARCINOIDS

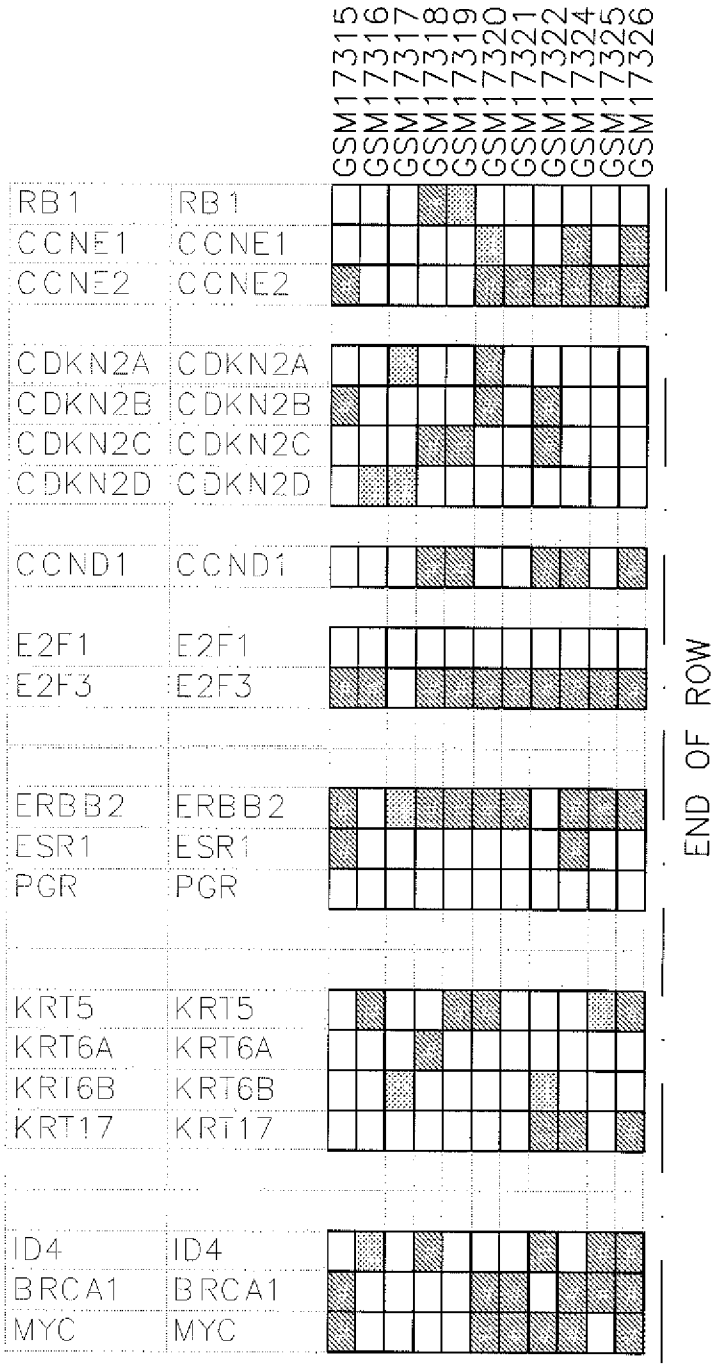
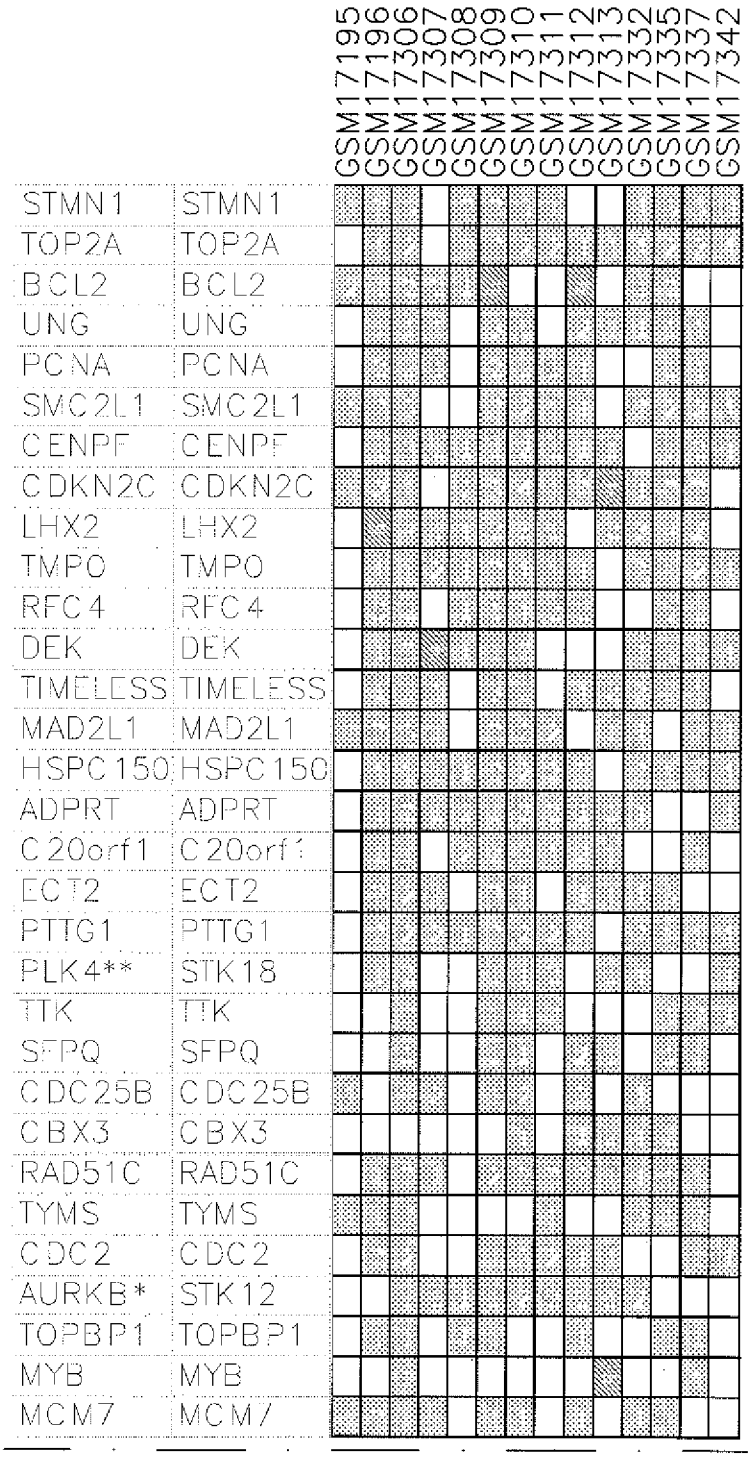


FIG. 14

PCA ERGO TUMOR LARGE CELL
NEUROENDOCRINE TUMOR CARCINOIDS

OVEREXPRESSED E2F-RESPONSIVE GENES

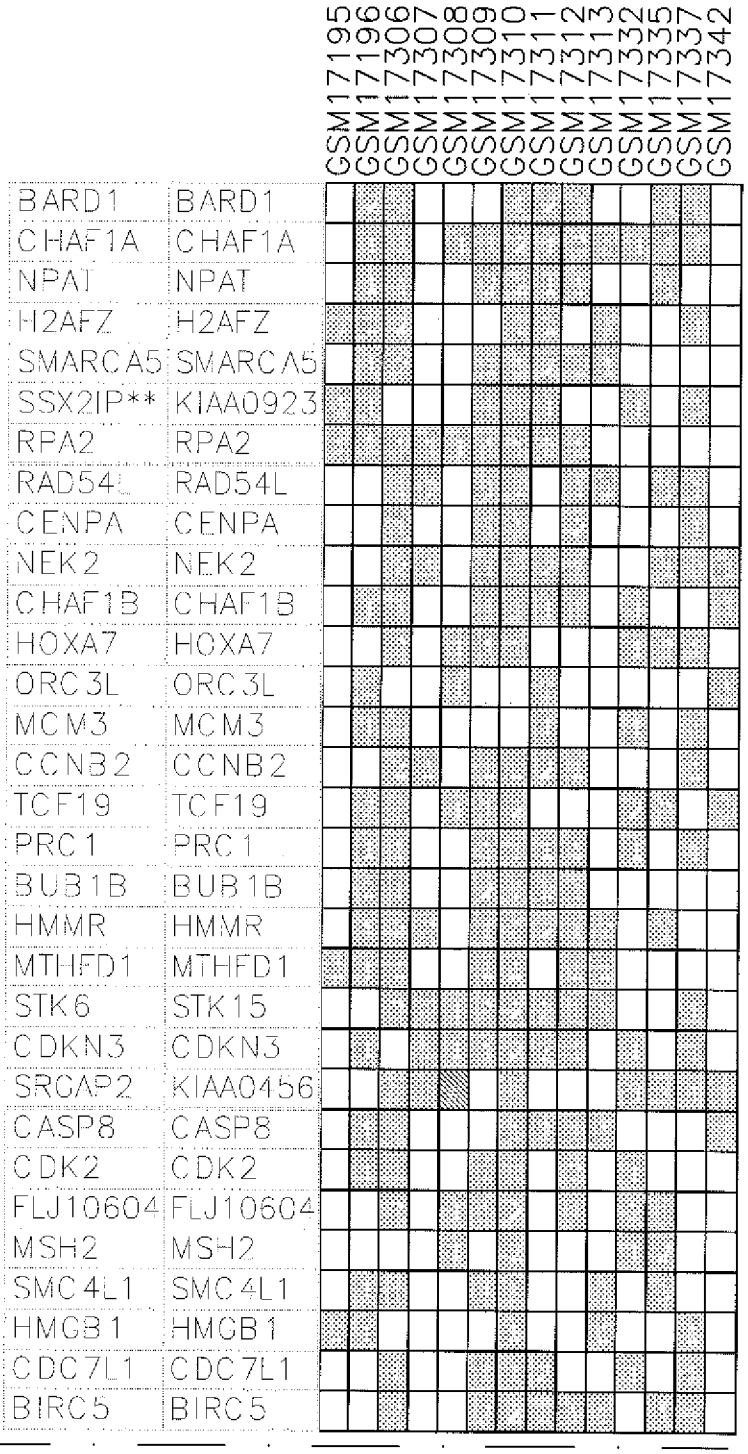


CONTINUED ON SHEET 5

FIG. 14

PCA ERαO TUMOR LARGE CELL
NEUROENDOCRINE TUMOR CARCINOIDS
CONTINUED FROM SHEET 4

OVEREXPRESSED E2F-RESPONSIVE GENES

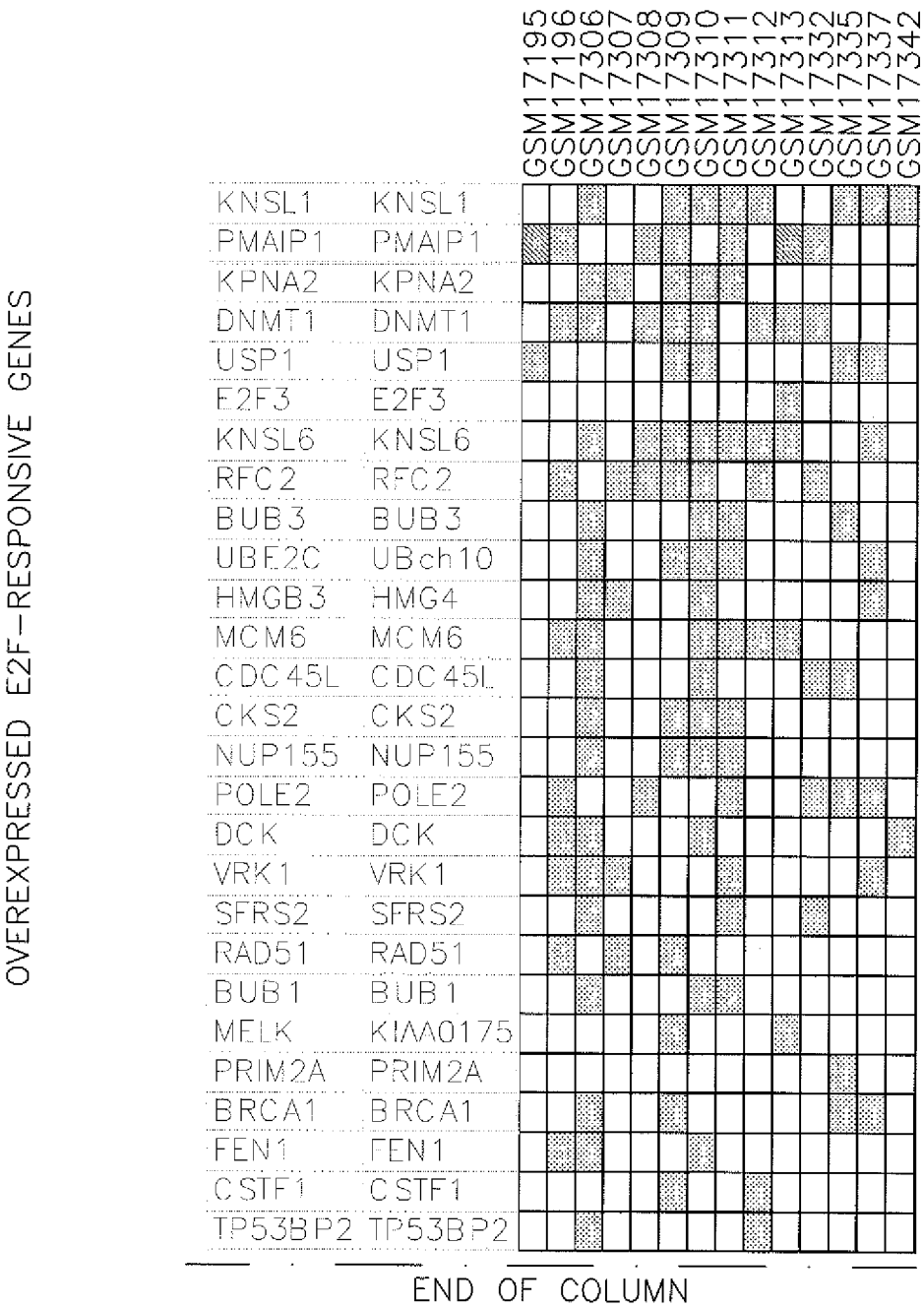


CONTINUED ON SHEET 6

FIG. 14

PCA ERGO TUMOR LARGE CELL
NEUROENDOCRINE TUMOR CARCINOIDS

CONTINUED FROM SHEET 5



END OF COLUMN

FIG. 14

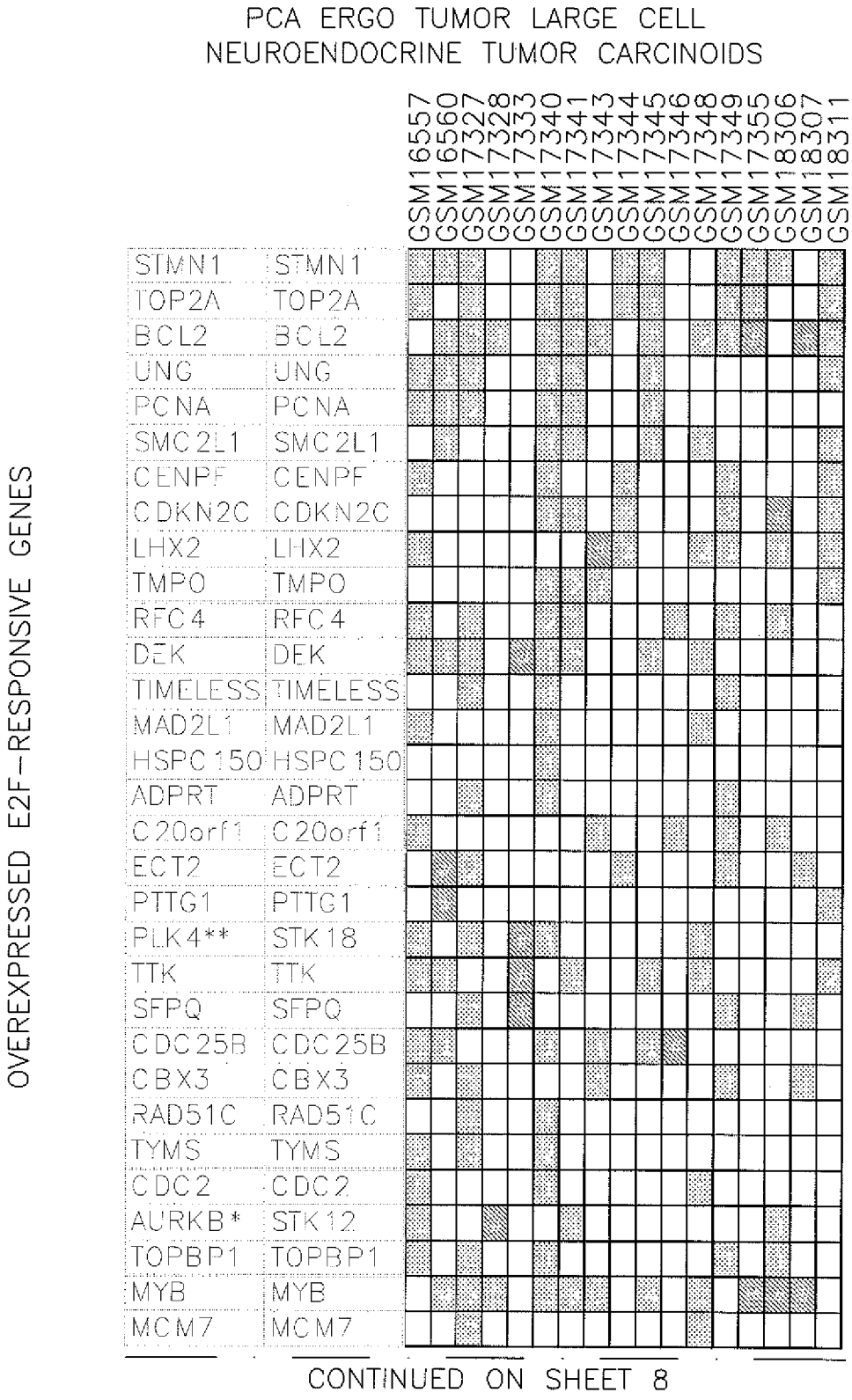
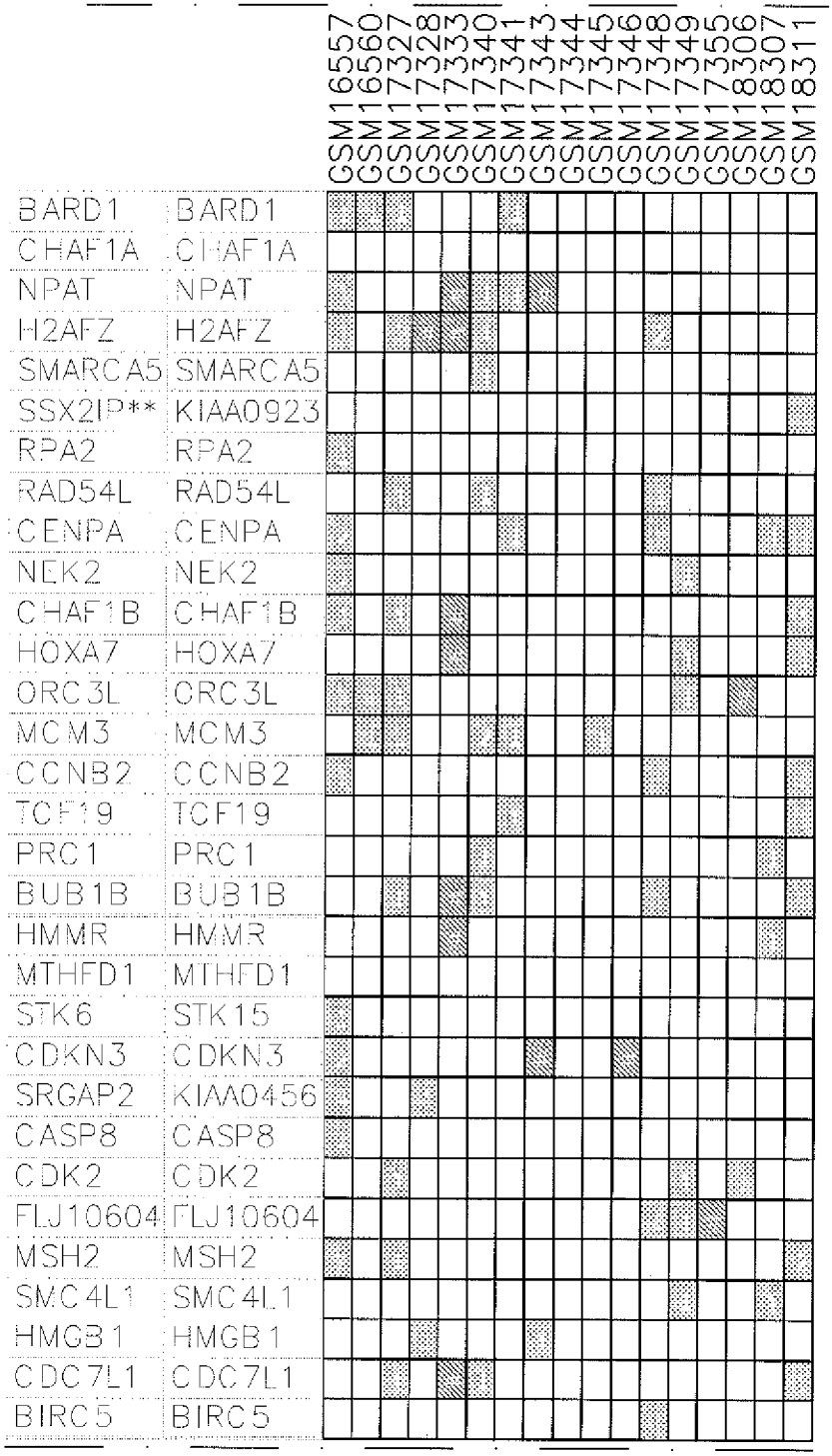

PCA ERGO TUMOR LARGE CELL
NEUROENDOCRINE TUMOR CARCINOIDS
OVEREXPRESSED E2F-RESPONSIVE GENES
GSM16557
GSM16560
GSM17327
GSM17328
GSM17333
GSM17340
GSM17341
GSM17343
GSM17344
GSM17345
GSM17346
GSM17348
GSM17349
GSM17355
GSM18306
GSM18307
GSM18311
STMN1 STMN1
TOP2A TOP2A
BCL2 BCL2
UNG UNG
PCNA PCNA
SMC2L1 SMC2L1
CENPF CENPF
CDKN2C CDKN2C
LHX2 LHX2
TMPO TMPO
RFC4 RFC4
DEK DEK
TIMELESS TIMELESS
MAD2L1 MAD2L1
HSPC150 HSPC150
ADPRT ADPRT
C20orf1 C20orf1
ECT2 ECT2
PTTG1 PTTG1
PLK4** STK18
TTK TTK
SFPQ SFPQ
CDC25B CDC25B
CBX3 CBX3
RAD51C RAD51C
TYMS TYMS
CDC2 CDC2
AURKB* STK12
TOPBP1 TOPBP1
MYB MYB
MCM7 MCM7
CONTINUED ON SHEET 8

FIG. 14

PCA ERGO TUMOR LARGE CELL
NEUROENDOCRINE TUMOR CARCINOIDS
CONTINUED FROM SHEET 7

OVEREXPRESSED E2F-RESPONSIVE GENES



CONTINUED ON SHEET 9

FIG. 14

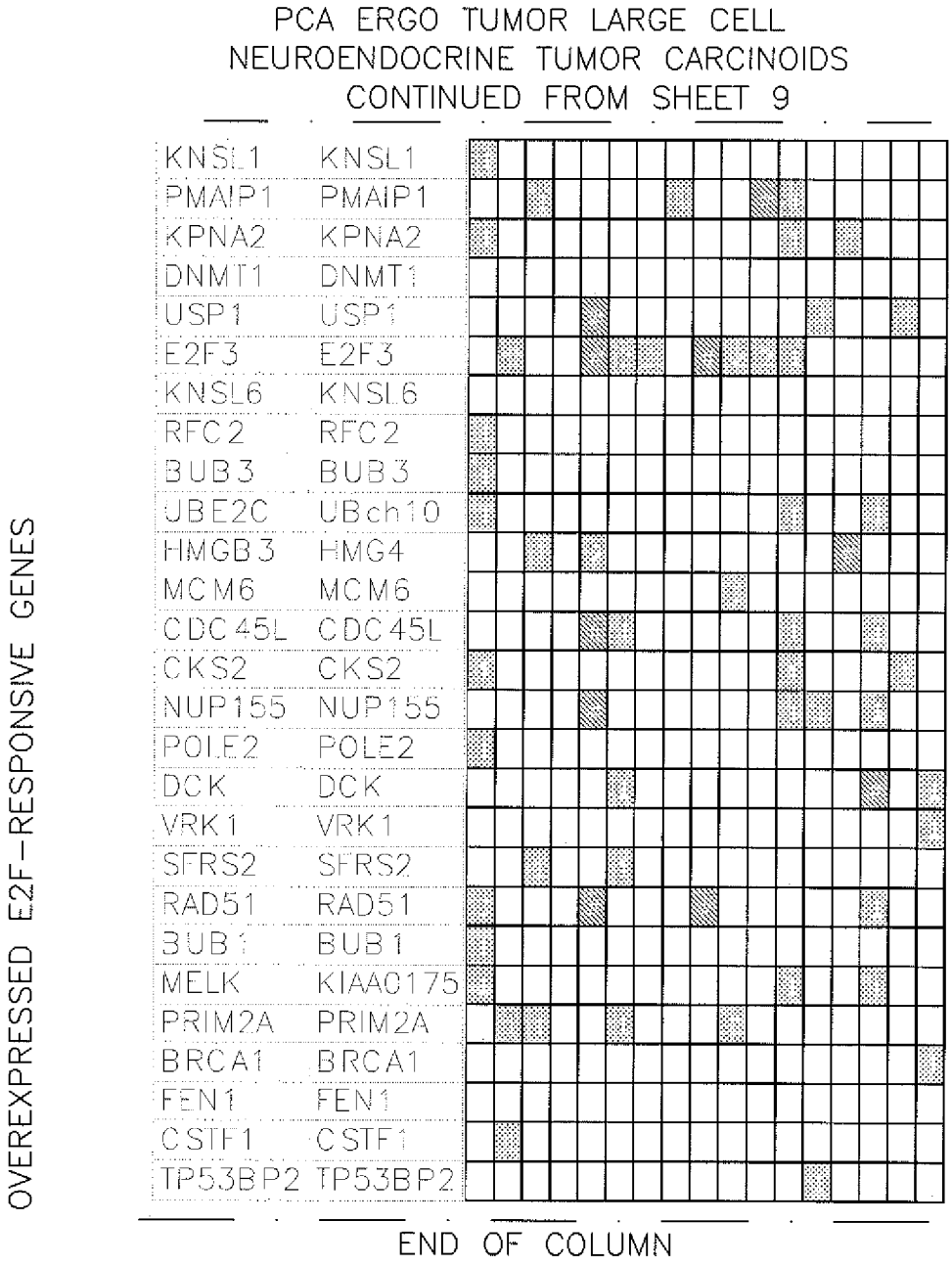

PCA ERGO TUMOR LARGE CELL
NEUROENDOCRINE TUMOR CARCINOIDS
CONTINUED FROM SHEET 9
OVEREXPRESSED E2F-RESPONSIVE GENES
KNSL1 KNSL1
PMAIP1 PMAIP1
KPNA2 KPNA2
DNMT1 DNMT1
USP1 USP1
E2F3 E2F3
KNSL6 KNSL6
RFC2 RFC2
BUB3 BUB3
UBE2C UBch10
HMGB3 HMG4
MCM6 MCM6
CDC45L CDC45L
CKS2 CKS2
NUP155 NUP155
POLE2 POLE2
DCK DCK
VRK1 VRK1
SFRS2 SFRS2
RAD51 RAD51
BUB1 BUB1
MELK KIAA0175
PRIM2A PRIM2A
BRCA1 BRCA1
FEN1 FEN1
CSTF1 CSTF1
TP53BP2 TP53BP2
END OF COLUMN

FIG. 14

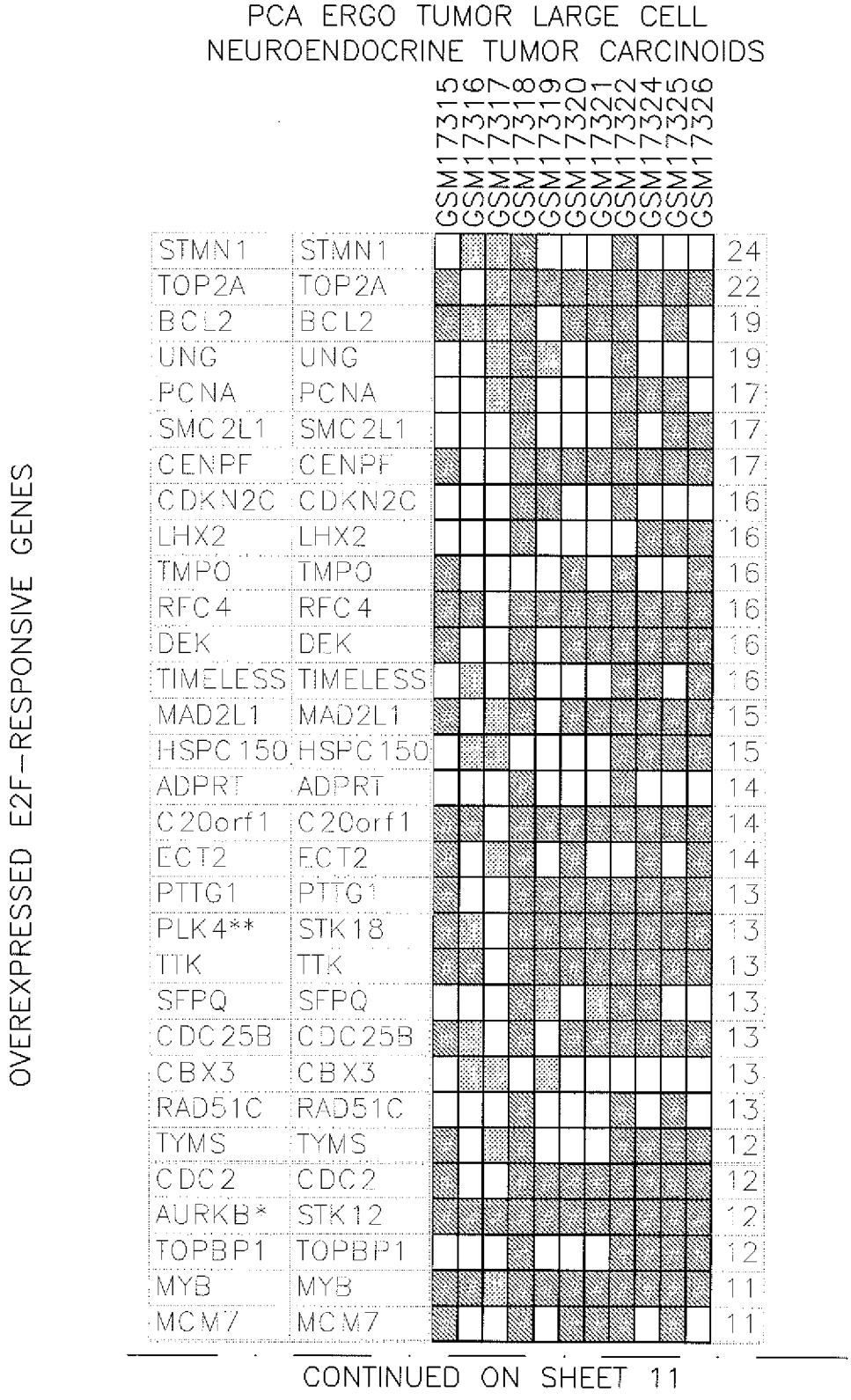
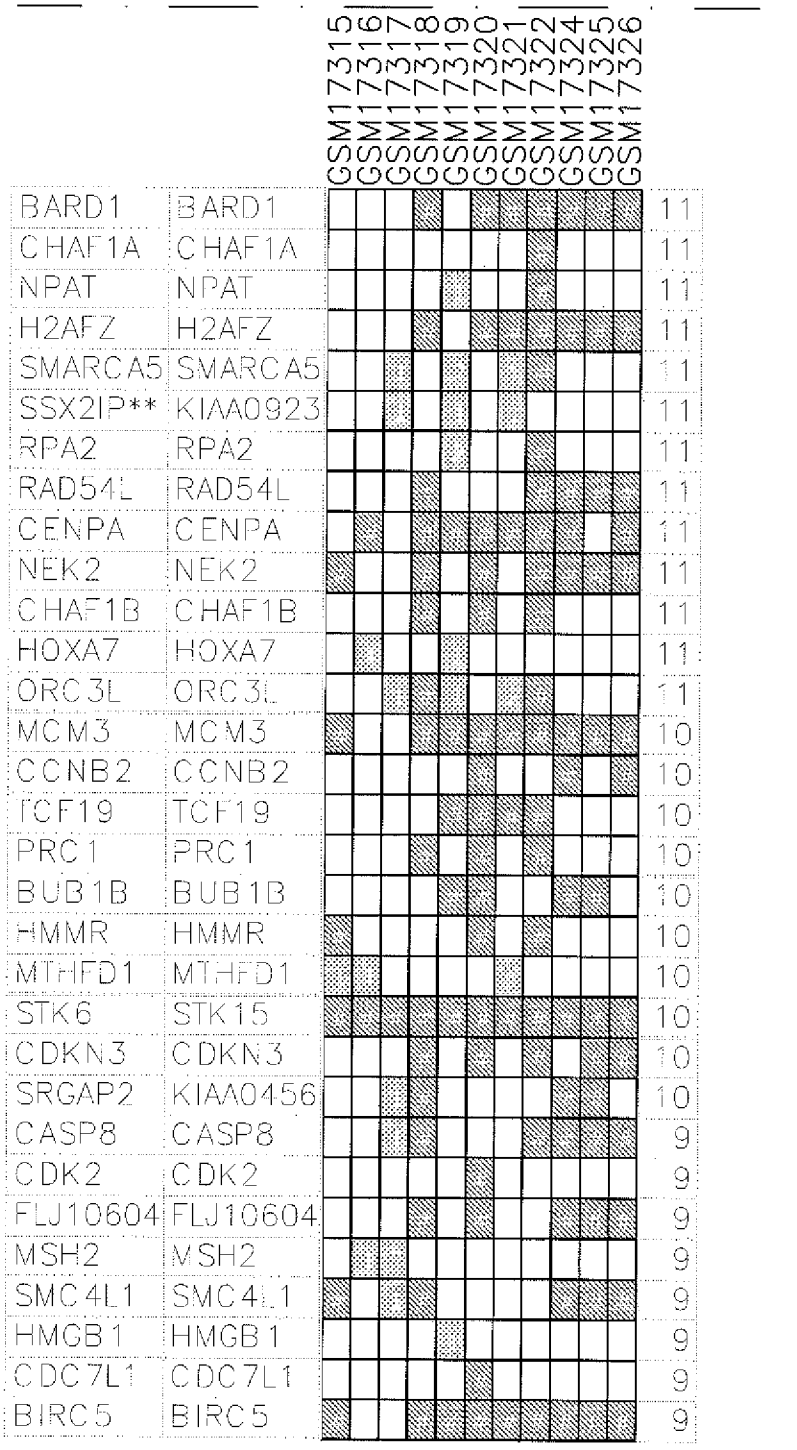

PCA ERGO TUMOR LARGE CELL
NEUROENDOCRINE TUMOR CARCINOIDS
GSM17315
GSM17316
GSM17317
GSM17318
GSM17319
GSM17320
GSM17321
GSM17322
GSM17324
GSM17325
GSM17326
OVEREXPRESSED E2F-RESPONSIVE GENES
STMN1 STMN1 24
TOP2A TOP2A 22
BCL2 BCL2 19
UNG UNG 19
PCNA PCNA 17
SMC2L1 SMC2L1 17
CENPF CENPF 17
CDKN2C CDKN2C 16
LHX2 LHX2 16
TMPO TMPO 16
RFC4 RFC4 16
DEK DEK 16
TIMELESS TIMELESS 16
MAD2L1 MAD2L1 15
HSPC150 HSPC150 15
ADPRT ADPRT 14
C20orf1 C20orf1 14
ECT2 ECT2 14
PTTG1 PTTG1 13
PLK4** STK18 13
TTK TTK 13
SFPQ SFPQ 13
CDC25B CDC25B 13
CBX3 CBX3 13
RAD51C RAD51C 13
TYMS TYMS 12
CDC2 CDC2 12
AURKB* STK12 12
TOPBP1 TOPBP1 12
MYB MYB 11
MCM7 MCM7 11
CONTINUED ON SHEET 11

FIG. 14

PCA ERGO TUMOR LARGE CELL
NEUROENDOCRINE TUMOR CARCINOIDS
CONTINUED FROM SHEET 10

OVEREXPRESSED E2F-RESPONSIVE GENES



CONTINUED ON SHEET 12

FIG. 14

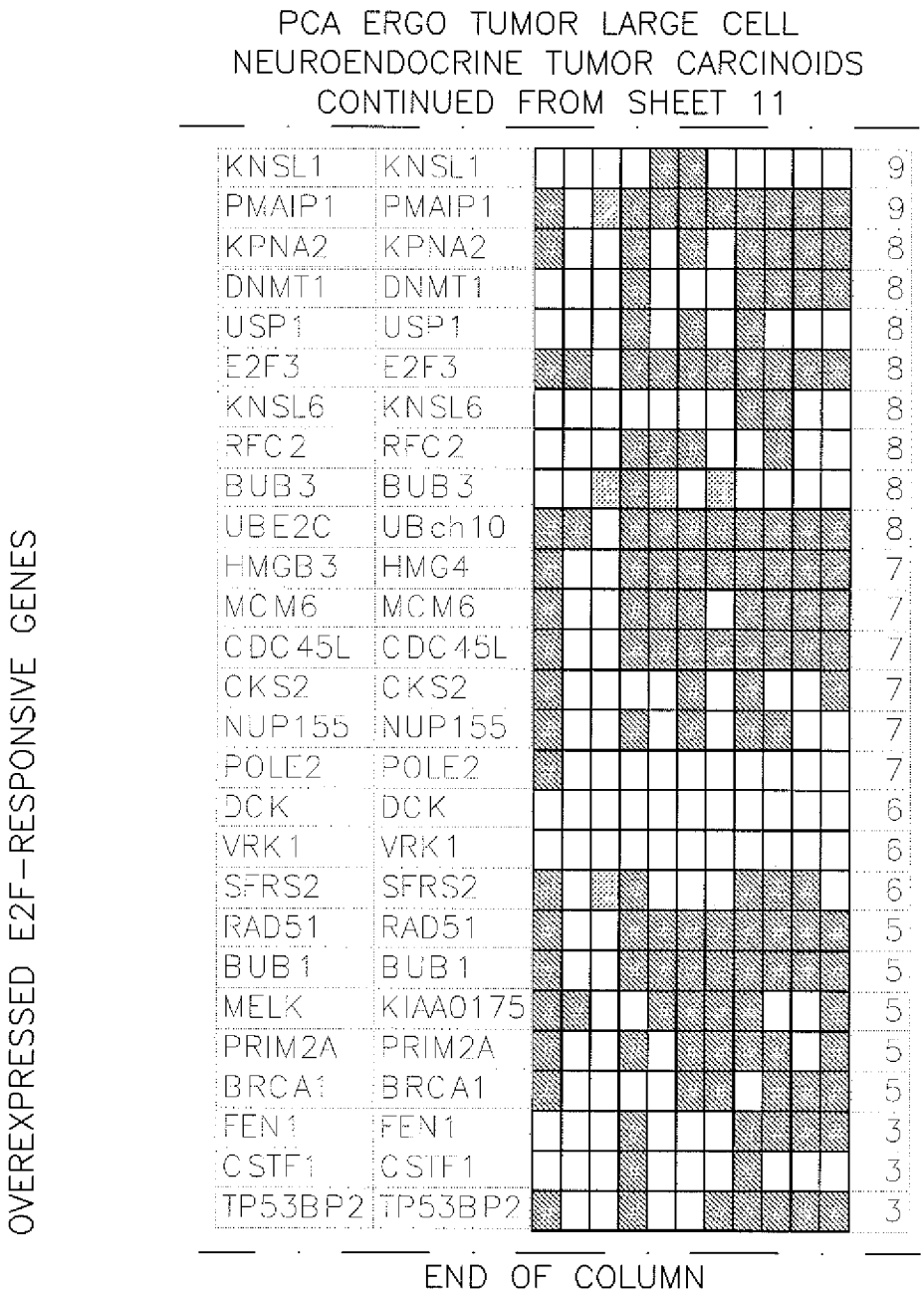

PCA ERGO TUMOR LARGE CELL
NEUROENDOCRINE TUMOR CARCINOIDS
CONTINUED FROM SHEET 11
OVEREXPRESSED E2F-RESPONSIVE GENES
KNSL1 KNSL1 9
PMAIP1 PMAIP1 9
KPNA2 KPNA2 8
DNMT1 DNMT1 8
USP1 USP1 8
E2F3 E2F3 8
KNSL6 KNSL6 8
RFC2 RFC2 8
BUB3 BUB3 8
UBE2C UBch10 8
HMGB3 HMG4 7
MCM6 MCM6 7
CDC45L CDC45L 7
CKS2 CKS2 7
NUP155 NUP155 7
POLE2 POLE2 7
DCK DCK 6
VRK1 VRK1 6
SFRS2 SFRS2 6
RAD51 RAD51 5
BUB1 BUB1 5
MELK KIAA0175 5
PRIM2A PRIM2A 5
BRCA1 BRCA1 5
FEN1 FEN1 3
CSTF1 CSTF1 3
TP53BP2 TP53BP2 3
END OF COLUMN

FIG. 14

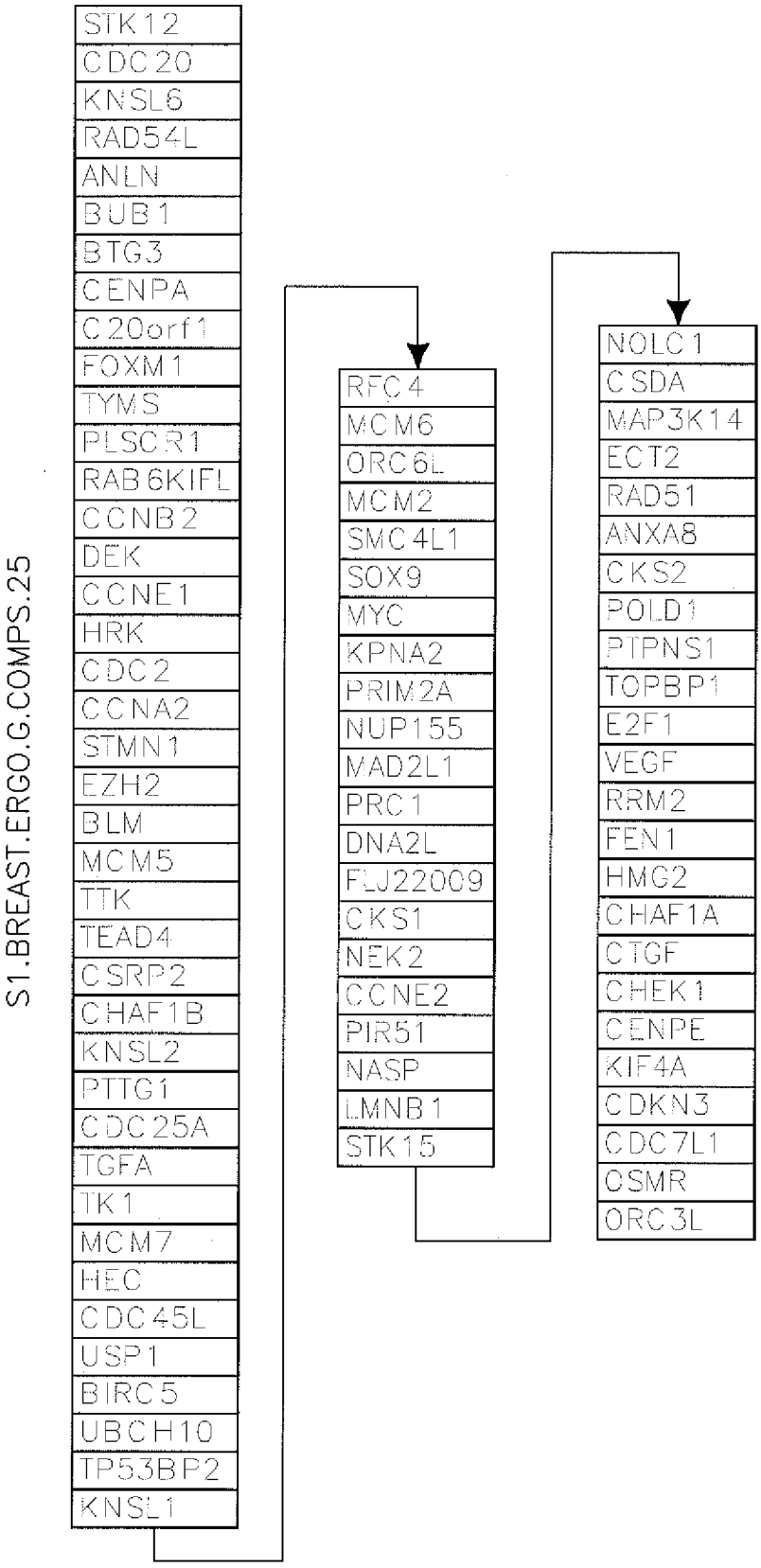

S1.BREAST.ERGO.G.COMPS.25
STK12
CDC20
KNSL6
RAD54L
ANLN
BUB1
BTG3
CENPA
C20orf1
FOXM1
TYMS
PLSCR1
RAB6KIFL
CCNB2
DEK
CCNE1
HRK
CDC2
CCNA2
STMN1
EZH2
BLM
MCM5
TTK
TEAD4
CSRP2
CHAF1B
KNSL2
PTTG1
CDC25A
TGFA
TK1
MCM7
HEC
CDC45L
USP1
BIRC5
UBCH10
TP53BP2
KNSL1
RFC4
MCM6
ORC6L
MCM2
SMC4L1
SOX9
MYC
KPNA2
PRIM2A
NUP155
MAD2L1
PRC1
DNA2L
FLJ22009
CKS1
NEK2
CCNE2
PIR51
NASP
LMNB1
STK15
NOLC1
CSDA
MAP3K14
ECT2
RAD51
ANXA8
CKS2
POLD1
PTPNS1
TOPBP1
E2F1
VEGF
RRM2
FEN1
HMG2
CHAF1A
CTGF
CHEK1
CENPE
KIF4A
CDKN3
CDC7L1
CSMR
ORC3L

FIG. 15

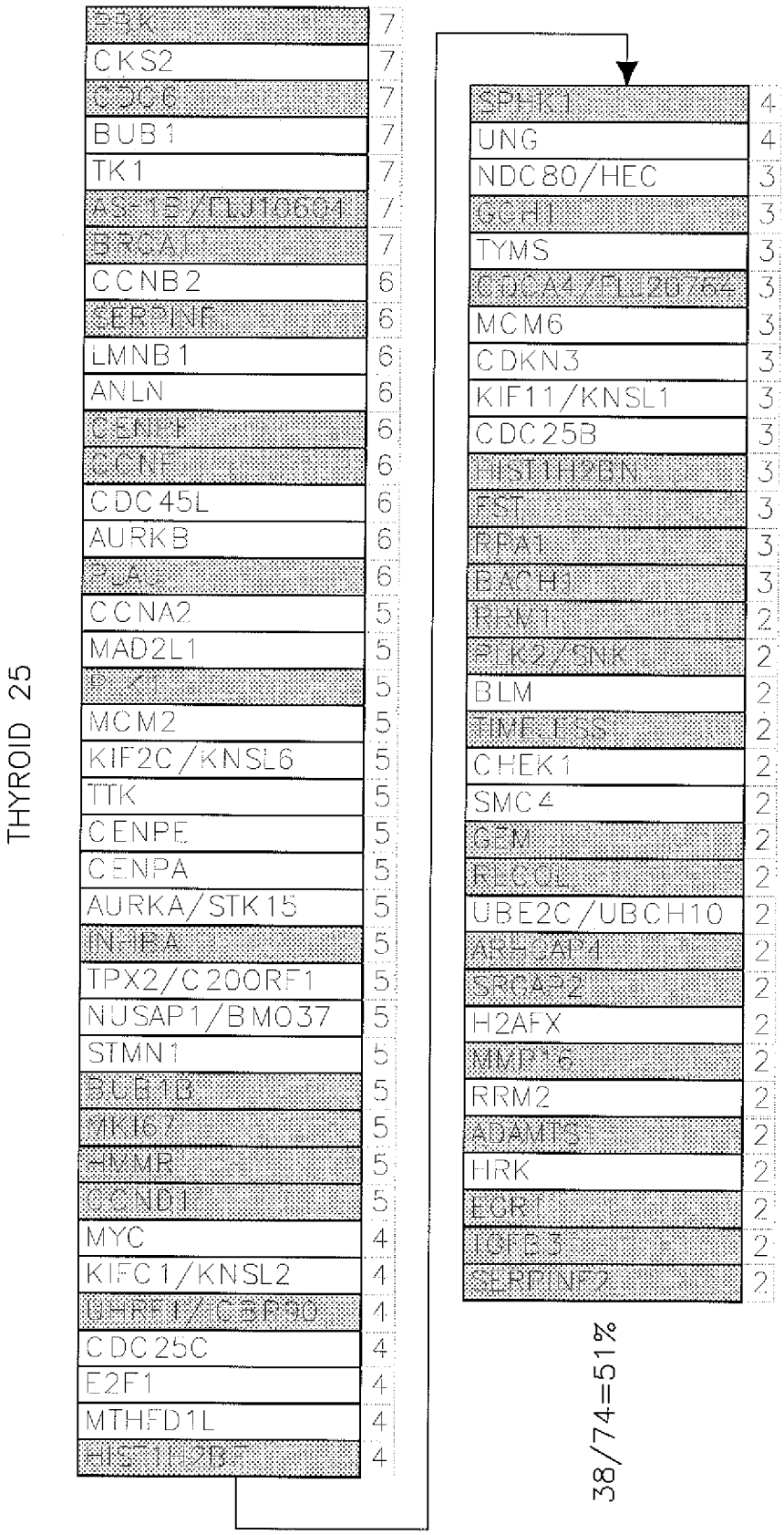

THYROID 25
PBK 7
CKS2 7
C20C6 7
BUB1 7
TK1 7
ASF1B/FLJ10604 7
BRCA1 7
CCNB2 6
SERPINF 6
LMNB1 6
ANLN 6
CENPF 6
CCNF 6
CDC45L 6
AURKB 6
PLAC 6
CCNA2 5
MAD2L1 5
PCT 5
MCM2 5
KIF2C/KNSL6 5
TTK 5
CENPE 5
CENPA 5
AURKA/STK15 5
INHBA 5
TPX2/C20ORF1 5
NUSAP1/BM037 5
STMN1 5
BUB1B 5
MKI67 5
HMMR 5
CCND1 5
MYC 4
KIFC1/KNSL2 4
UHRF1/C3P90 4
CDC25C 4
E2F1 4
MTHFD1L 4
HIST1H2BF 4
SPHK1 4
UNG 4
NDC80/HEC 3
GCH1 3
TYMS 3
CDCA4/FLJ20764 3
MCM6 3
CDKN3 3
KIF11/KNSL1 3
CDC25B 3
HIST1H2BN 3
FET 3
RPA1 3
BACH1 3
RRM1 2
PLK2/SNK 2
BLM 2
TIMELESS 2
CHEK1 2
SMC4 2
GEM 2
RLGCL 2
UBE2C/UBCH10 2
ARL7AP4 2
SRCAP2 2
H2AFX 2
MMP16 2
RRM2 2
ADAMTS 2
HRK 2
EGR1 2
IGFBP3 2
SERPINF2 2
38/74=51%

FIG. 15

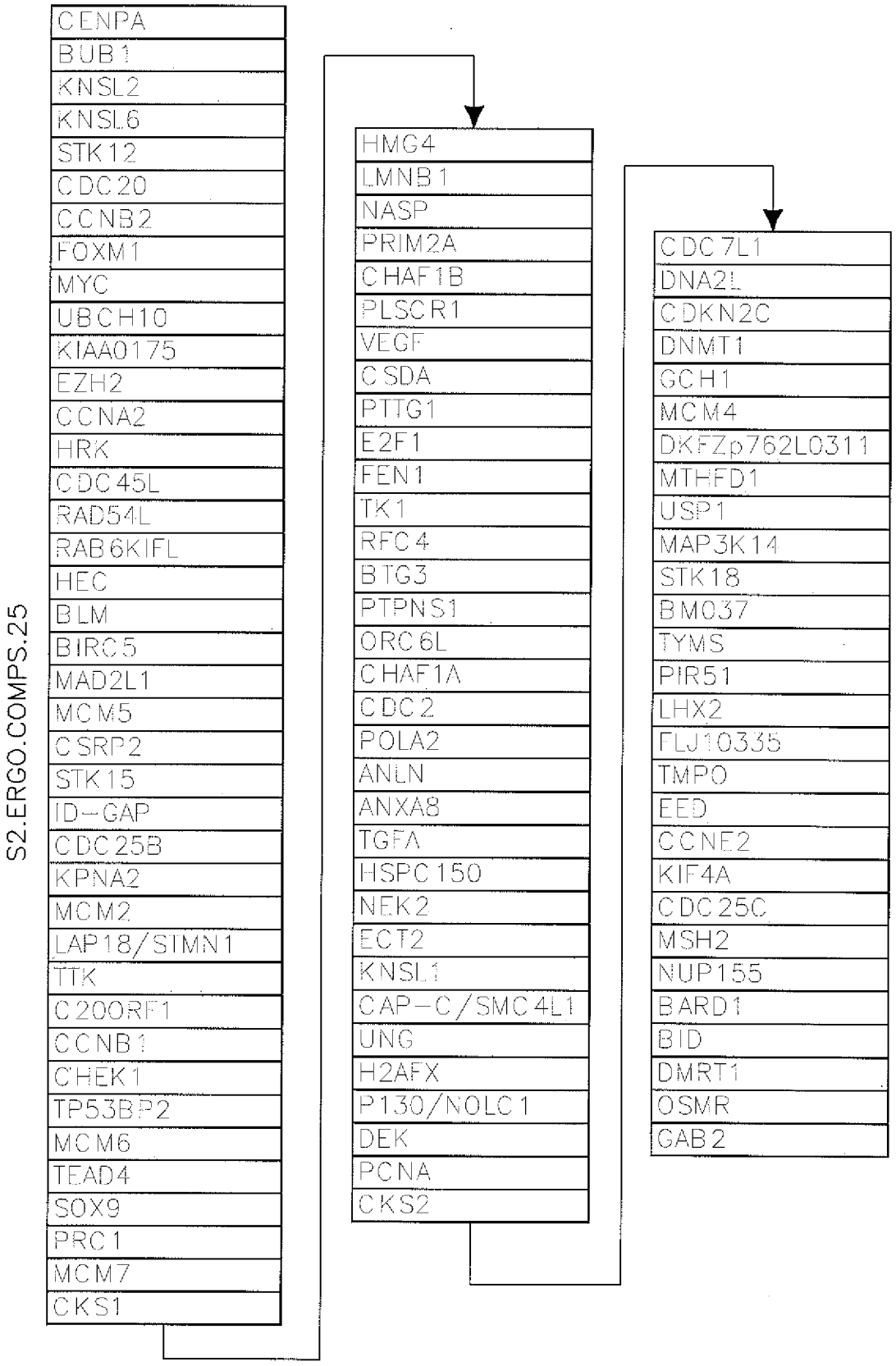

S2.ERGO.COMPS.25
CENPA
BUB1
KNSL2
KNSL6
STK12
CDC20
CCNB2
FOXM1
MYC
UBCH10
KIAA0175
EZH2
CCNA2
HRK
CDC45L
RAD54L
RAB6KIFL
HEC
BLM
BIRC5
MAD2L1
MCM5
CSRP2
STK15
ID-GAP
CDC25B
KPNA2
MCM2
LAP18/STMN1
TTK
C20ORF1
CCNB1
CHEK1
TP53BP2
MCM6
TEAD4
SOX9
PRC1
MCM7
CKS1
HMG4
LMNB1
NASP
PRIM2A
CHAF1B
PLSCR1
VEGF
CSDA
PTTG1
E2F1
FEN1
TK1
RFC4
BTG3
PTPNS1
ORC6L
CHAF1A
CDC2
POLA2
ANLN
ANXA8
TGFA
HSPC150
NEK2
ECT2
KNSL1
CAP-C/SMC4L1
UNG
H2AFX
P130/NOLC1
DEK
PCNA
CKS2
CDC7L1
DNA2L
CDKN2C
DNMT1
GCH1
MCM4
DKFZp762L0311
MTHFD1
USP1
MAP3K14
STK18
BM037
TYMS
PIR51
LHX2
FLJ10335
TMPO
EED
CCNE2
KIF4A
CDC25C
MSH2
NUP155
BARD1
BID
DMRT1
OSMR
GAB2

FIG. 15

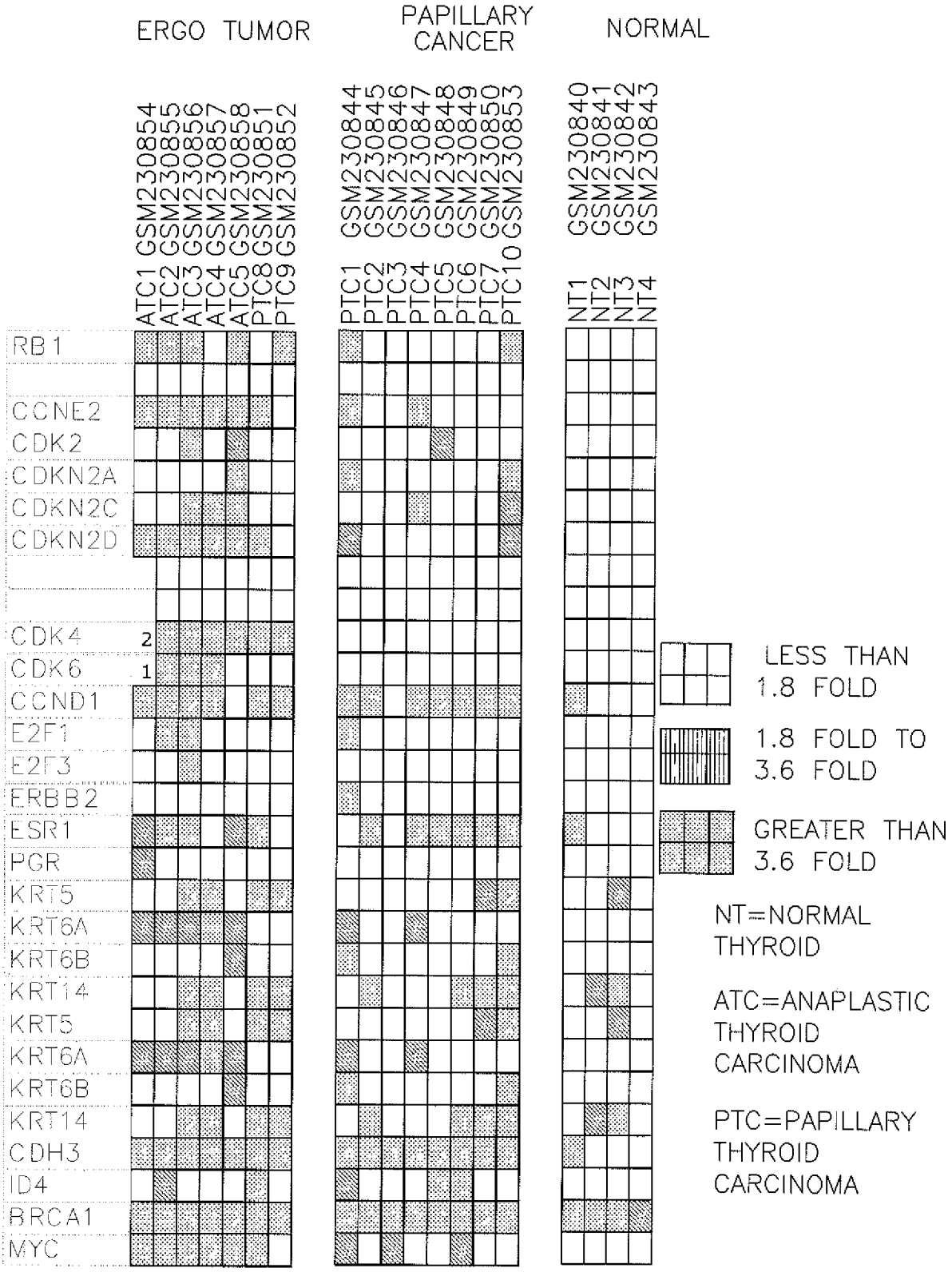
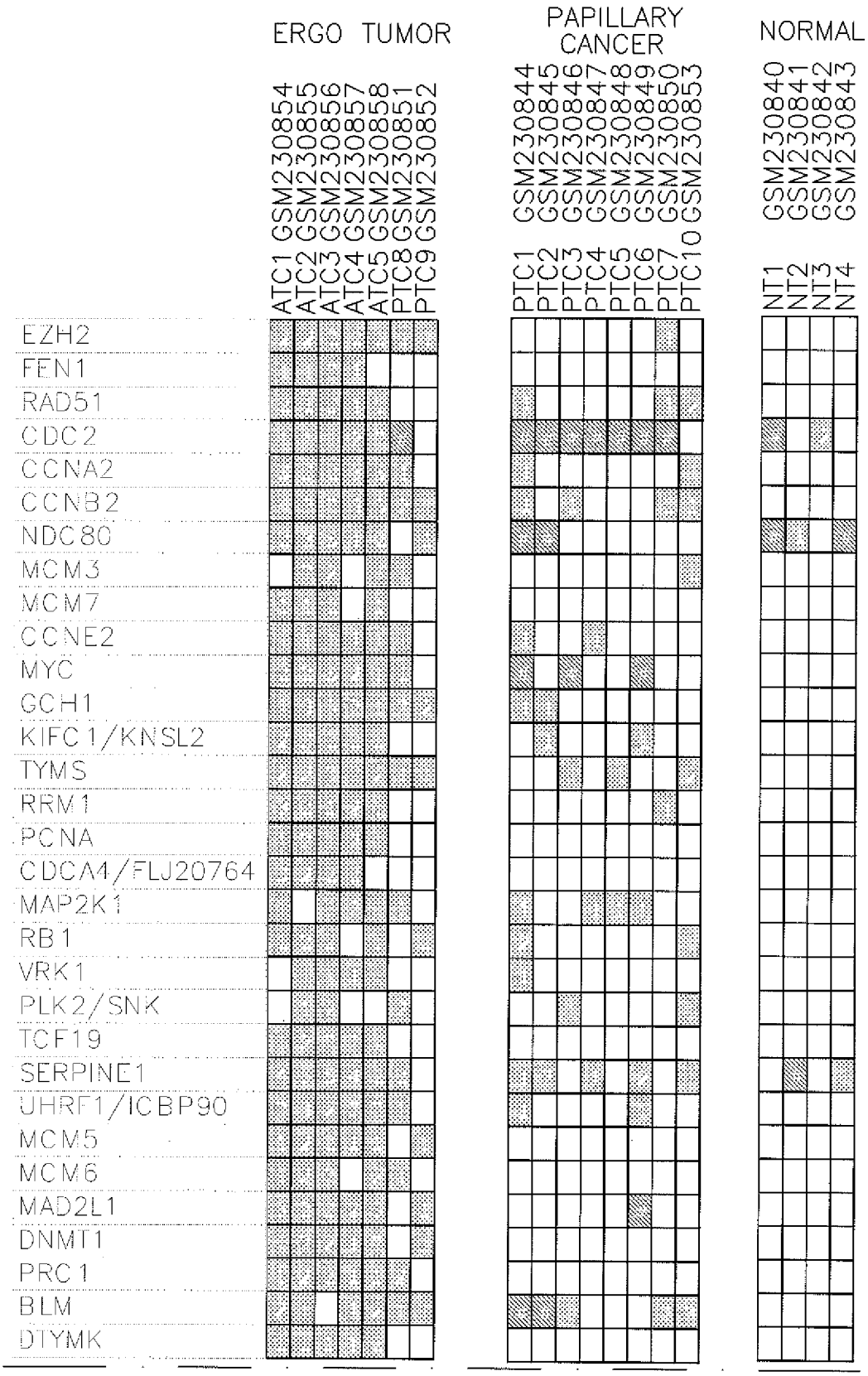
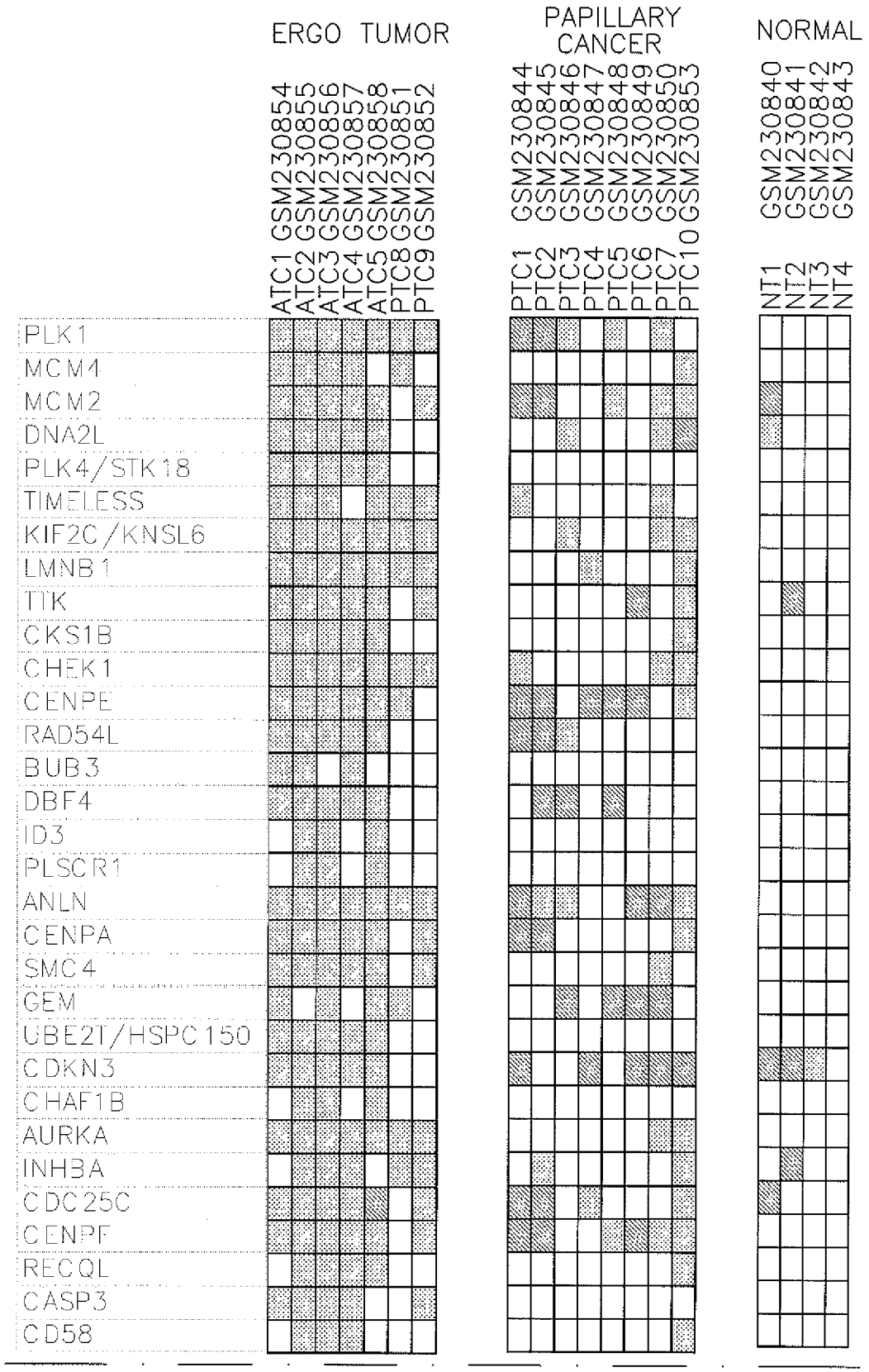

ERGO TUMOR
PAPILLARY CANCER
NORMAL
ATC1 GSM230854
ATC2 GSM230855
ATC3 GSM230856
ATC4 GSM230857
ATC5 GSM230858
PTC8 GSM230851
PTC9 GSM230852
PTC1 GSM230844
PTC2 GSM230845
PTC3 GSM230846
PTC4 GSM230847
PTC5 GSM230848
PTC6 GSM230849
PTC7 GSM230850
PTC10 GSM230853
NT1 GSM230840
NT2 GSM230841
NT3 GSM230842
NT4 GSM230843
RB1
CCNE2
CDK2
CDKN2A
CDKN2C
CDKN2D
CDK4
CDK6
CCND1
E2F1
E2F3
ERBB2
ESR1
PGR
KRT5
KRT6A
KRT6B
KRT14
KRT5
KRT6A
KRT6B
KRT14
CDH3
ID4
BRCA1
MYC
2
1
LESS THAN 1.8 FOLD
1.8 FOLD TO 3.6 FOLD
GREATER THAN 3.6 FOLD
NT=NORMAL THYROID
ATC=ANAPLASTIC THYROID CARCINOMA
PTC=PAPILLARY THYROID CARCINOMA

FIG. 16



CONTINUED ON SHEET 3

FIG. 16 2



CONTINUED ON SHEET 4

FIG. 16 3

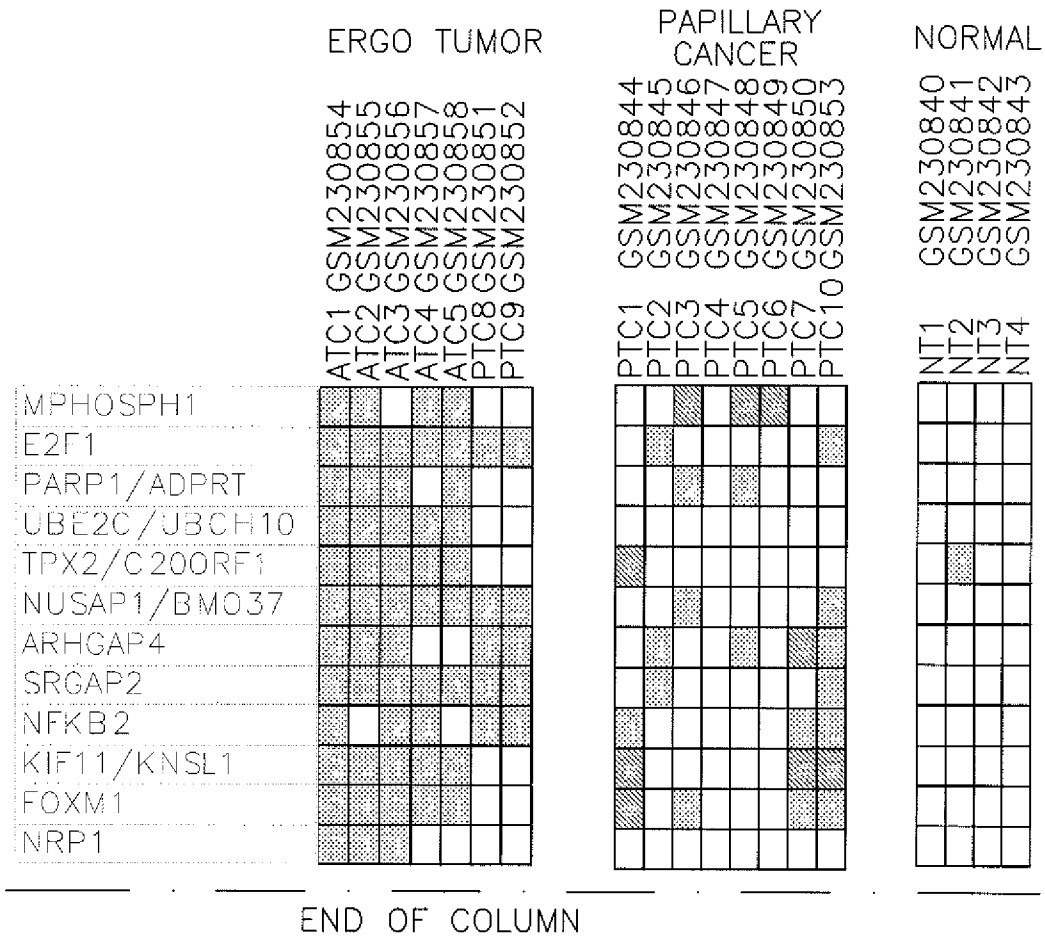

ERGO TUMOR
PAPILLARY CANCER
NORMAL
ATC1 GSM230854
ATC2 GSM230855
ATC3 GSM230856
ATC4 GSM230857
ATC5 GSM230858
PTC8 GSM230851
PTC9 GSM230852
PTC1 GSM230844
PTC2 GSM230845
PTC3 GSM230846
PTC4 GSM230847
PTC5 GSM230848
PTC6 GSM230849
PTC7 GSM230850
PTC10 GSM230853
NT1 GSM230840
NT2 GSM230841
NT3 GSM230842
NT4 GSM230843
MPHOSPH1
E2F1
PARP1/ADPRT
UBE2C/UBCH10
TPX2/C20ORF1
NUSAP1/BMO37
ARHGAP4
SRGAP2
NFKB2
KIF11/KNSL1
FOXM1
NRP1
END OF COLUMN

FIG. 16

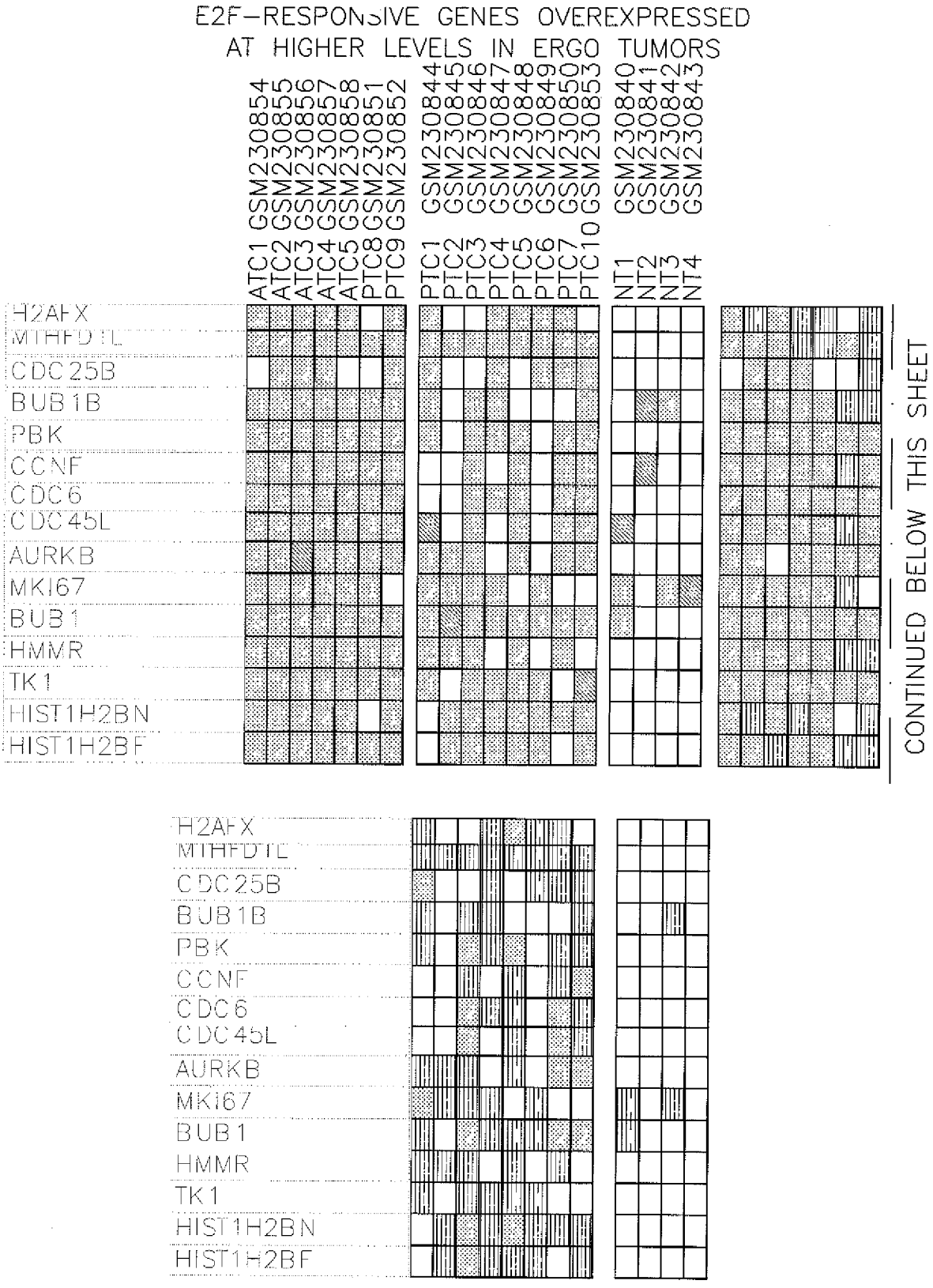
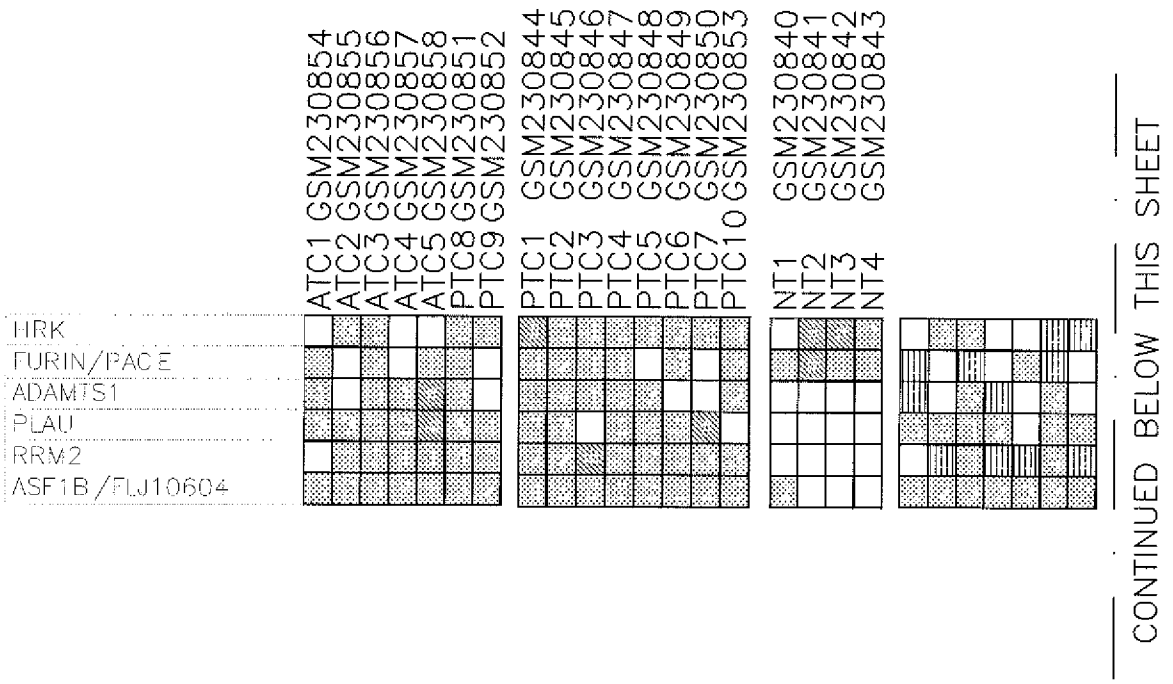

E2F-RESPONSIVE GENES OVEREXPRESSED
AT HIGHER LEVELS IN ERGO TUMORS
ATC1 GSM230854
ATC2 GSM230855
ATC3 GSM230856
ATC4 GSM230857
ATC5 GSM230858
PTC8 GSM230851
PTC9 GSM230852
PTC1 GSM230844
PTC2 GSM230845
PTC3 GSM230846
PTC4 GSM230847
PTC5 GSM230848
PTC6 GSM230849
PTC7 GSM230850
PTC10 GSM230853
NT1 GSM230840
NT2 GSM230841
NT3 GSM230842
NT4 GSM230843
H2AFX
MTHFD1L
CDC25B
BUB1B
PBK
CCNF
CDC6
CDC45L
AURKB
MKI67
BUB1
HMMR
TK1
HIST1H2BN
HIST1H2BF
CONTINUED BELOW THIS SHEET
H2AFX
MTHFD1L
CDC25B
BUB1B
PBK
CCNF
CDC6
CDC45L
AURKB
MKI67
BUB1
HMMR
TK1
HIST1H2BN
HIST1H2BF

FIG. 16

E2F-RESPONSIVE GENES OVEREXPRESSED AT SIMILAR LEVELS IN ERGO TUMORS AND NON-ERGO TUMORS



CONTINUED BELOW THIS SHEET

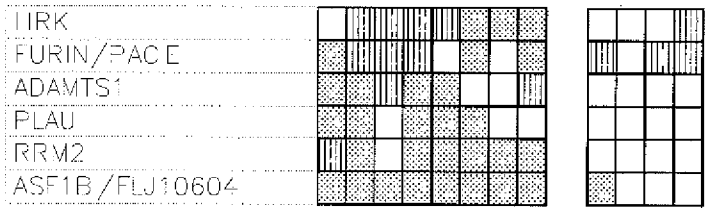


FIG. 16

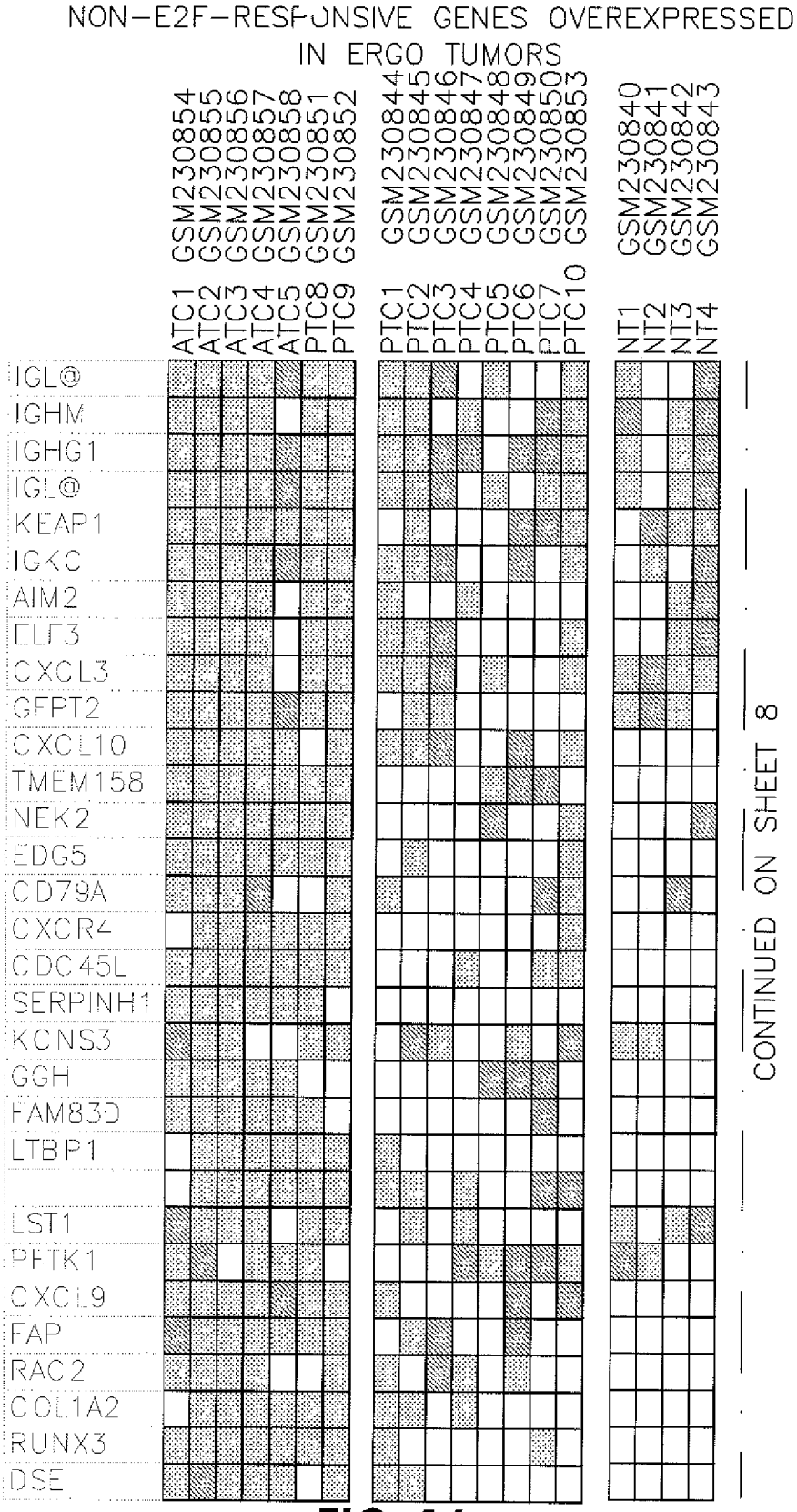

NON-E2F-RESPONSIVE GENES OVEREXPRESSED IN ERGO TUMORS
GSM230854 GSM230855 GSM230856 GSM230857 GSM230858 GSM230851 GSM230852
GSM230844 GSM230845 GSM230846 GSM230847 GSM230848 GSM230849 GSM230850 GSM230853
GSM230840 GSM230841 GSM230842 GSM230843
ATC1 ATC2 ATC3 ATC4 ATC5 PTC8 PTC9
PTC1 PTC2 PTC3 PTC4 PTC5 PTC6 PTC7 PTC10
NT1 NT2 NT3 NT4
IGL@
IGHM
IGHG1
IGL@
KEAP1
IGKC
AIM2
ELF3
CXCL3
GFPT2
CXCL10
TMEM158
NEK2
EDG5
CD79A
CXCR4
CDC45L
SERPINH1
KCNS3
GGH
FAM83D
LTBP1
LST1
PFTK1
CXCL9
FAP
RAC2
COL1A2
RUNX3
DSE
CONTINUED ON SHEET 8

FIG. 16

NON-E2F-RESPONSIVE GENES OVEREXPRESSED IN ERGO TUMORS

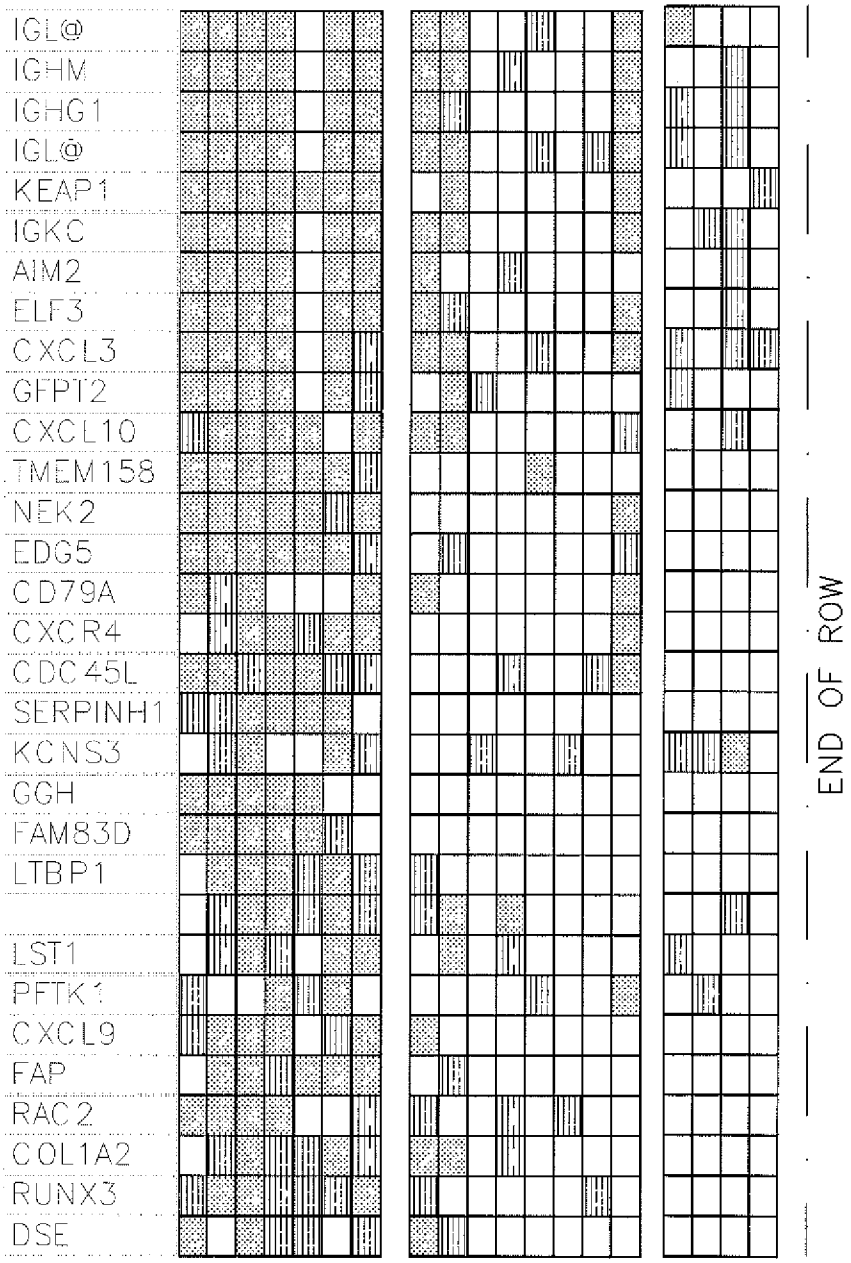


FIG. 16

NON-E2F-RESPONSIVE GENES OVEREXPRESSED AT HIGHER LEVELS IN ERGO TUMORS

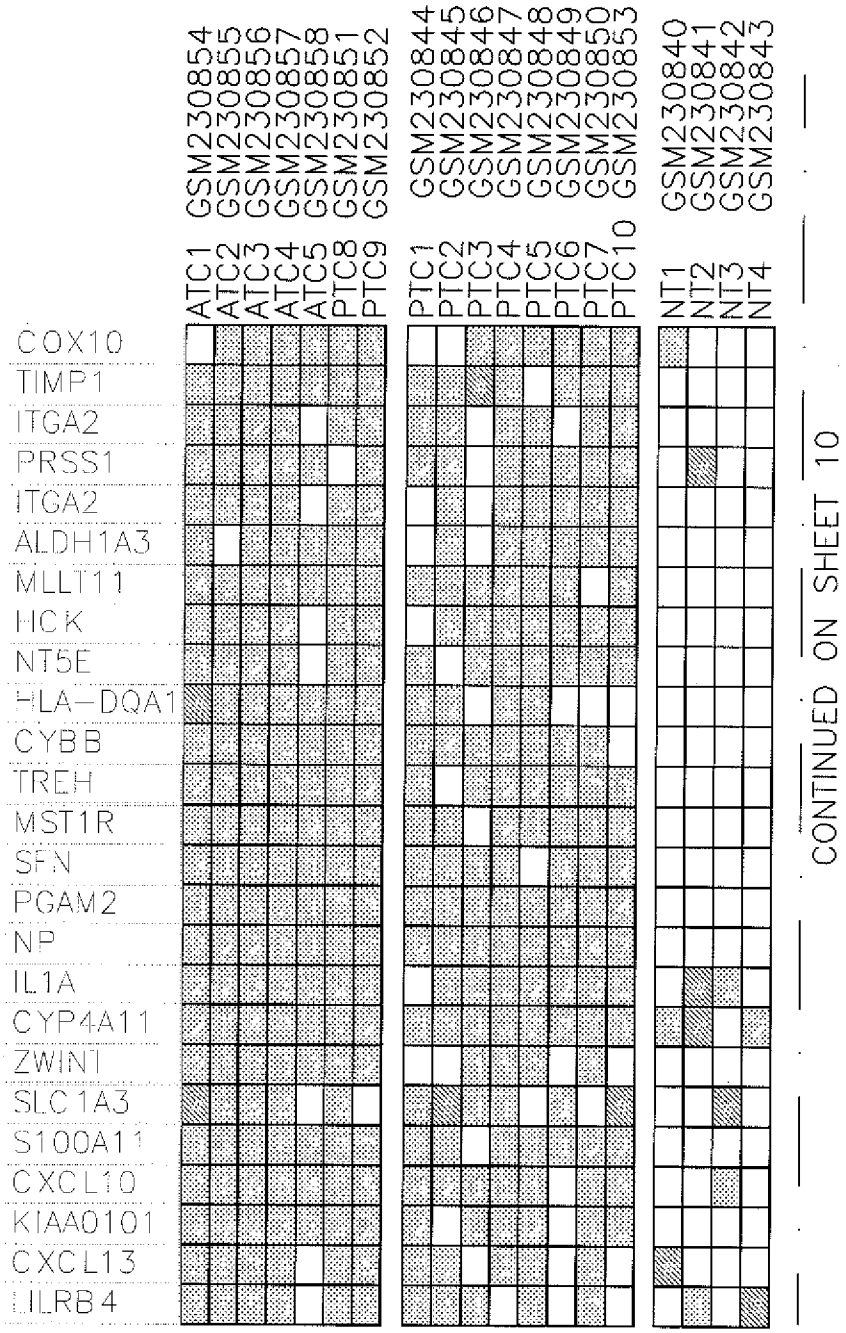


FIG. 16

NON-E2F-RESPONSIVE GENES OVEREXPRESSED AT HIGHER LEVELS IN ERGO TUMORS

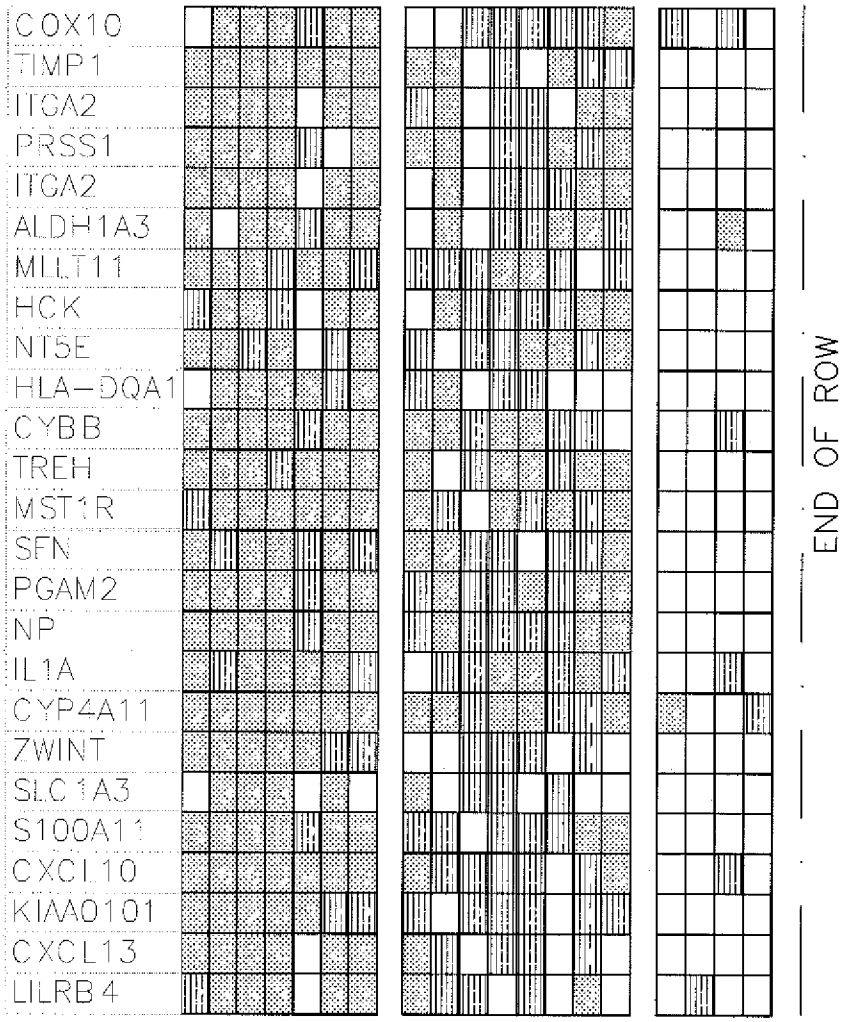


FIG. 16

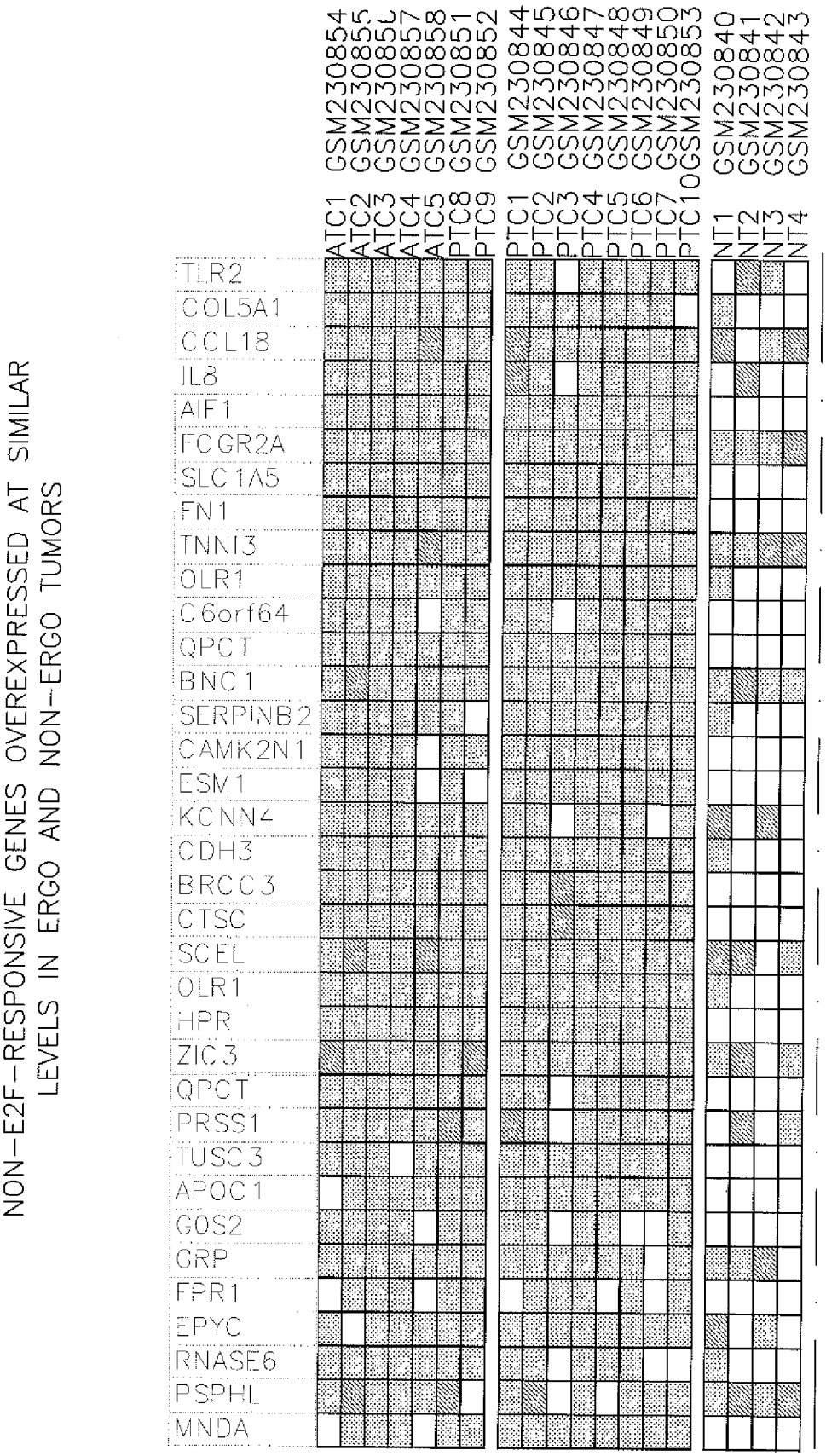

NON-E2F-RESPONSIVE GENES OVEREXPRESSED AT SIMILAR LEVELS IN ERGO AND NON-ERGO TUMORS
ATC1 GSM230854
ATC2 GSM230855
ATC3 GSM230856
ATC4 GSM230857
ATC5 GSM230858
PTC8 GSM230851
PTC9 GSM230852
PTC1 GSM230844
PTC2 GSM230845
PTC3 GSM230846
PTC4 GSM230847
PTC5 GSM230848
PTC6 GSM230849
PTC7 GSM230850
PTC10 GSM230853
NT1 GSM230840
NT2 GSM230841
NT3 GSM230842
NT4 GSM230843
TLR2
COL5A1
CCL18
IL8
AIF1
FCGR2A
SLC1A5
FN1
TNNI3
OLR1
C6orf64
QPCT
BNC1
SERPINB2
CAMK2N1
ESM1
KCNN4
CDH3
BRCC3
CTSC
SCEL
OLR1
HPR
ZIC3
QPCT
PRSS1
TUSC3
APOC1
G0S2
CRP
FPR1
EPYC
RNASE6
PSPHL
MNDA
CONTINUED ON SHEET 12

FIG. 16

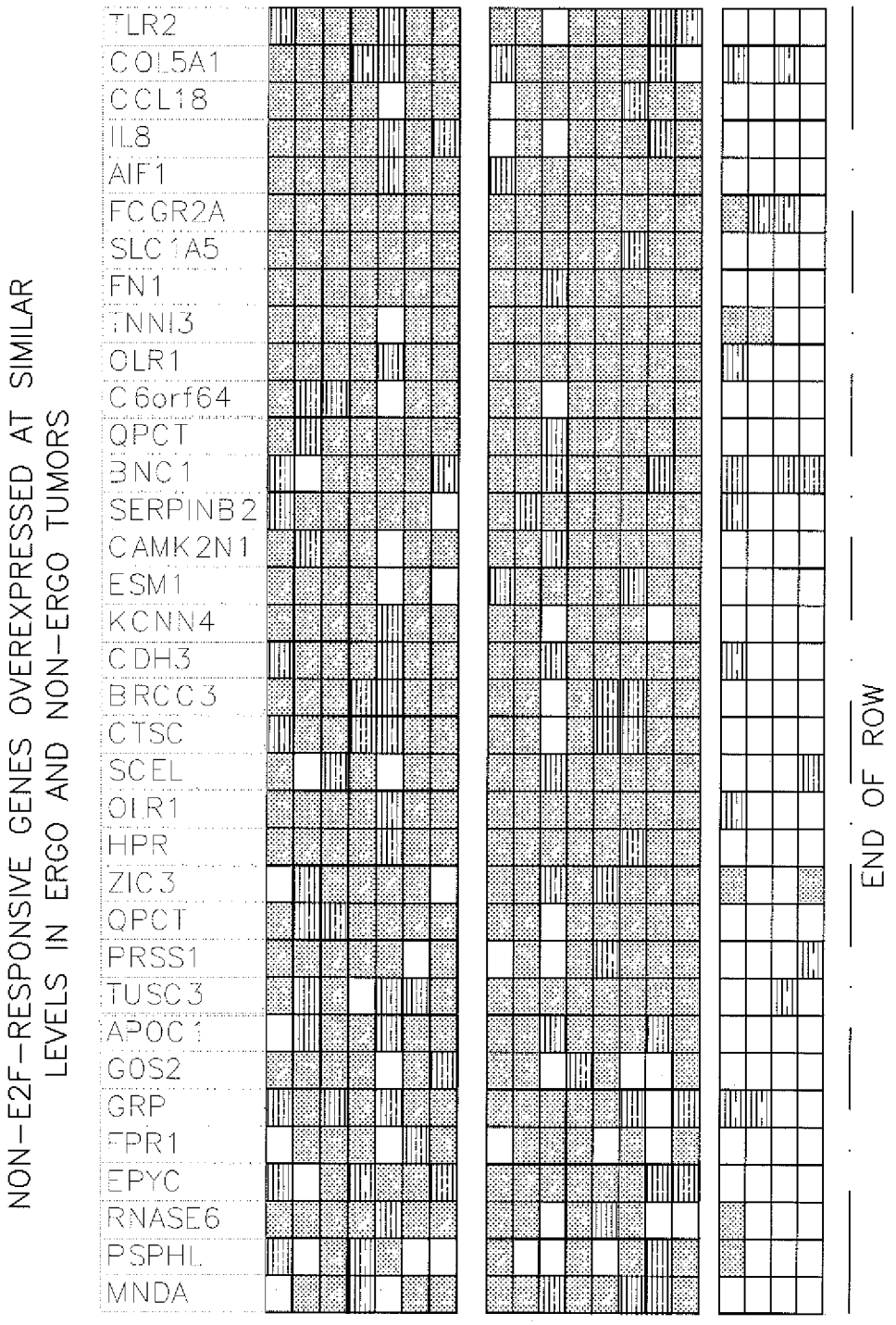

NON-E2F-RESPONSIVE GENES OVEREXPRESSED AT SIMILAR LEVELS IN ERGO AND NON-ERGO TUMORS
TLR2
COL5A1
CCL18
IL8
AIF1
FCGR2A
SLC1A5
FN1
TNNI3
OLR1
C6orf64
QPCT
BNC1
SERPINB2
CAMK2N1
ESM1
KCNN4
CDH3
BRCC3
CTSC
SCEL
OLR1
HPR
ZIC3
QPCT
PRSS1
TUSC3
APOC1
G0S2
GRP
FPR1
EPYC
RNASE6
PSPHL
MNDA
END OF ROW

FIG. 16

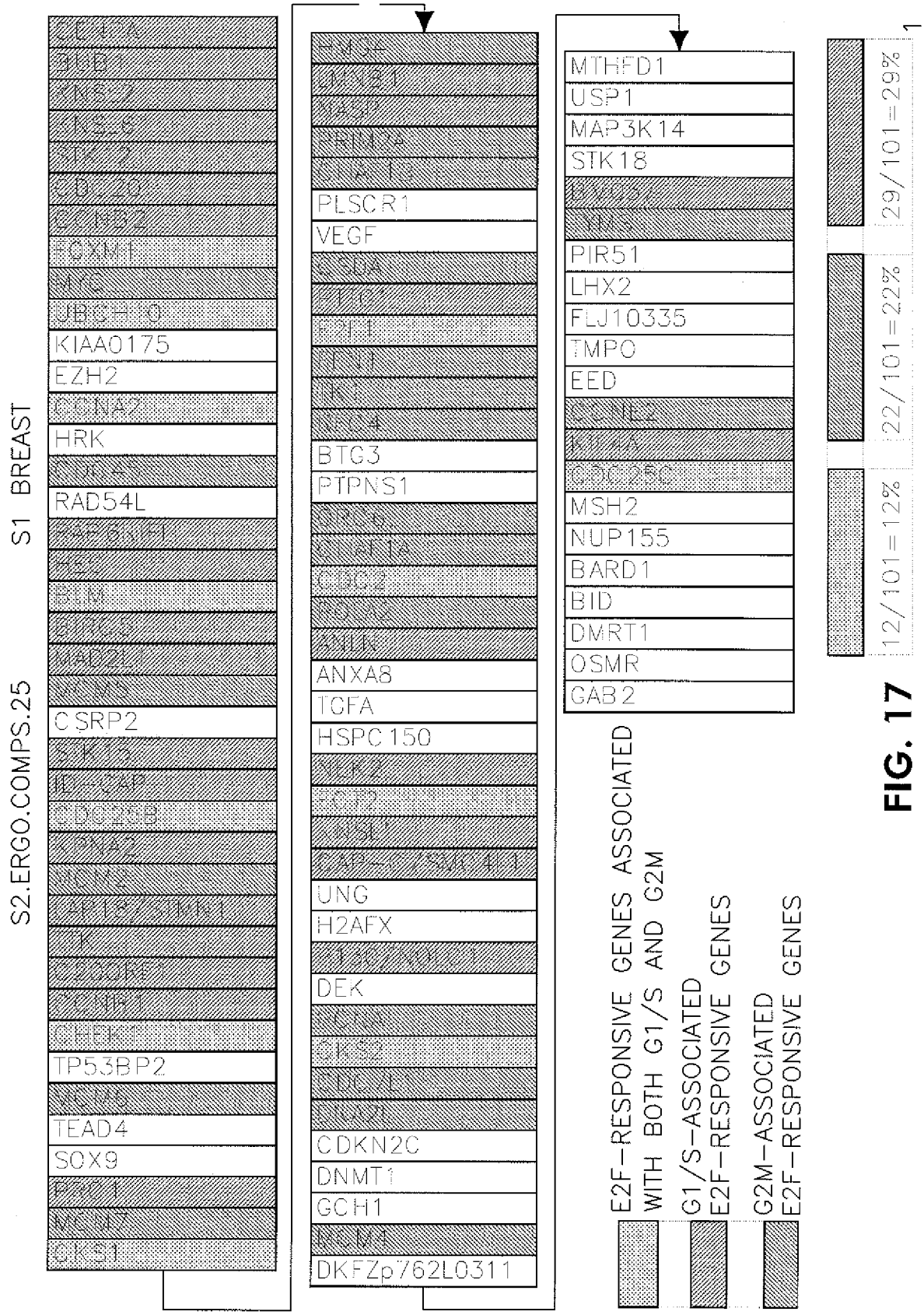

S1 BREAST
S2.ERGO.COMPS.25
KIAA0175
EZH2
HRK
RAD54L
CSRP2
PLSCR1
VEGF
BTG3
PTPNS1
ANXA8
TCFA
HSPC150
DEK
CDKN2C
DNMT1
GCH1
DKFZp762L0311
MTHFD1
USP1
MAP3K14
STK18
PIR51
LHX2
FLJ10335
TMPO
EED
MSH2
NUP155
BARD1
BID
DMRT1
OSMR
GAB2
E2F-RESPONSIVE GENES ASSOCIATED WITH BOTH G1/S AND G2M
G1/S-ASSOCIATED E2F-RESPONSIVE GENES
G2M-ASSOCIATED E2F-RESPONSIVE GENES
12/101=12%
22/101=22%
29/101=29%
1

FIG. 17

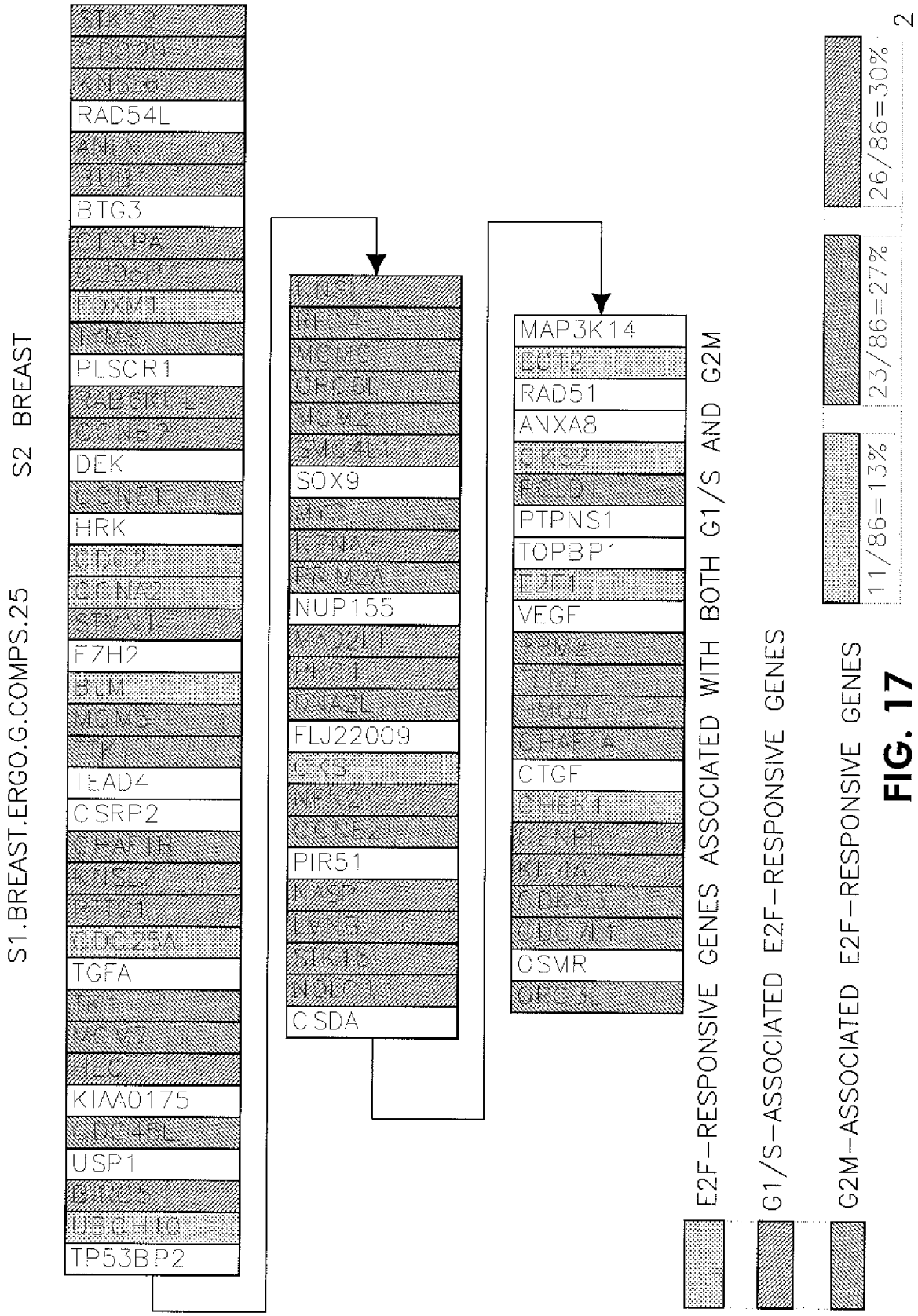

S1.BREAST.ERGO.G.COMPS.25
S2 BREAST
RAD54L
BTG3
PLSCR1
DEK
HRK
EZH2
TEAD4
CSRP2
TGFA
KIAA0175
USP1
TP53BP2
SOX9
NUP155
FLJ22009
PIR51
CSDA
MAP3K14
RAD51
ANXA8
PTPNS1
TOPBP1
VEGF
CTGF
E2F-RESPONSIVE GENES ASSOCIATED WITH BOTH G1/S AND G2M
G1/S-ASSOCIATED E2F-RESPONSIVE GENES
G2M-ASSOCIATED E2F-RESPONSIVE GENES
11/86=13%
23/86=27%
26/86=30%
2

FIG. 17

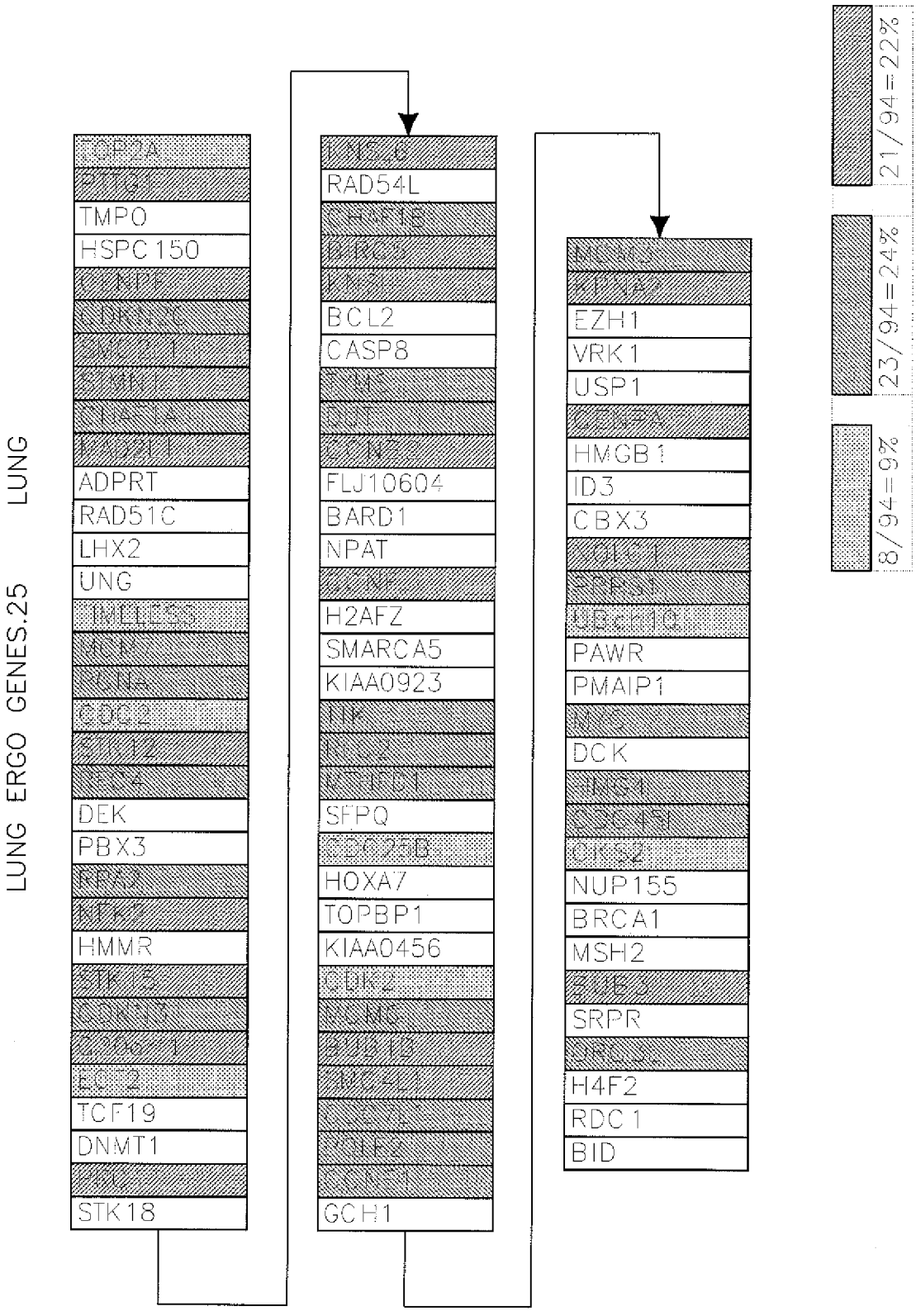

LUNG ERGO GENES.25 LUNG
TOP2A
PTTG1
TMPO
HSPC150
CENPF
KNTC2
MCM10
CHEK1
CHAF1A
KIAA0101
ADPRT
RAD51C
LHX2
UNG
MLF1IP
MCM7
PCNA
CDC2
STIL
PRC1
DEK
PBX3
RPA3
NTHL1
HMMR
TTK
CDKN3
C21orf1
EIF2
TCF19
DNMT1
PRC1
STK18
MCM6
RAD54L
CHAF1B
DIRC2
MCM4
BCL2
CASP8
TYMS
CDC7
CCNE2
FLJ10604
BARD1
NPAT
CCNF
H2AFZ
SMARCA5
KIAA0923
NEK6
RFC4
MCM3
SFPQ
C20orf20
HOXA7
TOPBP1
KIAA0456
CDK2
NUMA1
CDC10
MCM2
CCNA2
POLE2
CDC1
GCH1
MCM3
KPNA2
EZH1
VRK1
USP1
CENPA
HMGB1
ID3
CBX3
QIL1
SPAG7
UBE2C
PAWR
PMAIP1
MYC
DCK
ING1
CDC45
CIR
NUP155
BRCA1
MSH2
SUB1
SRPR
ORC6
H4F2
RDC1
BID
8/94=9%
23/94=24%
21/94=22%

FIG. 17

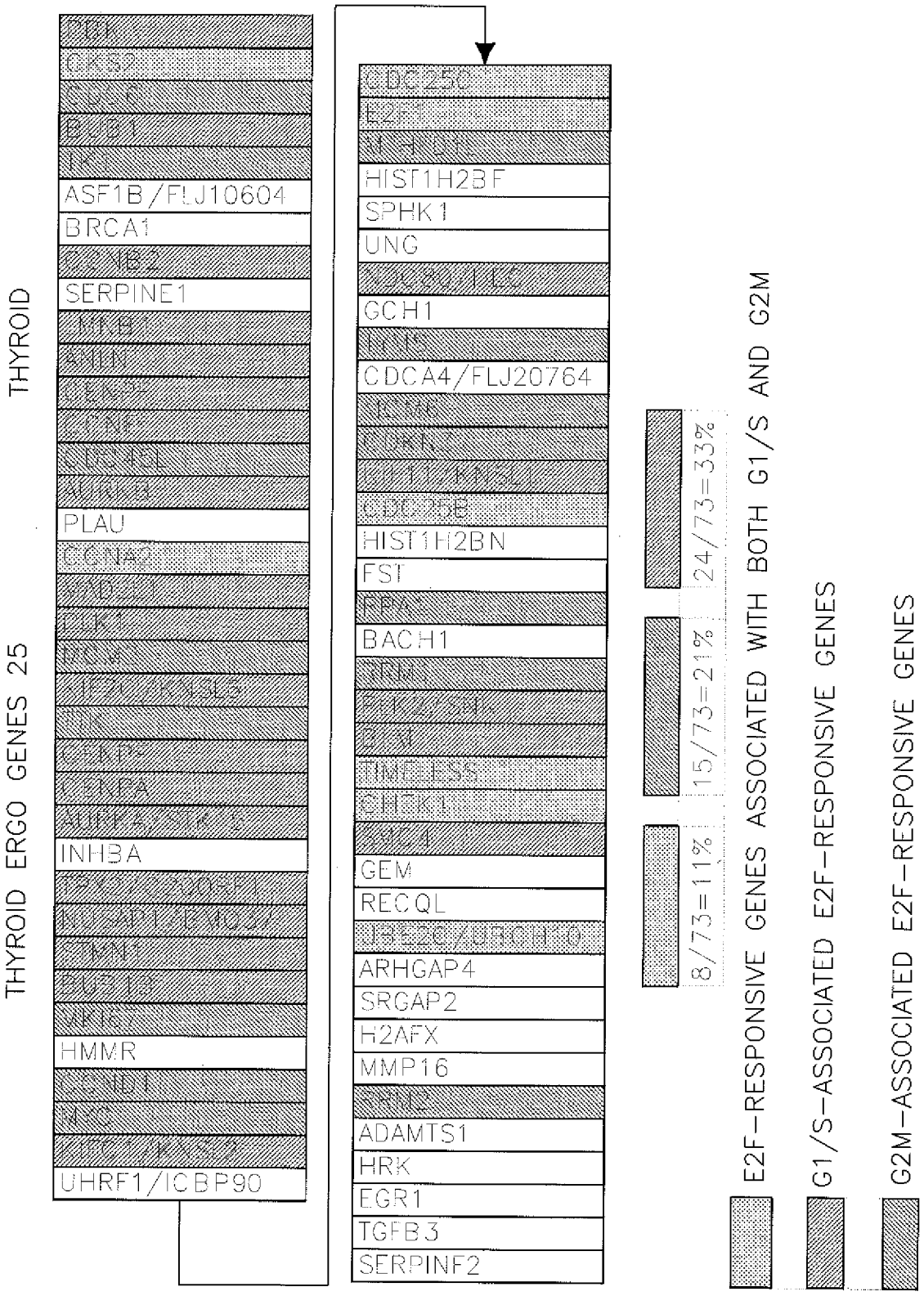

THYROID
THYROID ERGO GENES 25
ASF1B/FLJ10604
BRCA1
SERPINE1
PLAU
INHBA
HMMR
UHRF1/ICBP90
CDC25C
HIST1H2BF
SPHK1
UNG
GCH1
CDCA4/FLJ20764
HIST1H2BN
FST
BACH1
TIMELESS
GEM
RECQL
ARHGAP4
SRGAP2
H2AFX
MMP16
ADAMTS1
HRK
EGR1
TGFB3
SERPINF2
8/73=11%
15/73=21%
24/73=33%
E2F-RESPONSIVE GENES ASSOCIATED WITH BOTH G1/S AND G2M
G1/S-ASSOCIATED E2F-RESPONSIVE GENES
G2M-ASSOCIATED E2F-RESPONSIVE GENES

FIG. 17

BASAL-LIKE, PCA NON BASAL-LIKE
TOP 25 PUBLISHED BASAL-LIKE MARKERS
GENE NAME
TYPE
CDH3 dx/prog
KRT17 dx/prog
CRYAB dx/prog
SNL/fasc dx
ID4 dx
KRT5 dx/prog
VIM dx/prog
ACTG2 dx
CCNE1 dx/prog
EZH2 dx/prog
LAMB3 dx
KRT6B dx/prog
KRT14 dx/prog
MSN dx/prog
ANXA8 dx/prog
CCNE2 dx/prog
CD44 dx
ITGB4 dx/prog
S100A9 dx/prog
MCAM/cd dx/prog
KIT dx
KRT6A dx/prog
P63 dx
EGFR dx
TGFBR2 prog
SEE SHEET 2 FOR CONTINUATION

FIG. 18

BASAL-LIKE, PCA NON BASAL-LIKE
TOP 25 PUBLISHED BASAL-LIKE MARKERS
GENE NAME
TYPE
CDH3 dx/prog
KRT17 dx/prog
CRYAB dx/prog
SNL/fasc dx
ID4 dx
KRT5 dx/prog
VIM dx/prog
ACTG2 dx
CCNE1 dx/prog
EZH2 dx/prog
LAMB3 dx
KRT16B dx/prog
KRT14 dx/prog
MSN dx/prog
ANXA8 dx/prog
CCNE2 dx/prog
CD44 dx
ITGB4 dx/prog
S100A9 dx/prog
MCAM/cd dx/prog
KIT dx
KRT6A dx/prog
P63 dx
EGFR dx
TGFBR2 prog
SEE SHEET 3 FOR CONTINUATION

FIG. 18

BASAL–LIKE, PCA NON BASAL–LIKE
TOP 25 PUBLISHED BASAL–LIKE MARKERS

CDH3	dx/prog
KRT17	dx/prog
CRYAB	dx/prog
SNL/fosc	dx
ID4	dx
KRT5	dx/prog
VIM	dx/prog
ACTG2	dx
CCNE1	dx/prog
EZH2	dx/prog
LAMB3	dx
KRT6B	dx/prog
KRT14	dx/prog
MSN	dx/prog
ANXA8	dx/prog
CCNE2	dx/prog
CD44	dx
ITGB4	dx/prog
S100A9	dx/prog
MCAM/cc	dx/prog
KIT	dx
KRT6A	dx/prog
P63	dx
EGFR	dx
TGFBR2	prog

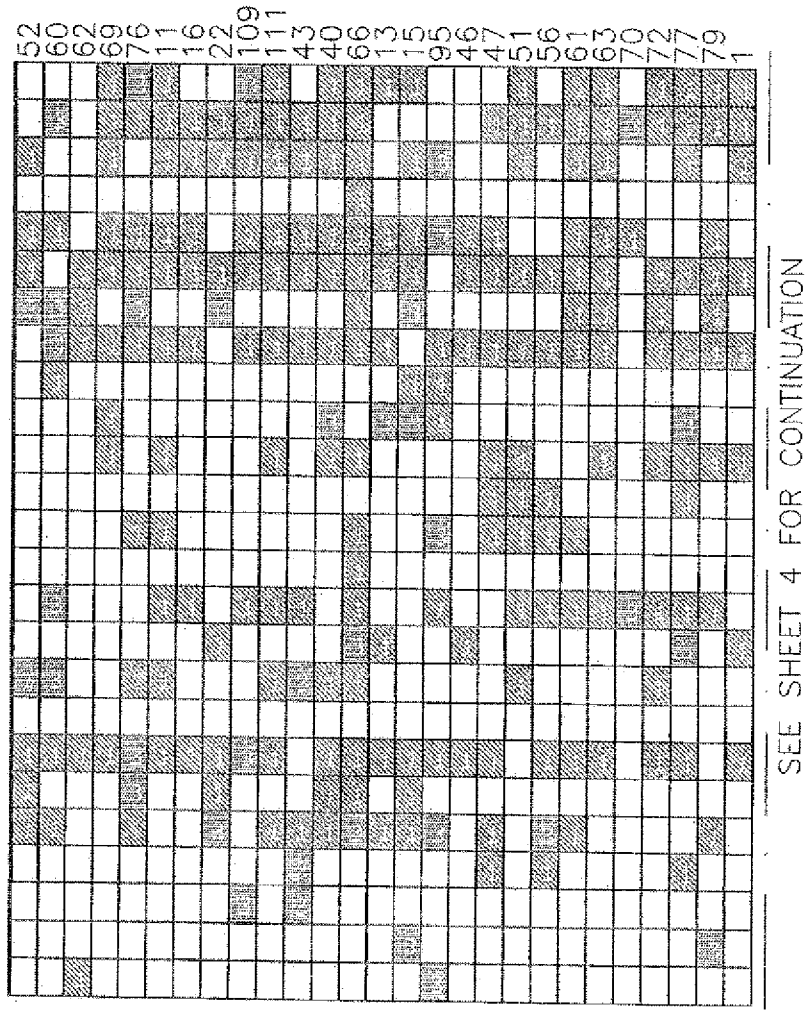


FIG. 18

WO 2010/056931 PCT/US2009/064294

BASAL-LIKE, PCA NON BASAL-LIKE
TOP 25 PUBLISHED BASAL-LIKE MARKERS

CDH3	dx/prog
KRT17	dx/prog
CRYAB	dx/prog
SNL/fosc	dx
ID4	dx
KRT5	dx/prog
VIM	dx/prog
ACTG2	dx
CCNE1	dx/prog
EZH2	dx/prog
LAMB3	dx
KRT6B	dx/prog
KRT14	dx/prog
MSN	dx/prog
ANXA8	dx/prog
CCNE2	dx/prog
CD44	dx
ITGB4	dx/prog
S100A9	dx/prog
MCAM/cc	dx/prog
KIT	dx
KRT6A	dx/prog
P63	dx
EGFR	dx
TGFBR2	prog

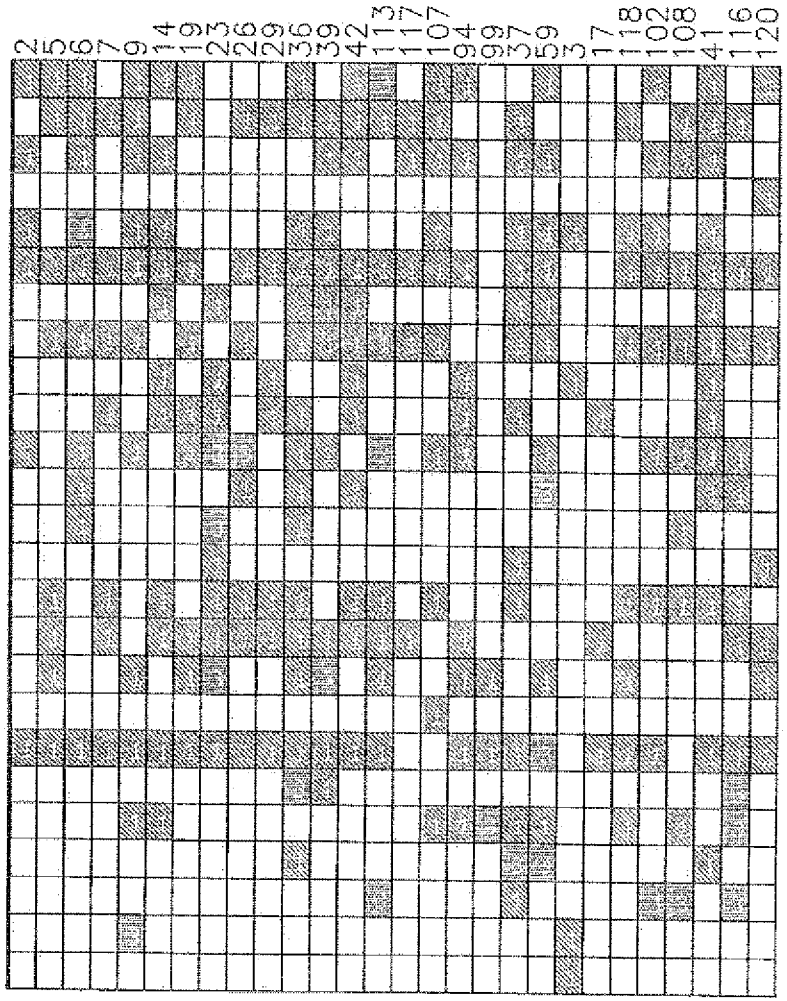


FIG. 18

BASAL-LIKE, PCA NON BASAL-LIKE
TOP 25 PUBLISHED BASAL-LIKE MARKERS

CDH3	dx/prog
KRT17	dx/prog
CRYAB	dx/prog
SNL/fasc	dx
ID4	dx
KRT5	dx/prog
VIM	dx/prog
ACTG2	dx
CCNE1	dx/prog
EZH2	dx/prog
LAMB3	dx
KRT6B	dx/prog
KRT14	dx/prog
MSN	dx/prog
ANXA8	dx/prog
CCNE2	dx/prog
CD44	dx
ITGB4	dx/prog
S100A9	dx/prog
MCAM/cc	dx/prog
KIT	dx
KRT6A	dx/prog
P63	dx
EGFR	dx
TGFBR2	prog

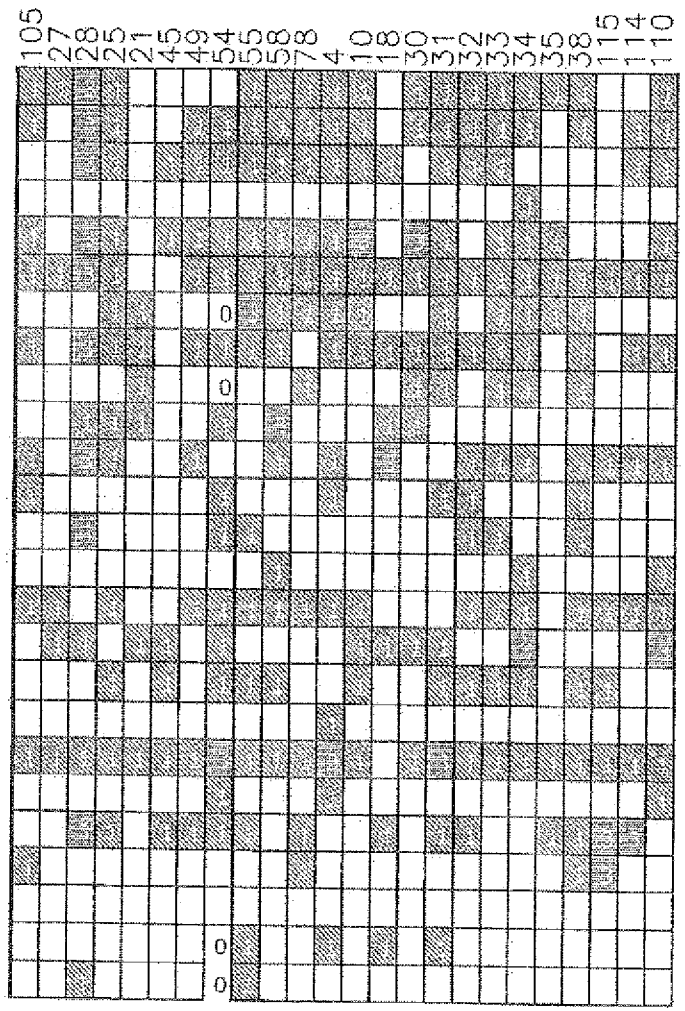
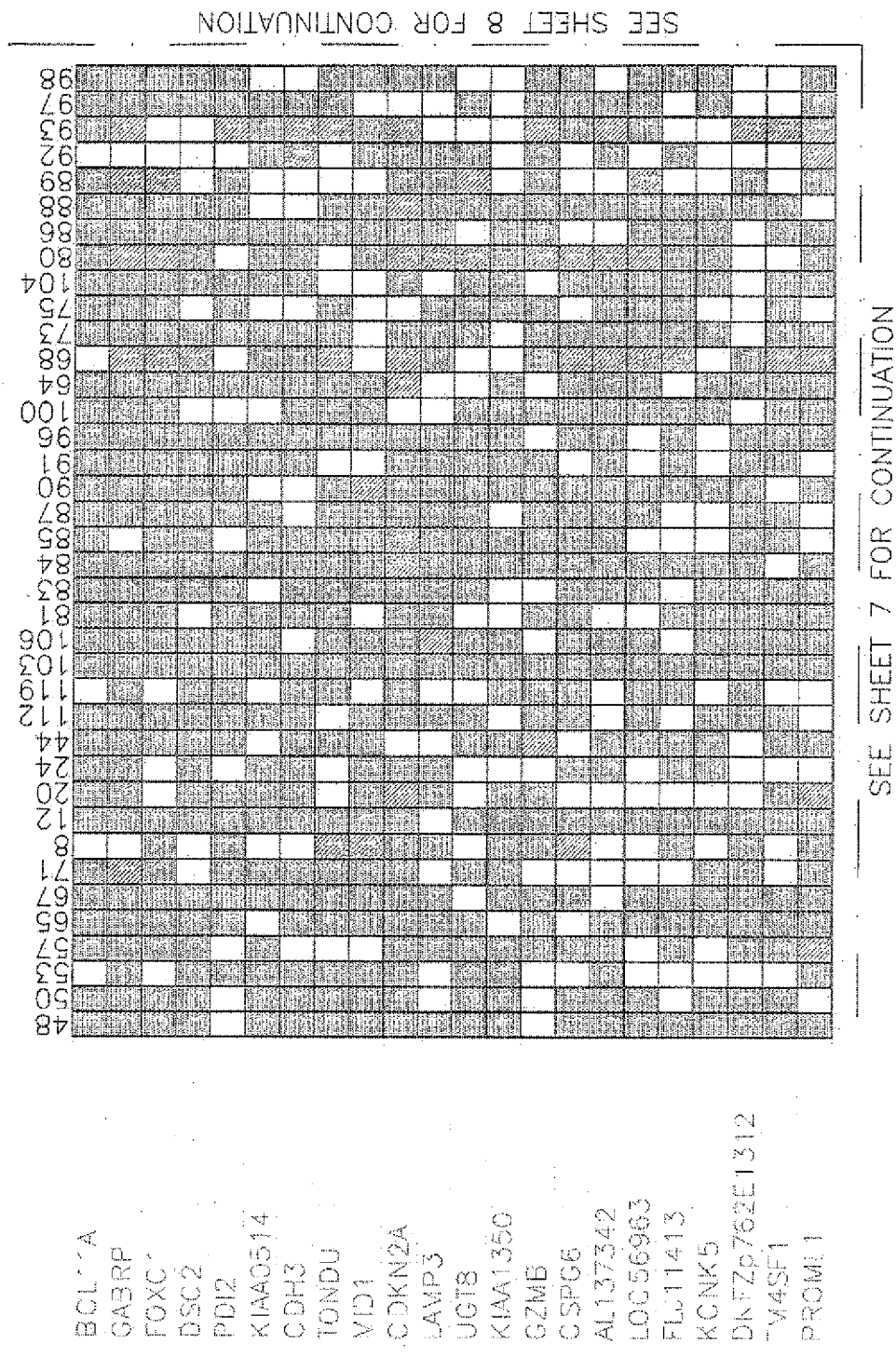


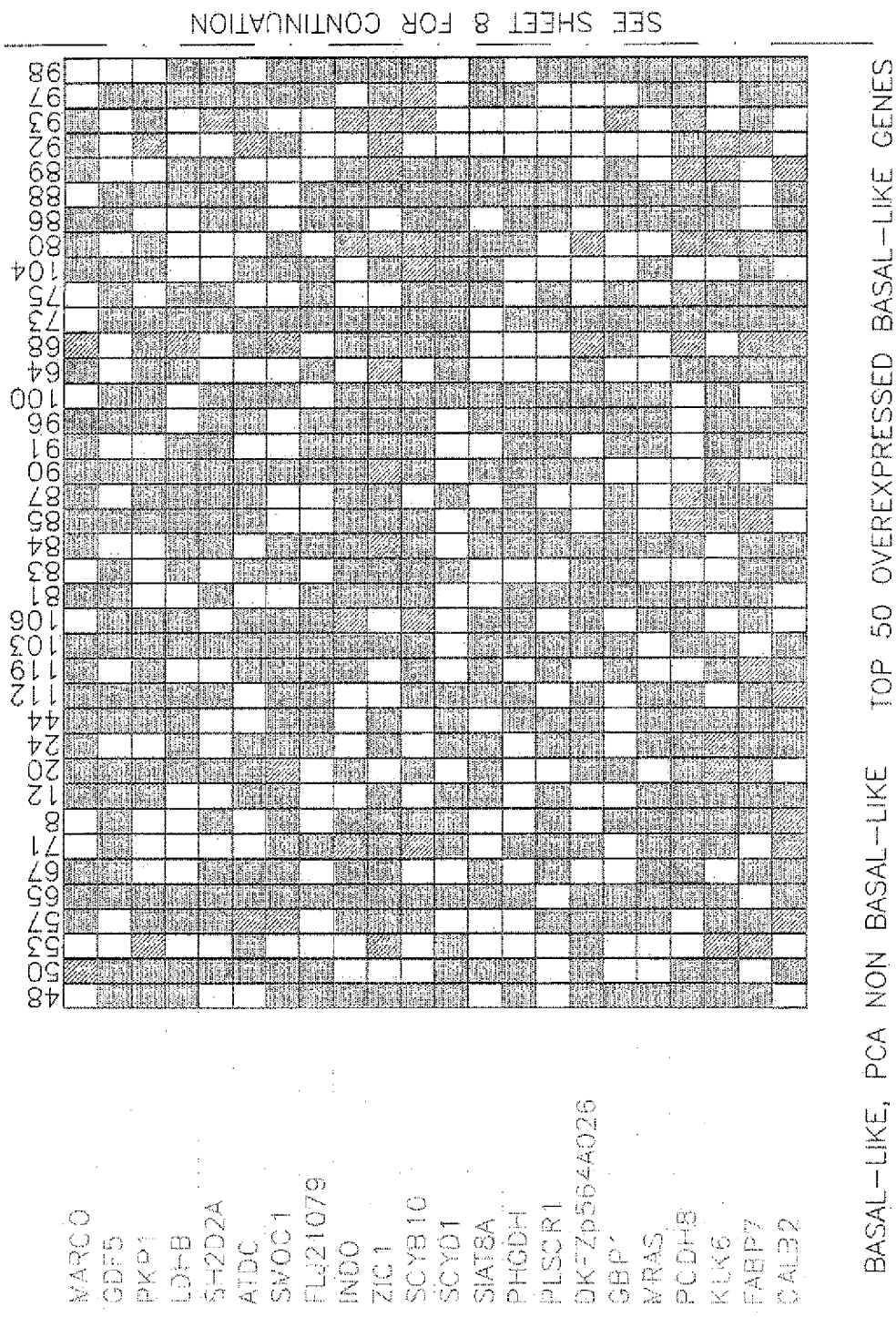
FIG. 18

WO 2010/056931 PCT/US2009/064294



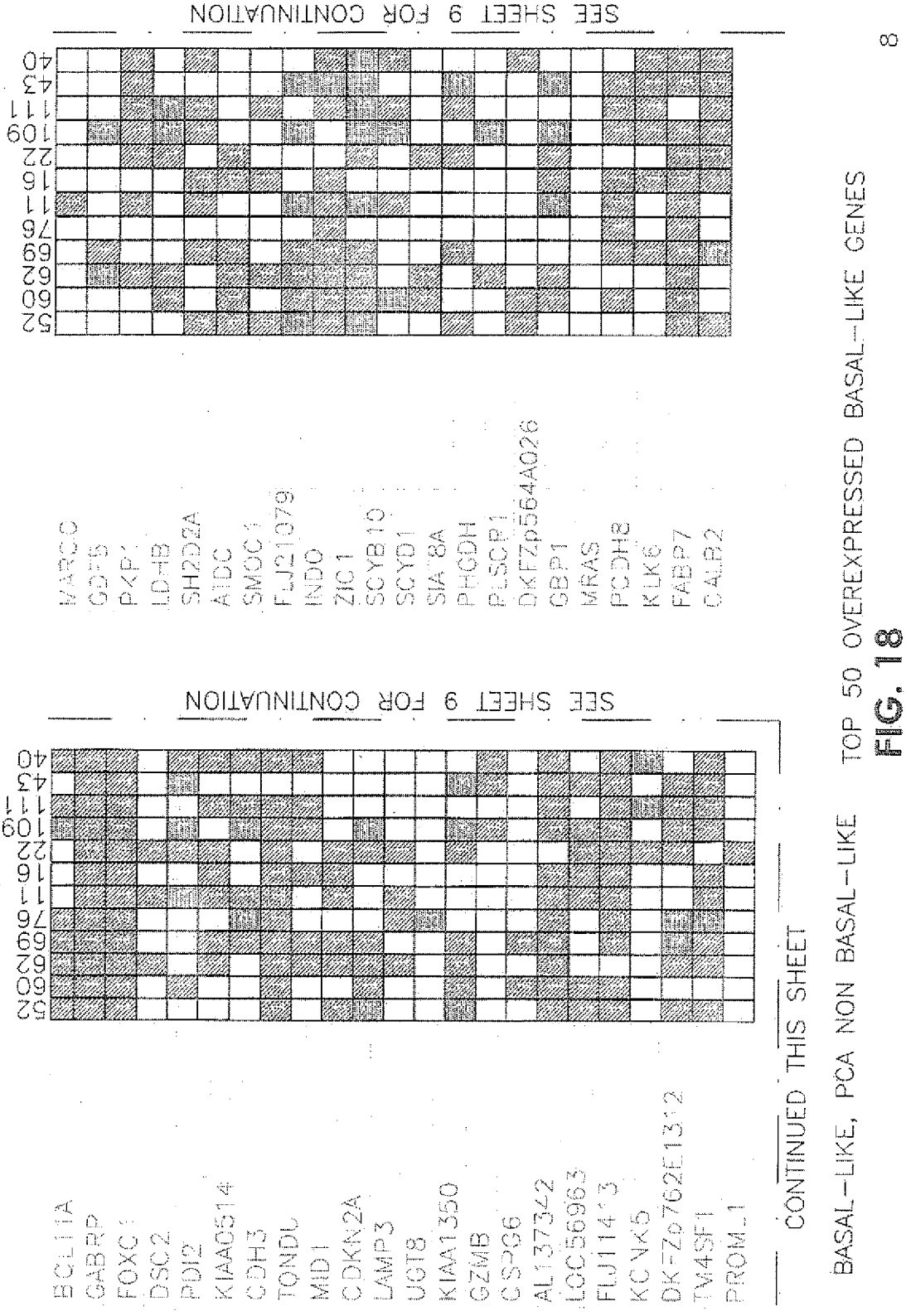
BASAL-LIKE, PCA NON BASAL-LIKE TOP 50 OVEREXPRESSED BASAL-LIKE GENES

FIG. 18



BASAL-LIKE, PCA NON BASAL-LIKE TOP 50 OVEREXPRESSED BASAL-LIKE GENES

FIG. 18



BASAL-LIKE, PCA NON BASAL-LIKE TOP 50 OVEREXPRESSED BASAL-LIKE GENES

FIG. 18

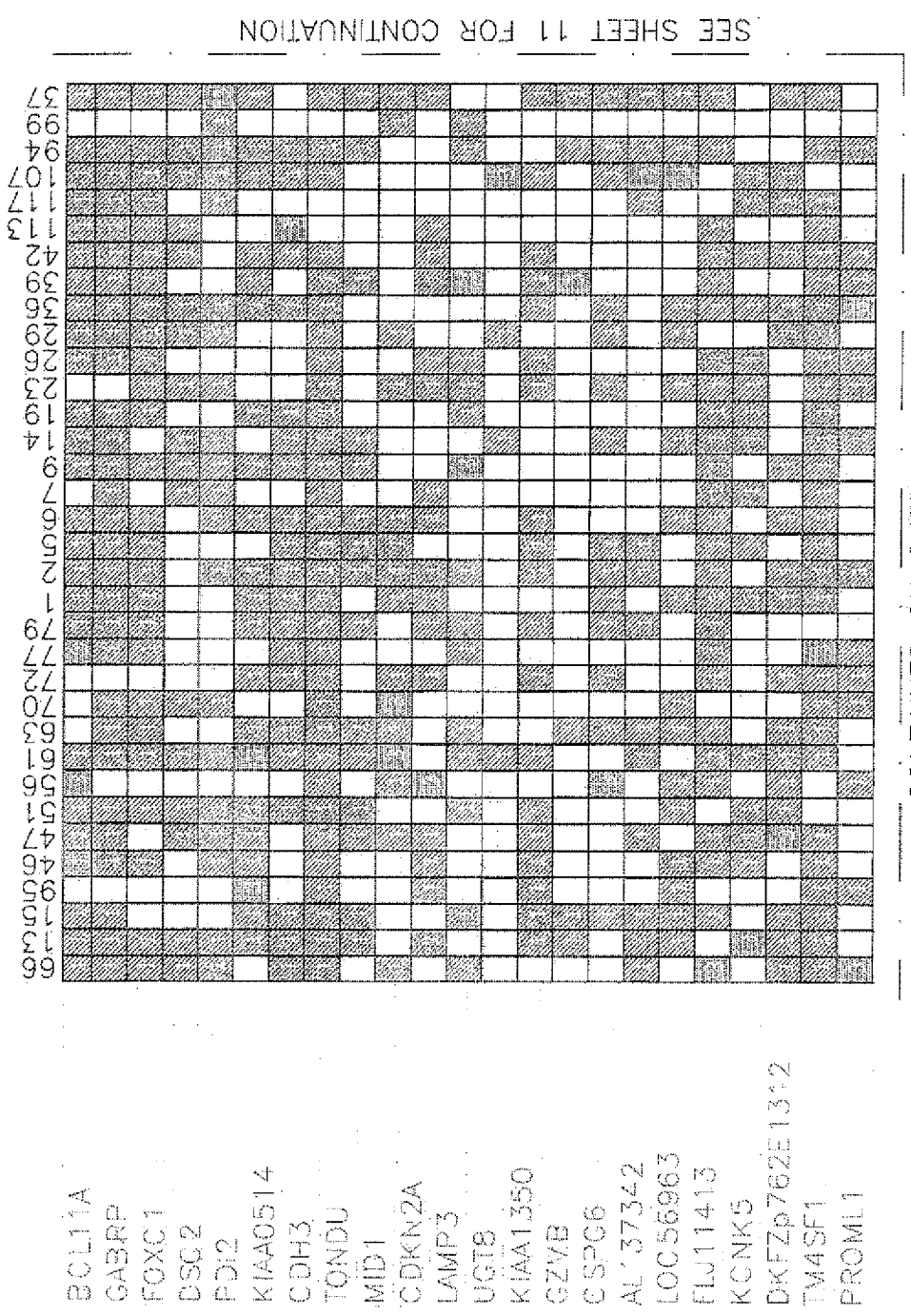
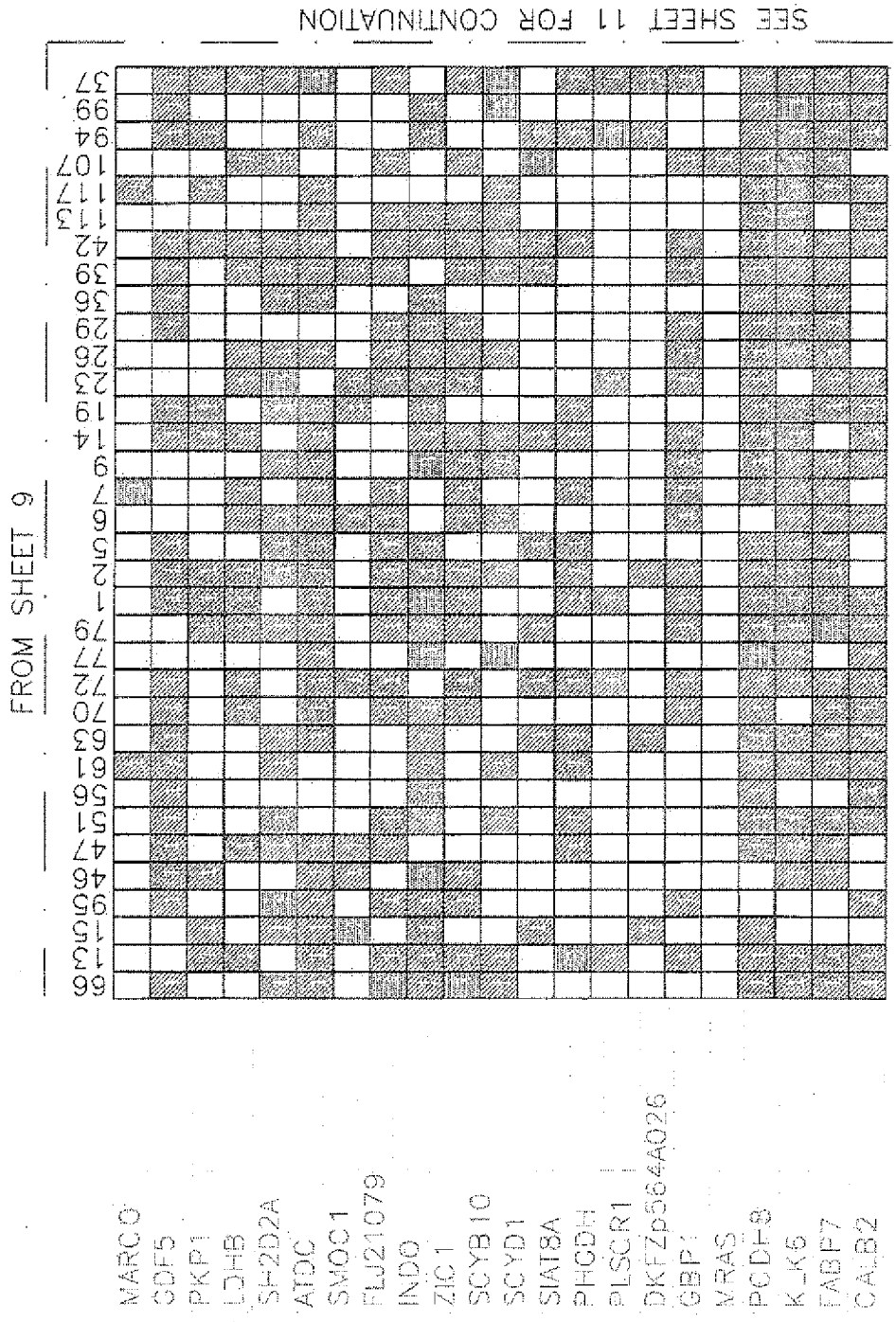
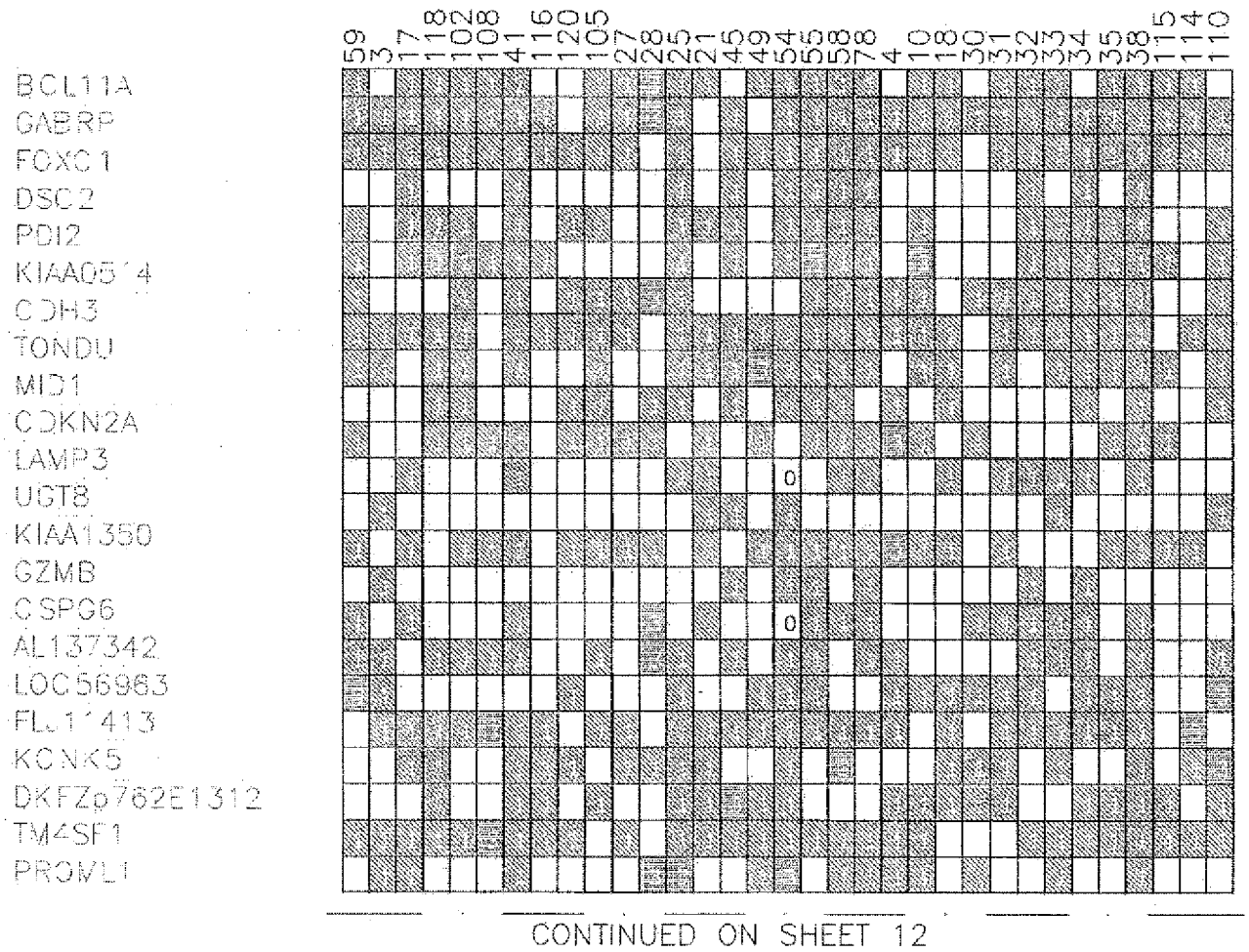

SEE SHEET 11 FOR CONTINUATION
BCL11A
GABRP
FOXC1
DSC2
PDI2
KIAA0514
CDH3
TONDU
MID1
CDKN2A
LAMP3
UGT8
KIAA1350
GZMB
CSPG6
AL137342
LOC56963
FLJ11413
KCNK5
DKFZp762E1312
TM4SF1
PROML1
CONTINUED ON SHEET 10
BASAL-LIKE, PCA NON BASAL-LIKE TOP 50 OVEREXPRESSED BASAL-LIKE GENES

FIG. 18



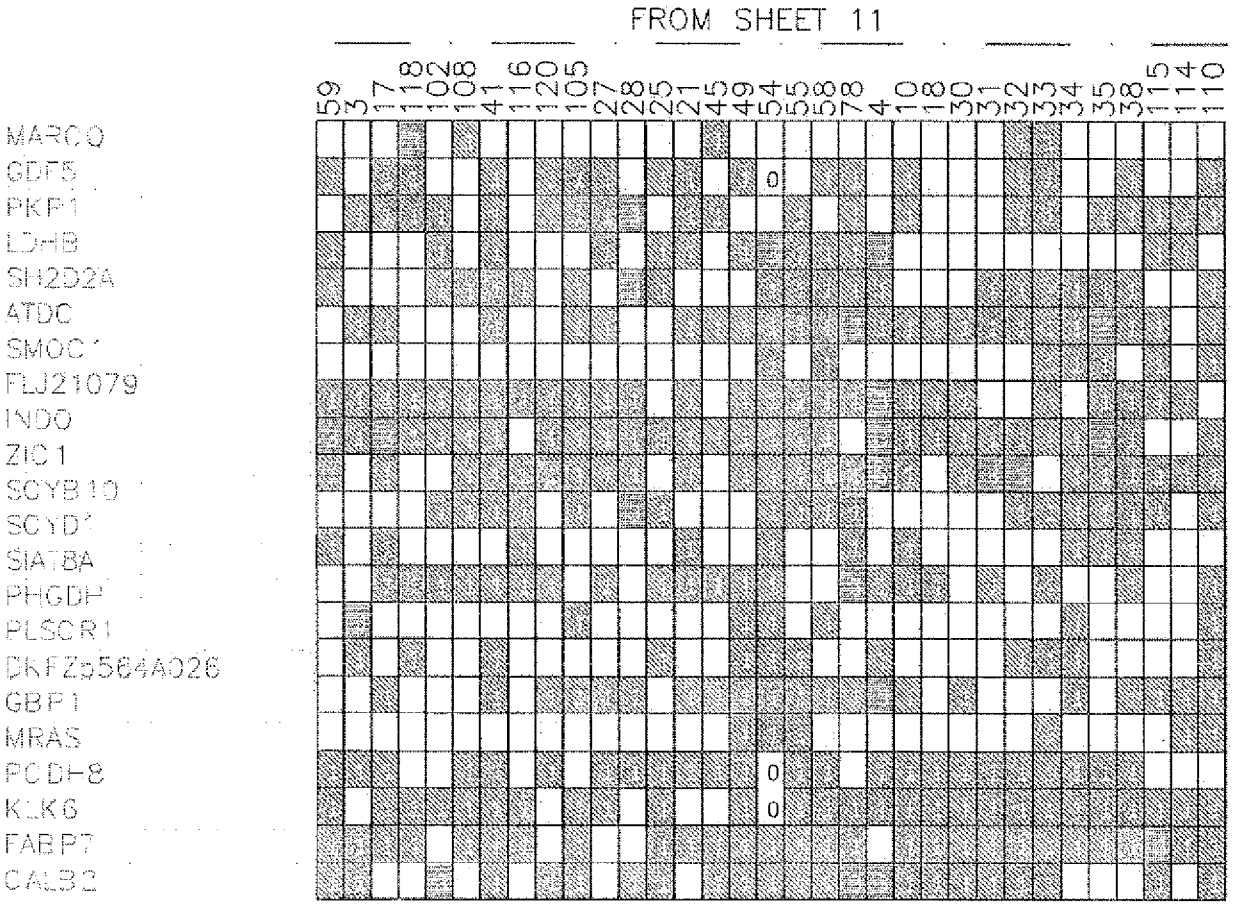
BASAL-LIKE, PCA NON BASAL-LIKE TOP 50 OVEREXPRESSED BASAL-LIKE GENES

FIG. 18



BASAL-LIKE, PCA NON BASAL-LIKE TOP 50 OVEREXPRESSED BASAL-LIKE GENES

FIG. 18



BASAL–LIKE, PCA NON BASAL–LIKE TOP 50 OVEREXPRESSED BASAL–LIKE GENES

FIG. 18

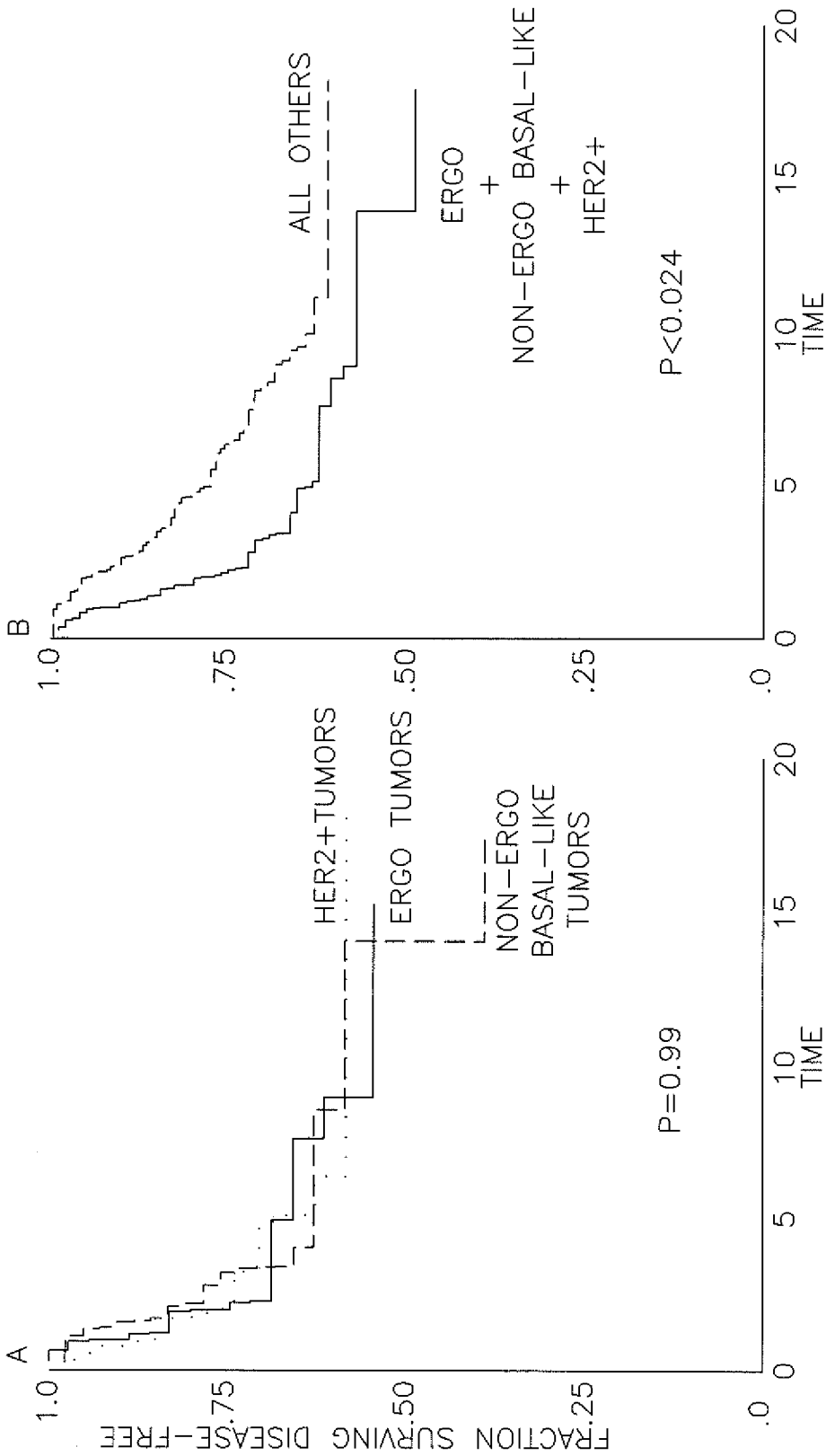

A
B
1.0
.75
.50
.25
.0
FRACTION SURVIVING DISEASE-FREE
0
5
10
15
20
TIME
TIME, YEARS
HER2+TUMORS
ERGO TUMORS
NON-ERGO BASAL-LIKE TUMORS
P=0.99
ALL OTHERS
ERGO + NON-ERGO BASAL-LIKE + HER2+
P<0.024

FIG. 19

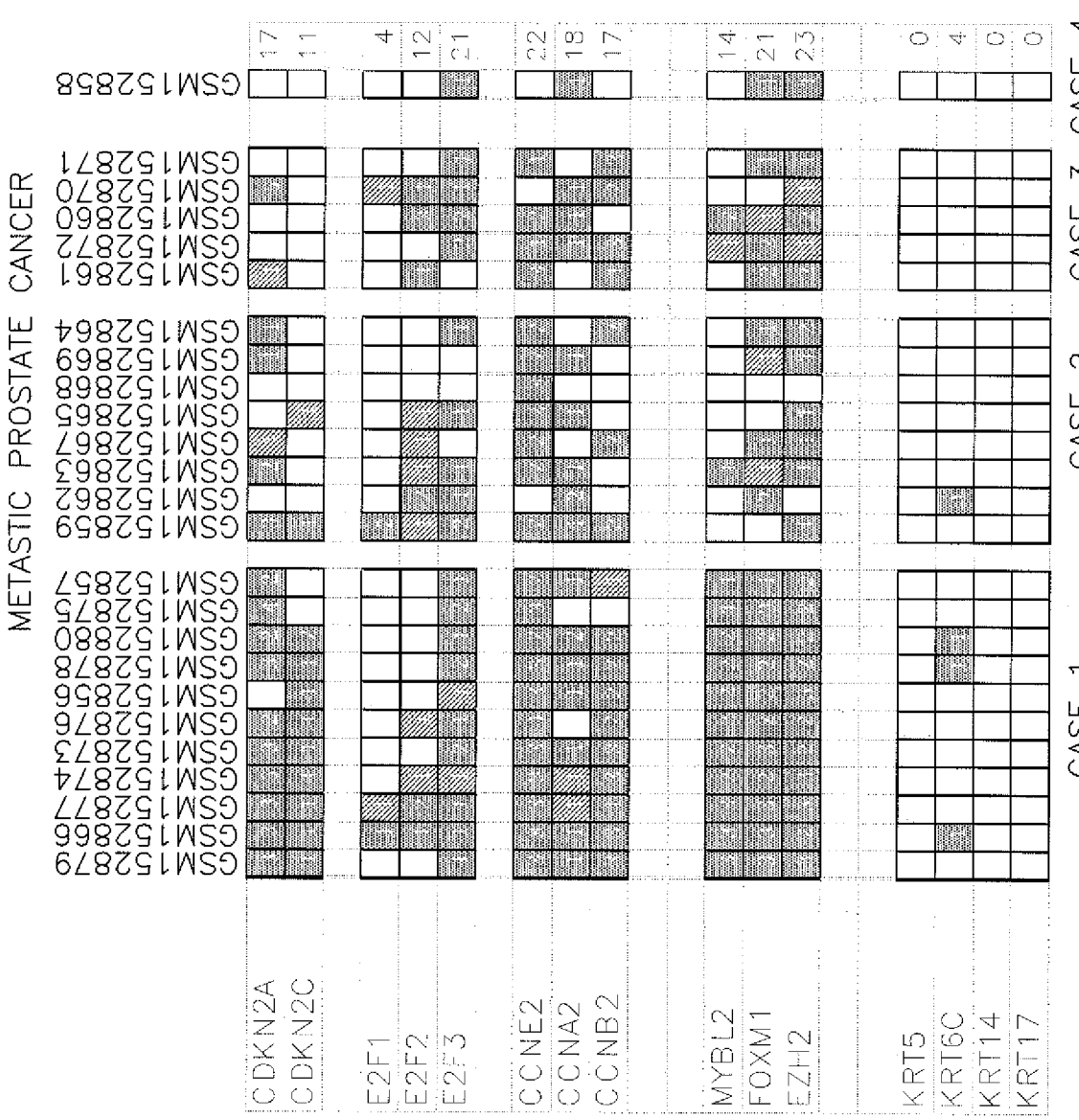

SEE SHEET 2 FOR CONTINUATION
METASTIC PROSTATE CANCER
GSM152879
GSM152866
GSM152877
GSM152874
GSM152873
GSM152876
GSM152856
GSM152878
GSM152880
GSM152875
GSM152857
GSM152859
GSM152862
GSM152863
GSM152867
GSM152865
GSM152868
GSM152869
GSM152864
GSM152861
GSM152872
GSM152860
GSM152870
GSM152871
GSM152858
CDKN2A
CDKN2C
E2F1
E2F2
E2F3
CCNE2
CCNA2
CCNB2
MYBL2
FOXM1
EZH2
KRT5
KRT6C
KRT14
KRT17
17 11
4 12 21
22 18 17
14 21 23
0 4 0 0
CASE 1
CASE 2
CASE 3
CASE 4

FIG. 20

ADVANCED ERGO PCA PATTERN(DOTS)
TRANSITIONAL PCA PATTERN (WHITE)
SEE SHEET 3 FOR CONTINUATION
PRIMARY PROSTATE CANCER
GG:=GLEASON GRADE
CDKN2A
CDKN2C
E2F1
E2F2
E2F3
CCNE2
CCNA2
CCNB2
MYBL2
FOXM1
EZH2
KRT5
KRT6C
KRT14
KRT17

FIG. 20

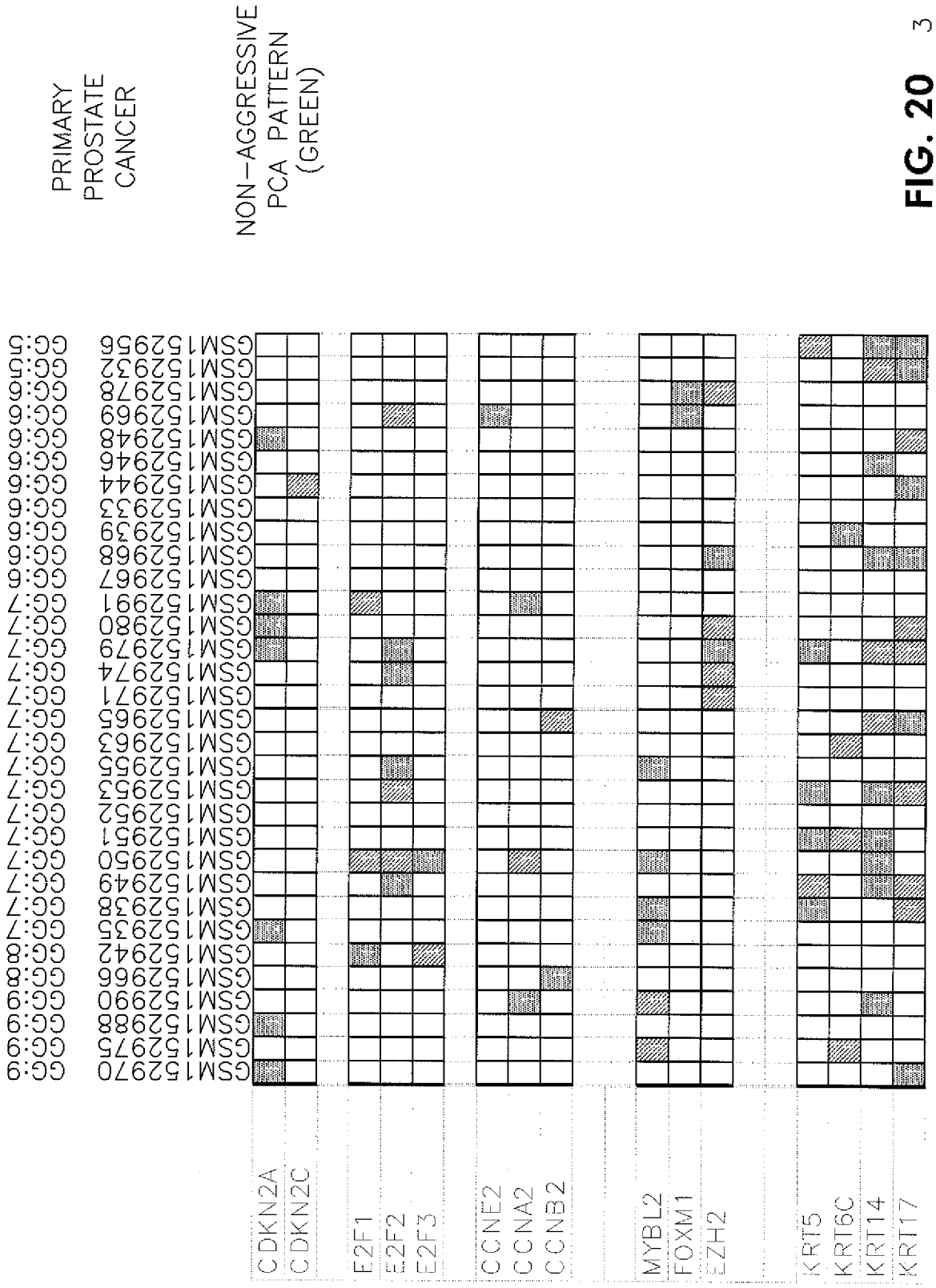
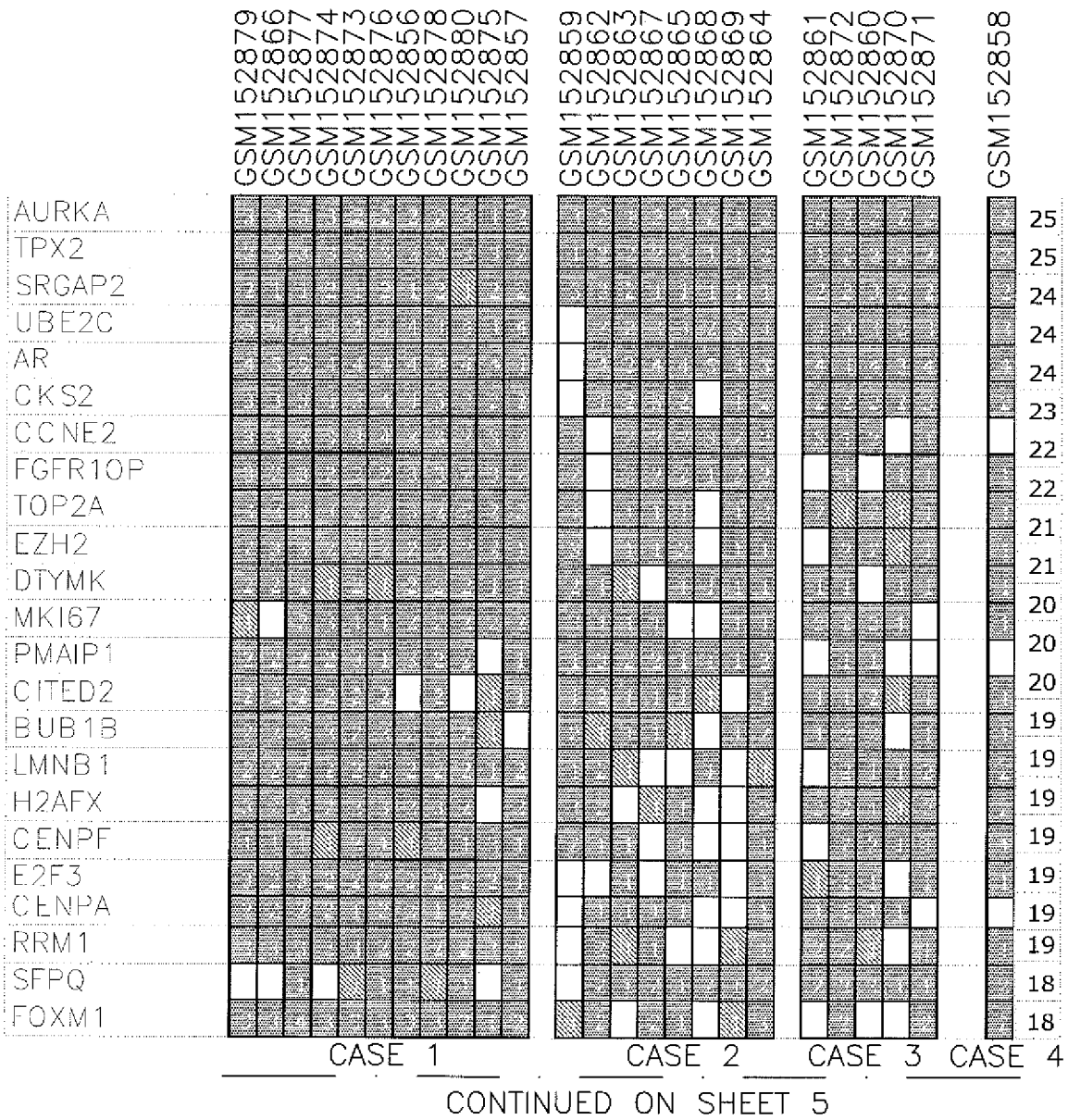
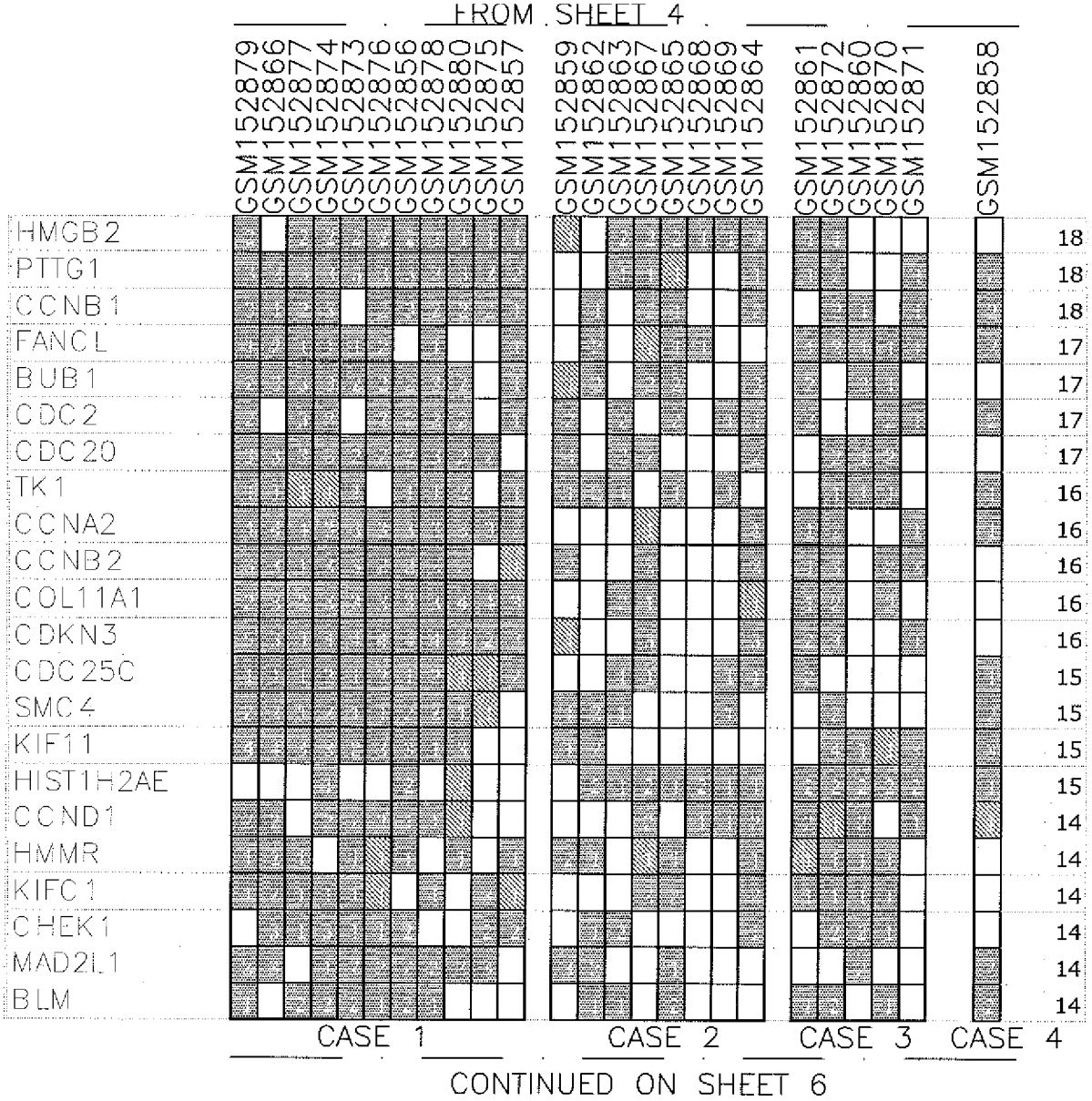

PRIMARY PROSTATE CANCER
NON–AGGRESSIVE PCA PATTERN (GREEN)
GSM152970 GG:9
GSM152975 GG:9
GSM152988 GG:9
GSM152990 GG:9
GSM152966 GG:8
GSM152942 GG:8
GSM152955 GG:7
GSM152958 GG:7
GSM152949 GG:7
GSM152950 GG:7
GSM152951 GG:7
GSM152952 GG:7
GSM152953 GG:7
GSM152955 GG:7
GSM152963 GG:7
GSM152965 GG:7
GSM152971 GG:7
GSM152974 GG:7
GSM152979 GG:7
GSM152980 GG:7
GSM152991 GG:7
GSM152967 GG:6
GSM152968 GG:6
GSM152939 GG:6
GSM152953 GG:6
GSM152944 GG:6
GSM152946 GG:6
GSM152948 GG:6
GSM152969 GG:6
GSM152978 GG:6
GSM152932 GG:6
GSM152956 GG:6
CDKN2A
CDKN2C
E2F1
E2F2
E2F3
CCNE2
CCNA2
CCNB2
MYBL2
FOXM1
EZH2
KRT5
KRT6C
KRT14
KRT17

FIG. 20 3



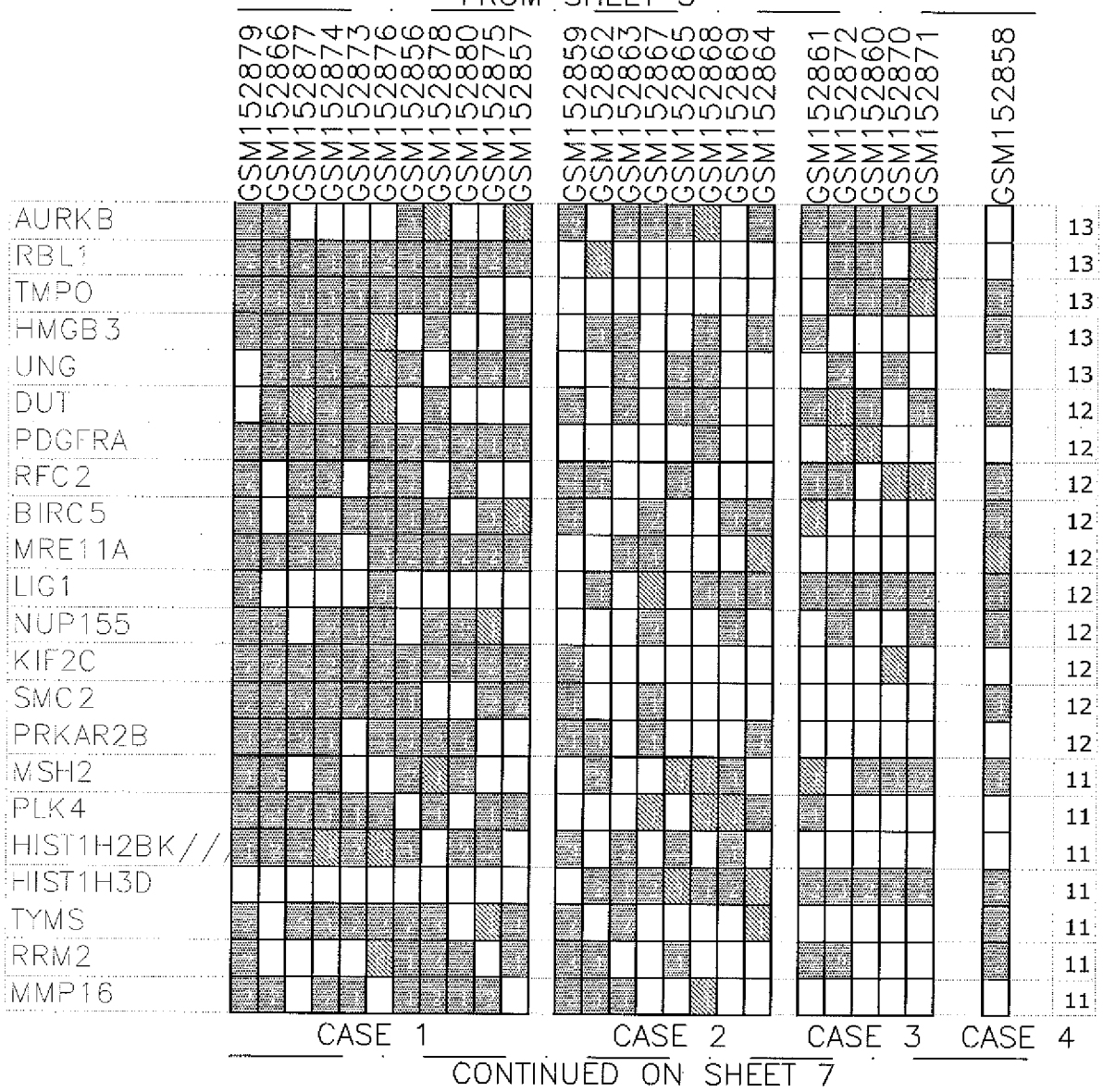
METASTIC PROSTATE CANCER

FIG. 20



METASTIC PROSTATE CANCER

FIG. 20



METASTIC PROSTATE CANCER

FIG. 20

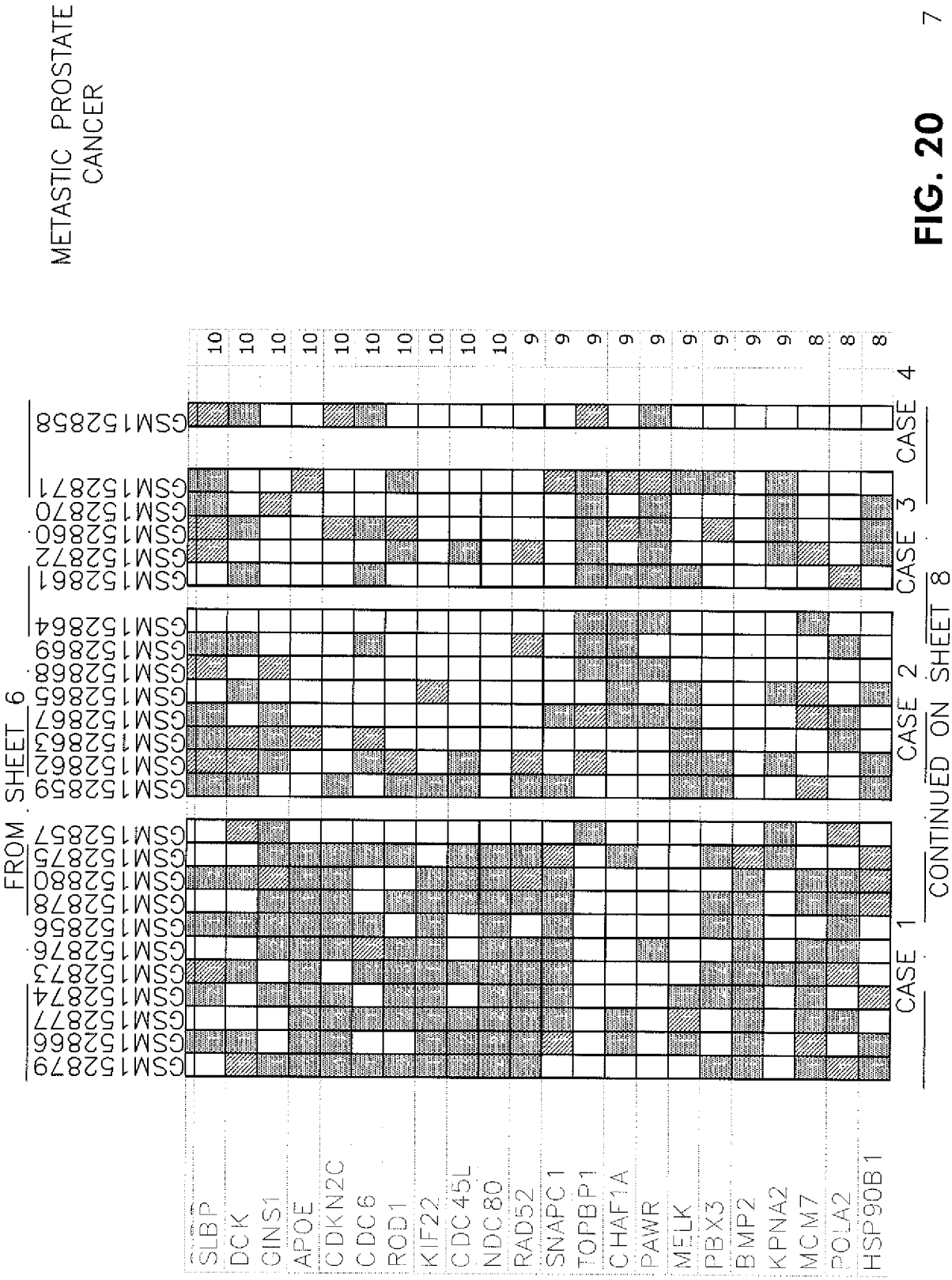

METASTIC PROSTATE CANCER
FROM SHEET 6
CONTINUED ON SHEET 8
CASE 1
CASE 2
CASE 3
CASE 4
SLBP
DCK
CINS1
APOE
CDKN2C
CDC6
ROD1
KIF22
CDC45L
NDC80
RAD52
SNAPC1
TOPBP1
CHAF1A
PAWR
MELK
PBX3
BMP2
KPNA2
MCM7
POLA2
HSP90B1

FIG. 20

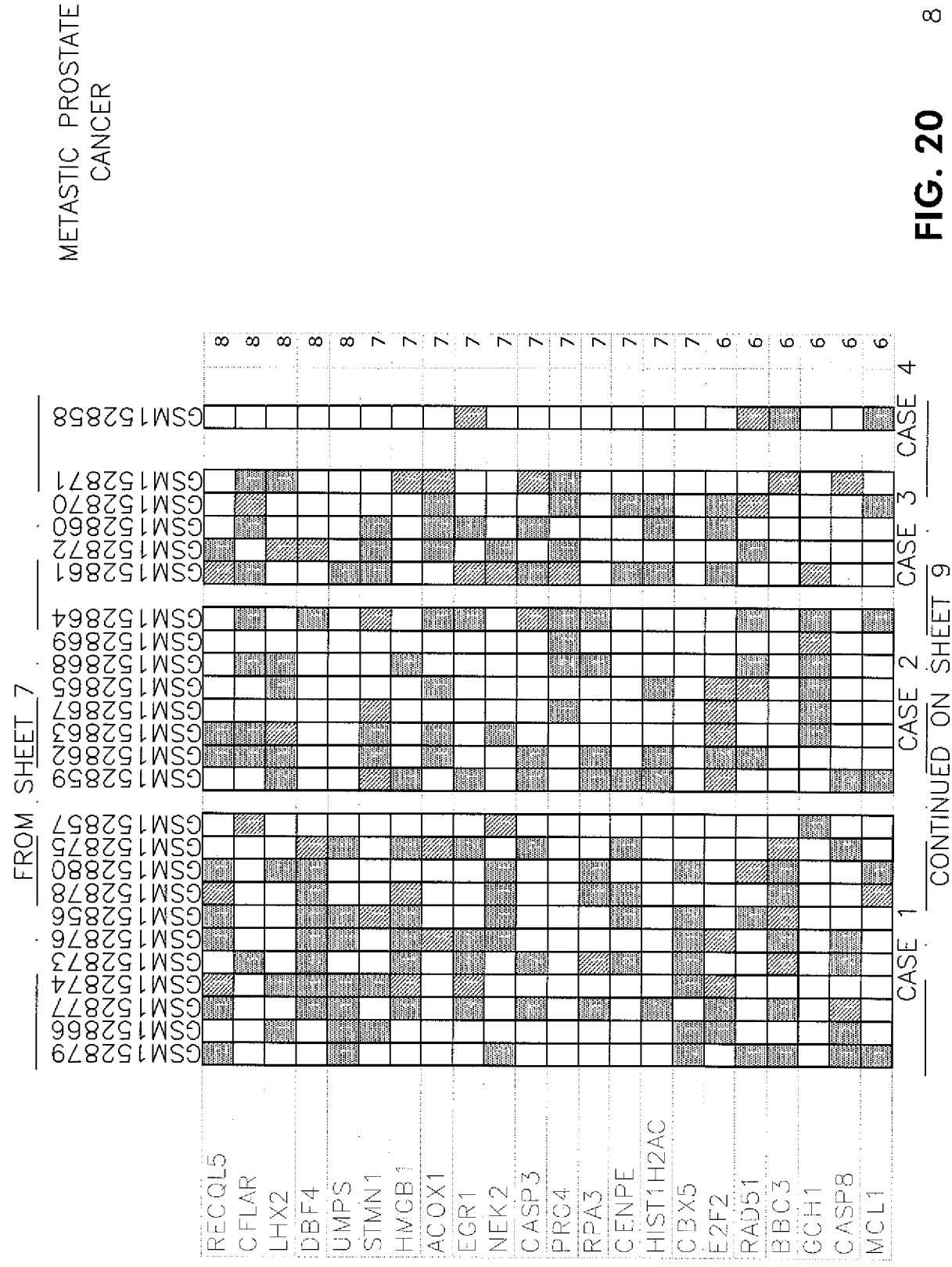
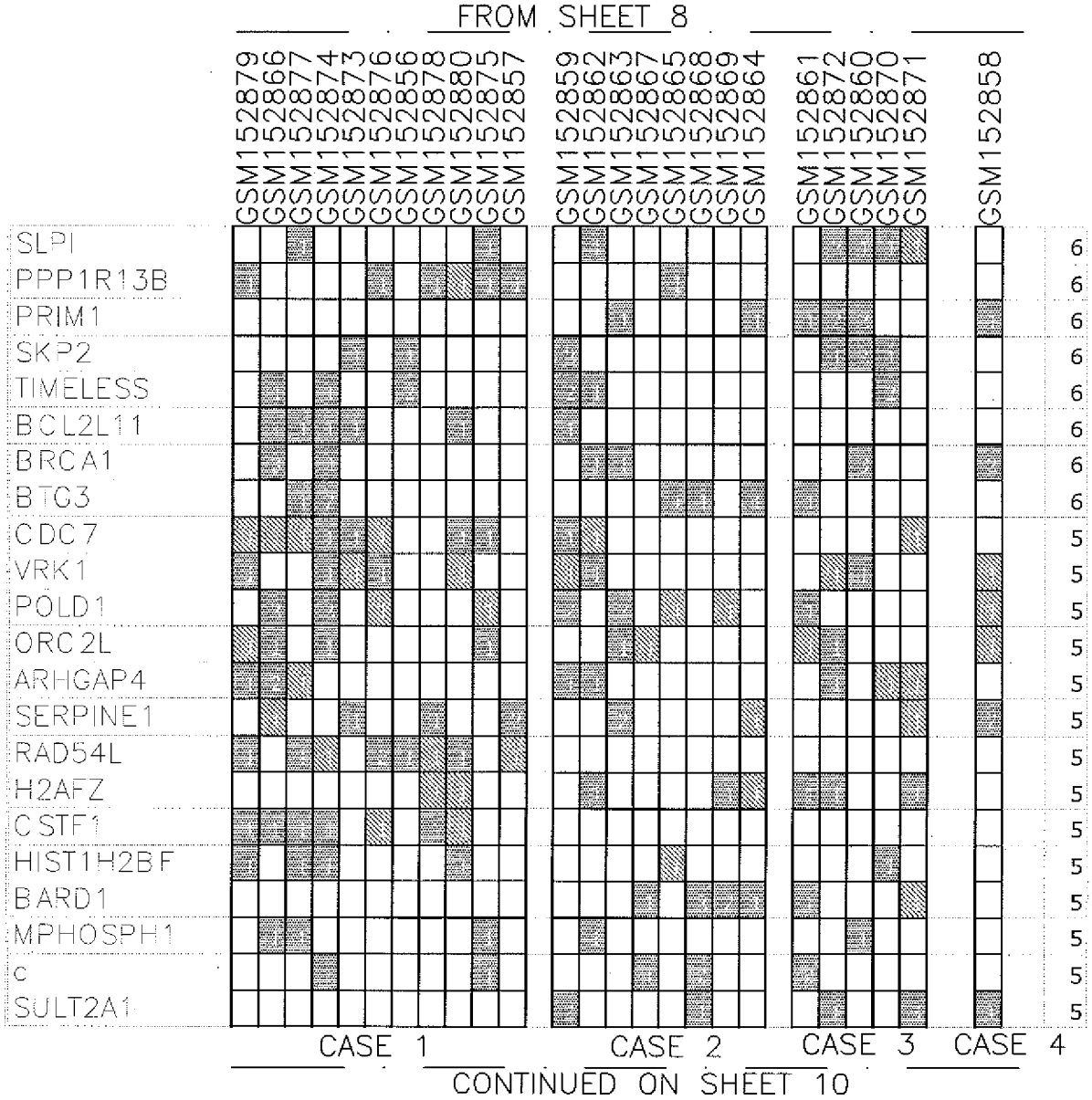

METASTIC PROSTATE CANCER
FROM SHEET 7
CONTINUED ON SHEET 9
CASE 1
CASE 2
CASE 3
CASE 4
RECQL5
CFLAR
LHX2
DBF4
UMPS
STMN1
HMGB1
ACOX1
EGR1
NEK2
CASP3
PRC4
RPA3
CENPE
HIST1H2AC
CBX5
E2F2
RAD51
BBC3
GCH1
CASP8
MCL1

FIG. 20



METASTIC PROSTATE CANCER

FIG. 20

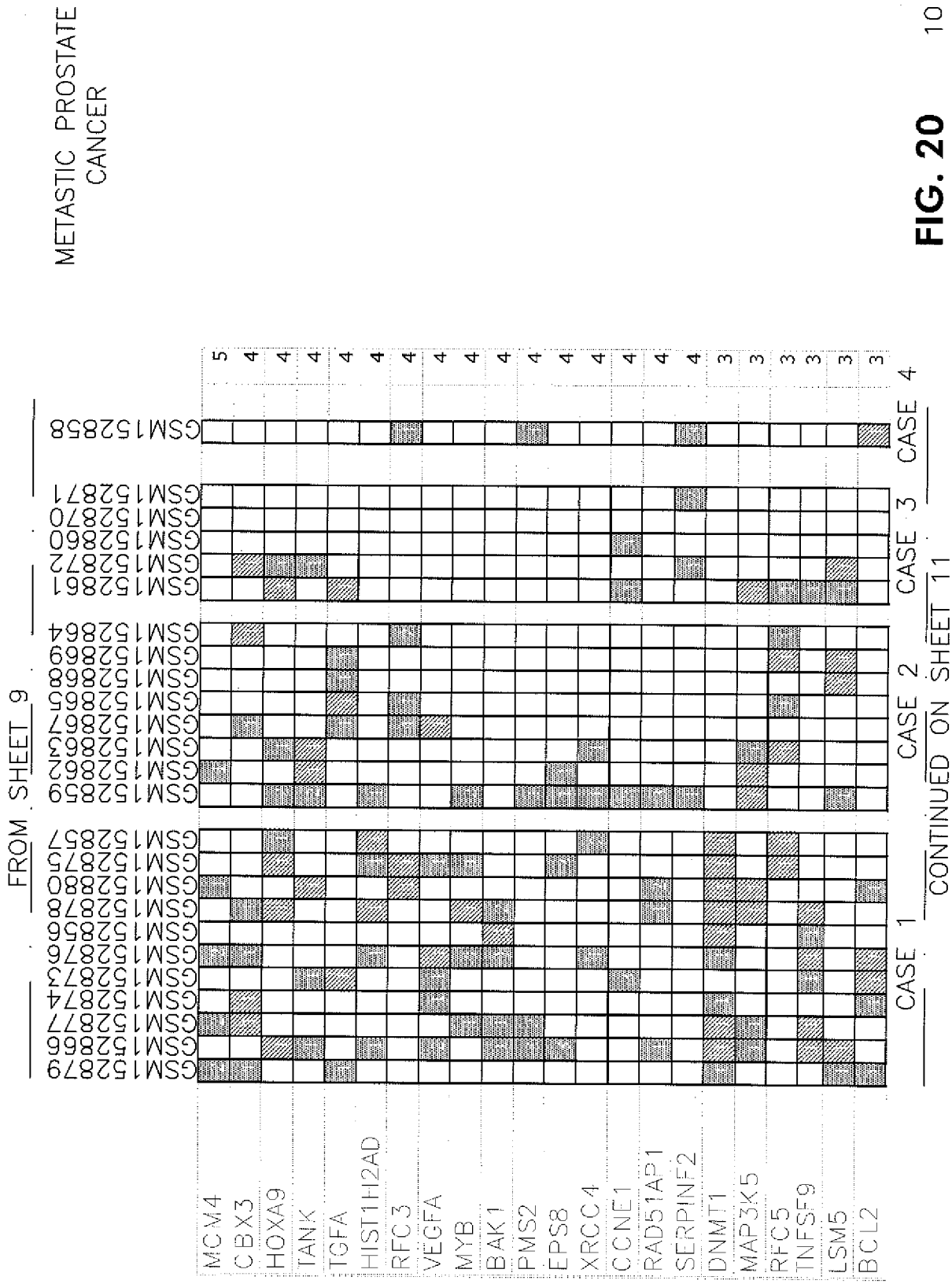
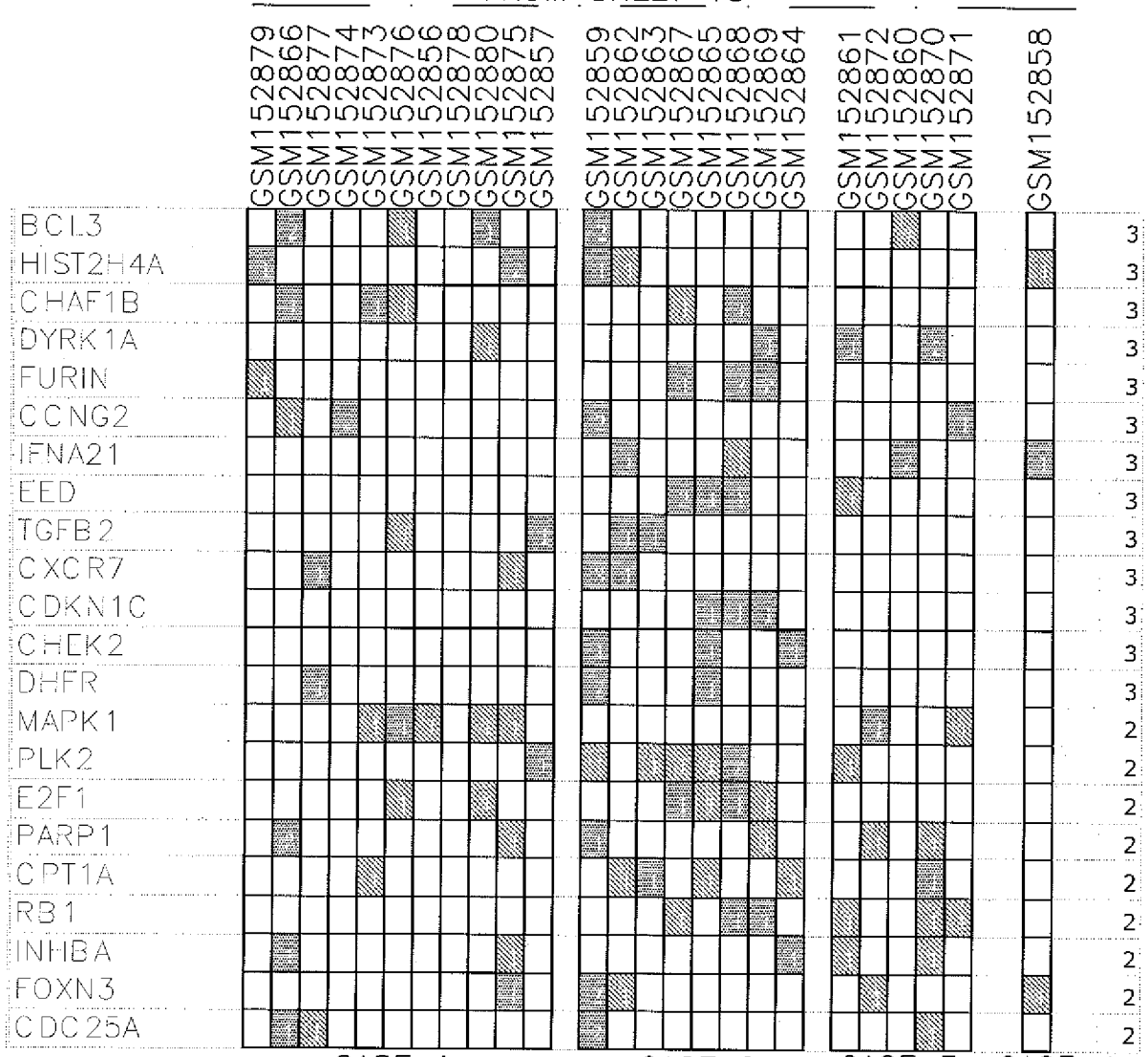

METASTIC PROSTATE CANCER
FROM SHEET 9
CONTINUED ON SHEET 11
CASE 1
CASE 2
CASE 3
CASE 4
MCM4
CBX3
HOXA9
TANK
TGFA
HIST1H2AD
RFC3
VEGFA
MYB
BAK1
PMS2
EPS8
XRCC4
CCNE1
RAD51AP1
SERPINF2
DNMT1
MAP3K5
RFC5
TNFSF9
LSM5
BCL2

FIG. 20

FROM SHEET 10



METASTIC PROSTATE CANCER

CONTINUED ON SHEET 12

FIG. 20

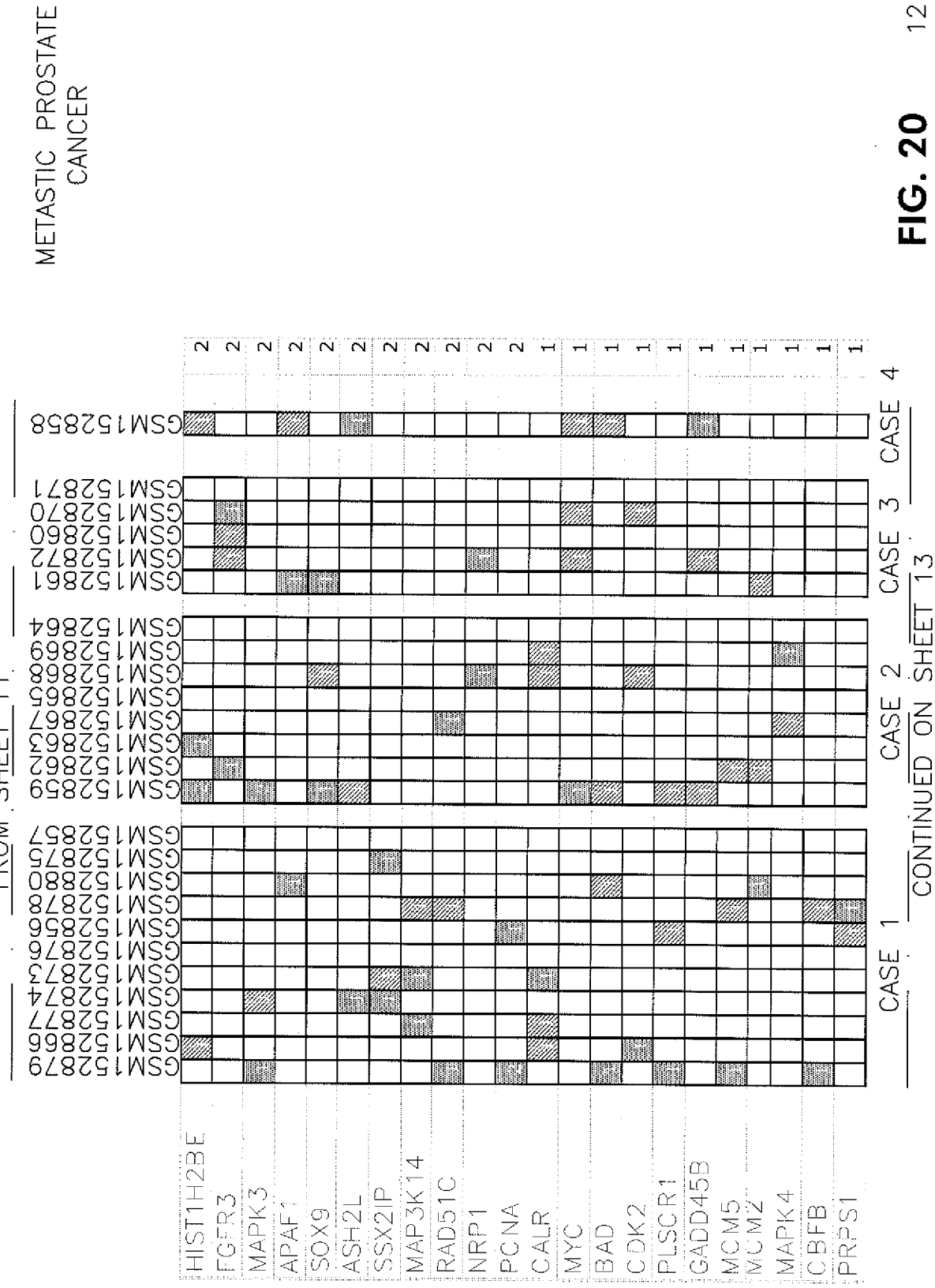
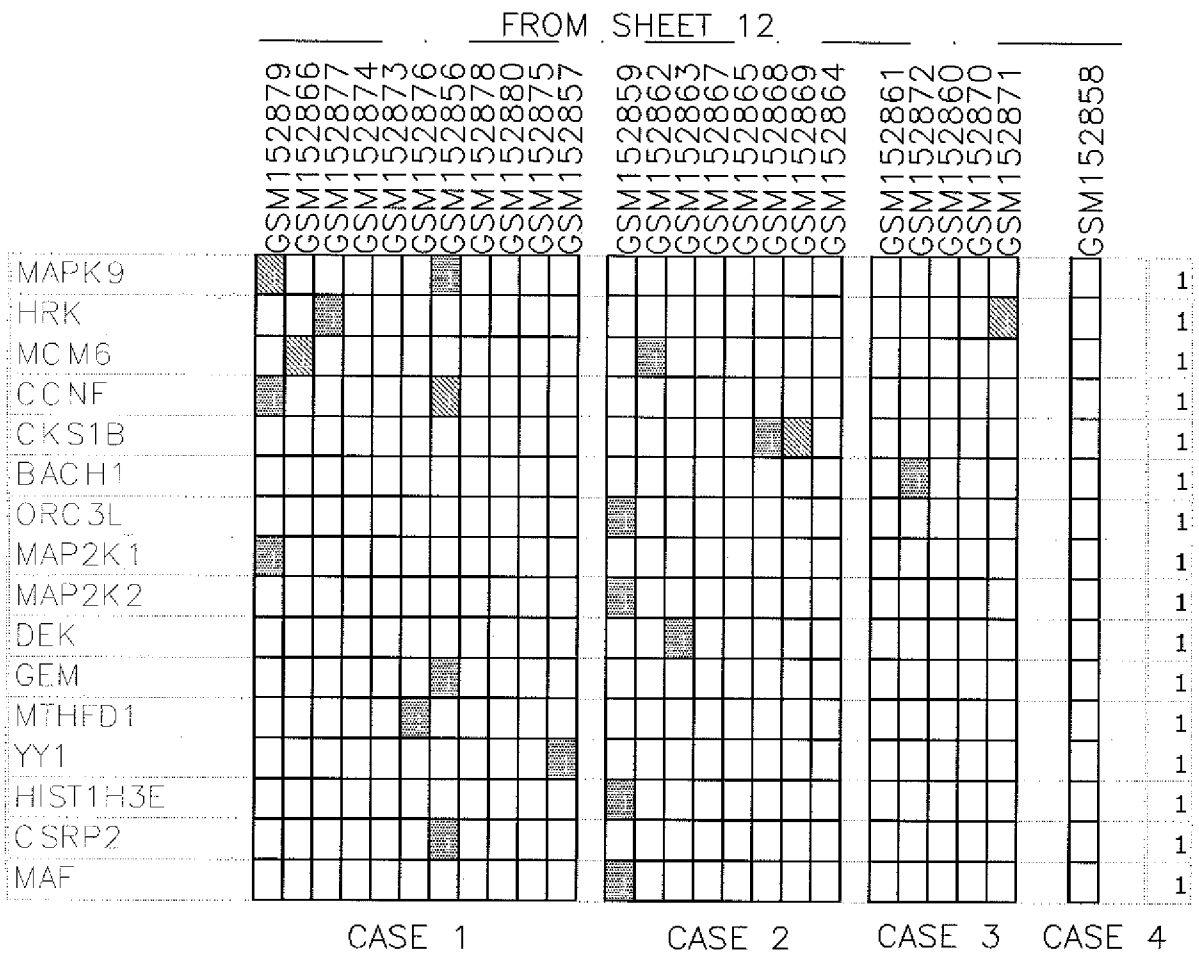
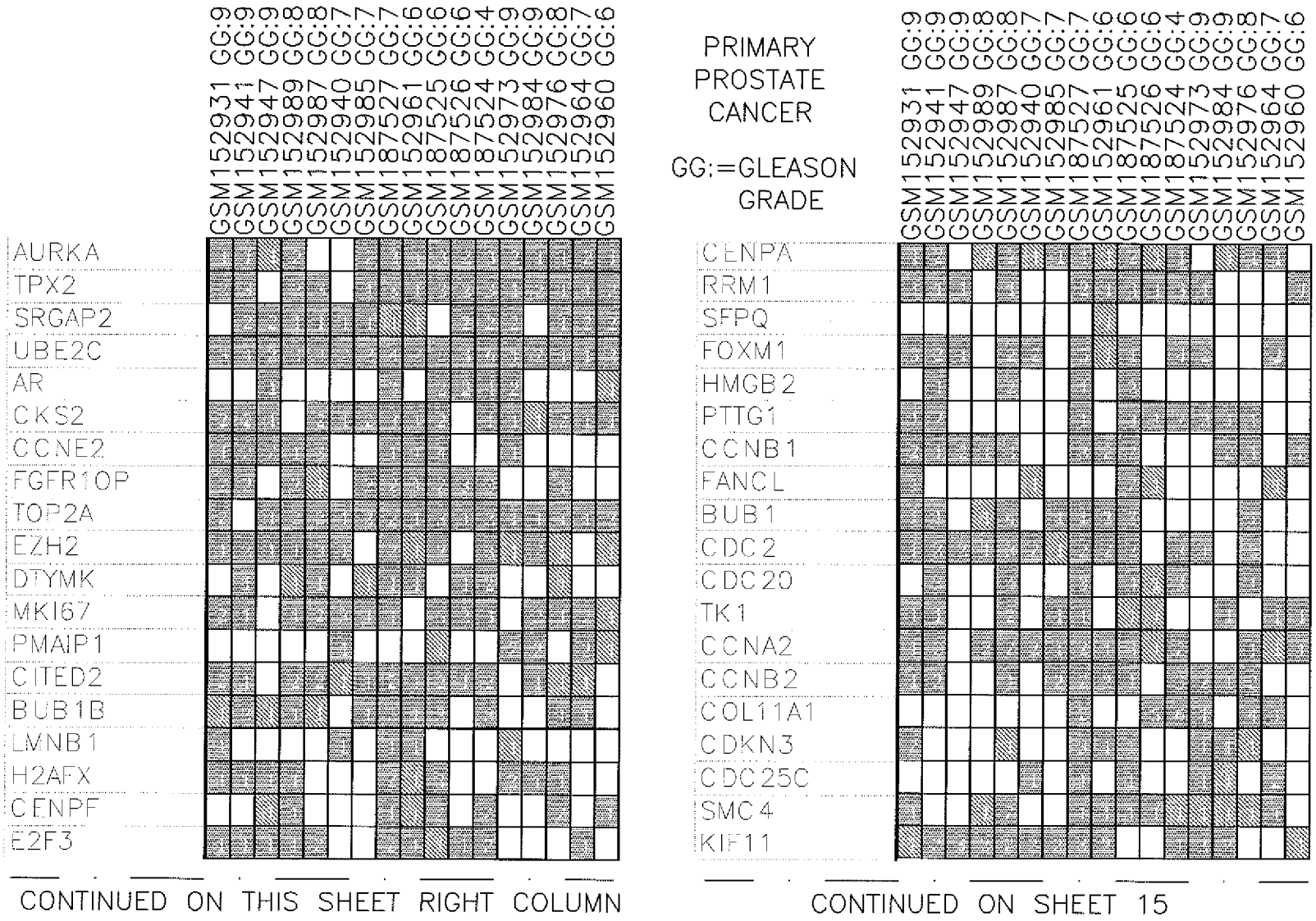

METASTIC PROSTATE CANCER
FROM SHEET 11
CONTINUED ON SHEET 13
CASE 1
CASE 2
CASE 3
CASE 4
HIST1H2BE
FGFR3
MAPK3
APAF1
SOX9
ASH2L
SSX2IP
MAP3K14
RAD51C
NRP1
PCNA
CALR
MYC
BAD
CDK2
PLSCR1
GADD45B
MCM5
MCM2
MAPK4
CBFB
PRPS1

FIG. 20



METASTIC PROSTATE CANCER

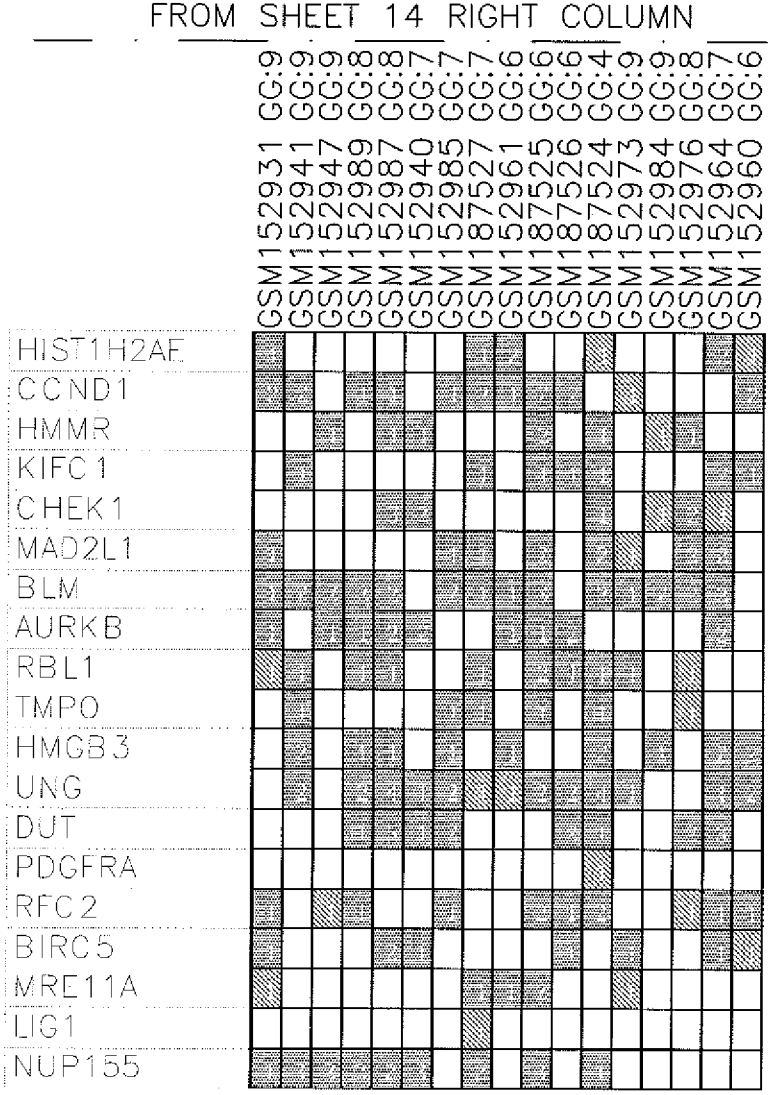
FIG. 20



ADVANCED ERGO PCA PATTERN(DOTS)

FIG. 20

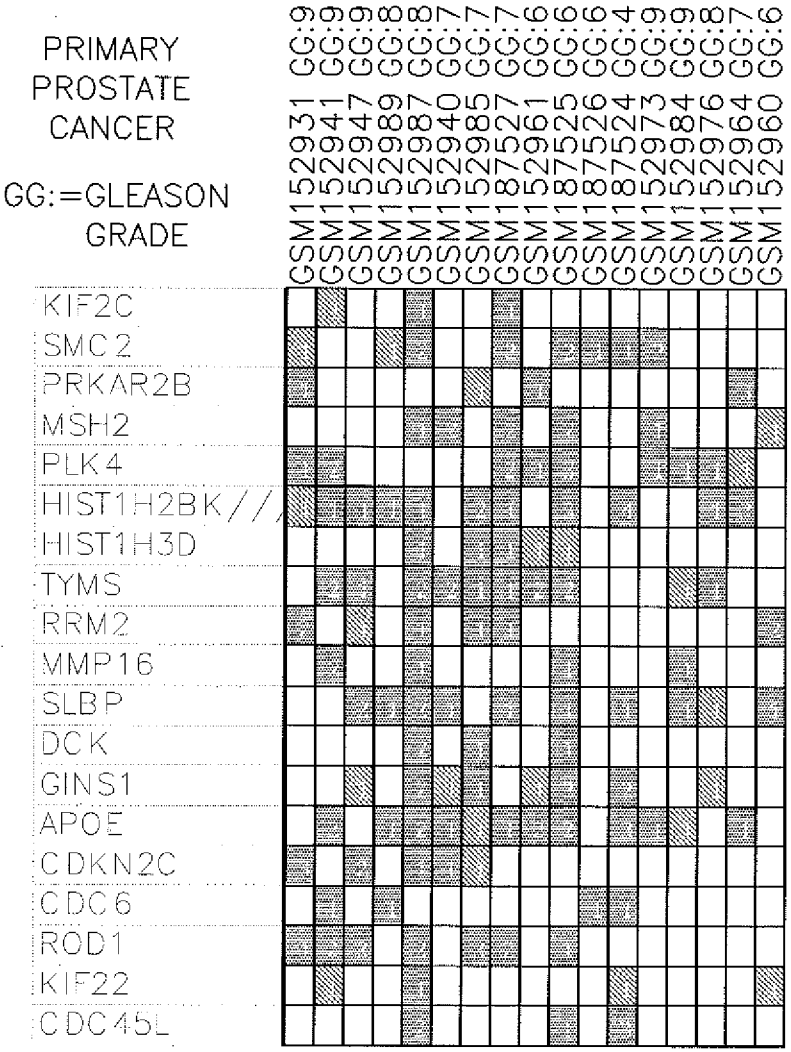
FROM SHEET 14 RIGHT COLUMN



CONTINUED ON THIS SHEET RIGHT COLUMN

PRIMARY PROSTATE CANCER

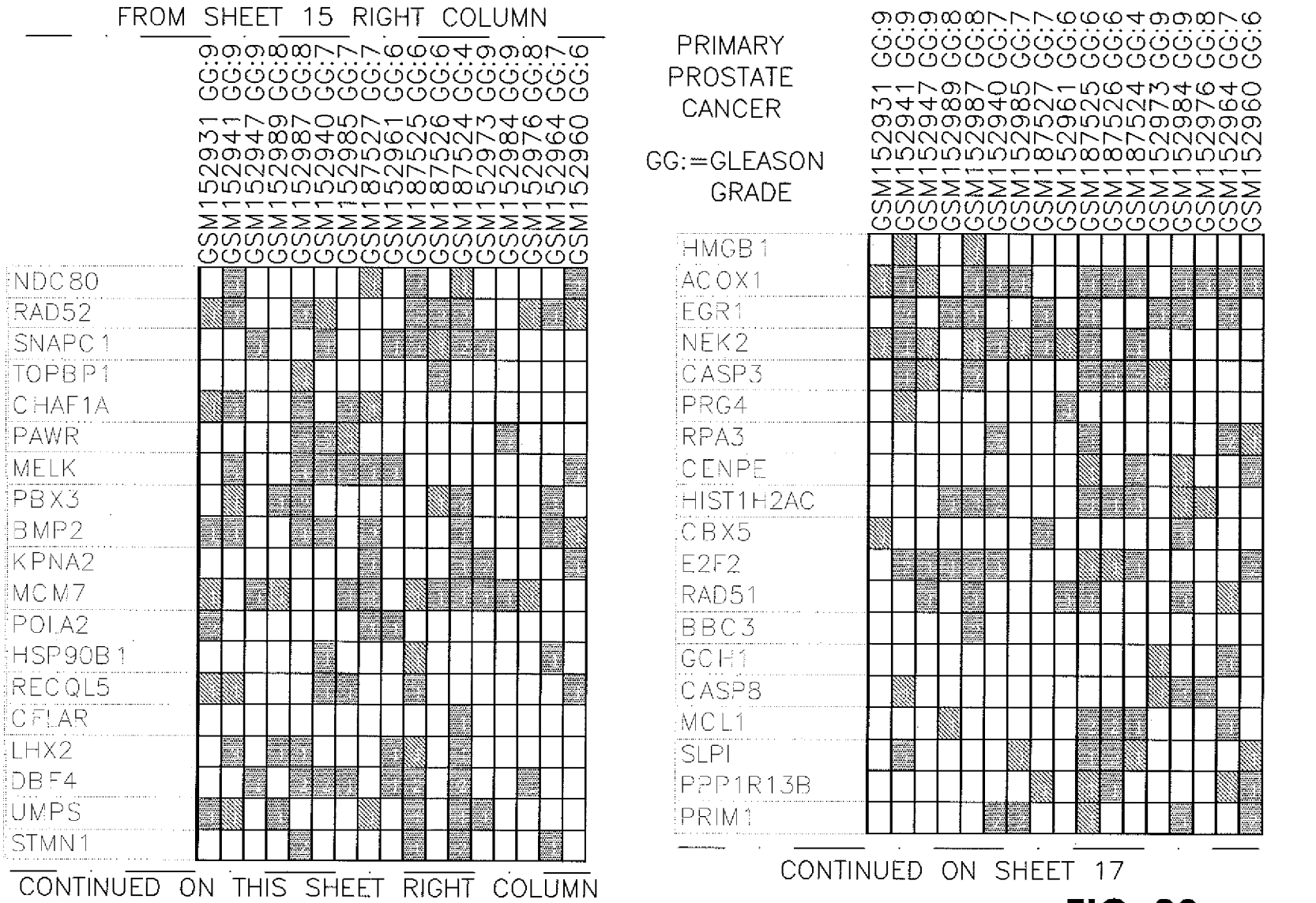
GG:=GLEASON GRADE



CONTINUED ON SHEET 16

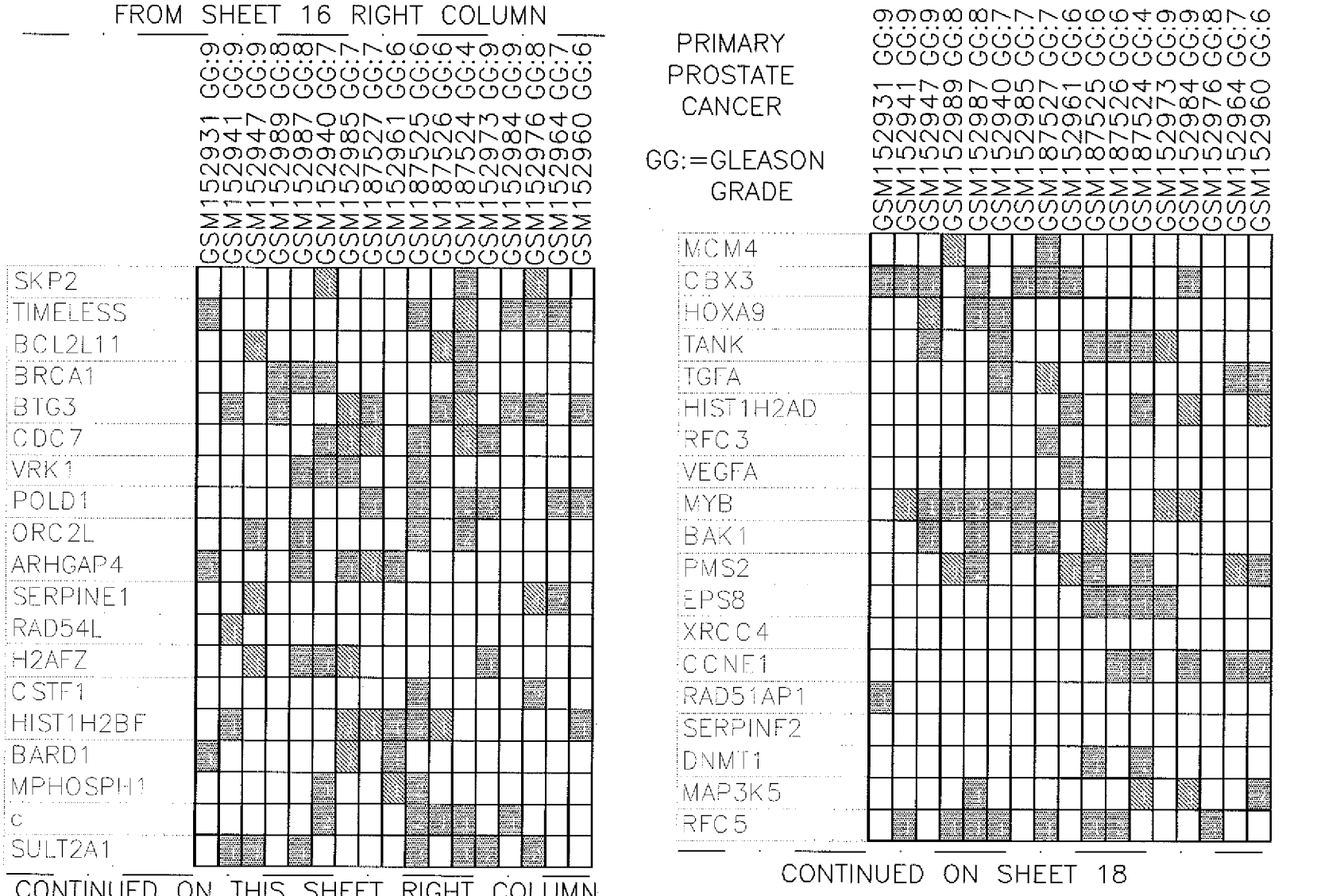
ADVANCED ERGO PCA PATTERN(DOTS)

FIG. 20



ADVANCED ERGO PCA PATTERN(DOTS)

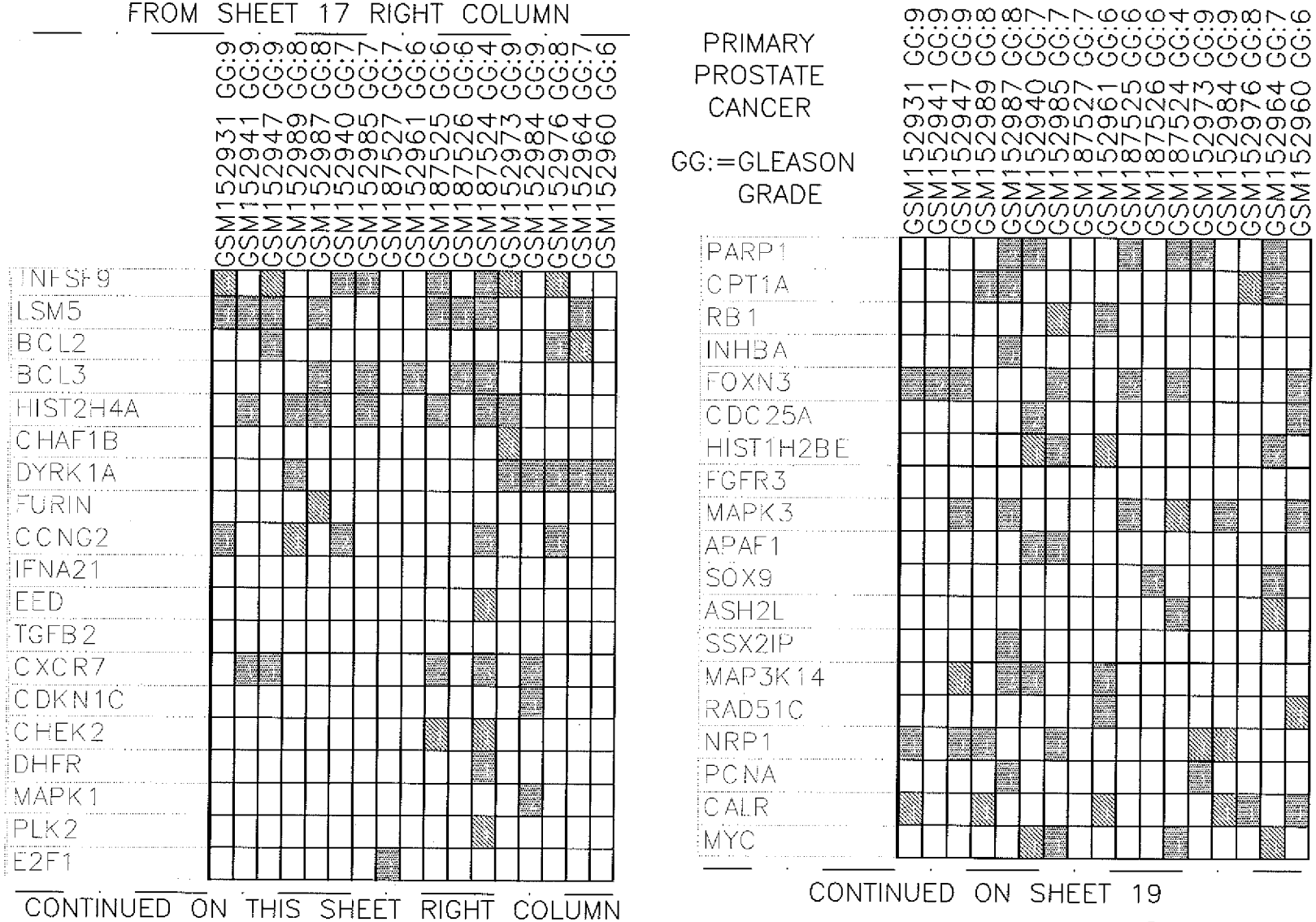
FIG. 20



ADVANCED ERGO PCA PATTERN(DOTS)

FIG. 20

FROM SHEET 17 RIGHT COLUMN

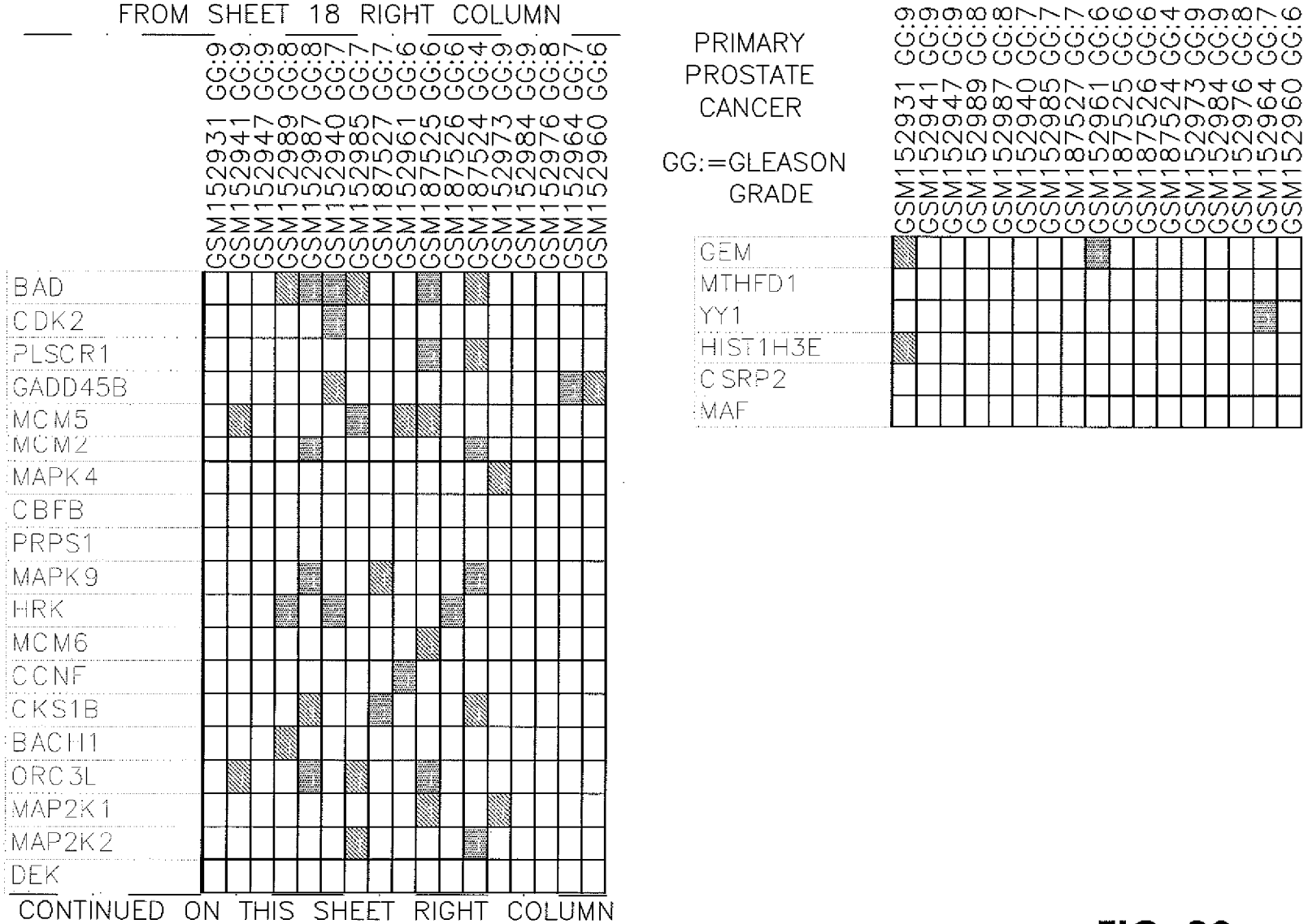


CONTINUED ON THIS SHEET RIGHT COLUMN

CONTINUED ON SHEET 19

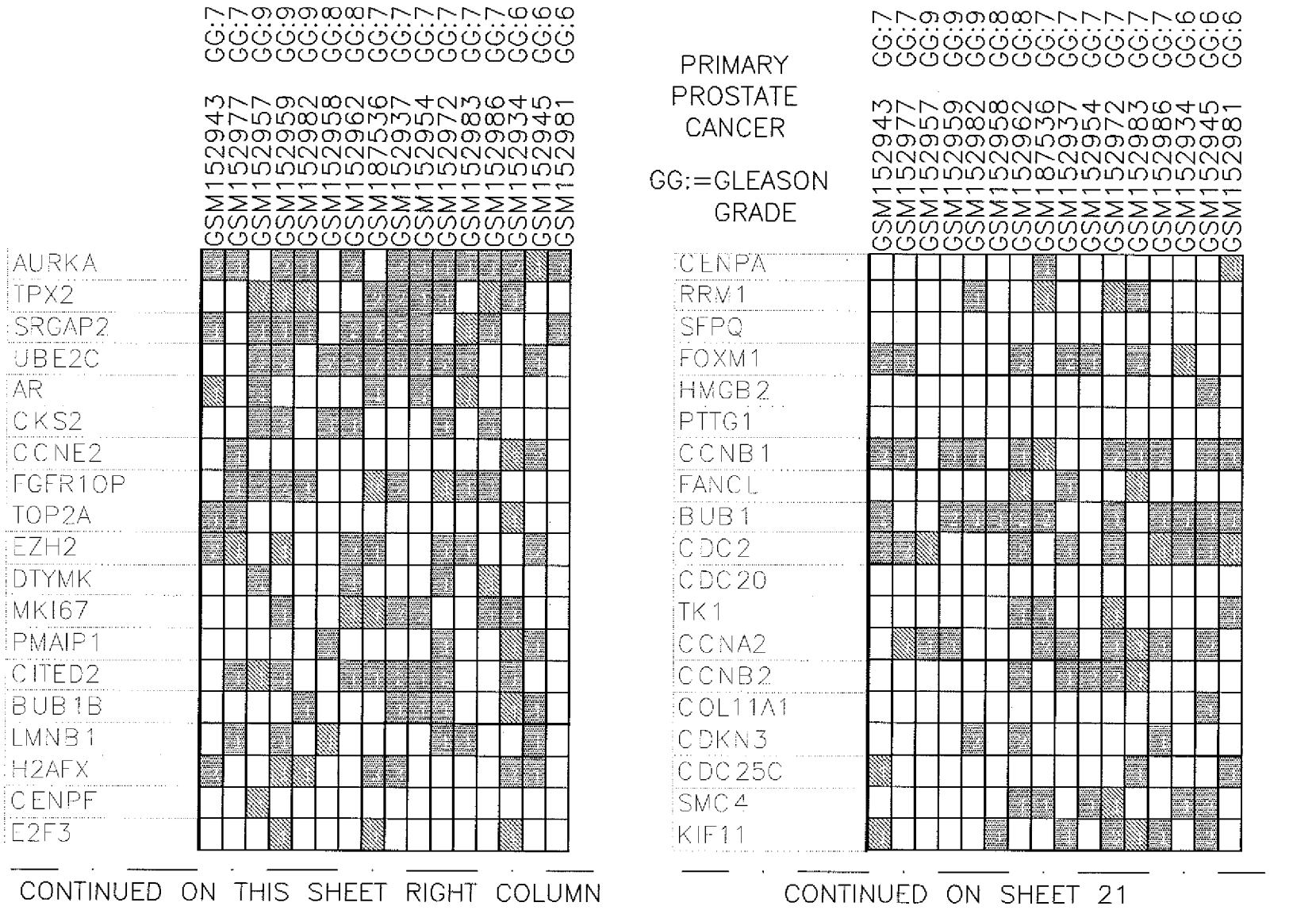
ADVANCED ERGO PCA PATTERN(DOTS)

FIG. 20



ADVANCED ERGO PCA PATTERN(DOTS)

FIG. 20



TRANSITIONAL PCA PATTERN (WHITE)

FIG. 20

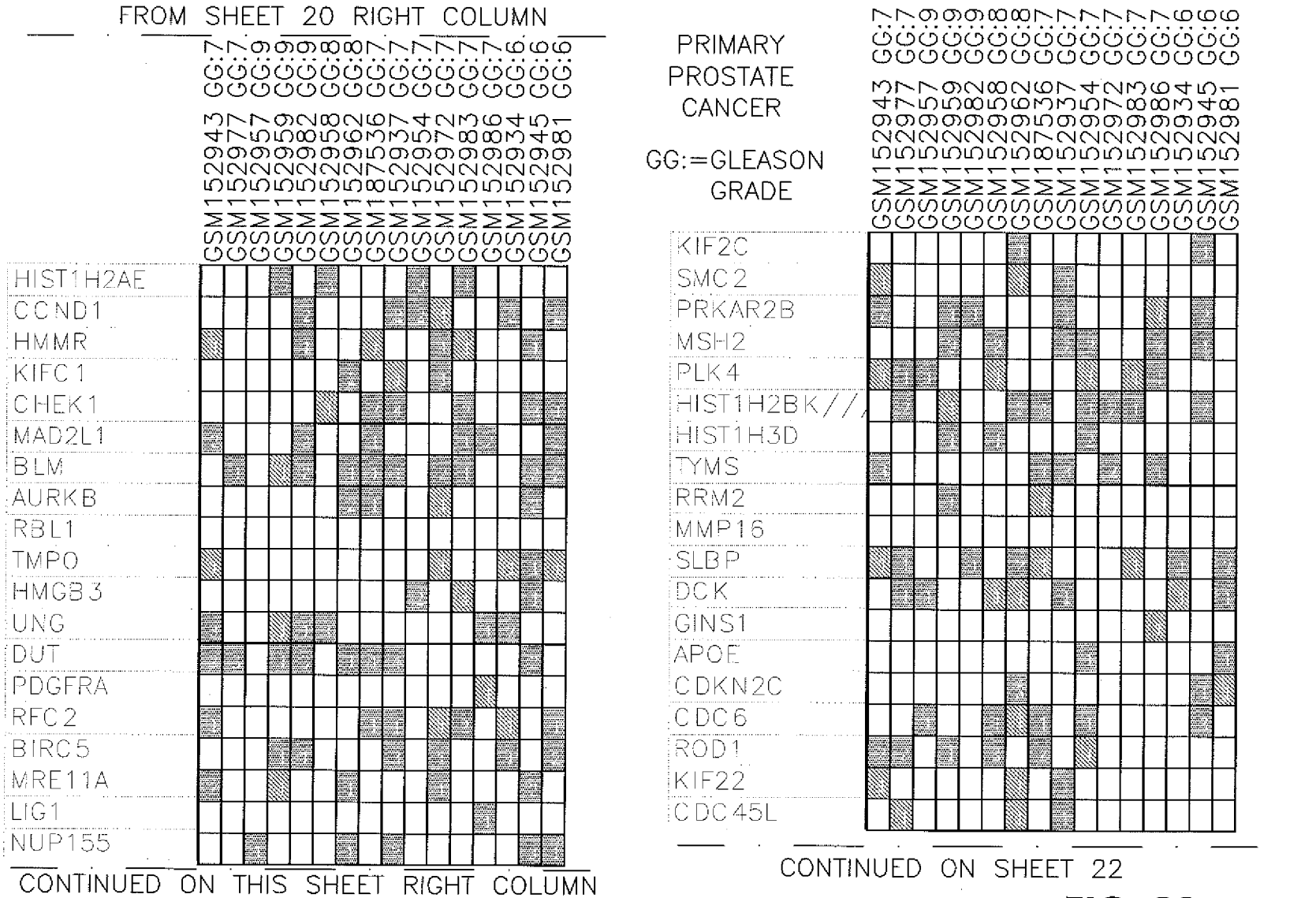
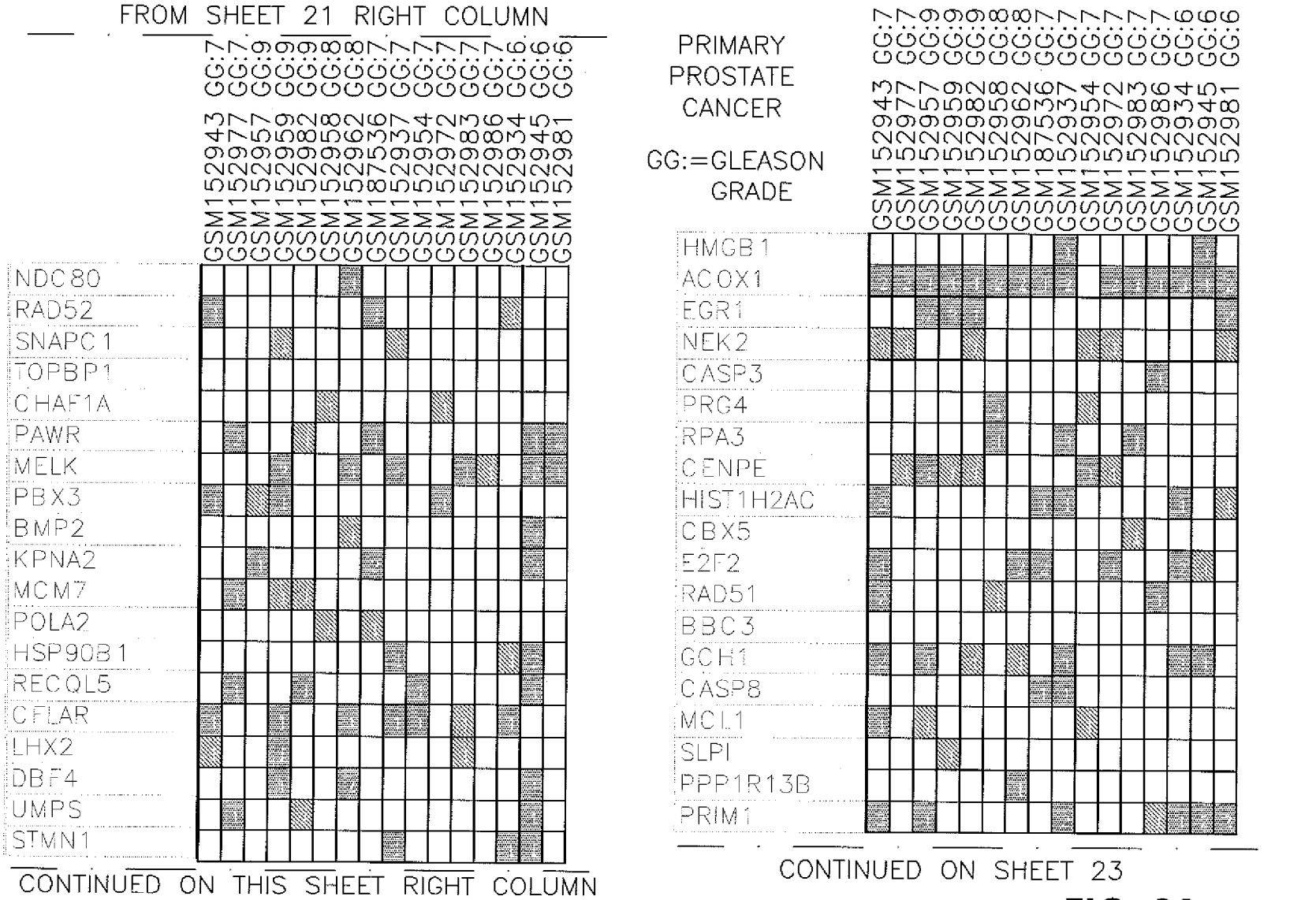
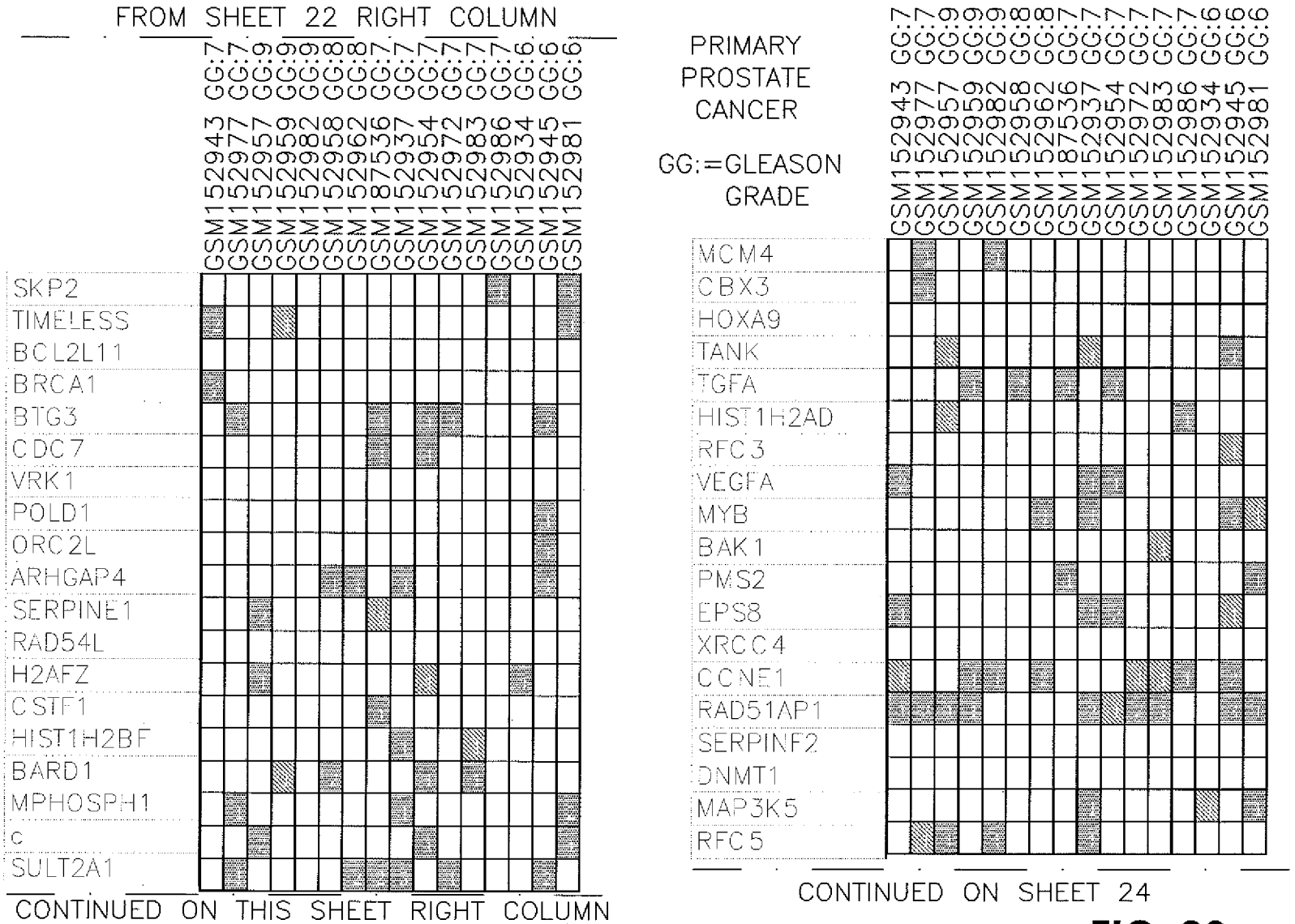

FROM SHEET 20 RIGHT COLUMN
GG:7 GG:7 GG:9 GG:9 GG:9 GG:8 GG:8 GG:7 GG:7 GG:7 GG:7 GG:7 GG:6 GG:6 GG:6
GSM1529943 GSM1529977 GSM1529957 GSM1529959 GSM1529982 GSM1529958 GSM1529962 GSM1875336 GSM1529937 GSM1529954 GSM1529972 GSM1529983 GSM1529986 GSM1529934 GSM1529945 GSM1529981
HIST1H2AE
CCND1
HMMR
KIFC1
CHEK1
MAD2L1
BLM
AURKB
RBL1
TMPO
HMGB3
UNG
DUT
PDGFRA
RFC2
BIRC5
MRE11A
LIG1
NUP155
CONTINUED ON THIS SHEET RIGHT COLUMN
PRIMARY PROSTATE CANCER
GG:=GLEASON GRADE
GG:7 GG:7 GG:9 GG:9 GG:9 GG:8 GG:8 GG:7 GG:7 GG:7 GG:7 GG:7 GG:6 GG:6 GG:6
GSM1529943 GSM1529977 GSM1529957 GSM1529959 GSM1529982 GSM1529958 GSM1529962 GSM1875336 GSM1529937 GSM1529954 GSM1529972 GSM1529983 GSM1529986 GSM1529934 GSM1529945 GSM1529981
KIF2C
SMC2
PRKAR2B
MSH2
PLK4
HIST1H2BK//
HIST1H3D
TYMS
RRM2
MMP16
SLBP
DCK
GINS1
APOE
CDKN2C
CDC6
ROD1
KIF22
CDC45L
CONTINUED ON SHEET 22
TRANSITIONAL PCA PATTERN (WHITE)

FIG. 20



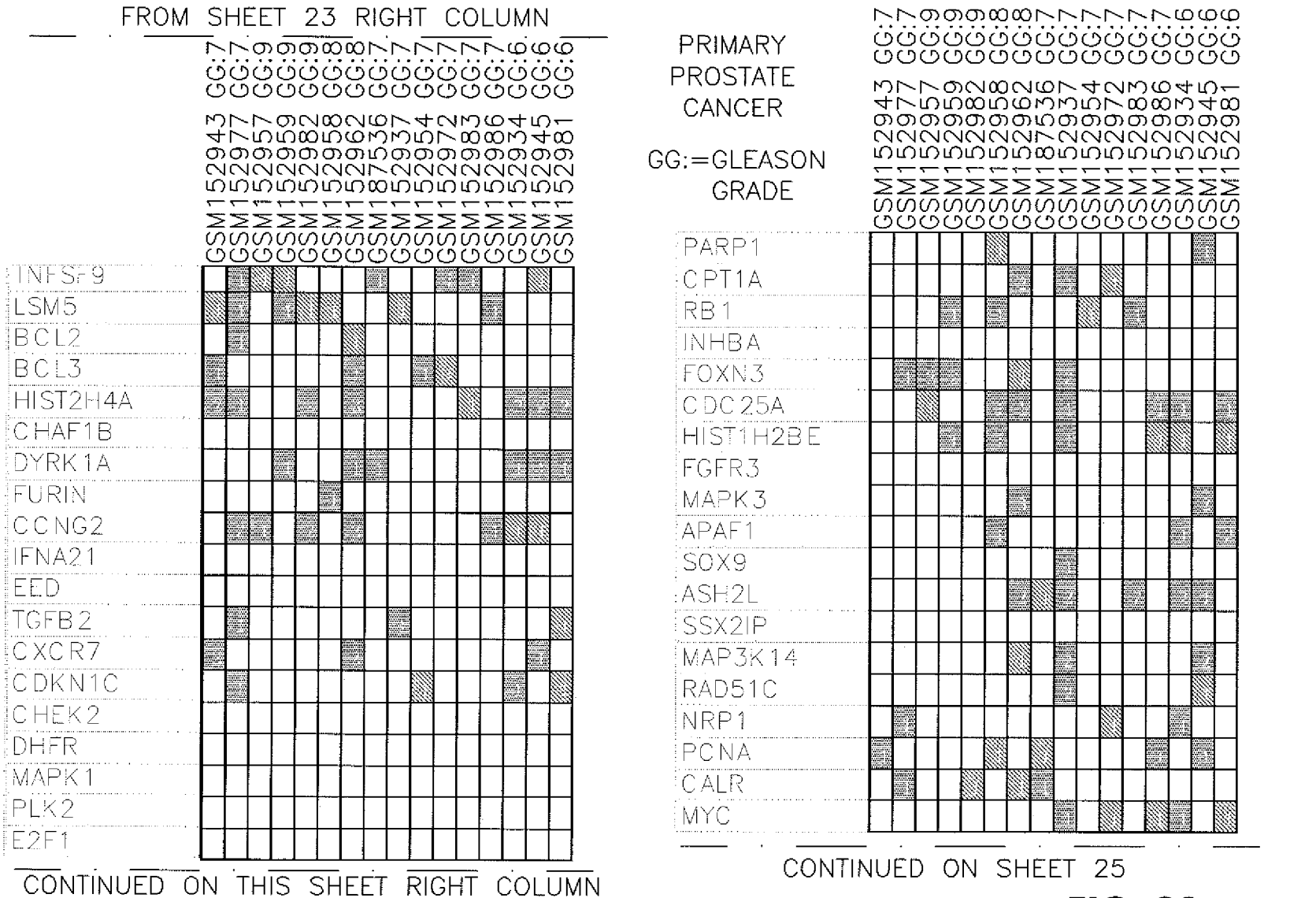
TRANSITIONAL PCA PATTERN (WHITE)

FIG. 20



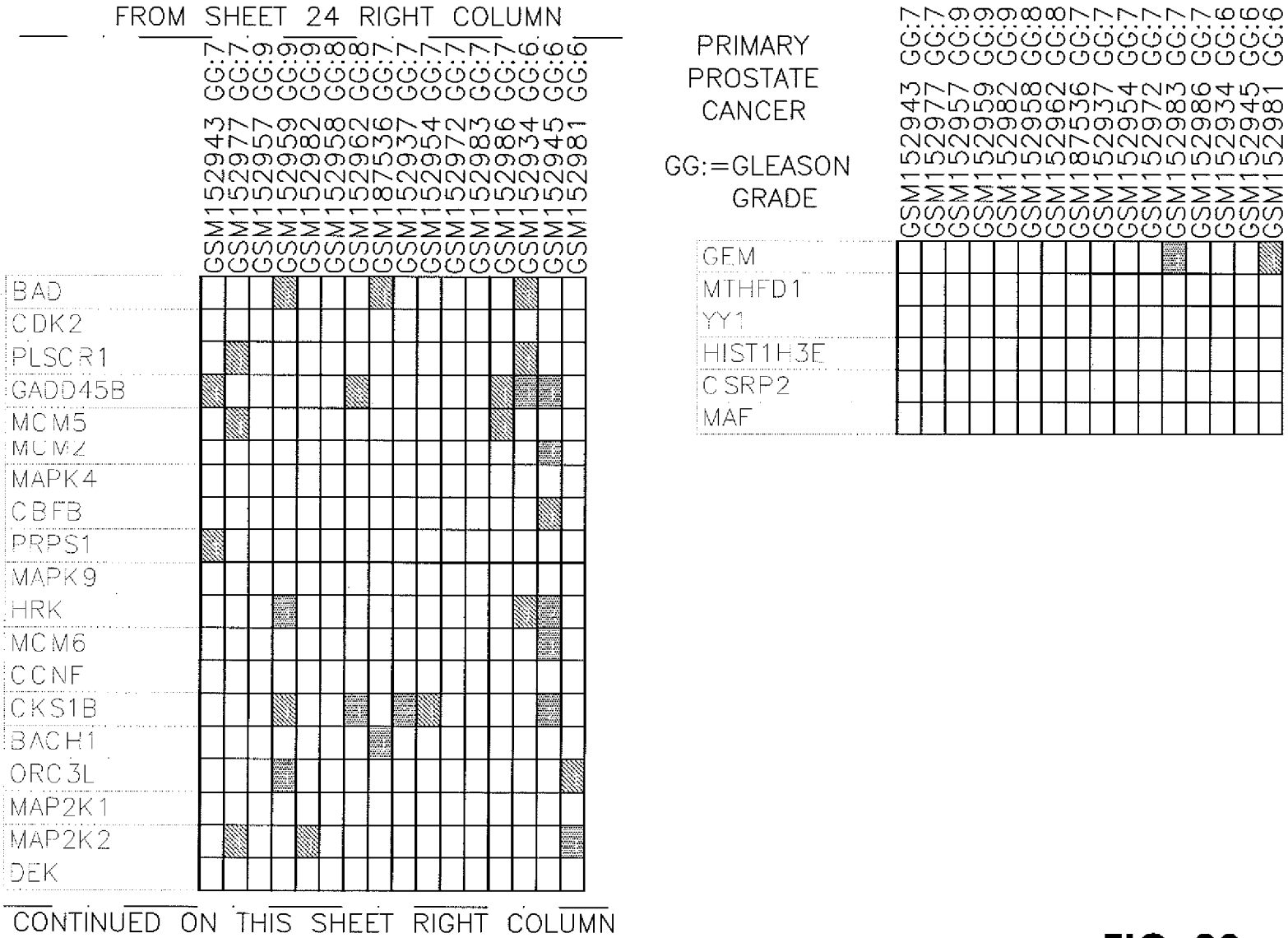
TRANSITIONAL PCA PATTERN (WHITE)

FIG. 20



TRANSITIONAL PCA PATTERN (WHITE)

FIG. 20



TRANSITIONAL PCA PATTERN (WHITE)

FIG. 20

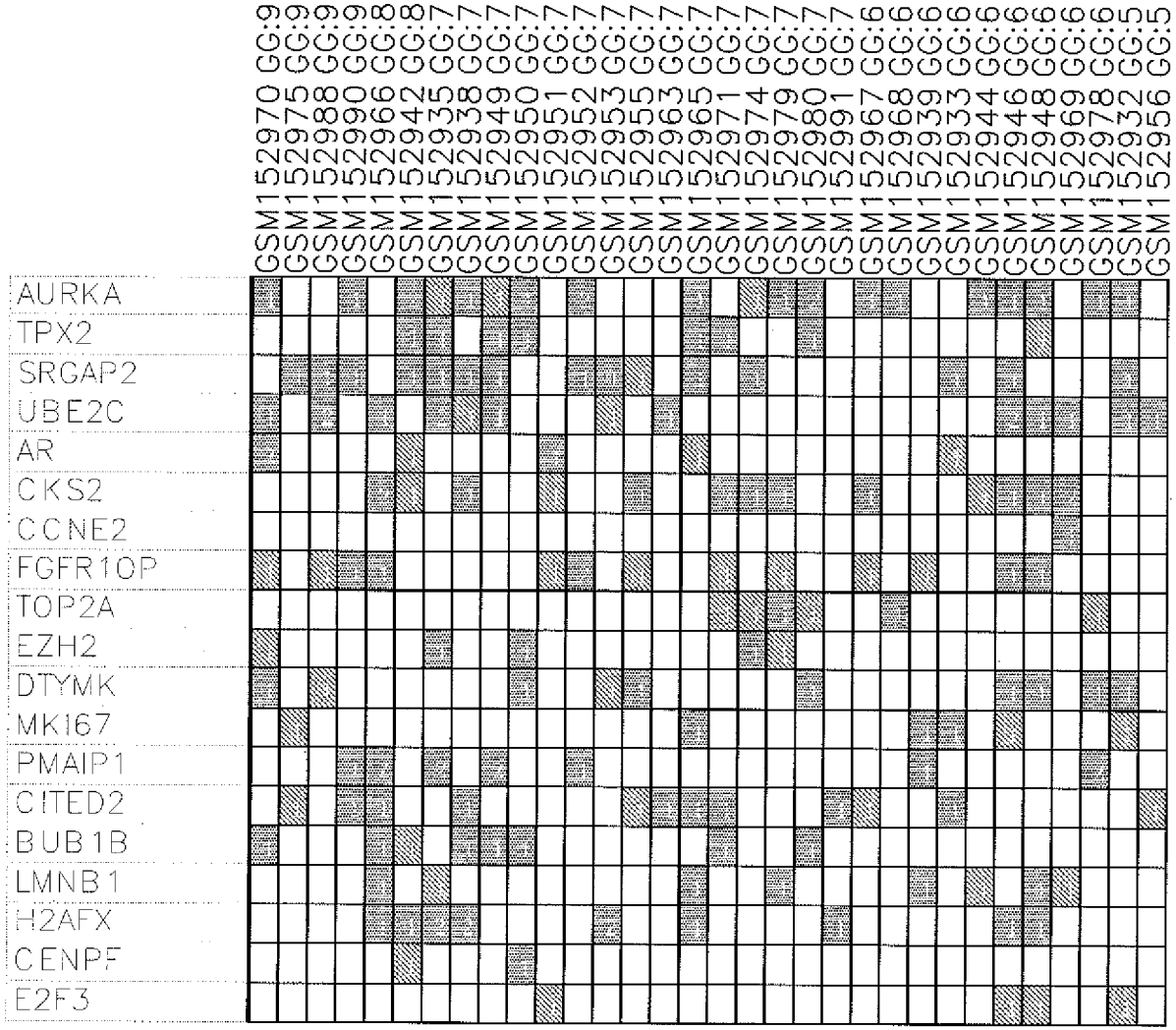

GSM1529970 GG:9
GSM1529975 GG:9
GSM1529988 GG:9
GSM1529990 GG:9
GSM1529966 GG:8
GSM1529942 GG:8
GSM1529935 GG:7
GSM1529938 GG:7
GSM1529949 GG:7
GSM1529950 GG:7
GSM1529951 GG:7
GSM1529952 GG:7
GSM1529953 GG:7
GSM1529955 GG:7
GSM1529963 GG:7
GSM1529965 GG:7
GSM1529971 GG:7
GSM1529974 GG:7
GSM1529979 GG:7
GSM1529980 GG:7
GSM1529991 GG:7
GSM1529967 GG:6
GSM1529968 GG:6
GSM1529939 GG:6
GSM1529933 GG:6
GSM1529944 GG:6
GSM1529946 GG:6
GSM1529948 GG:6
GSM1529969 GG:6
GSM1529978 GG:6
GSM1529932 GG:5
GSM1529956 GG:5
AURKA
TPX2
SRGAP2
UBE2C
AR
CKS2
CCNE2
FGFR1OP
TOP2A
EZH2
DTYMK
MKI67
PMAIP1
CITED2
BUB1B
LMNB1
H2AFX
CENPF
E2F3
PRIMARY PROSTATE CANCER
NON–AGGRESSIVE PCA PATTERN (GREEN)
CONTINUED ON SHEET 27

FIG. 20

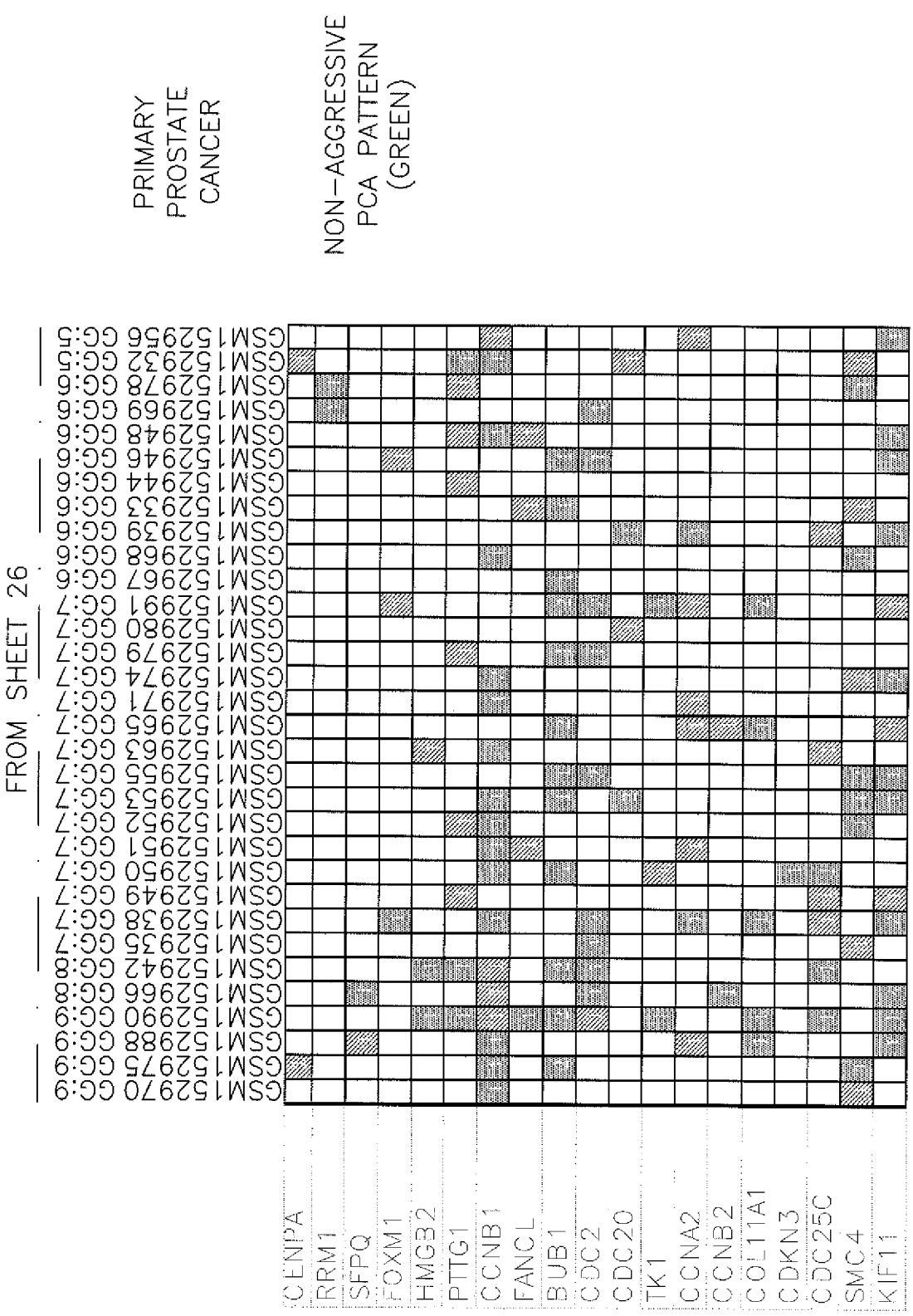

PRIMARY PROSTATE CANCER
NON-AGGRESSIVE PCA PATTERN (GREEN)
FROM SHEET 26
CONTINUED ON SHEET 28
CENPA
RRM1
SFPQ
FOXM1
HMGB2
PTTG1
CCNB1
FANCL
BUB1
CDC2
CDC20
TK1
CCNA2
CCNB2
COL11A1
CDKN3
CDC25C
SMC4
KIF11

FIG. 20

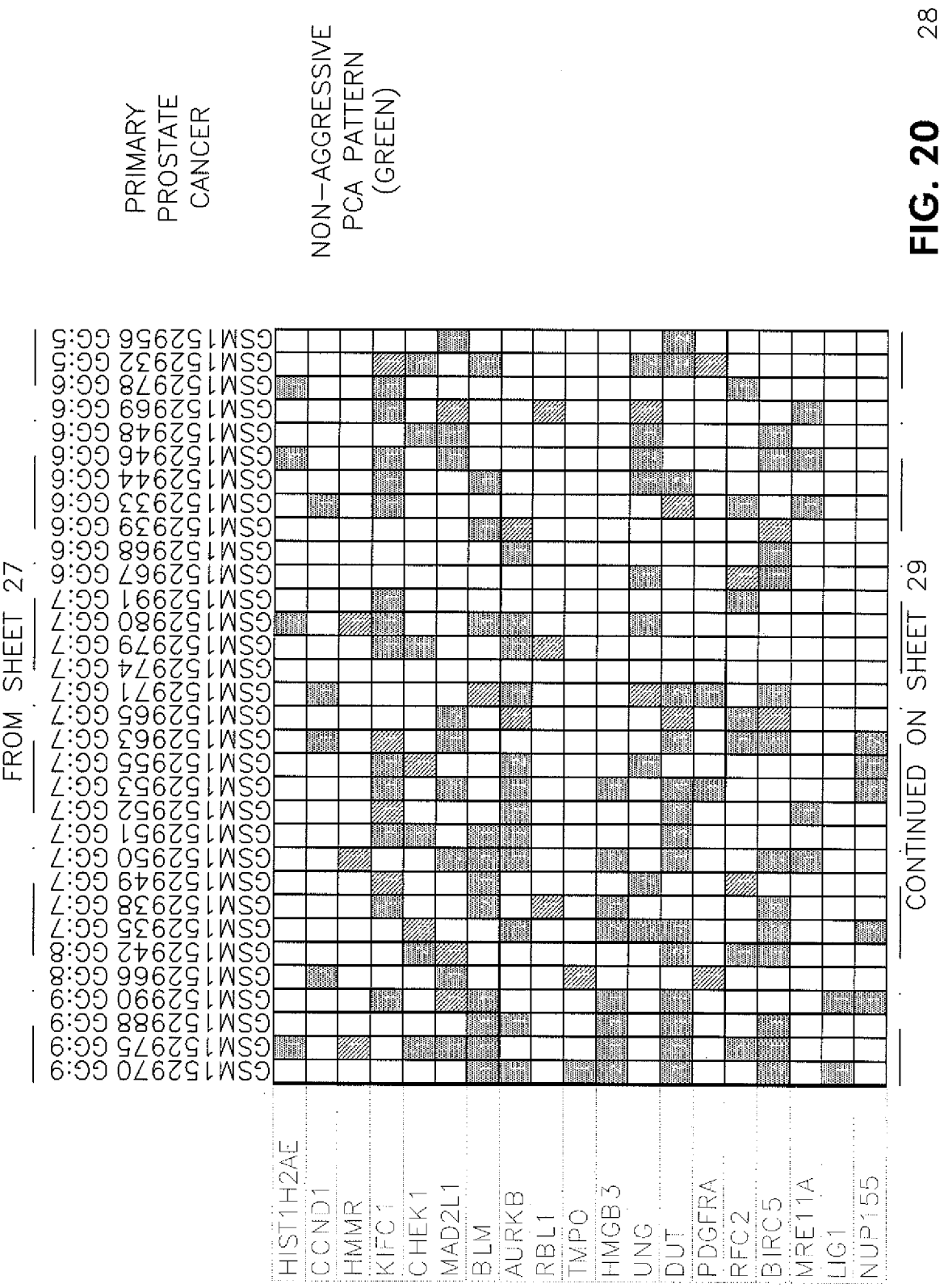

FROM SHEET 27
PRIMARY PROSTATE CANCER
NON–AGGRESSIVE PCA PATTERN (GREEN)
HIST1H2AE
CCND1
HMMR
KIFC1
CHEK1
MAD2L1
BLM
AURKB
RBL1
TMPO
HMGB3
UNG
DUT
PDGFRA
RFC2
BIRC5
MRE11A
LIG1
NUP155
GSM152970 GG:9
GSM152975 GG:9
GSM152988 GG:9
GSM152990 GG:9
GSM152966 GG:8
GSM152942 GG:8
GSM152935 GG:7
GSM152938 GG:7
GSM152949 GG:7
GSM152950 GG:7
GSM152951 GG:7
GSM152952 GG:7
GSM152953 GG:7
GSM152955 GG:7
GSM152963 GG:7
GSM152965 GG:7
GSM152971 GG:7
GSM152974 GG:7
GSM152979 GG:7
GSM152980 GG:7
GSM152991 GG:7
GSM152967 GG:6
GSM152968 GG:6
GSM152939 GG:6
GSM152933 GG:6
GSM152944 GG:6
GSM152946 GG:6
GSM152948 GG:6
GSM152969 GG:6
GSM152978 GG:6
GSM152932 GG:6
GSM152956 GG:5
CONTINUED ON SHEET 29

FIG. 20

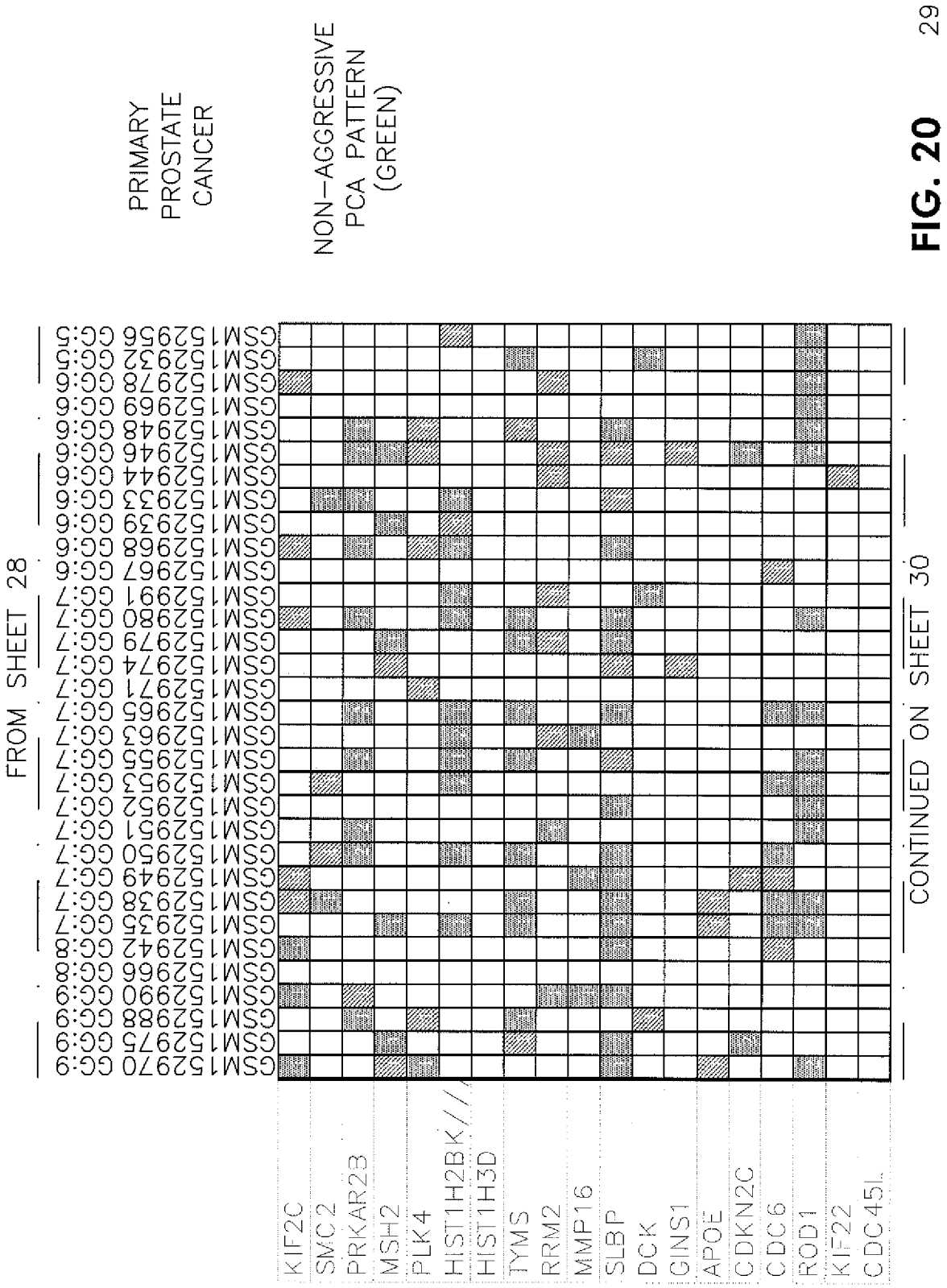
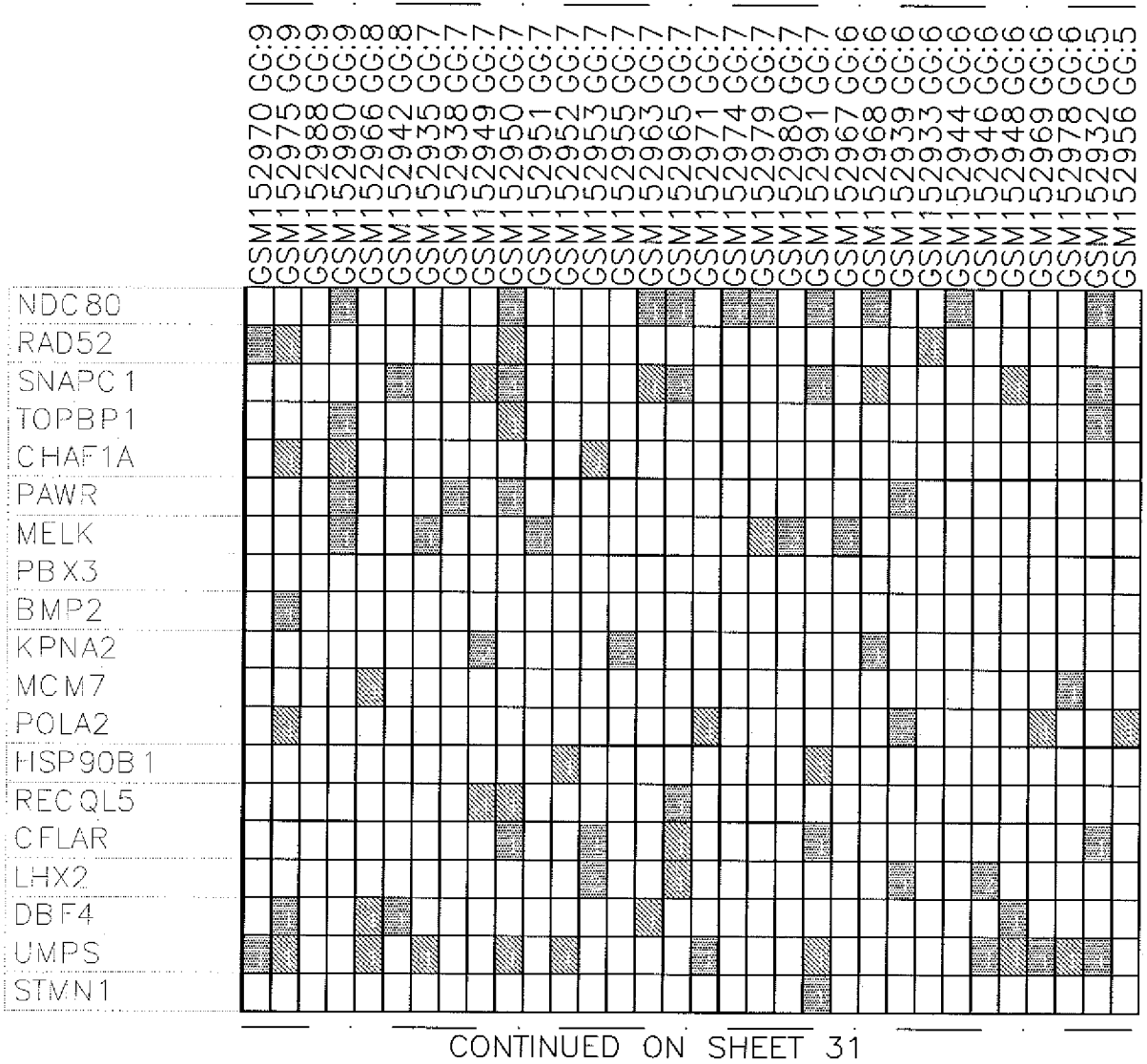

FROM SHEET 28
PRIMARY PROSTATE CANCER
NON-AGGRESSIVE PCA PATTERN (GREEN)
KIF2C
SMC2
PRKAR2B
MSH2
PLK4
HIST1H2BK
HIST1H3D
TYMS
RRM2
MMP16
SLBP
DCK
GINS1
APOE
CDKN2C
CDC6
ROD1
KIF22
CDC45L
CONTINUED ON SHEET 30

FIG. 20

FROM SHEET 29



CONTINUED ON SHEET 31

PRIMARY PROSTATE CANCER

NON–AGGRESSIVE PCA PATTERN (GREEN)

FIG. 20

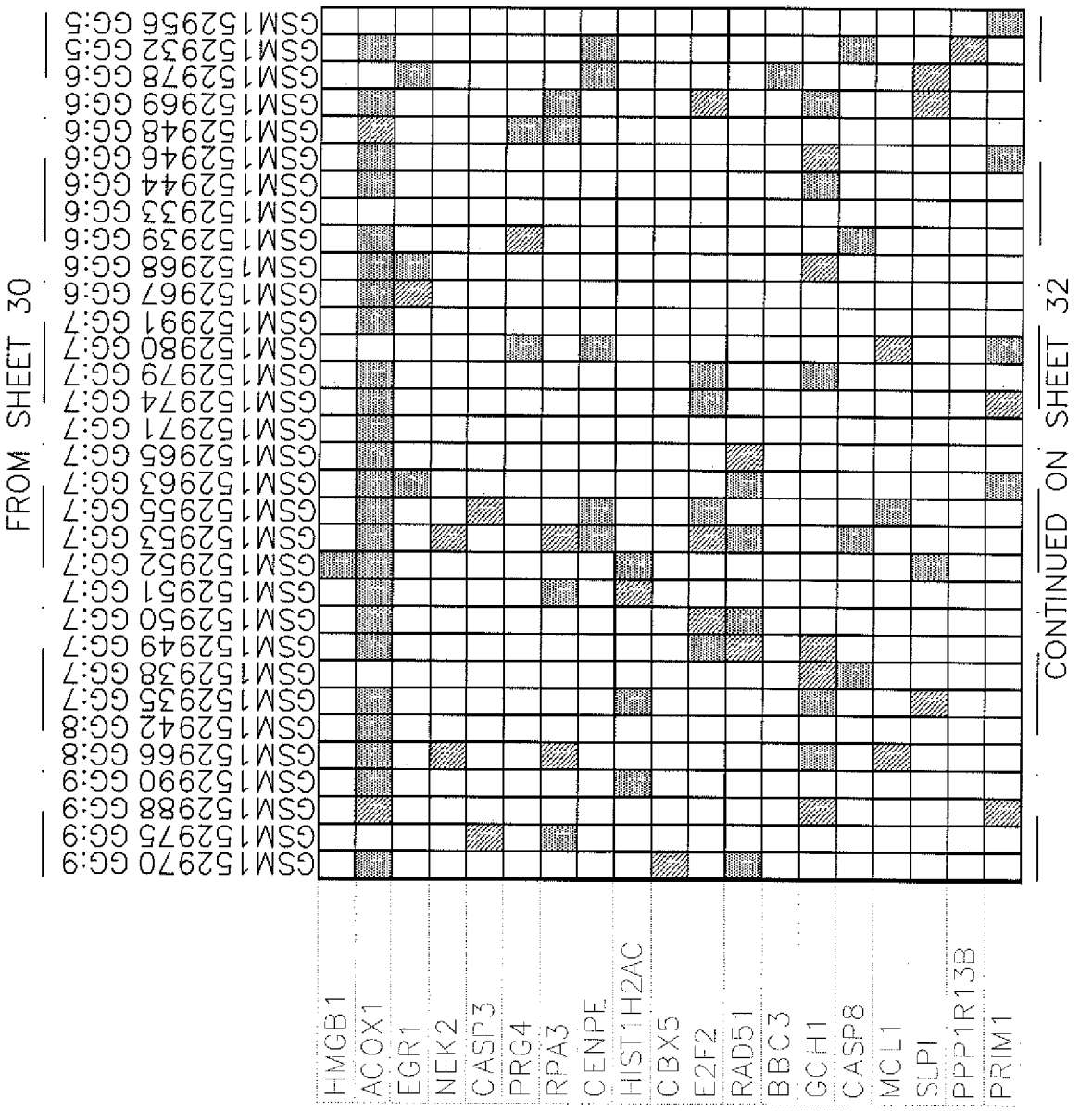

FROM SHEET 30
PRIMARY PROSTATE CANCER
NON-AGGRESSIVE PCA PATTERN (GREEN)
HMGB1
ACOX1
EGR1
NEK2
CASP3
PRG4
RPA3
CENPE
HIST1H2AC
CBX5
E2F2
RAD51
BBC3
GCH1
CASP8
MCL1
SLPI
PPP1R13B
PRIM1
GSM152970 GG:9
GSM152975 GG:9
GSM152988 GG:9
GSM152990 GG:9
GSM152966 GG:8
GSM152942 GG:8
GSM152935 GG:7
GSM152938 GG:7
GSM152949 GG:7
GSM152950 GG:7
GSM152951 GG:7
GSM152952 GG:7
GSM152953 GG:7
GSM152955 GG:7
GSM152963 GG:7
GSM152965 GG:7
GSM152971 GG:7
GSM152974 GG:7
GSM152979 GG:7
GSM152980 GG:7
GSM152991 GG:7
GSM152967 GG:6
GSM152968 GG:6
GSM152939 GG:6
GSM152933 GG:6
GSM152944 GG:6
GSM152946 GG:6
GSM152948 GG:6
GSM152969 GG:6
GSM152978 GG:6
GSM152932 GG:6
GSM152956 GG:6
CONTINUED ON SHEET 32

FIG. 20

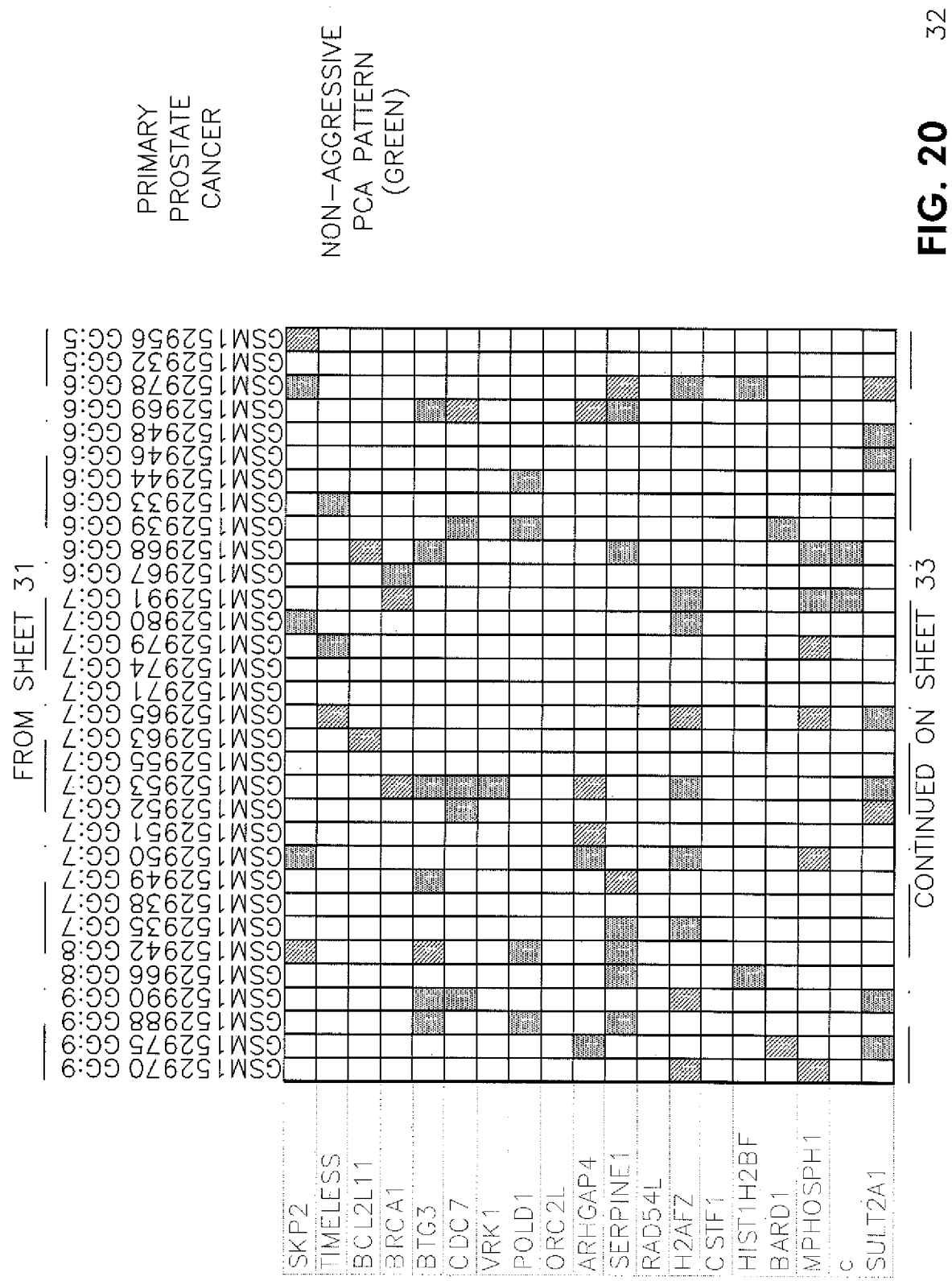

FROM SHEET 31
PRIMARY PROSTATE CANCER
NON-AGGRESSIVE PCA PATTERN (GREEN)
SKP2
TIMELESS
BCL2L11
BRCA1
BTG3
CDC7
VRK1
POLD1
ORC2L
ARHGAP4
SERPINE1
RAD54L
H2AFZ
CSTF1
HIST1H2BF
BARD1
MPHOSPH1
c
SULT2A1
CONTINUED ON SHEET 33

FIG. 20

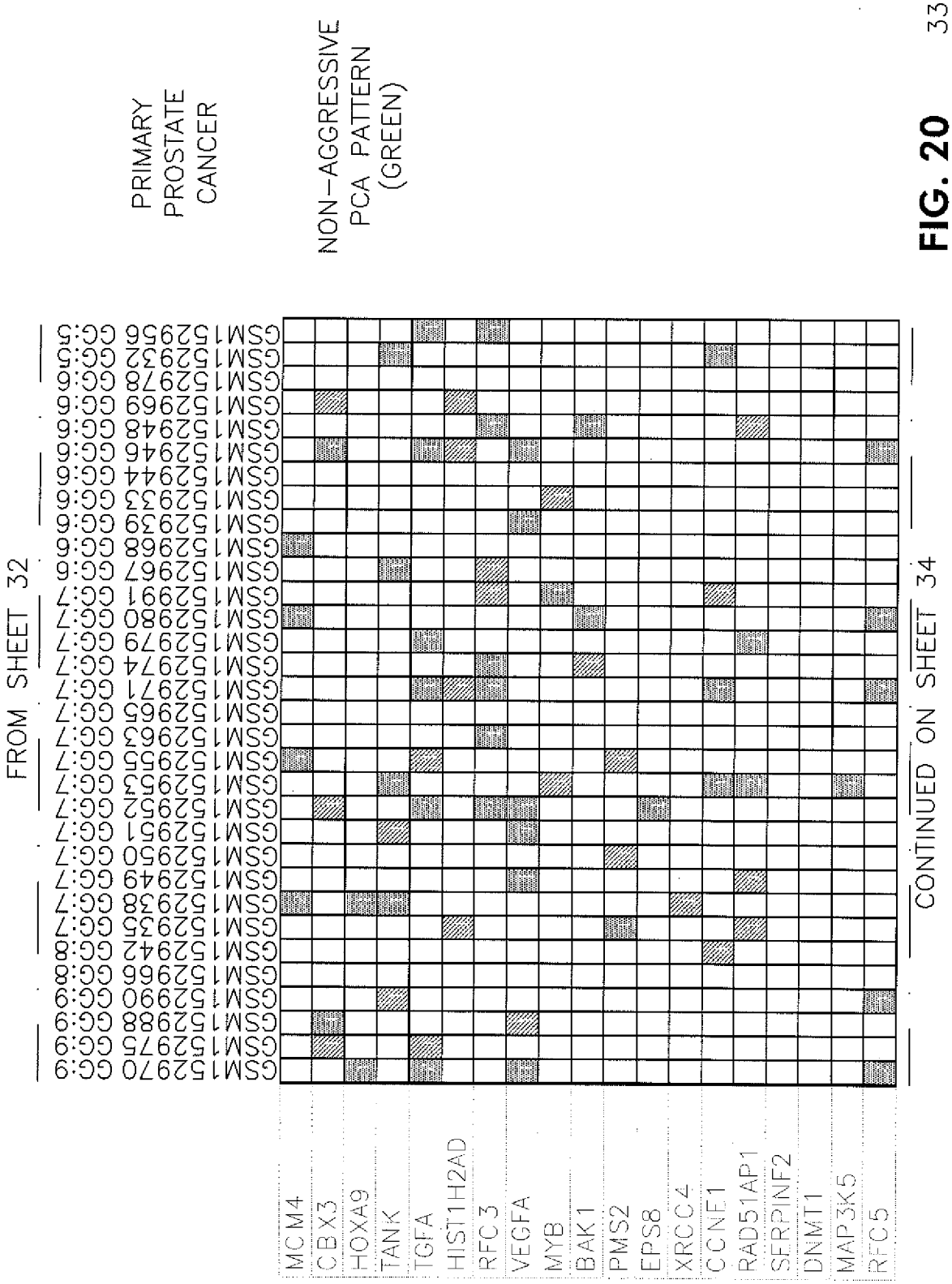

PRIMARY PROSTATE CANCER
NON-AGGRESSIVE PCA PATTERN (GREEN)
FROM SHEET 32
CONTINUED ON SHEET 34
MCM4
CBX3
HOXA9
TANK
TGFA
HIST1H2AD
RFC3
VEGFA
MYB
BAK1
PMS2
EPS8
XRCC4
CCNE1
RAD51AP1
SERPINF2
DNMT1
MAP3K5
RFC5

FIG. 20

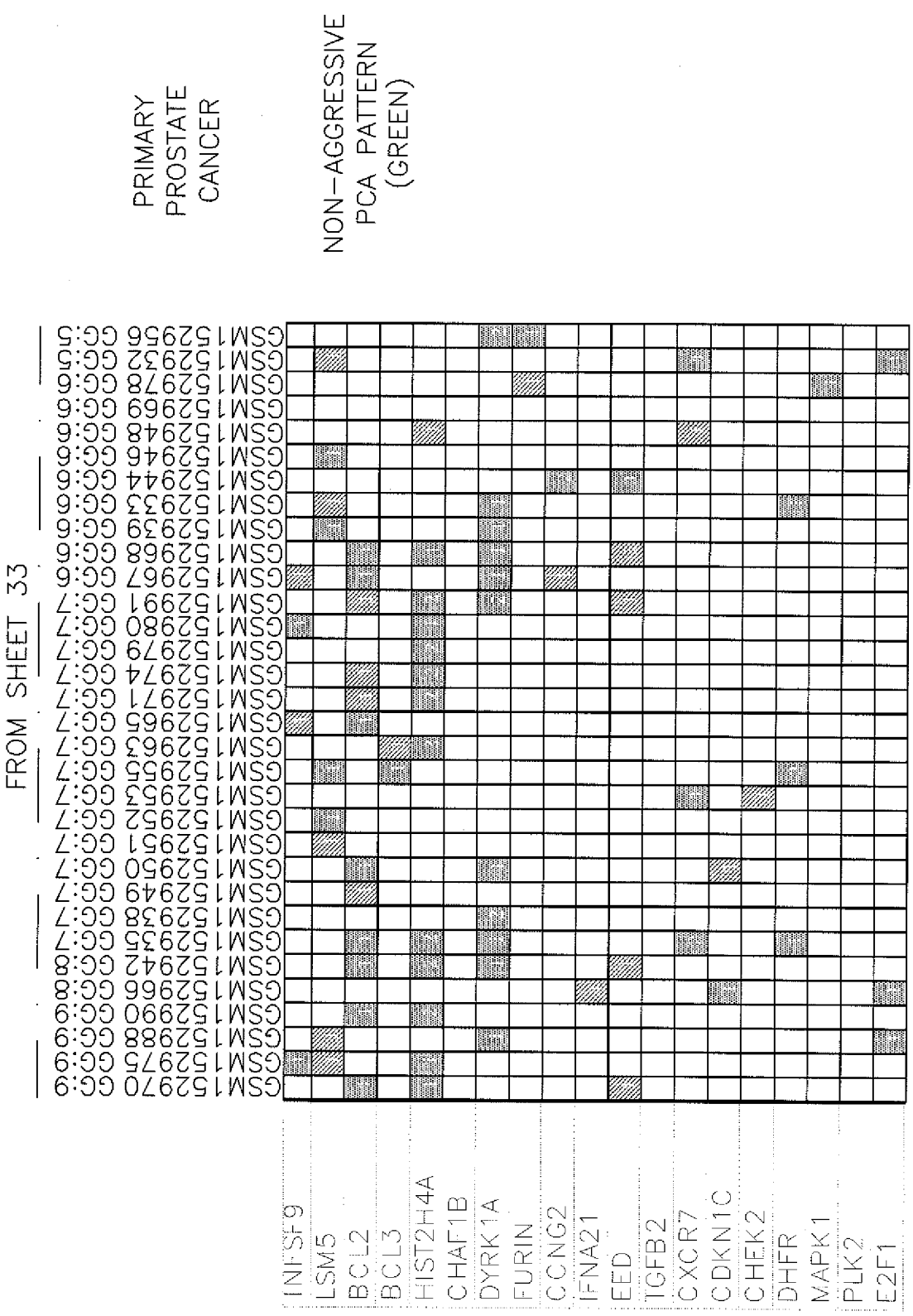

PRIMARY PROSTATE CANCER
NON-AGGRESSIVE PCA PATTERN (GREEN)
FROM SHEET 33
CONTINUED ON SHEET 35
INHBA
LSM5
BCL2
BCL3
HIST2H4A
CHAF1B
DYRK1A
FURIN
CCNG2
IFNA21
EED
TGFB2
CXCR7
CDKN1C
CHEK2
DHFR
MAPK1
PLK2
E2F1

FIG. 20

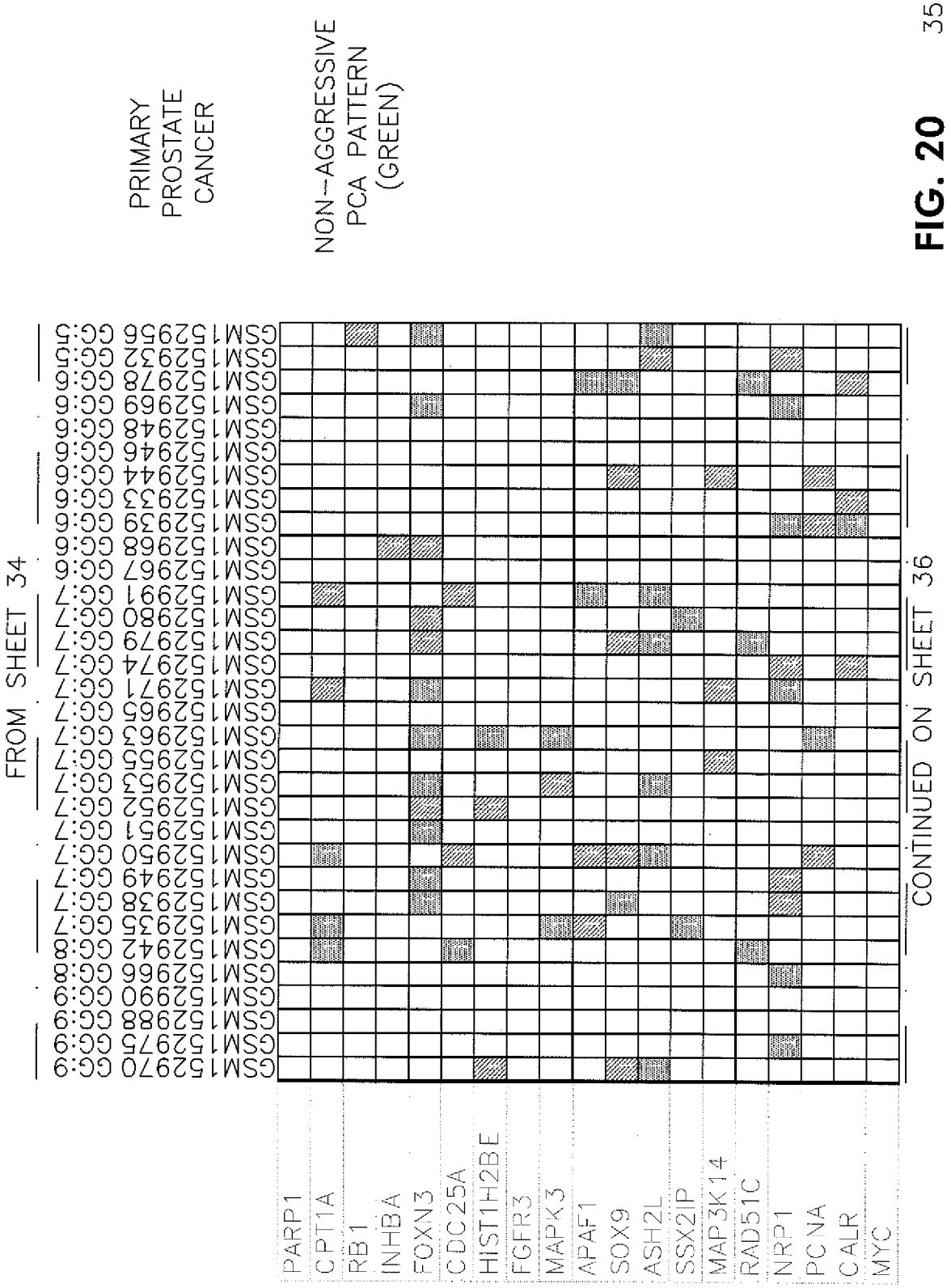
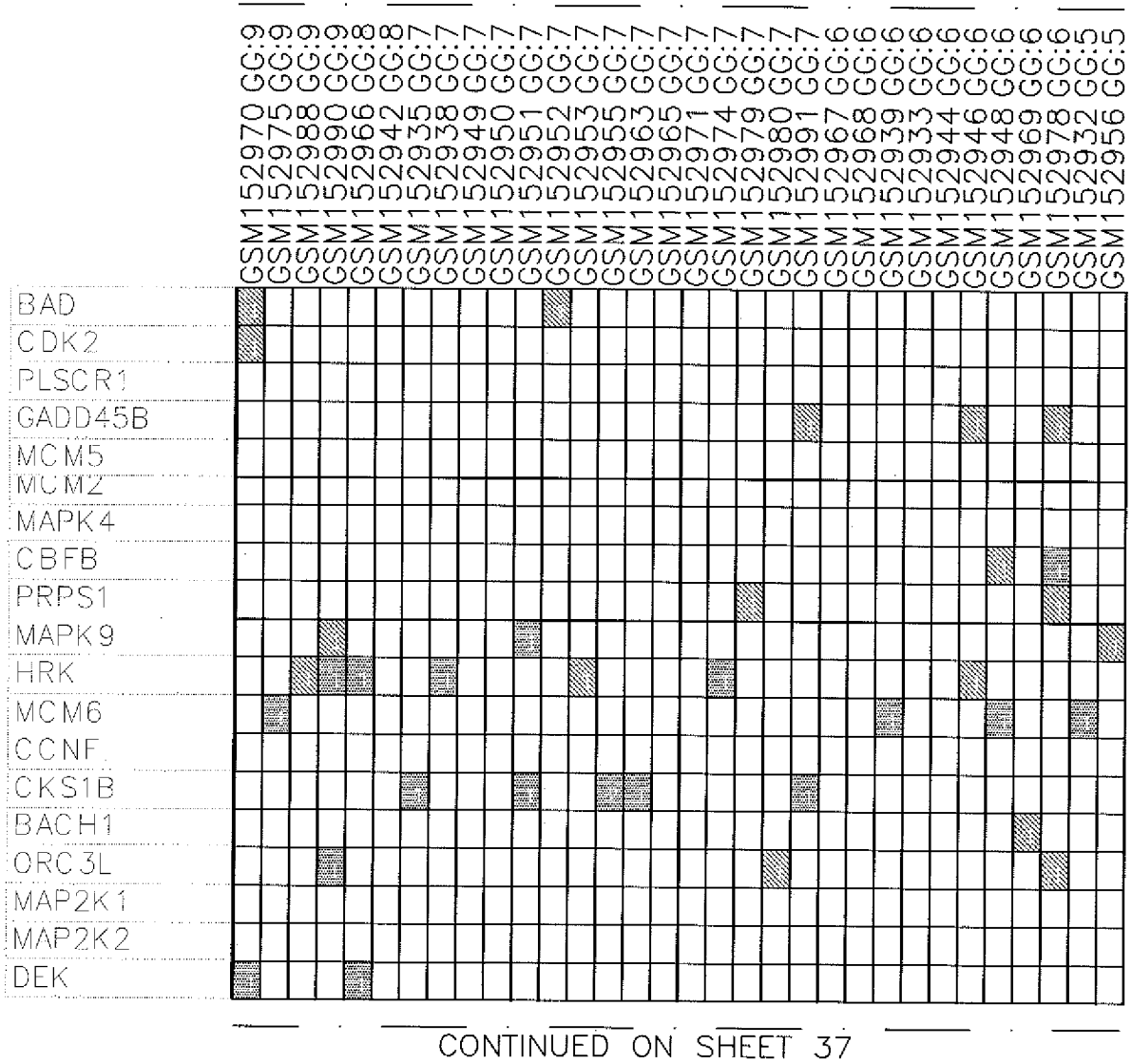

PRIMARY PROSTATE CANCER
NON-AGGRESSIVE PCA PATTERN (GREEN)
FROM SHEET 34
CONTINUED ON SHEET 36
PARP1
CPT1A
RB1
INHBA
FOXN3
CDC25A
HIST1H2BE
FGFR3
MAPK3
APAF1
SOX9
ASH2L
SSX2IP
MAP3K14
RAD51C
NRP1
PCNA
CALR
MYC

FIG. 20

FROM SHEET 35



PRIMARY PROSTATE CANCER

NON–AGGRESSIVE PCA PATTERN (GREEN)

CONTINUED ON SHEET 37

FIG. 20

PRIMARY
PROSTATE
CANCER
NON-AGGRESSIVE
PCA PATTERN
(GREEN)
FROM SHEET 36
GSM152970 GG:9
GSM152975 GG:9
GSM152988 GG:9
GSM152990 GG:9
GSM152966 GG:8
GSM152942 GG:8
GSM152935 GG:7
GSM152938 GG:7
GSM152949 GG:7
GSM152950 GG:7
GSM152951 GG:7
GSM152952 GG:7
GSM152953 GG:7
GSM152955 GG:7
GSM152963 GG:7
GSM152965 GG:7
GSM152971 GG:7
GSM152974 GG:7
GSM152979 GG:7
GSM152980 GG:7
GSM152991 GG:7
GSM152967 GG:6
GSM152968 GG:6
GSM152939 GG:6
GSM152933 GG:6
GSM152944 GG:6
GSM152946 GG:6
GSM152948 GG:6
GSM152969 GG:6
GSM152978 GG:6
GSM152932 GG:5
GSM152956 GG:5
GEM
MTHFD1
YY1
HIST1H3E
CSRP2
MAF

FIG. 20

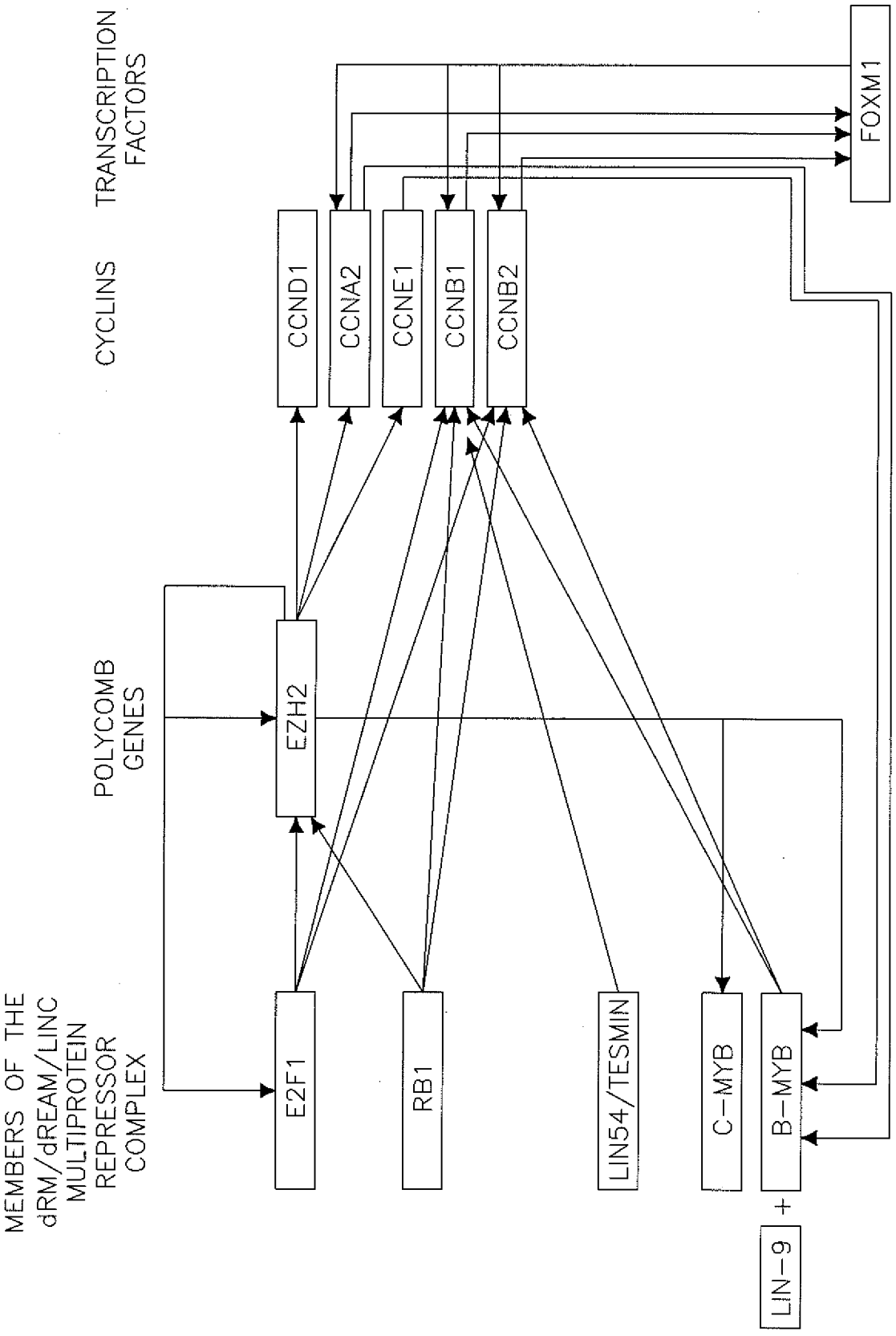

MEMBERS OF THE dRM/dREAM/LINC MULTIPROTEIN REPRESSOR COMPLEX
POLYCOMB GENES
CYCLINS
TRANSCRIPTION FACTORS
E2F1
RB1
LIN54/TESMIN
C-MYB
B-MYB
LIN-9
+
EZH2
CCND1
CCNA2
CCNE1
CCNB1
CCNB2
FOXM1

FIG. 21

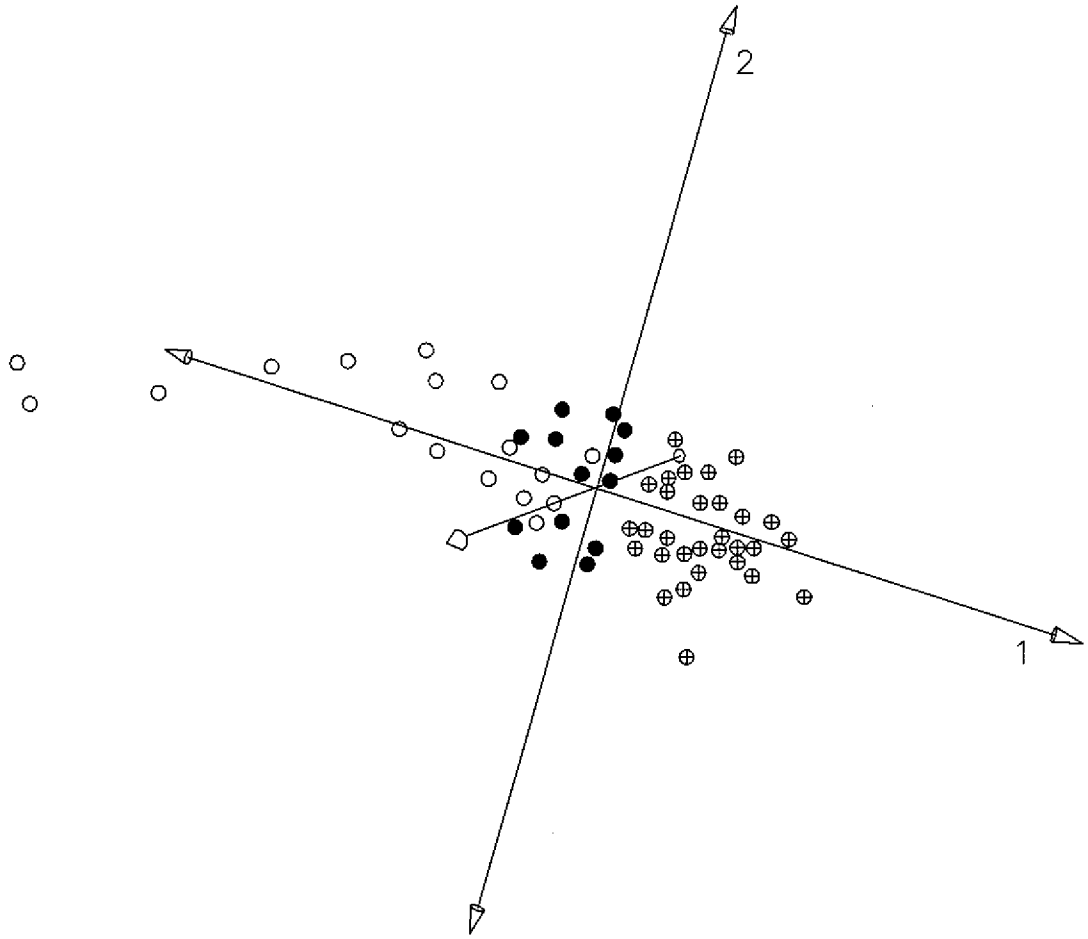


FIG. 22

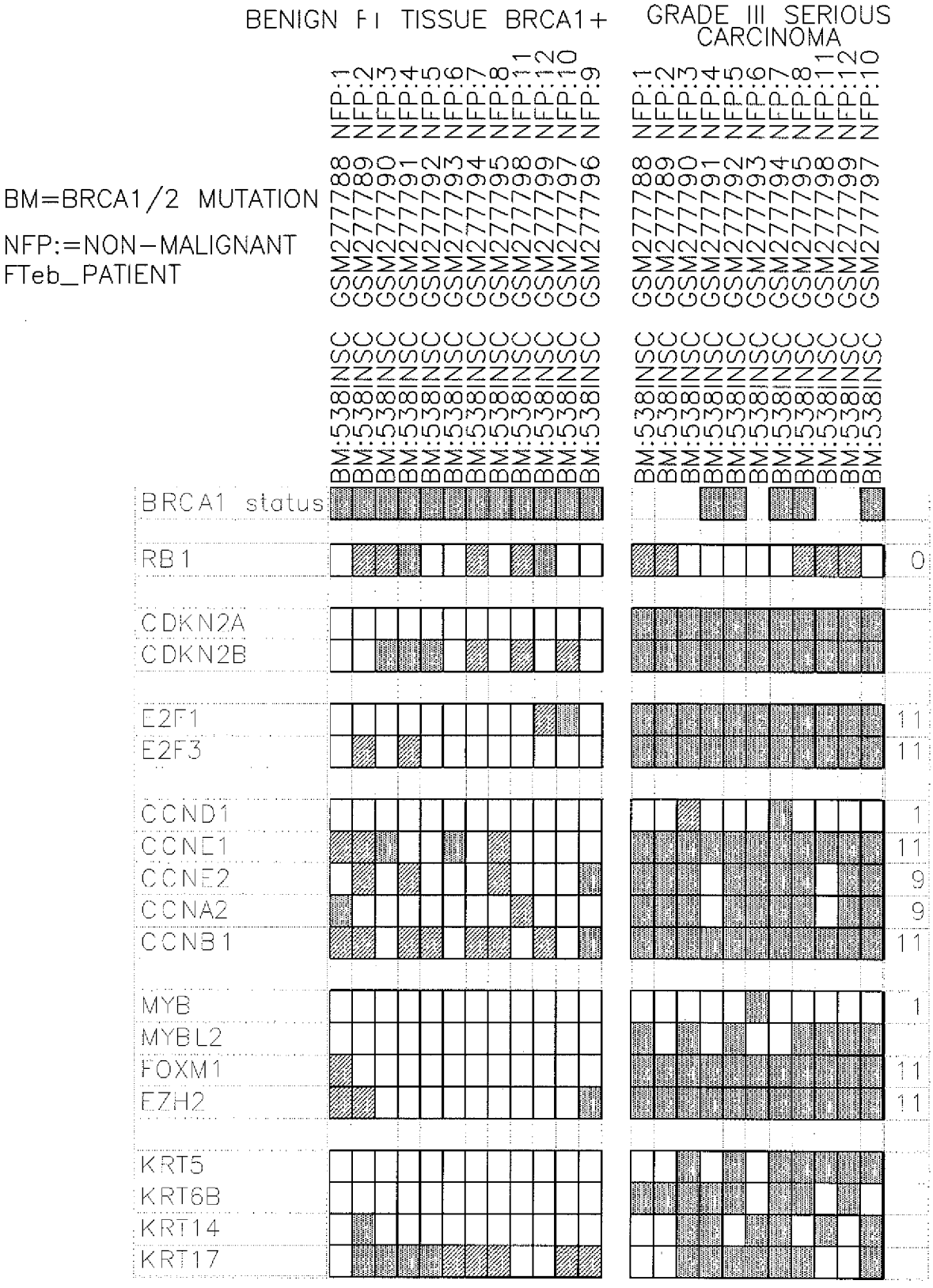
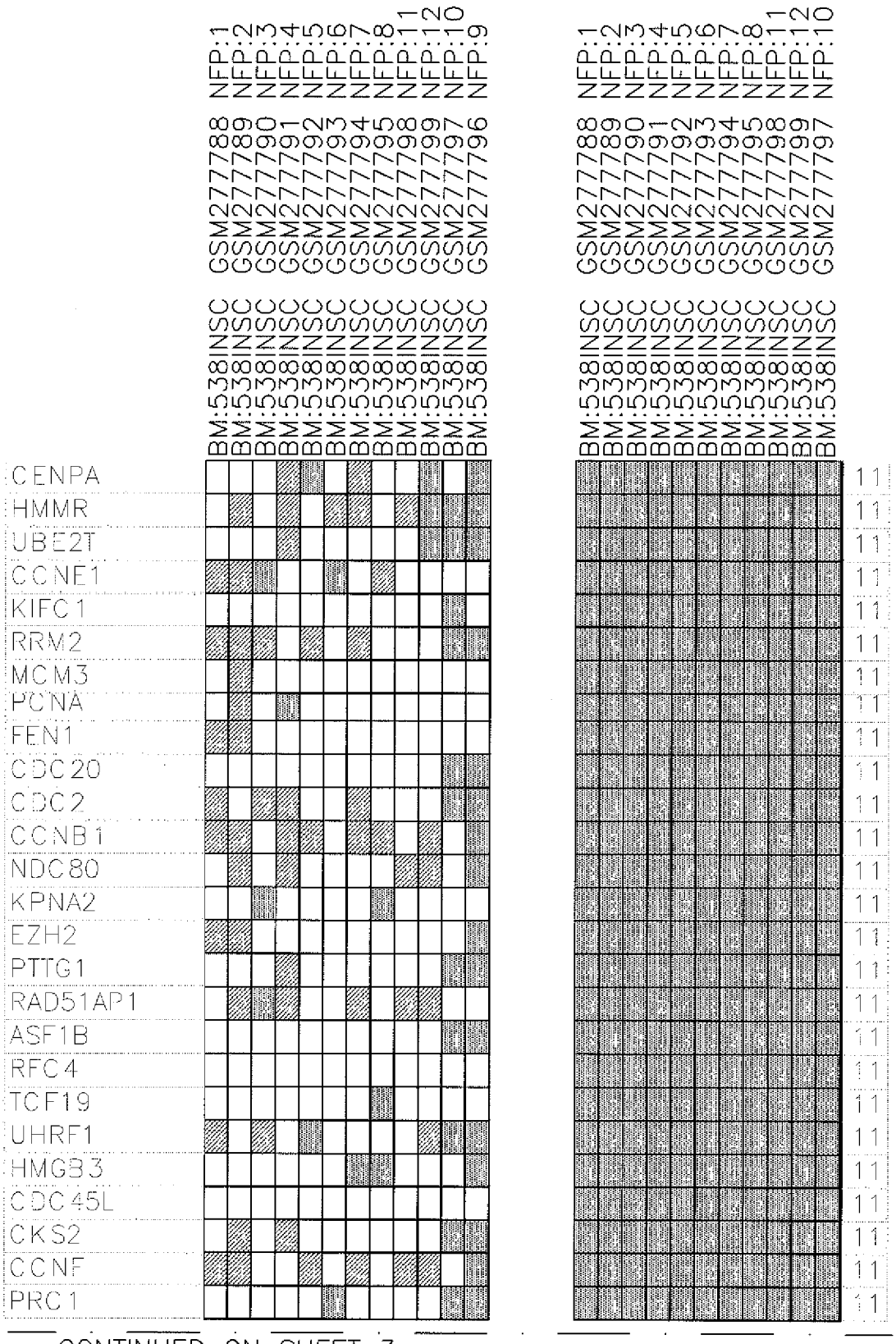
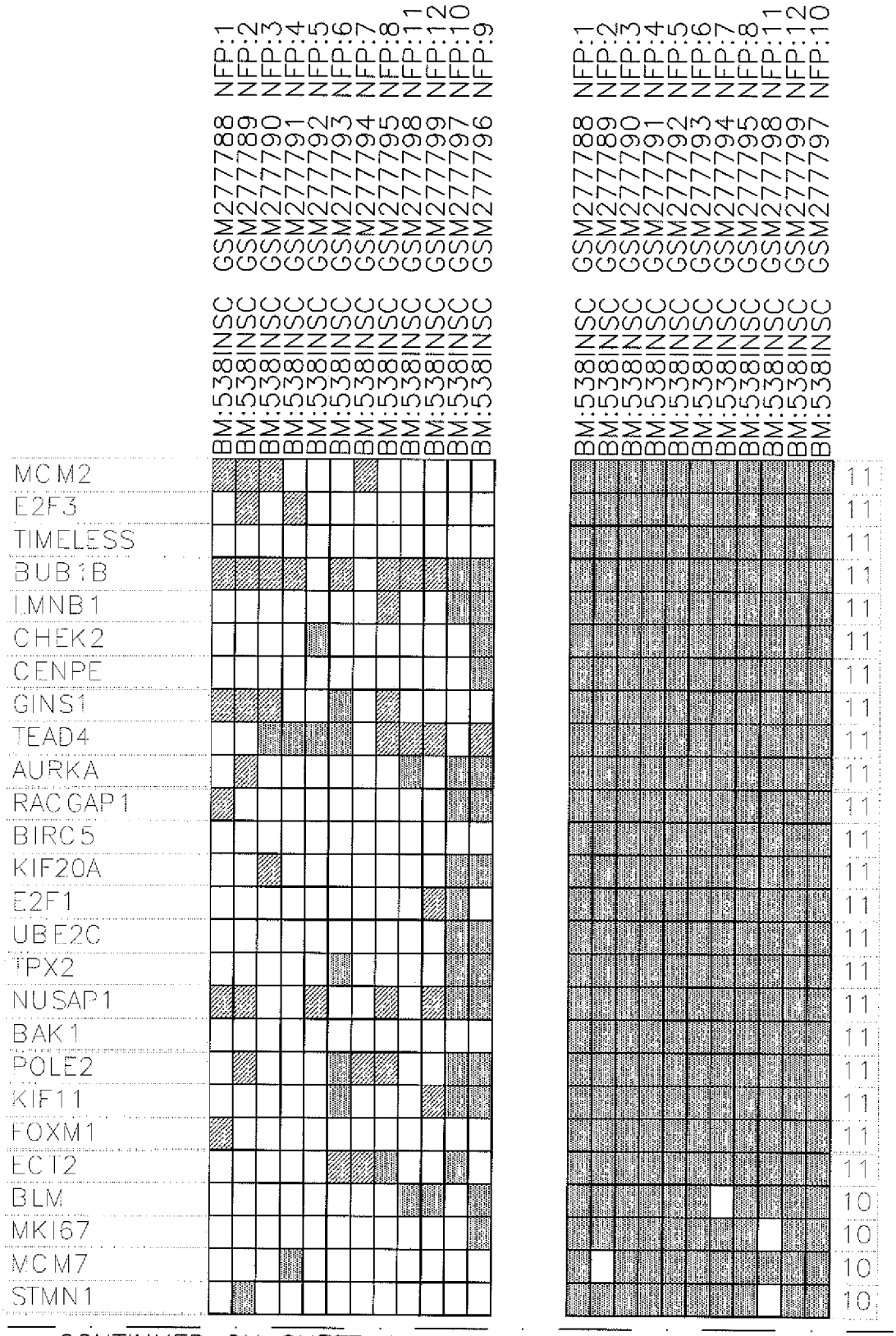

BENIGN FT TISSUE BRCA1+
GRADE III SERIOUS CARCINOMA
BM=BRCA1/2 MUTATION
NFP:=NON-MALIGNANT
FTeb_PATIENT
BRCA1 status
RB1
CDKN2A
CDKN2B
E2F1
E2F3
CCND1
CCNE1
CCNE2
CCNA2
CCNB1
MYB
MYBL2
FOXM1
EZH2
KRT5
KRT6B
KRT14
KRT17

FIG. 23



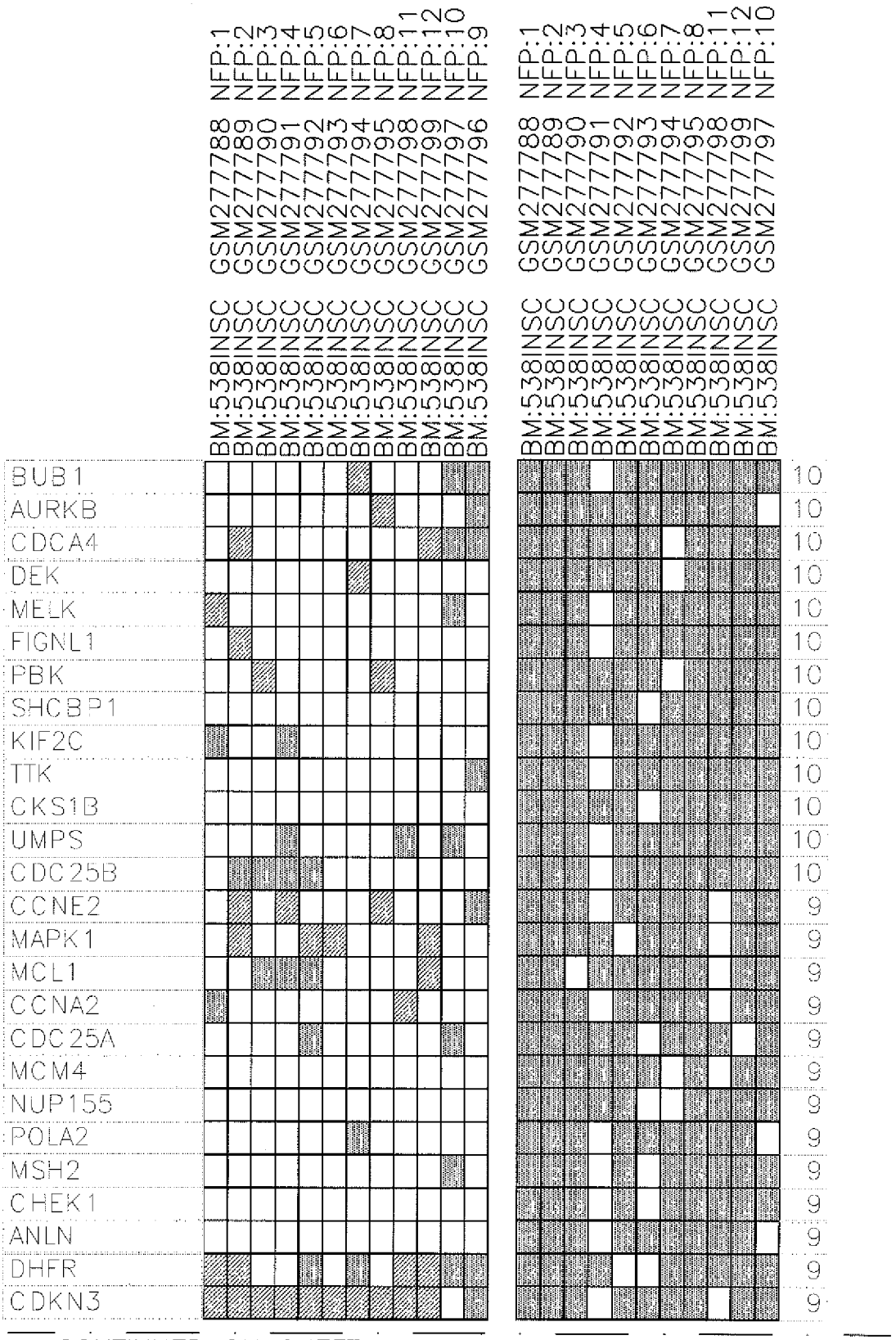
CONTINUED ON SHEET 3

FIG. 23



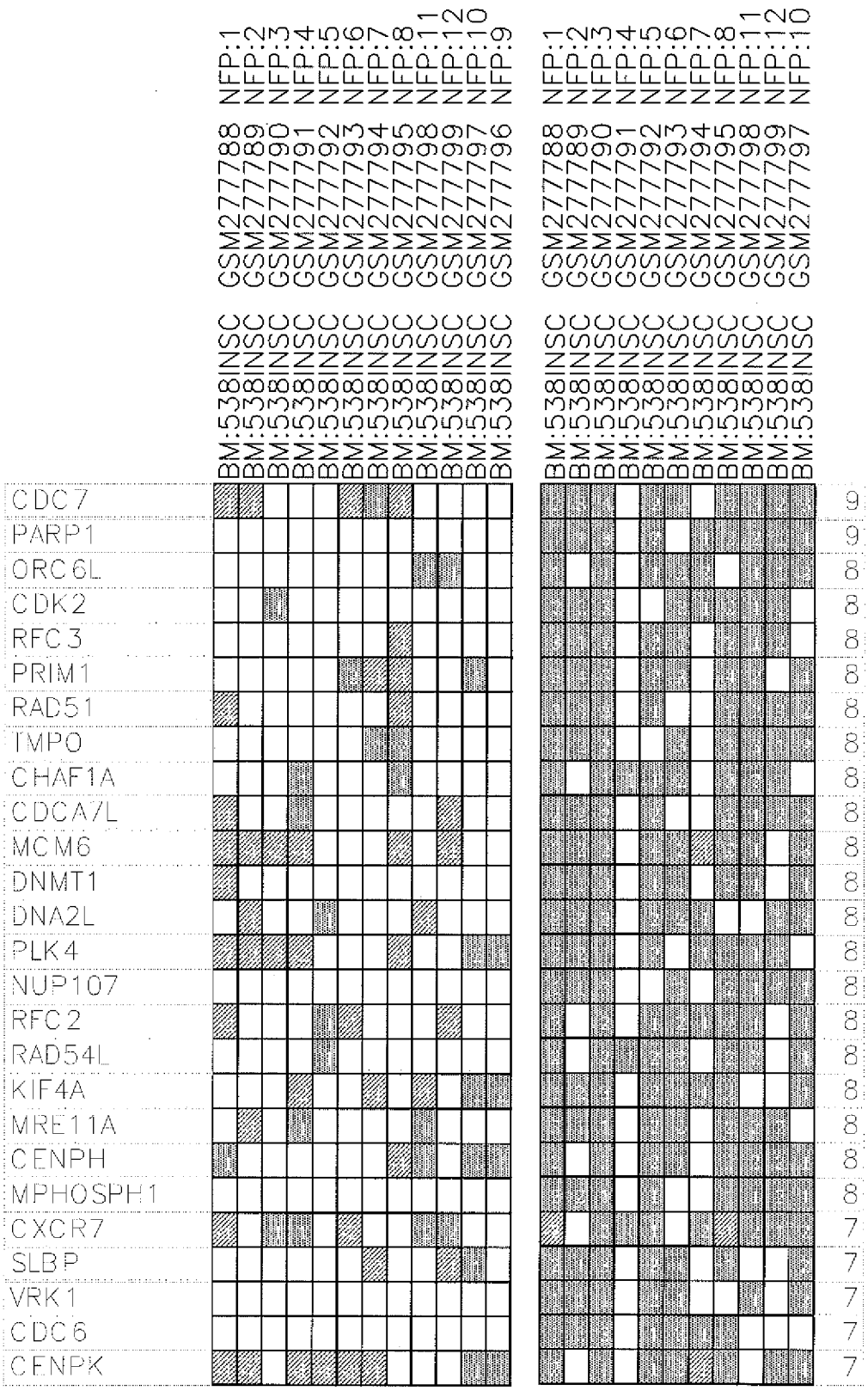
CONTINUED ON SHEET 4

FIG. 23



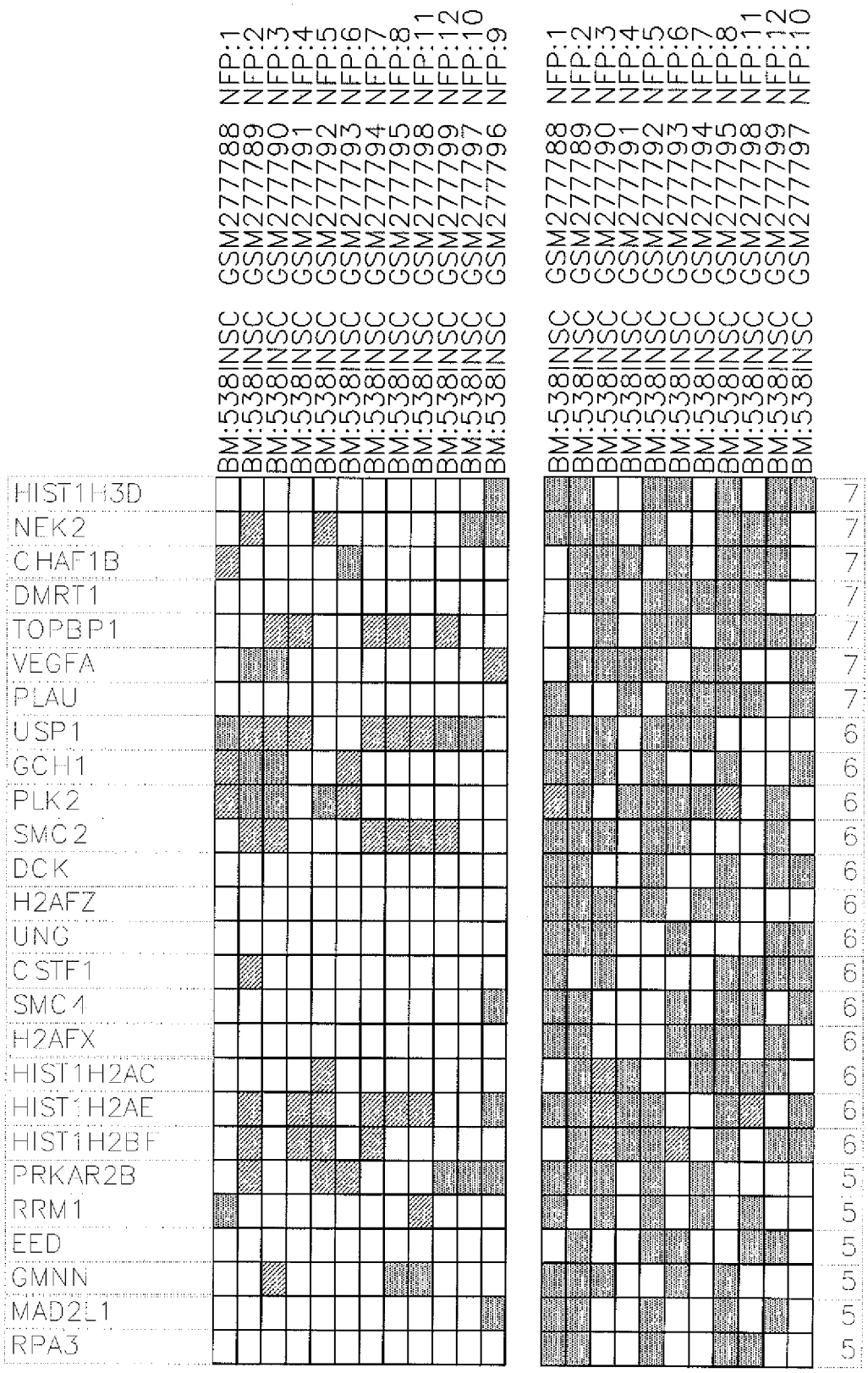
CONTINUED ON SHEET 5

FIG. 23



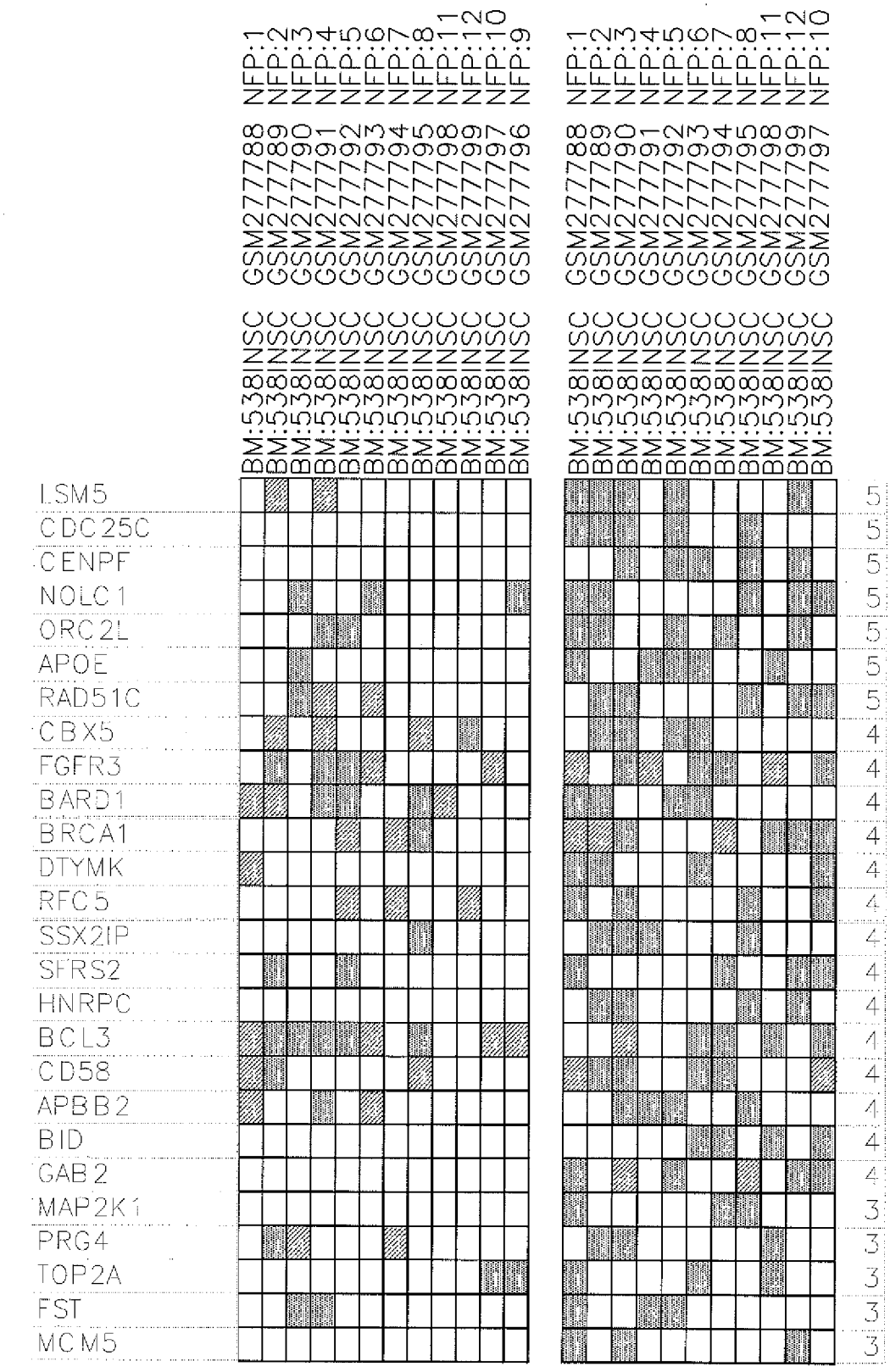
CONTINUED ON SHEET 6

FIG. 23



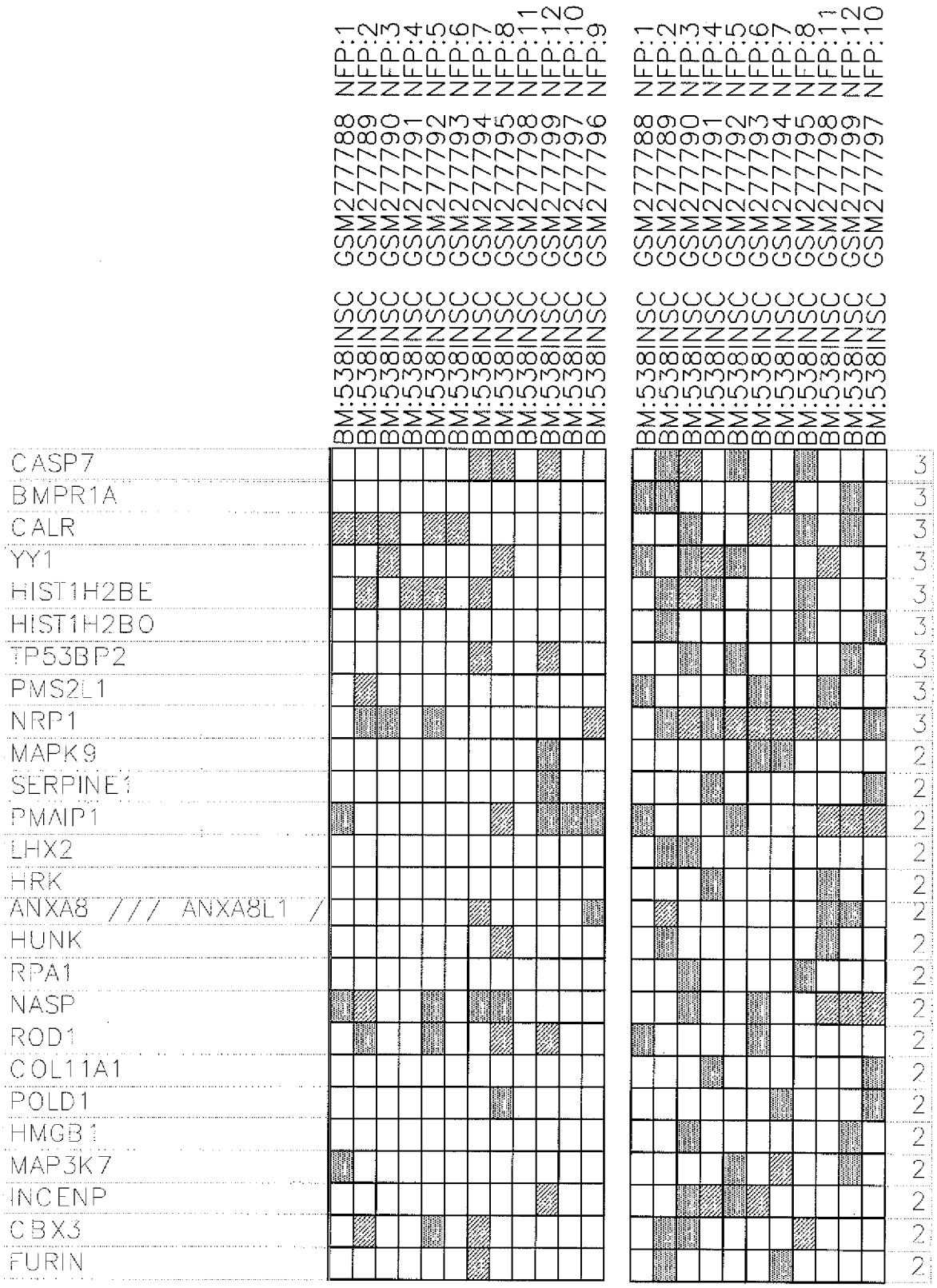
CONTINUED ON SHEET 7

FIG. 23



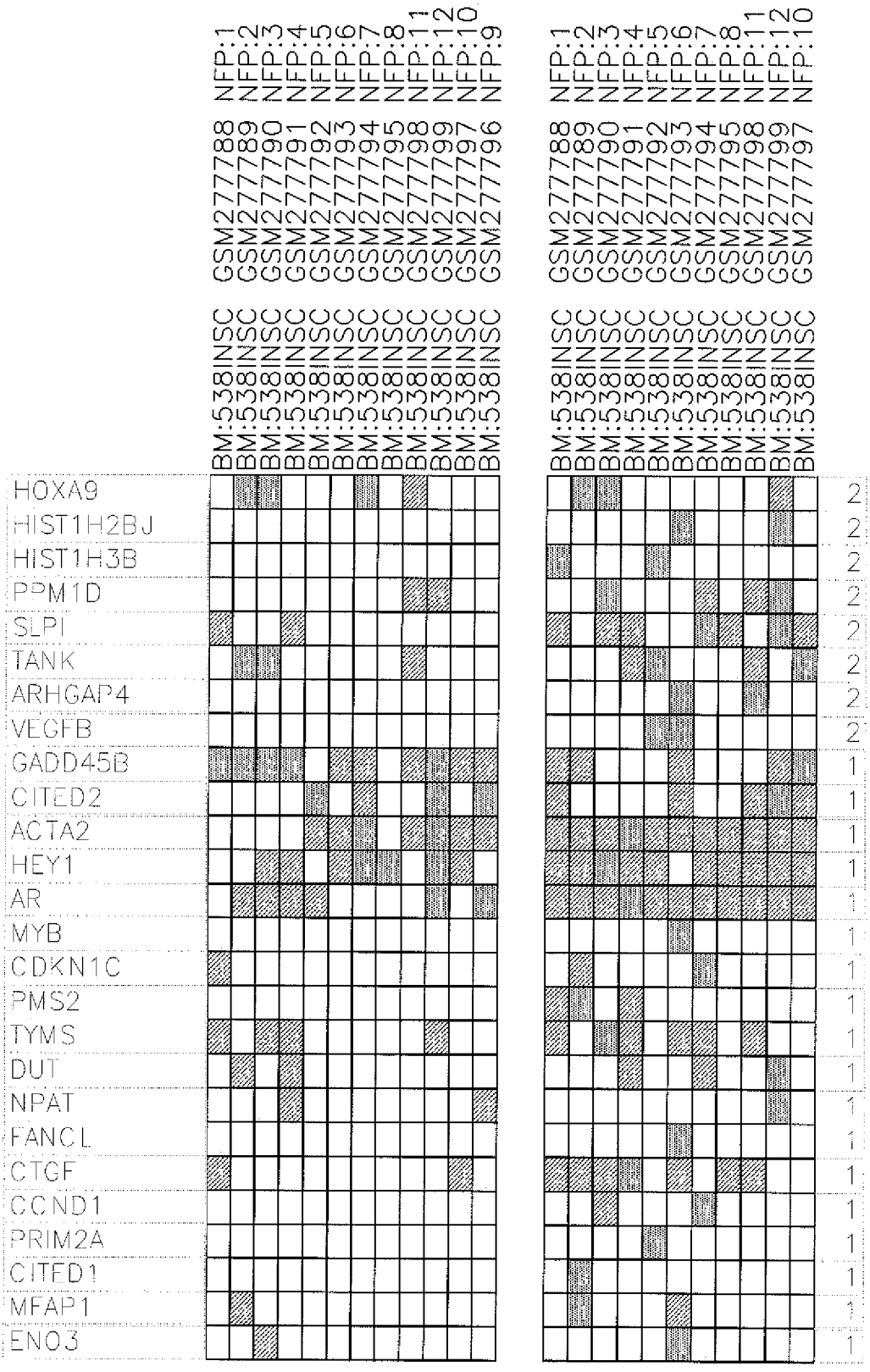
CONTINUED ON SHEET 8

FIG. 23



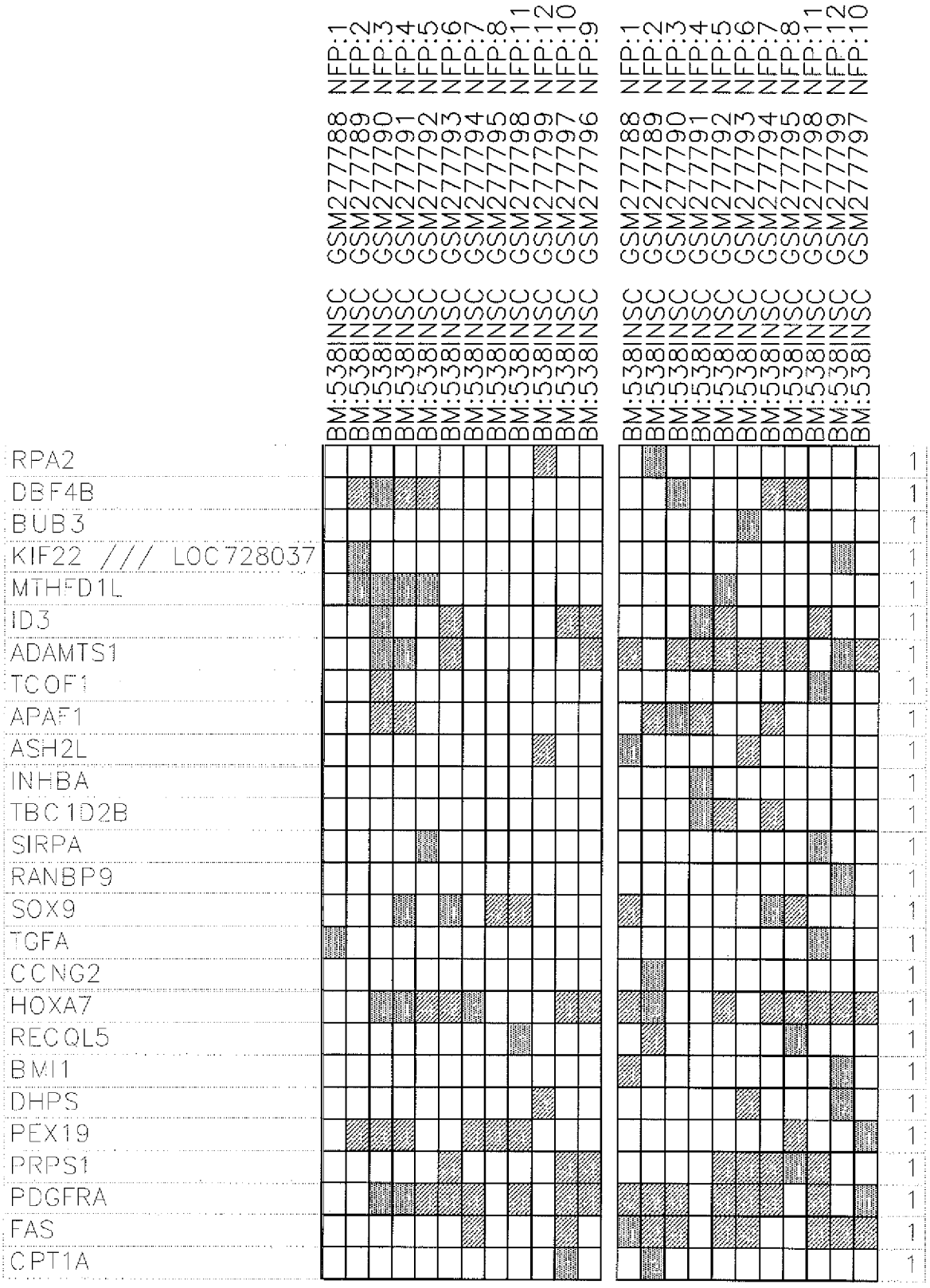
CONTINUED ON SHEET 9

FIG. 23



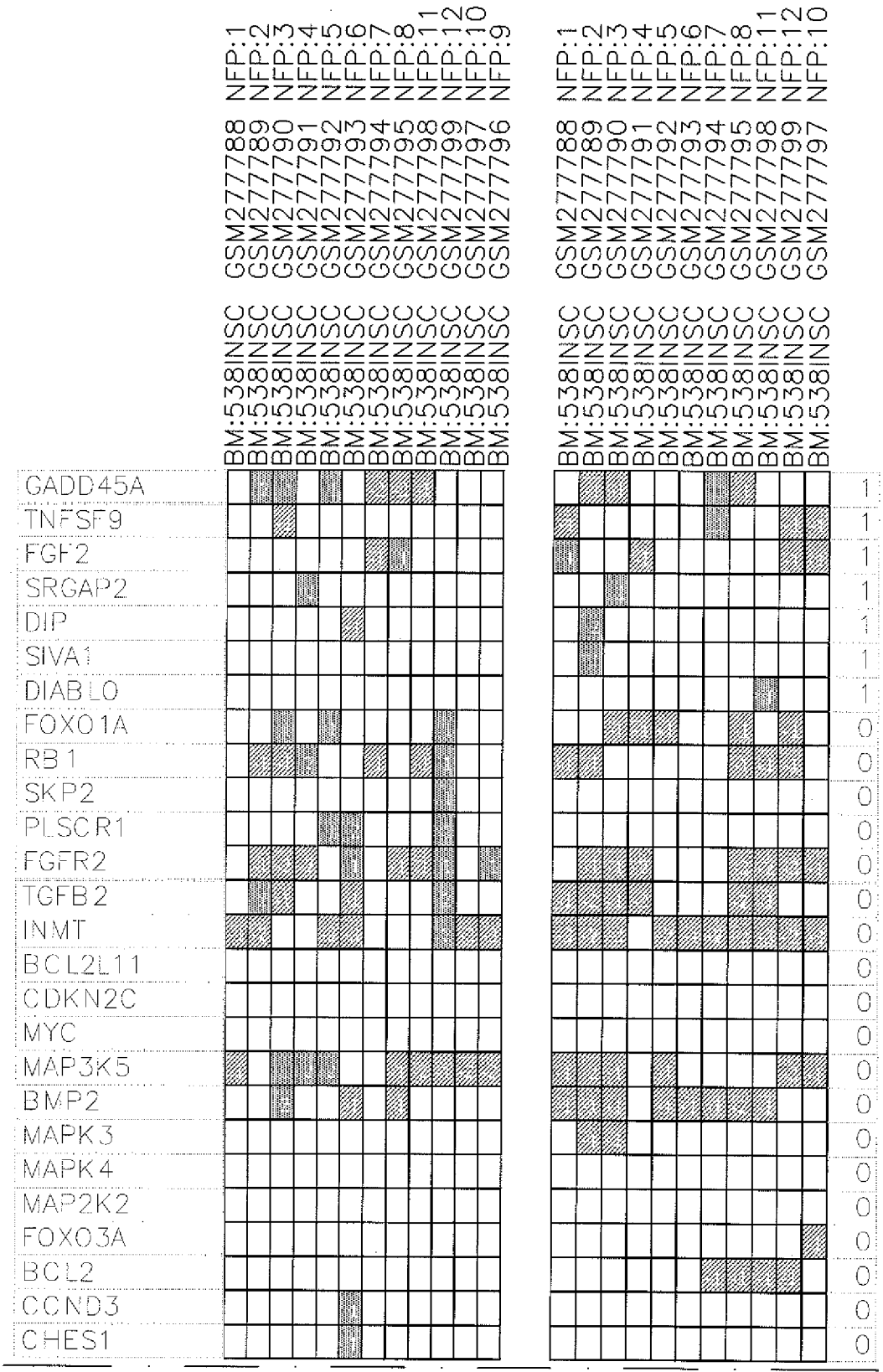
CONTINUED ON SHEET 10

FIG. 23



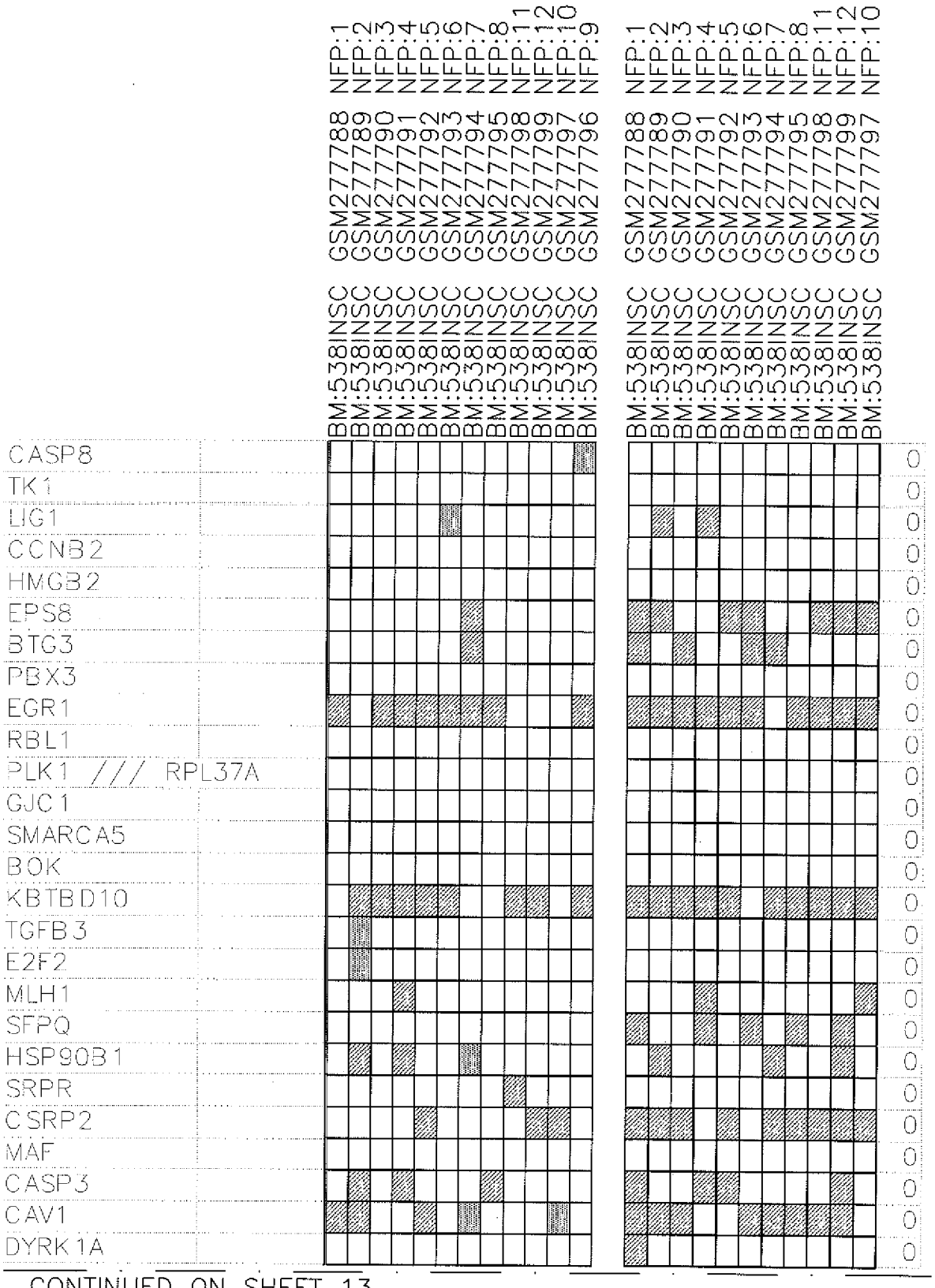
CONTINUED ON SHEET 11

FIG. 23



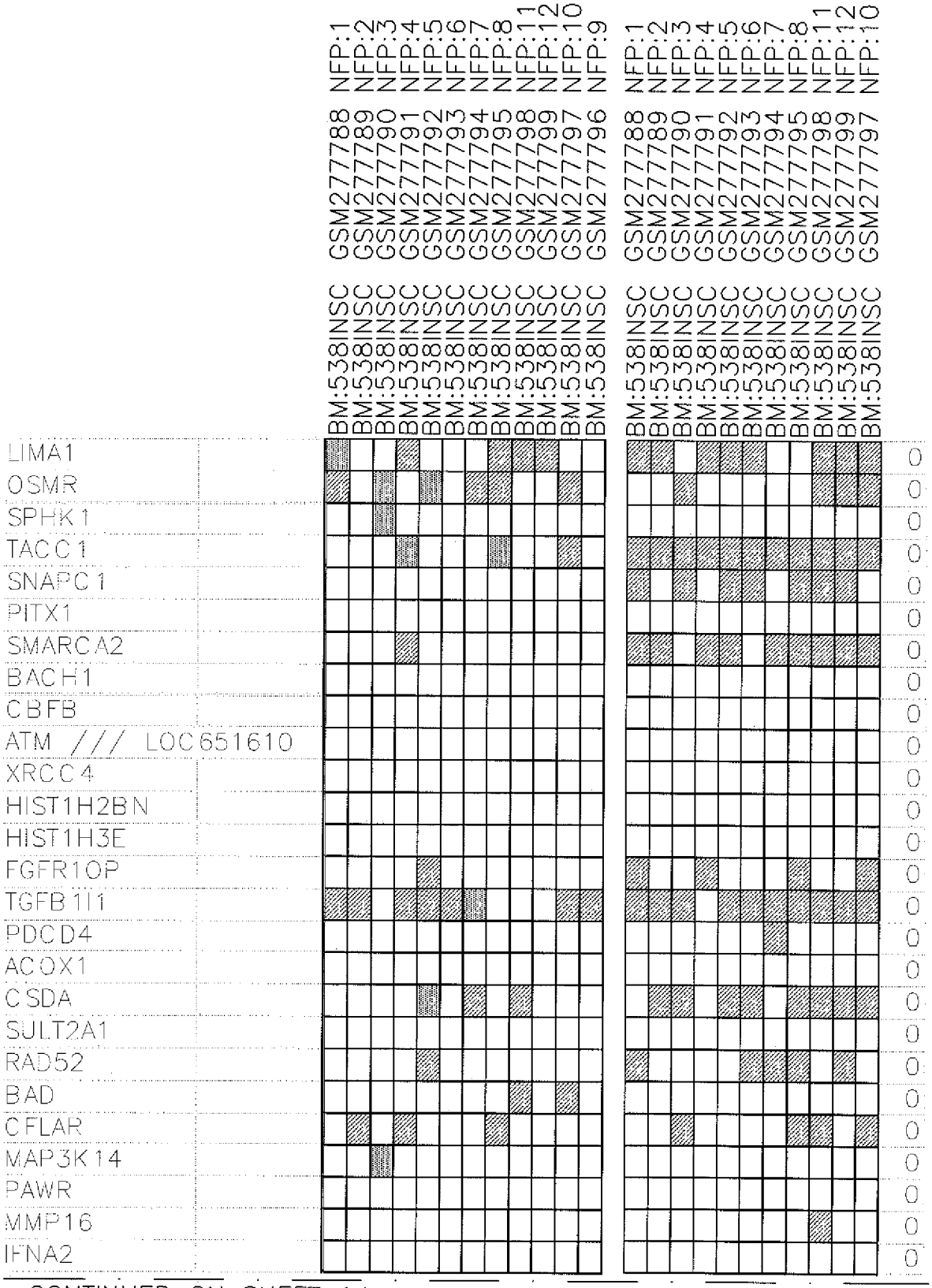
CONTINUED ON SHEET 12

FIG. 23



CONTINUED ON SHEET 13

FIG. 23



CONTINUED ON SHEET 14

FIG. 23

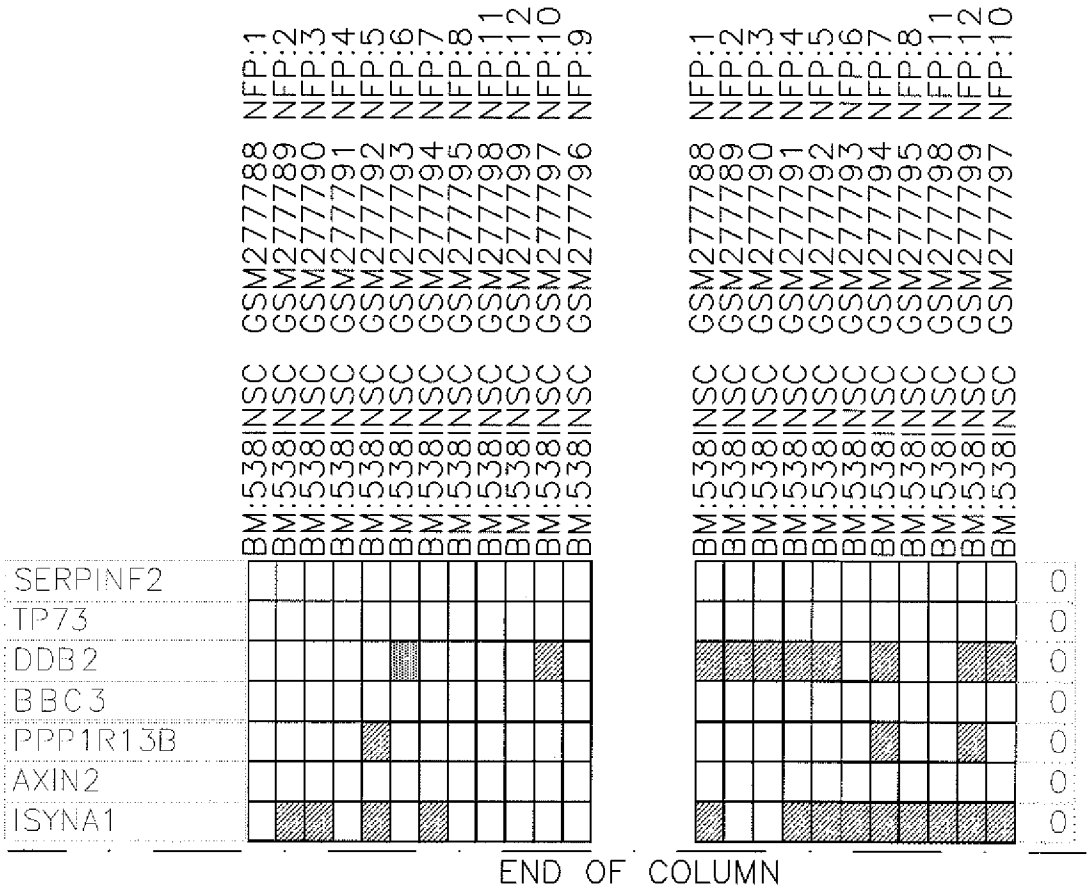

BM:538INSC NFP:1 GSM277788
BM:538INSC NFP:2 GSM277789
BM:538INSC NFP:3 GSM277790
BM:538INSC NFP:4 GSM277791
BM:538INSC NFP:5 GSM277792
BM:538INSC NFP:6 GSM277793
BM:538INSC NFP:7 GSM277794
BM:538INSC NFP:8 GSM277795
BM:538INSC NFP:11 GSM277798
BM:538INSC NFP:12 GSM277799
BM:538INSC NFP:10 GSM277797
BM:538INSC NFP:9 GSM277796
BM:538INSC NFP:1 GSM277788
BM:538INSC NFP:2 GSM277789
BM:538INSC NFP:3 GSM277790
BM:538INSC NFP:4 GSM277791
BM:538INSC NFP:5 GSM277792
BM:538INSC NFP:6 GSM277793
BM:538INSC NFP:7 GSM277794
BM:538INSC NFP:8 GSM277795
BM:538INSC NFP:11 GSM277798
BM:538INSC NFP:12 GSM277799
BM:538INSC NFP:10 GSM277797
SERPINF2
TP73
DDB2
BBC3
PPP1R13B
AXIN2
ISYNA1
0
0
0
0
0
0
0
END OF COLUMN

FIG. 23

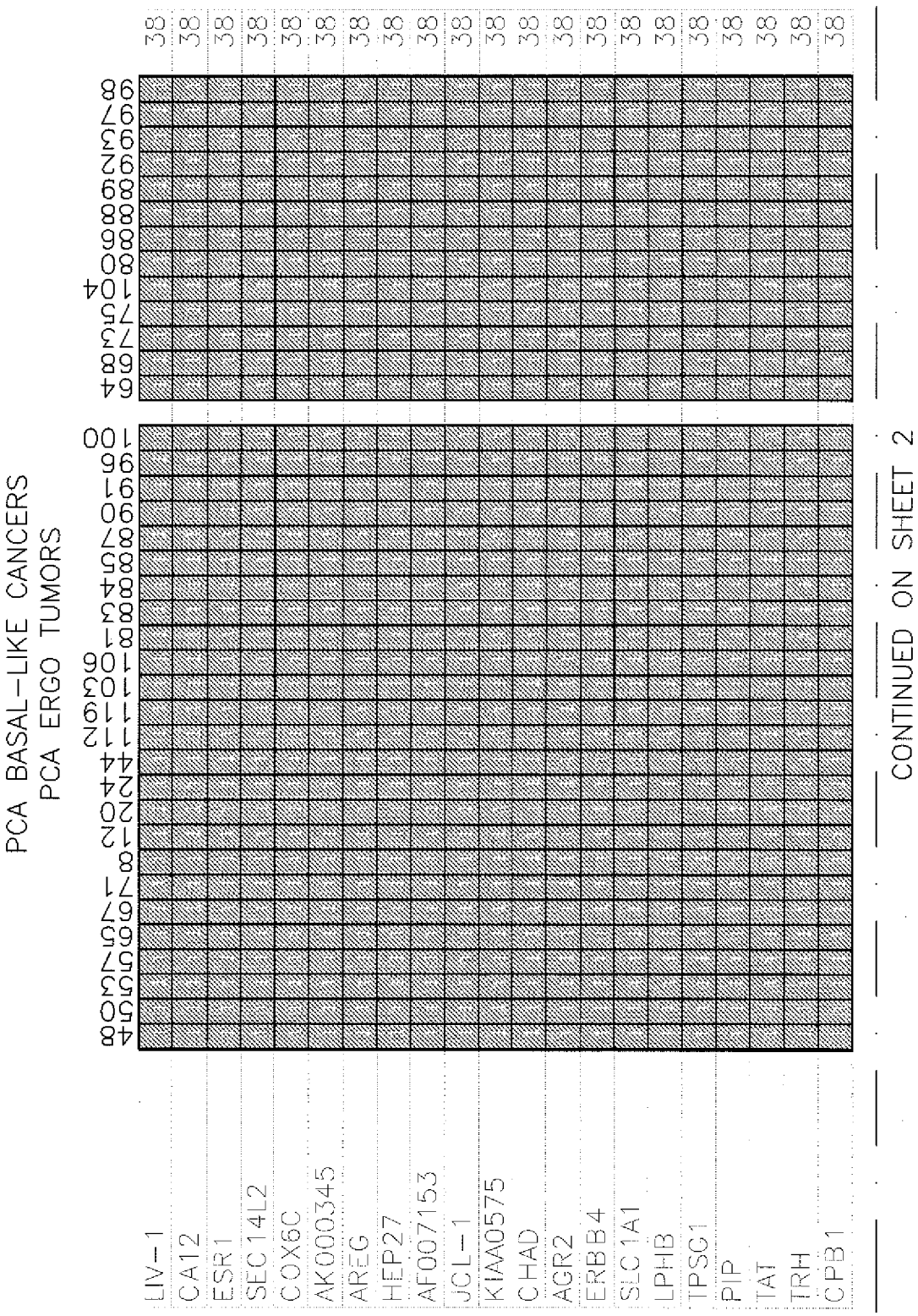

PCA BASAL-LIKE CANCERS
PCA ERGO TUMORS
LIV-1
CA12
ESR1
SEC14L2
COX6C
AK000345
AREG
HEP27
AF007153
JCL-1
KIAA0575
CHAD
AGR2
ERBB4
SLC1A1
LPHB
TPSG1
PIP
TAT
TRH
CPB1
CONTINUED ON SHEET 2

FIG. 24

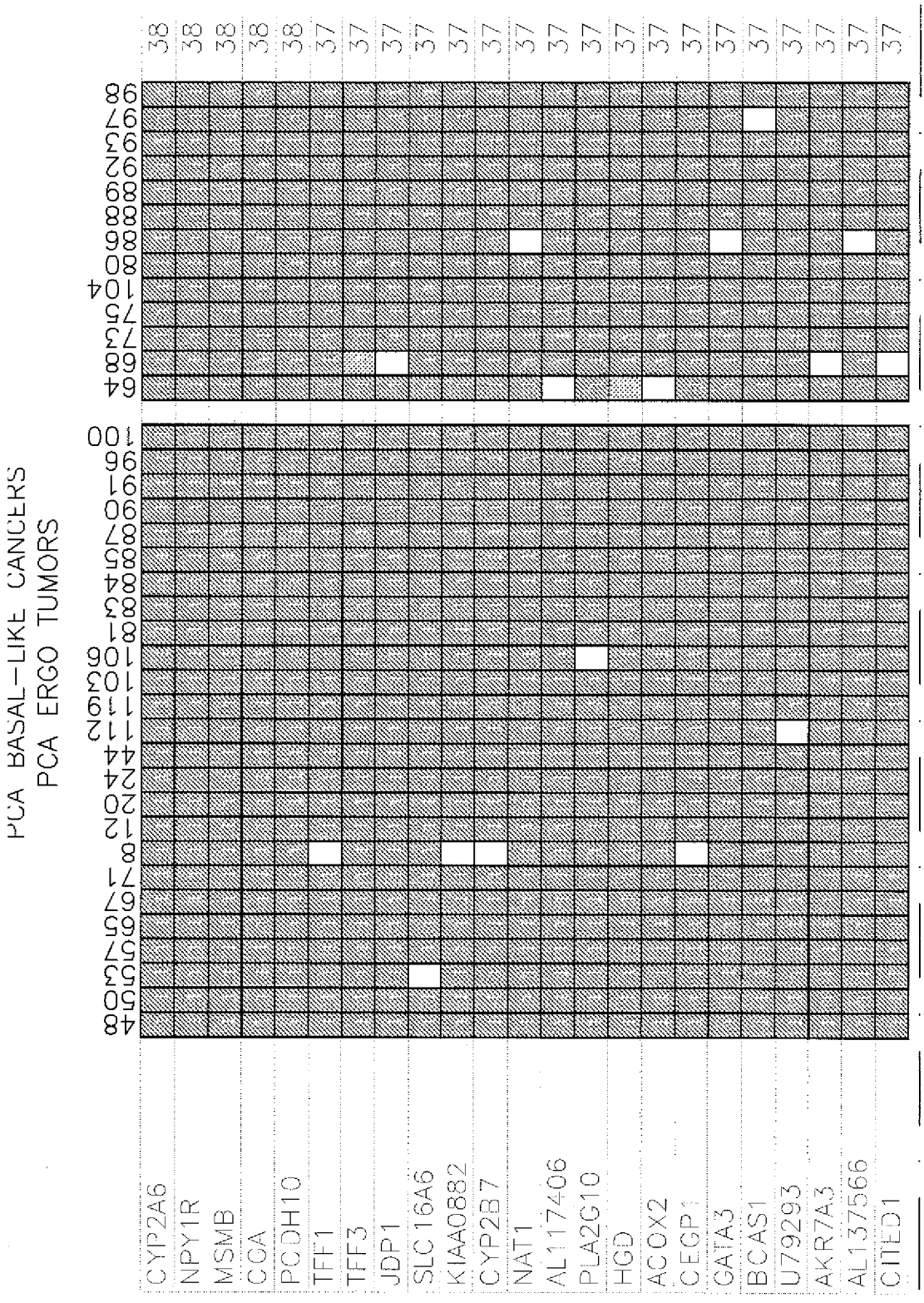

PCA BASAL-LIKE CANCERS
PCA ERGO TUMORS
CYP2A6
NPY1R
MSMB
CCA
PCDH10
TFF1
TFF3
JDP1
SLC16A6
KIAA0882
CYP2B7
NAT1
AL117406
PLA2G10
HGD
ACOX2
CEGP1
GATA3
BCAS1
U79293
AKR7A3
AL137566
CITED1
CONTINUED ON SHEET 3

FIG. 24

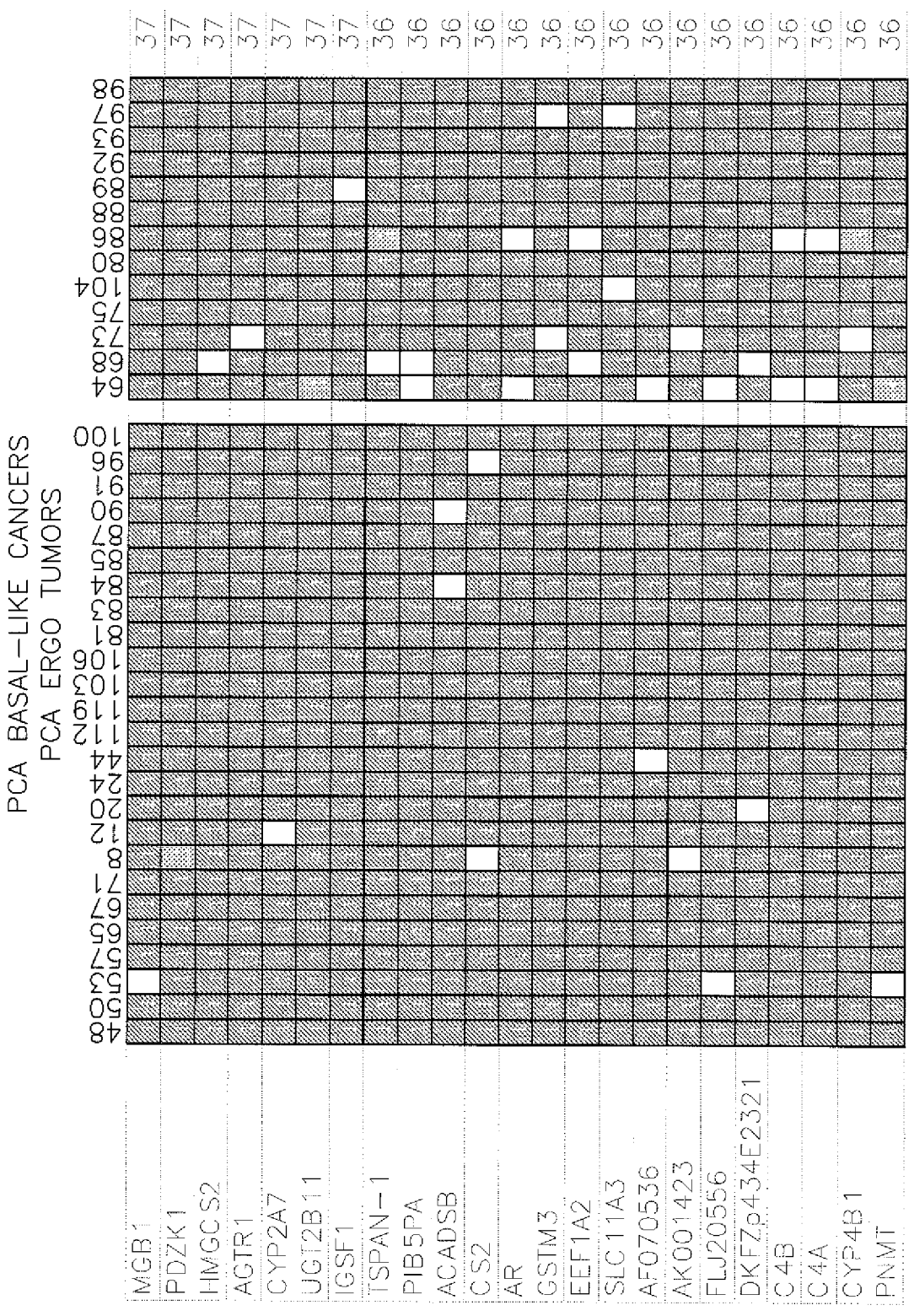

PCA BASAL-LIKE CANCERS
PCA ERGO TUMORS
MGB1
PDZK1
HMGCS2
AGTR1
CYP2A7
UGT2B11
IGSF1
TSPAN-1
PIB5PA
ACADSB
CS2
AR
GSTM3
EEF1A2
SLC11A3
AF070536
AK001423
FLJ20556
DKFZp434E2321
C4B
C4A
CYP4B1
PNMT
CONTINUED ON SHEET 4

FIG. 24

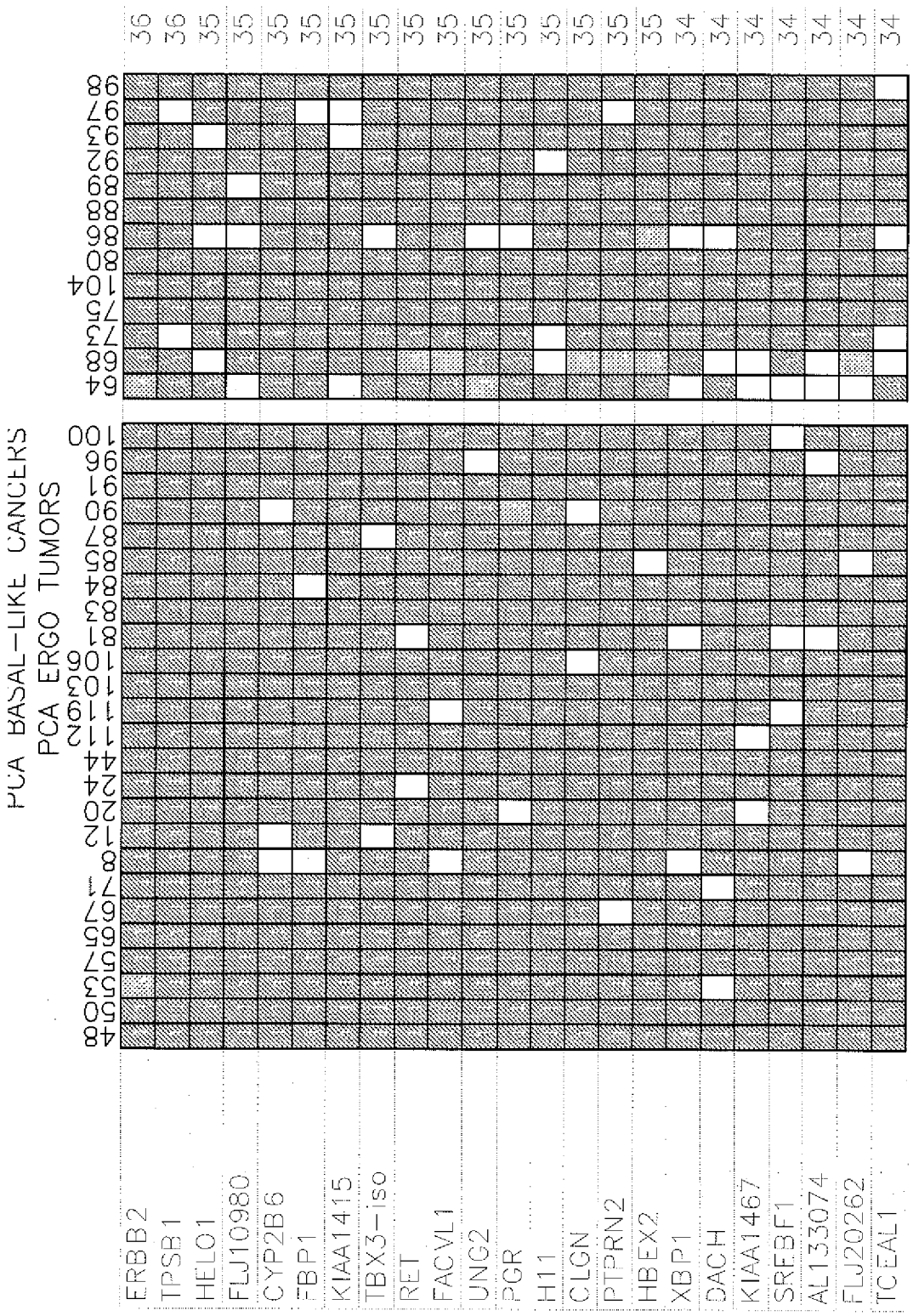
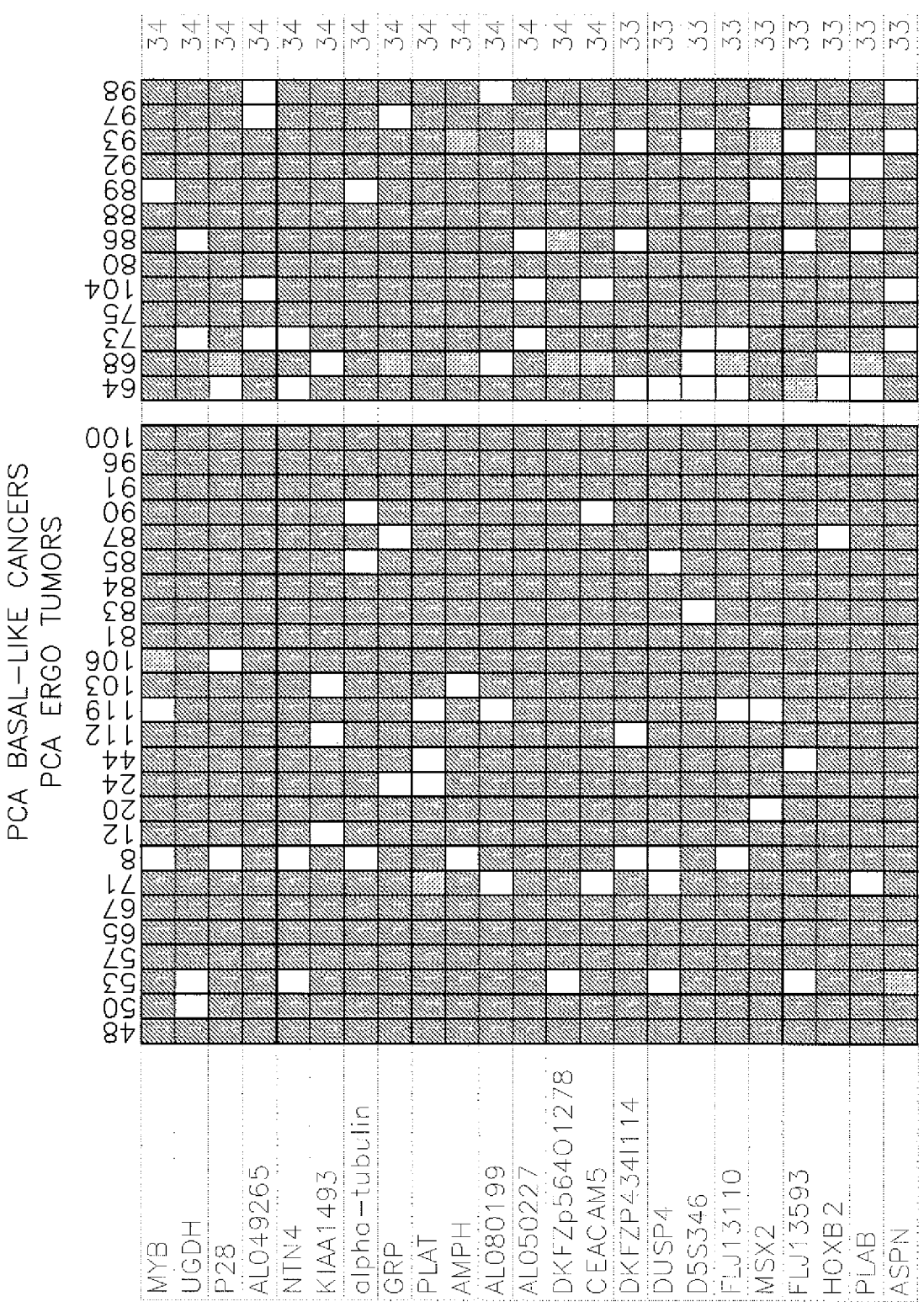

PCA BASAL-LIKE CANCERS
PCA ERGO TUMORS
ERBB2
TPSB1
HELO1
FLJ10980
CYP2B6
TBP1
KIAA1415
TBX3-iso
RET
FACVL1
UNG2
PGR
H11
CLGN
PTPRN2
HBEX2
XBP1
DACH
KIAA1467
SREBF1
AL133074
FLJ20262
TCEAL1
CONTINUED ON SHEET 5

FIG. 24



CONTINUED ON SHEET 6

FIG. 24

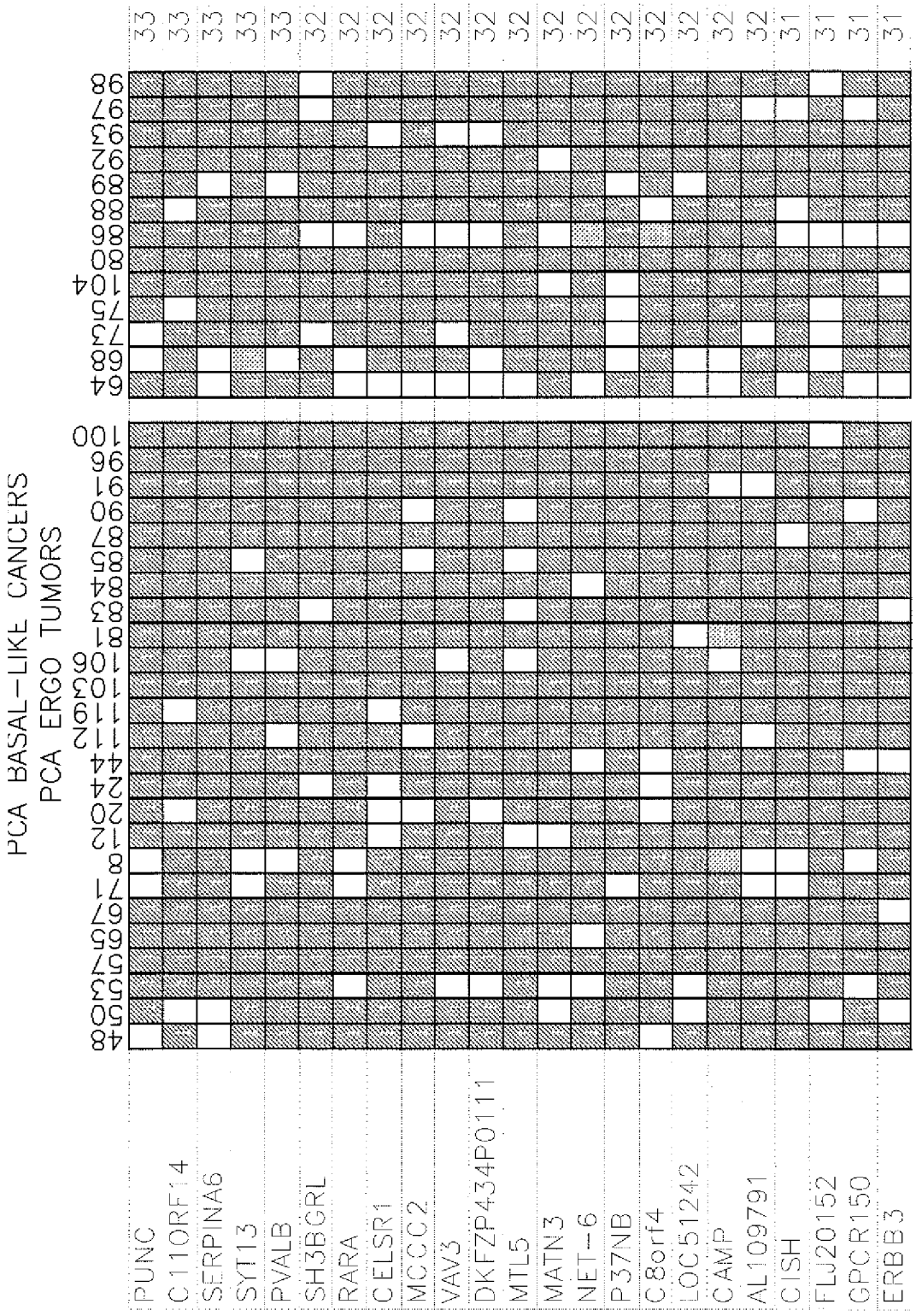

PCA BASAL-LIKE CANCERS
PCA ERGO TUMORS
PUNC
C11ORF14
SERPINA6
SYT13
PVALB
SH3BGRL
RARA
CELSR1
MCCC2
VAV3
DKFZP434P0111
MTL5
MATN3
NET-6
P37NB
C8orf4
LOC51242
CAMP
AL109791
CISH
FLJ20152
GPCR150
ERBB3
CONTINUED ON SHEET 7

FIG. 24

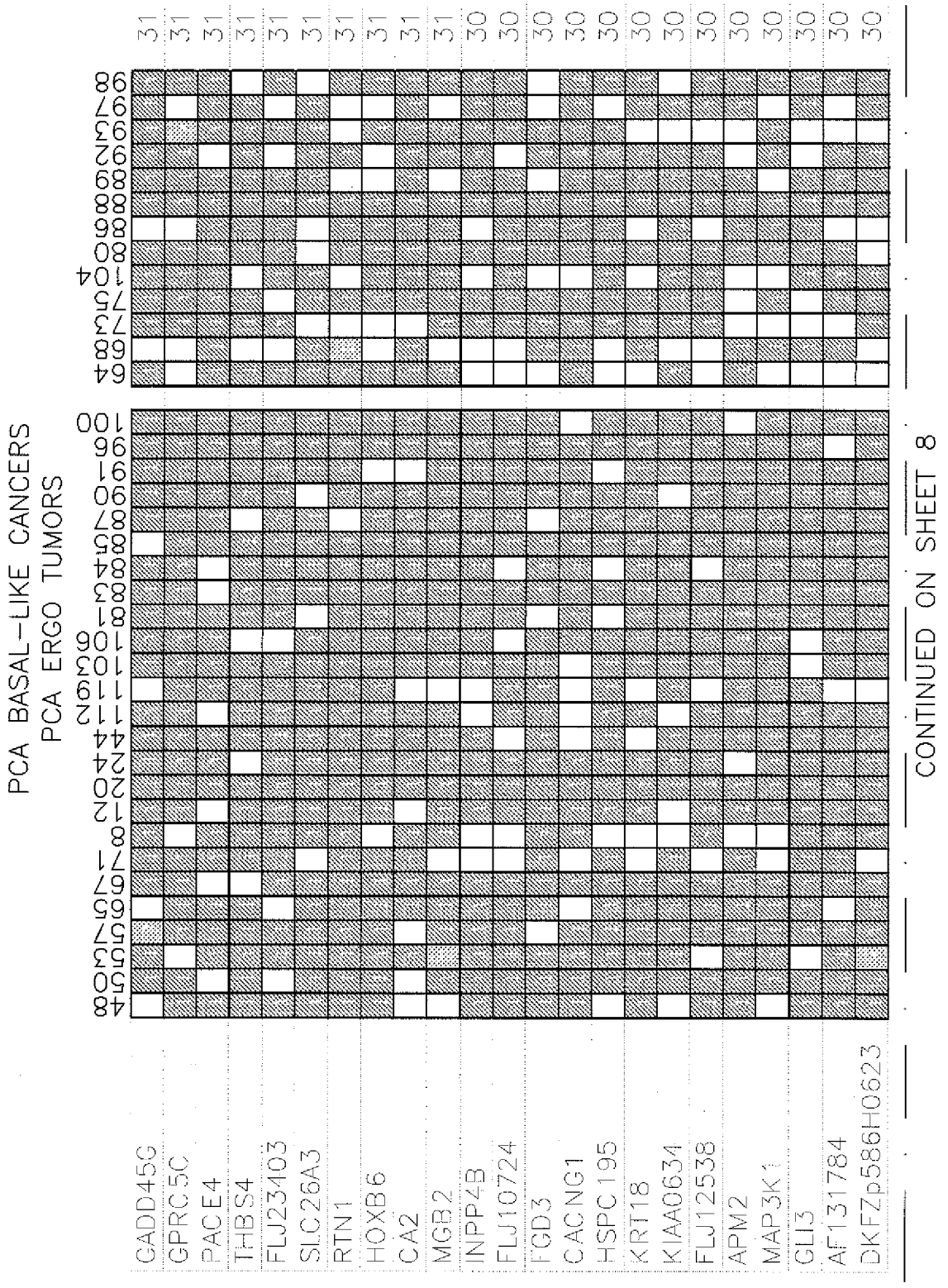

PCA BASAL-LIKE CANCERS
PCA ERGO TUMORS
GADD45G
GPRC5C
PACE4
THBS4
FLJ23403
SLC26A3
RTN1
HOXB6
CA2
MGB2
INPP4B
FLJ10724
FGD3
CACNG1
HSPC195
KRT18
KIAA0634
FLJ12538
APM2
MAP3K1
GLI3
AF131784
DKFZp586H0623
CONTINUED ON SHEET 8

FIG. 24

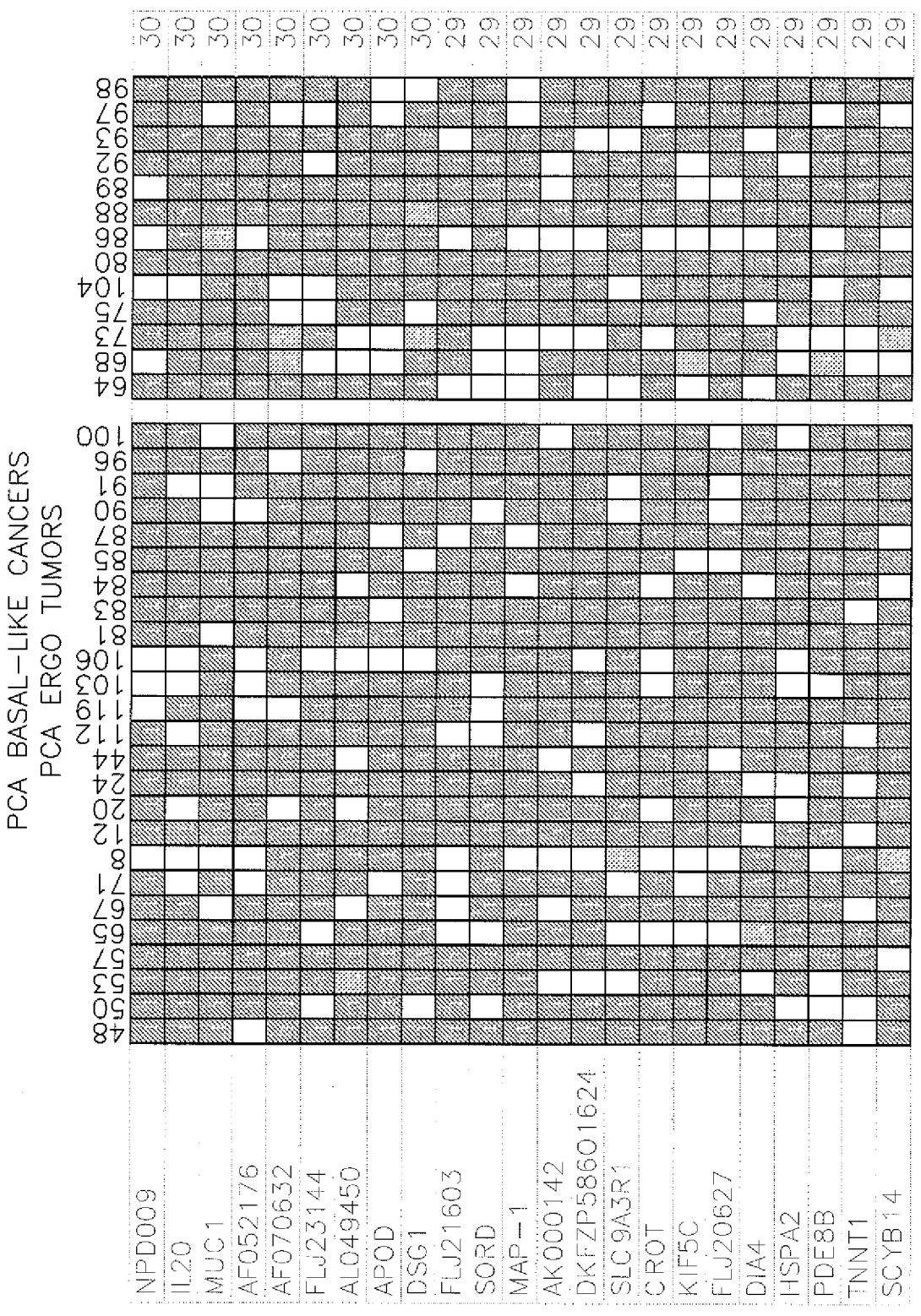

PCA BASAL-LIKE CANCERS
PCA ERGO TUMORS
NPD009
IL20
MUC1
AF052176
AF070632
FLJ23144
AL049450
APOD
DSG1
FLJ21603
SORD
MAP-1
AK000142
DKFZP586O1624
SLC9A3R1
CROT
KIF5C
FLJ20627
DIA4
HSPA2
PDE8B
TNNT1
SCYB14
CONTINUED ON SHEET 9

FIG. 24

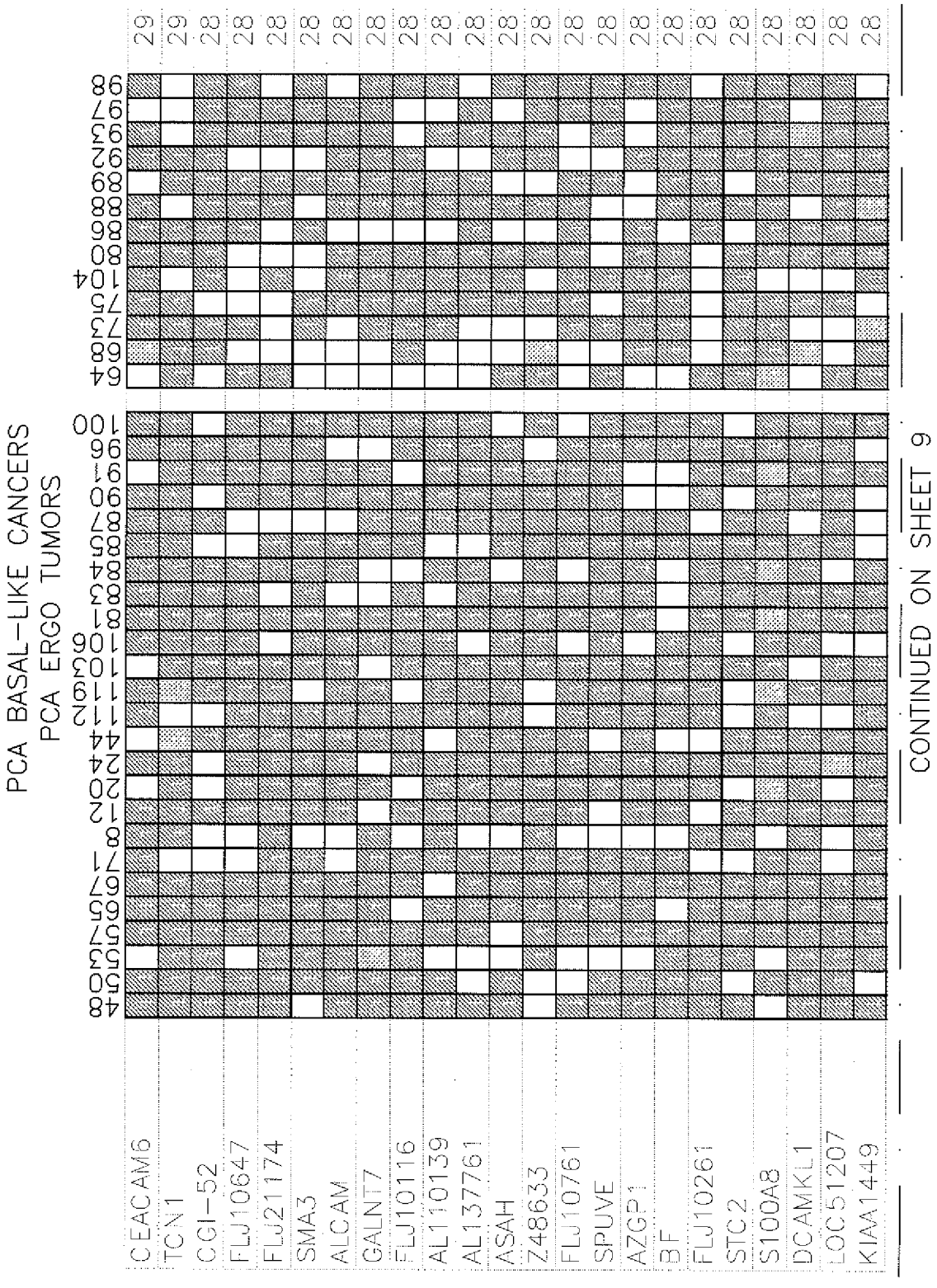

PCA BASAL-LIKE CANCERS
PCA ERGO TUMORS
CEACAM6
TCN1
CGI-52
FLJ10647
FLJ21174
SMA3
ALCAM
GALNT7
FLJ10116
AL110139
AL137761
ASAH
Z48633
FLJ10761
SPUVE
AZGP1
BF
FLJ10261
STC2
S100A8
DCAMKL1
LOC51207
KIAA1449
CONTINUED ON SHEET 9

FIG. 24

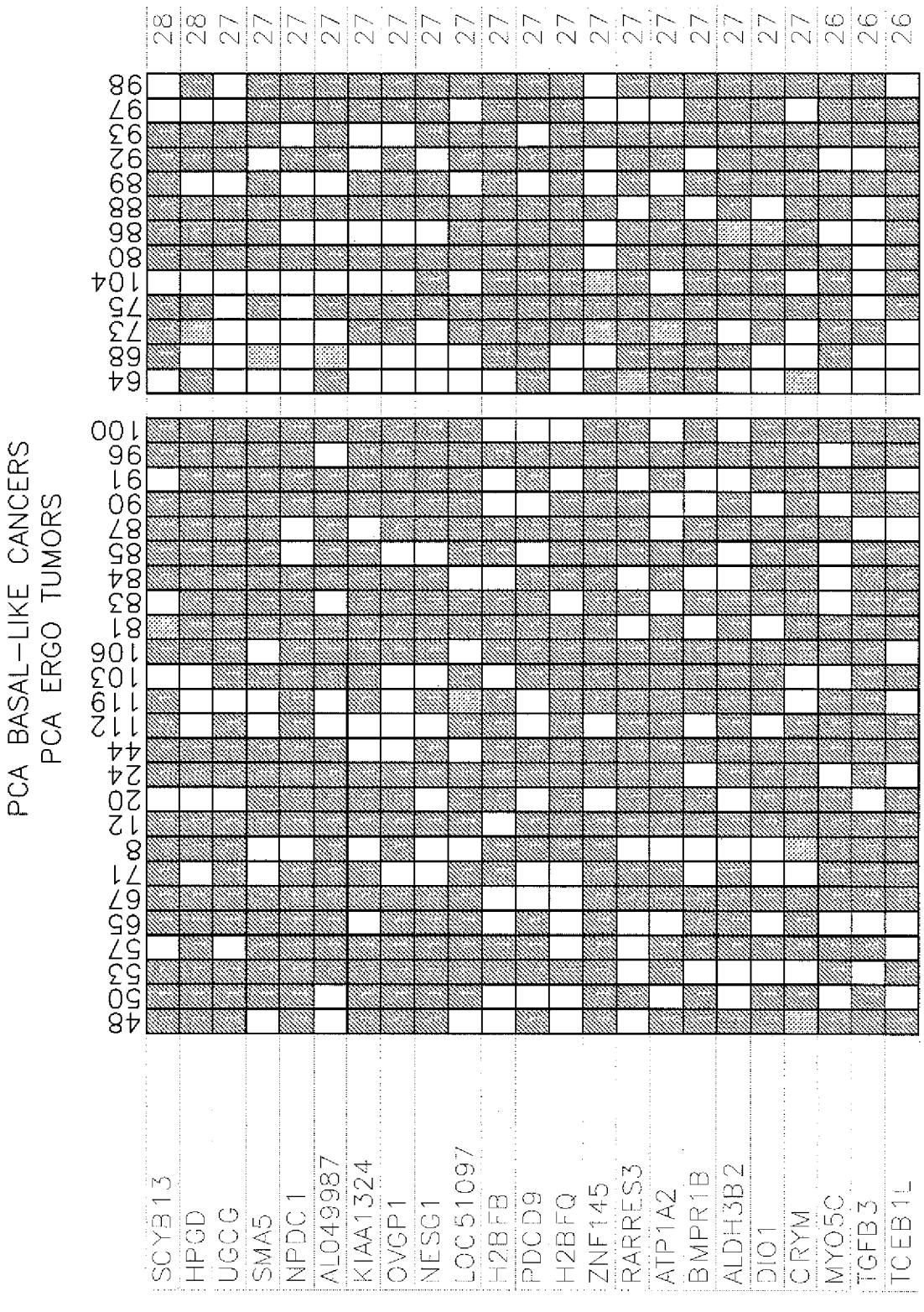

PCA BASAL-LIKE CANCERS
PCA ERGO TUMORS
SCYB13
HPGD
UGCG
SMA5
NPDC1
AL049987
KIAA1324
CVGP1
NESG1
LOC51097
H2BFB
PDCD9
H2BFQ
ZNF145
RARRES3
ATP1A2
BMPR1B
ALDH3B2
DIO1
CRYM
MYO5C
TGFB3
TCEB1L
CONTINUED ON SHEET 11

FIG. 24

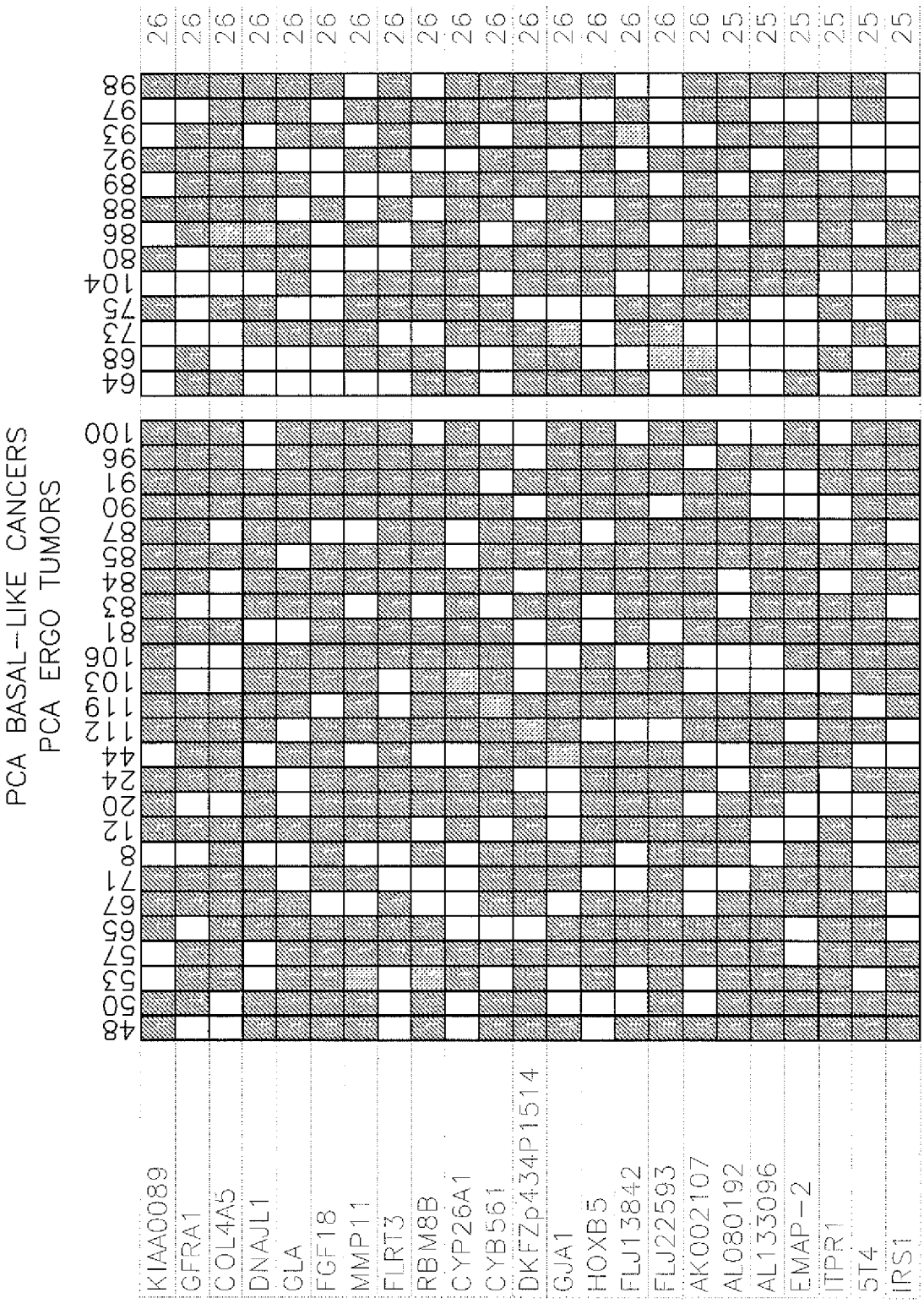

PCA BASAL-LIKE CANCERS
PCA ERGO TUMORS
KIAA0089
GFRA1
COL4A5
DNAJL1
GLA
FGF18
MMP11
FLRT3
RBM8B
CYP26A1
CYB561
DKFZp434P1514
GJA1
HOXB5
FLJ13842
FLJ22593
AK002107
AL080192
AL133096
EMAP-2
ITPR1
ST4
IRS1
CONTINUED ON SHEET 12

FIG. 24

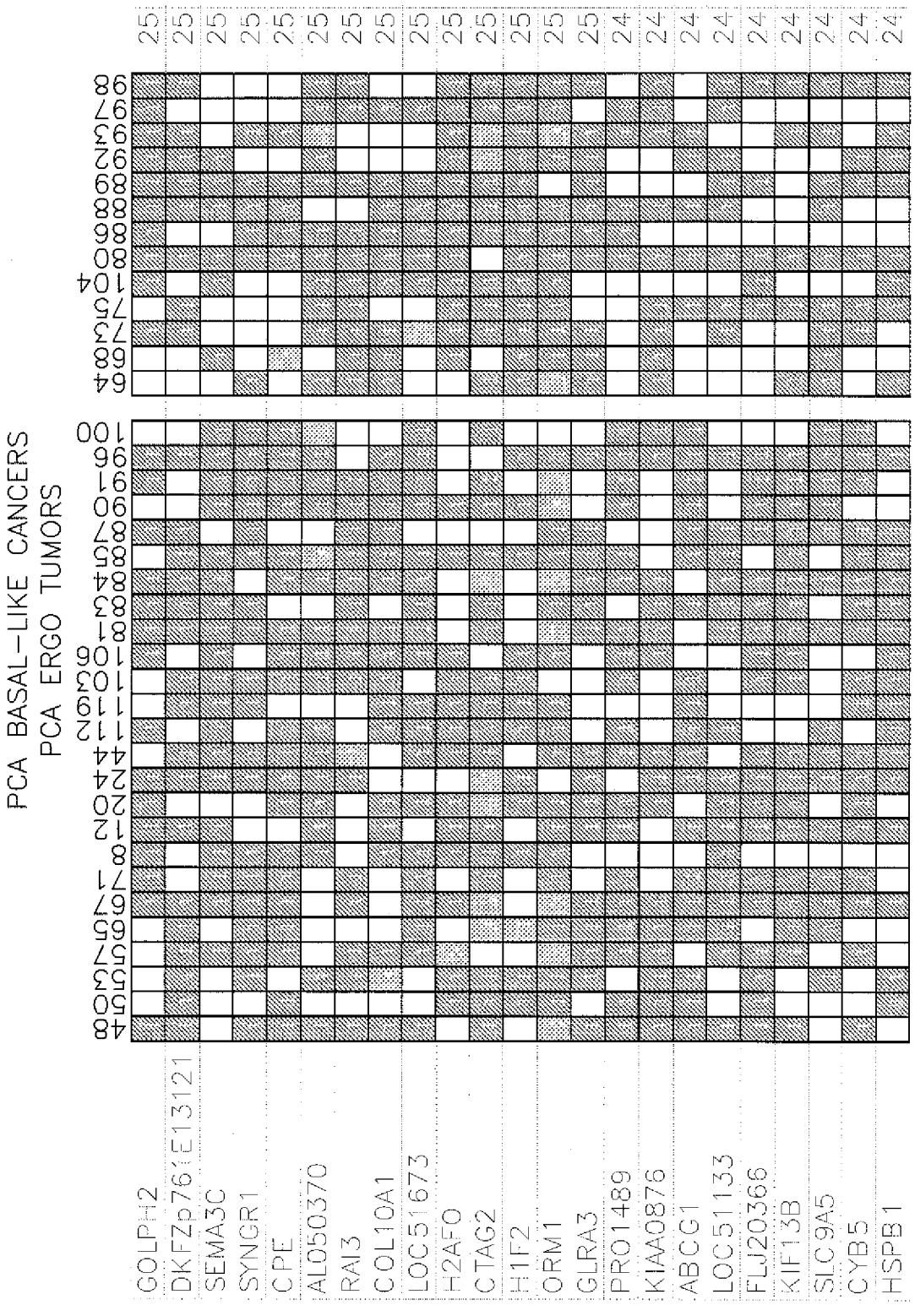

PCA BASAL-LIKE CANCERS
PCA ERGO TUMORS
GOLPH2
DKFZp761E13121
SEMA3C
SYNGR1
CPE
AL050370
RAI3
COL10A1
LOC51673
H2AFO
CTAG2
H1F2
ORM1
GLRA3
PRO1489
KIAA0876
ABCG1
LOC51133
FLJ20366
KIF13B
SLC9A5
CYB5
HSPB1
CONTINUED ON SHEET 13

FIG. 24

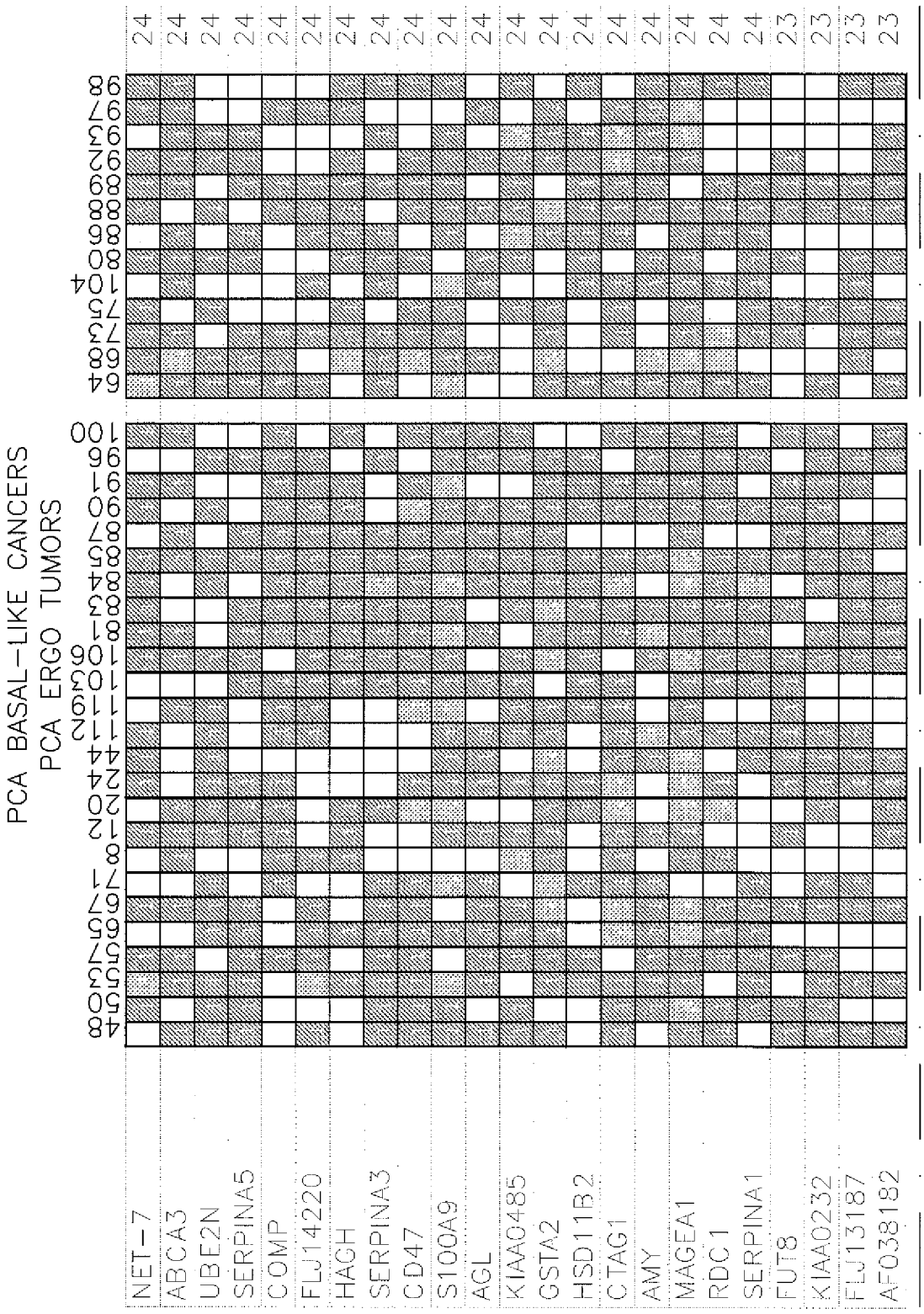

PCA BASAL-LIKE CANCERS
PCA ERGO TUMORS
NET-7
ABCA3
UBE2N
SERPINA5
COMP
FLJ14220
HAGH
SERPINA3
CD47
S100A9
AGL
KIAA0485
GSTA2
HSD11B2
CTAG1
AMY
MAGEA1
RDC1
SERPINA1
FUT8
KIAA0232
FLJ13187
AF038182
24
24
24
24
24
24
24
24
24
24
24
24
24
24
24
24
24
24
24
24
24
23
23
23
23
CONTINUED ON SHEET 14

FIG. 24

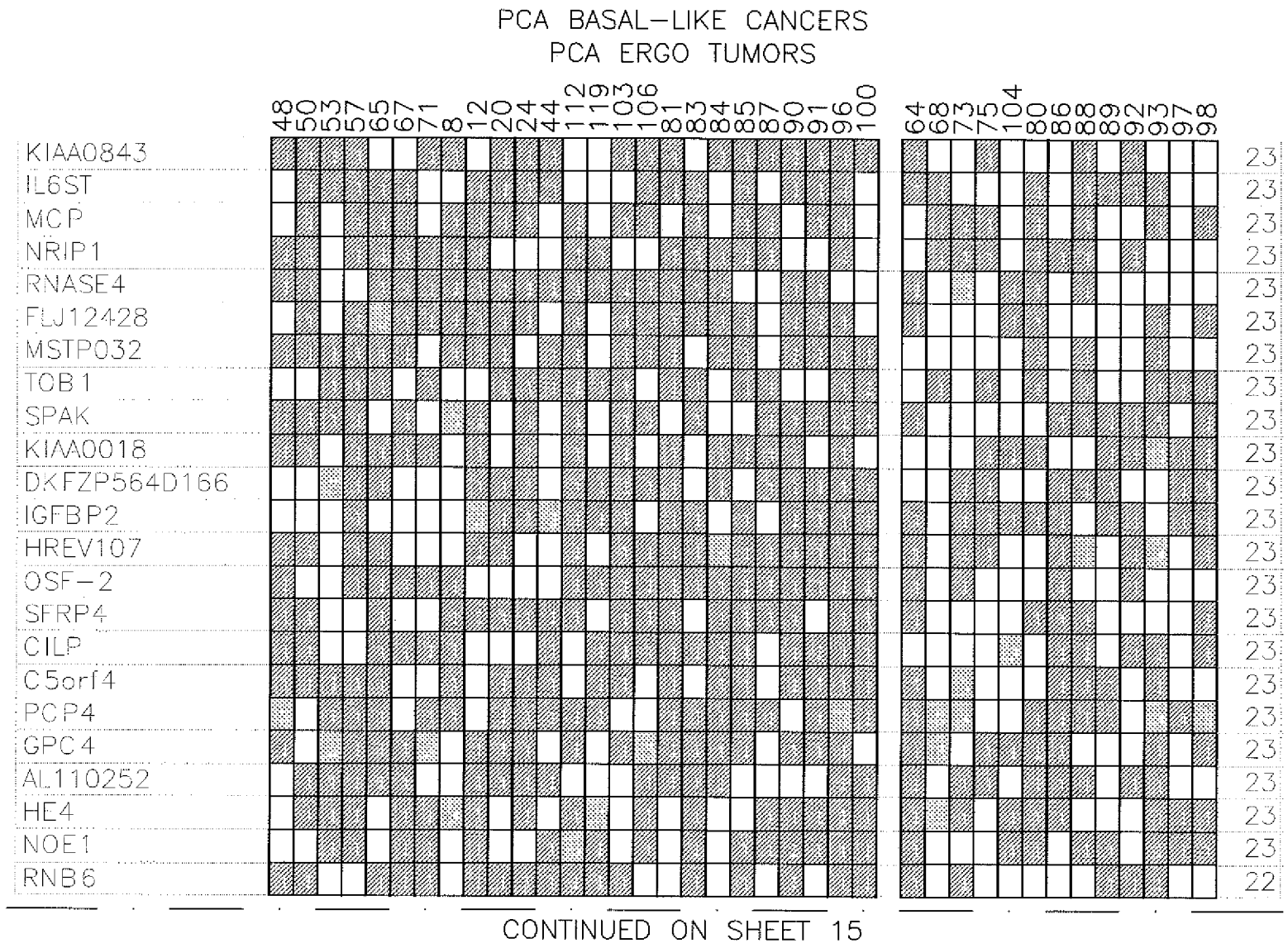

PCA BASAL–LIKE CANCERS
PCA ERGO TUMORS
48 50 53 57 65 67 71 8 12 20 24 44 112 119 103 106 81 83 84 85 87 90 91 96 100
64 68 73 75 104 80 86 88 89 92 93 97 98
KIAA0843 23
IL6ST 23
MCP 23
NRIP1 23
RNASE4 23
FLJ12428 23
MSTP032 23
TOB1 23
SPAK 23
KIAA0018 23
DKFZP564D166 23
IGFBP2 23
HREV107 23
OSF–2 23
SFRP4 23
CILP 23
C5orf4 23
PCP4 23
GPC4 23
AL110252 23
HE4 23
NOE1 23
RNB6 22
CONTINUED ON SHEET 15

FIG. 24

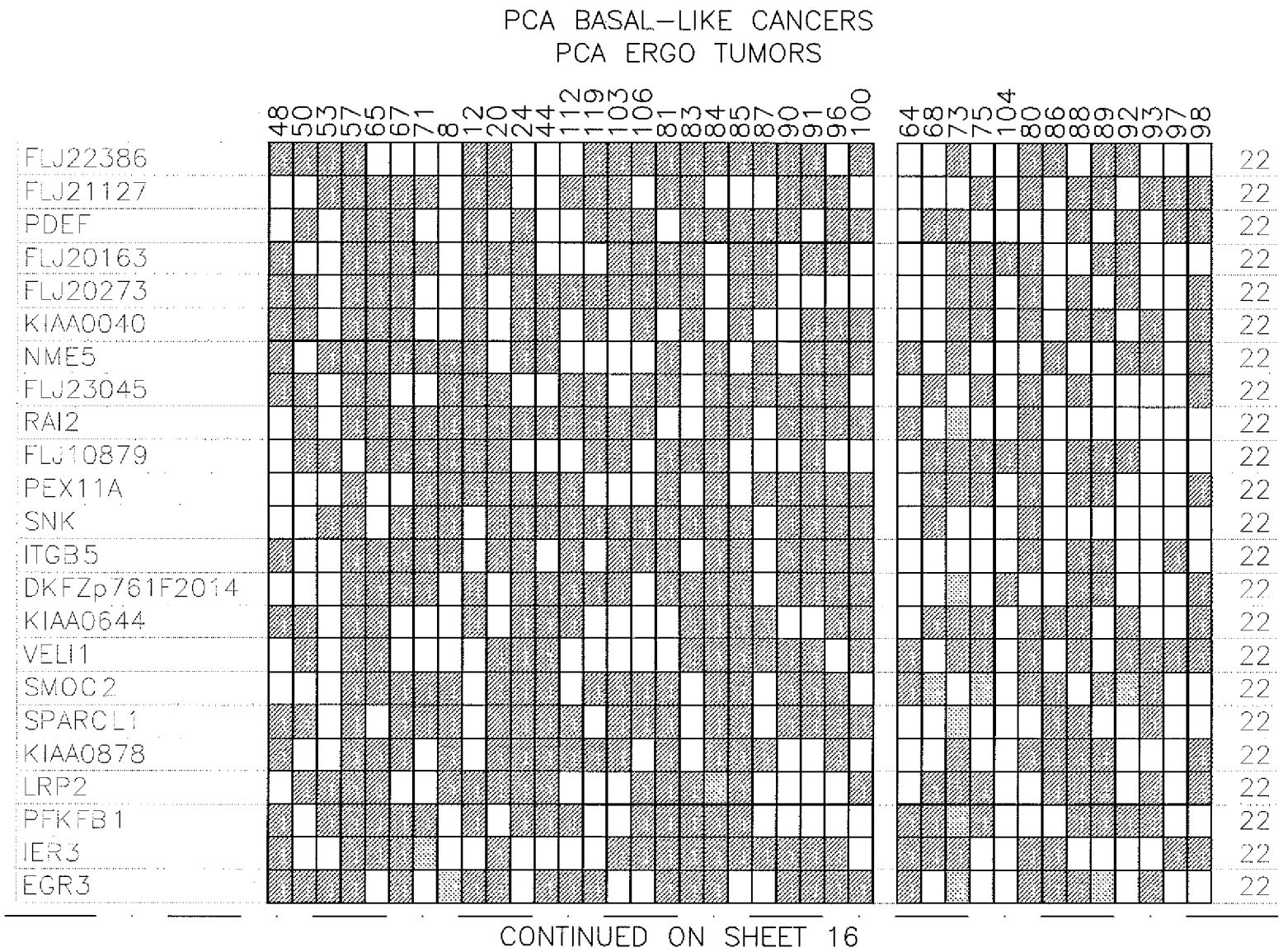

PCA BASAL–LIKE CANCERS
PCA ERGO TUMORS
48 50 53 57 65 67 71 8 12 20 24 44 112 119 103 106 81 83 84 85 87 90 91 96 100 64 68 73 75 104 80 86 88 89 92 93 97 98
FLJ22386 22
FLJ21127 22
PDEF 22
FLJ20163 22
FLJ20273 22
KIAA0040 22
NME5 22
FLJ23045 22
RAI2 22
FLJ10879 22
PEX11A 22
SNK 22
ITGB5 22
DKFZp761F2014 22
KIAA0644 22
VELI1 22
SMOC2 22
SPARCL1 22
KIAA0878 22
LRP2 22
PFKFB1 22
IER3 22
EGR3 22
CONTINUED ON SHEET 16

FIG. 24

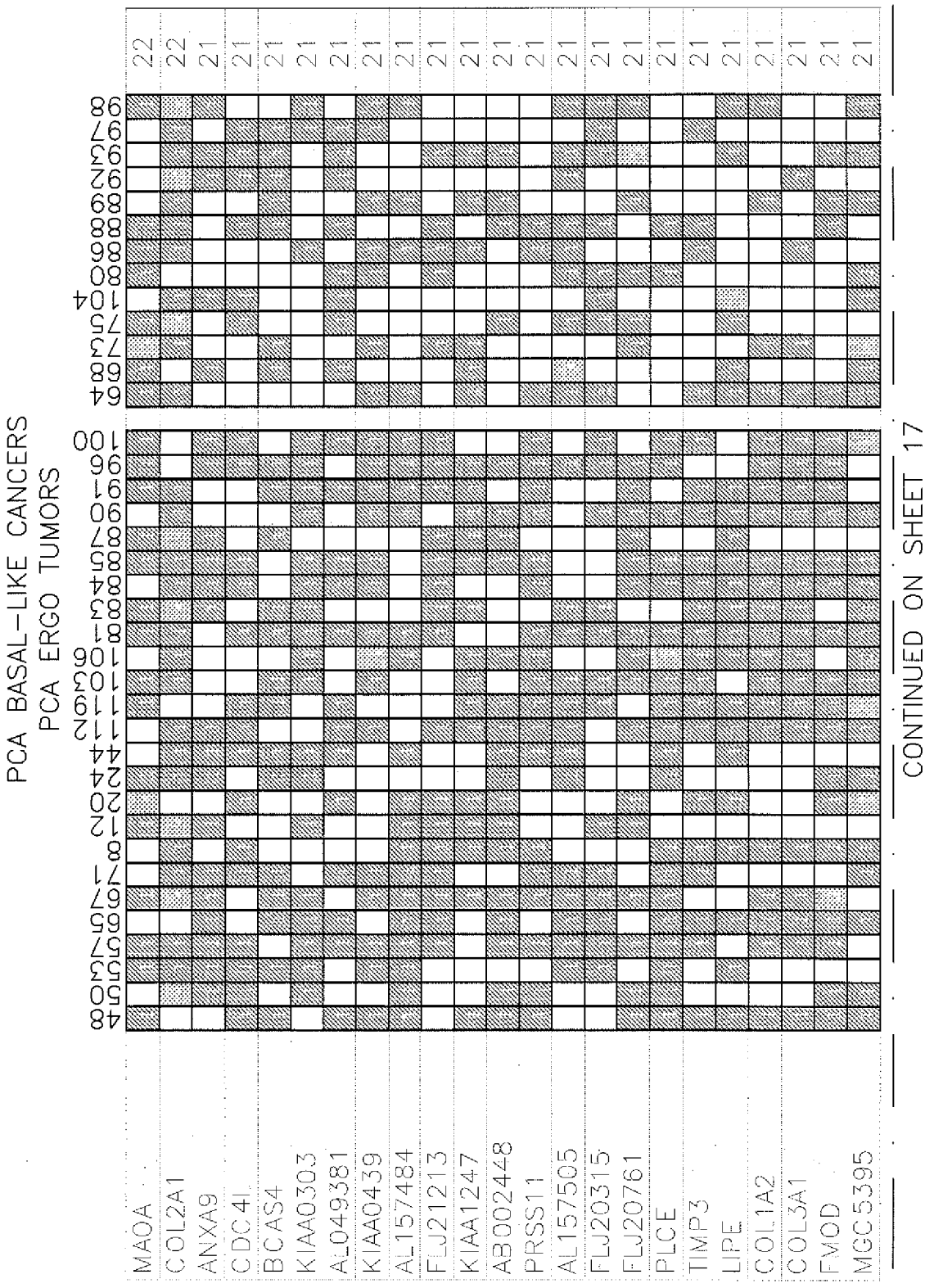

PCA BASAL-LIKE CANCERS
PCA ERGO TUMORS
MAOA
COL2A1
ANXA9
CDC4L
BCAS4
KIAA0303
AL049381
KIAA0439
AL157484
FLJ21213
KIAA1247
AB002448
PRSS11
AL157505
FLJ20315
FLJ20761
PLCE
TIMP3
LIPE
COL1A2
COL3A1
FVOD
MGC5395
CONTINUED ON SHEET 17

FIG. 24

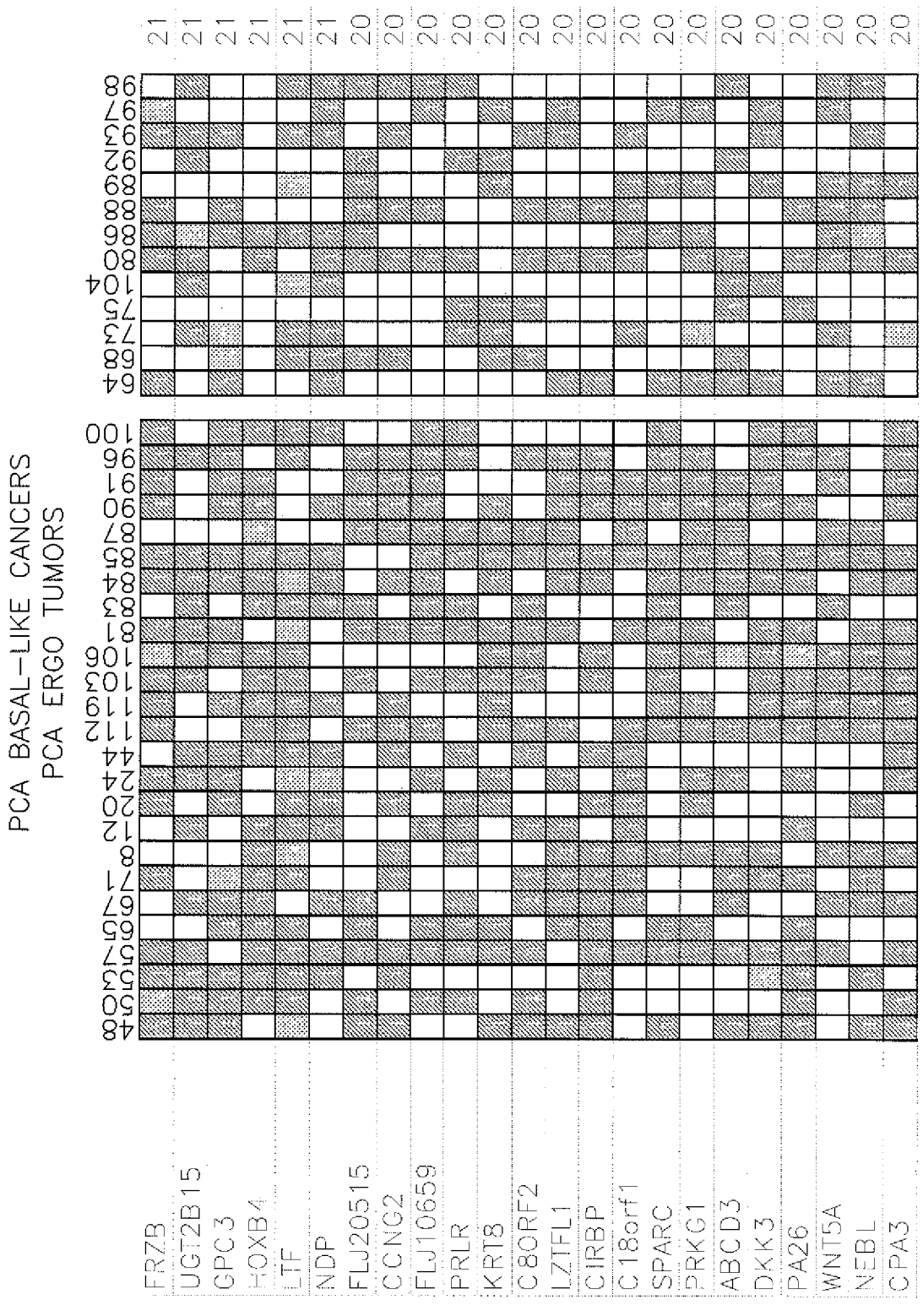

PCA BASAL-LIKE CANCERS
PCA ERGO TUMORS
FRZB
UGT2B15
GPC3
HOXB4
LTF
NDP
FLJ20515
CCNG2
FLJ10659
PRLR
KRT8
C8ORF2
LZTFL1
CIRBP
C18orf1
SPARC
PRKG1
ABCD3
DKK3
PA26
WNT5A
NEBL
CPA3
CONTINUED ON SHEET 18

FIG. 24

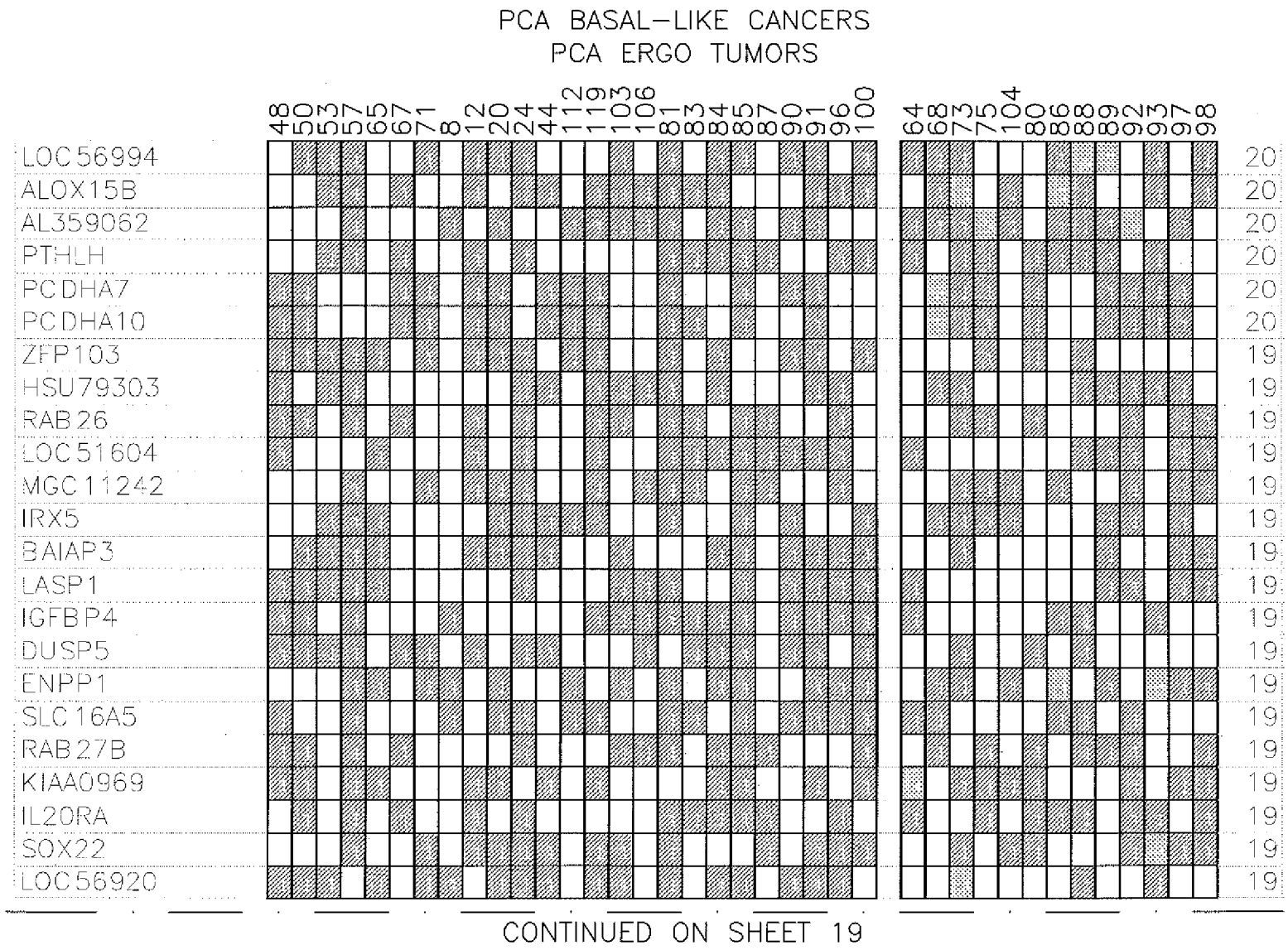

PCA BASAL–LIKE CANCERS
PCA ERGO TUMORS
48 50 53 57 65 67 71 8 12 20 24 44 112 119 103 106 81 83 84 85 87 90 91 96 100 64 68 73 75 104 80 86 88 89 92 93 97 98
LOC56994 20
ALOX15B 20
AL359062 20
PTHLH 20
PCDHA7 20
PCDHA10 20
ZFP103 19
HSU79303 19
RAB26 19
LOC51604 19
MGC11242 19
IRX5 19
BAIAP3 19
LASP1 19
IGFBP4 19
DUSP5 19
ENPP1 19
SLC16A5 19
RAB27B 19
KIAA0969 19
IL20RA 19
SOX22 19
LOC56920 19
CONTINUED ON SHEET 19

FIG. 24

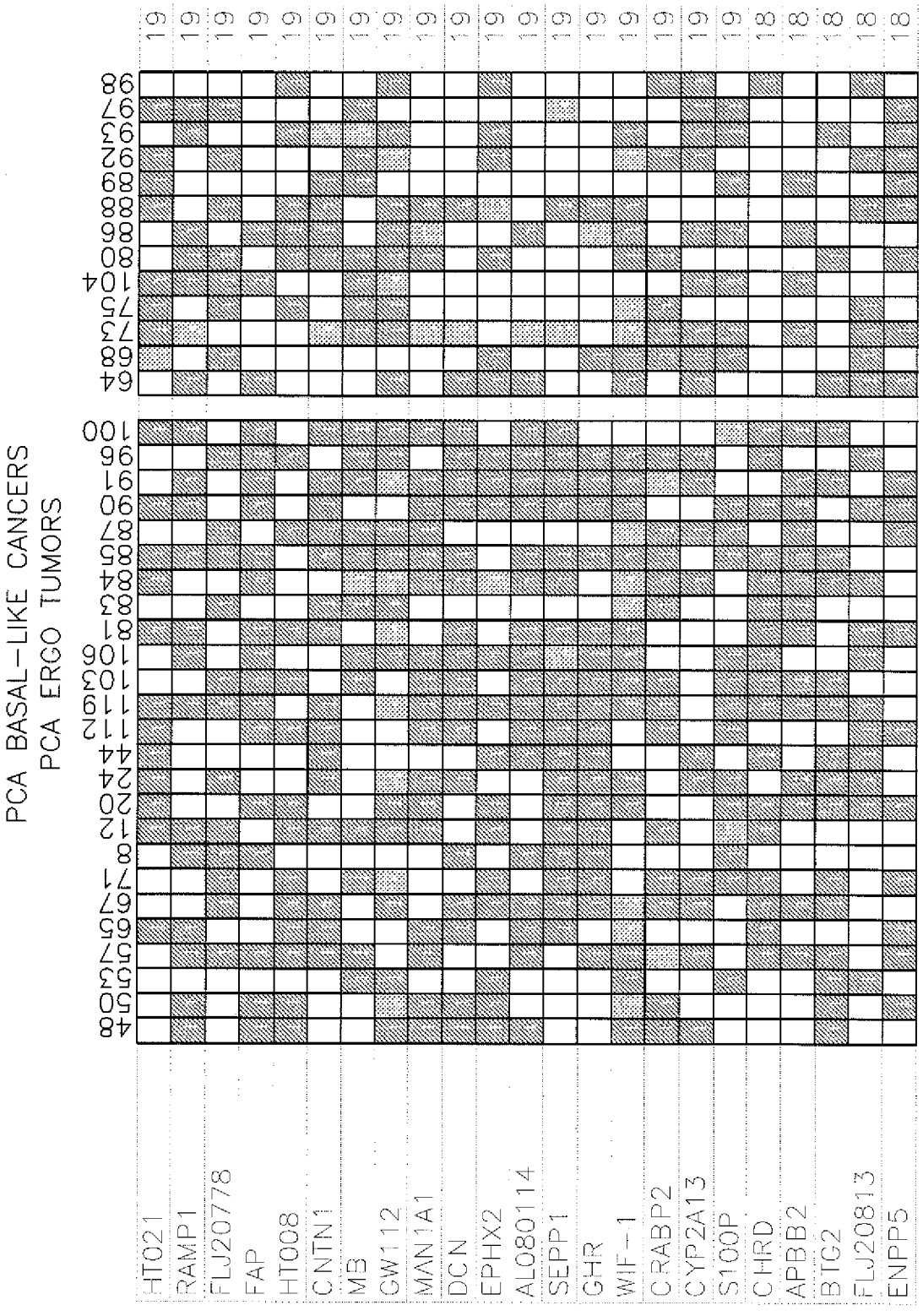

PCA BASAL-LIKE CANCERS
PCA ERGO TUMORS
HT021
RAMP1
FLJ20778
FAP
HT008
CNTN1
MB
GW112
MAN1A1
DCN
EPHX2
AL080114
SEPP1
GHR
WIF-1
CRABP2
CYP2A13
S100P
CHRD
APBB2
BTG2
FLJ20813
ENPP5
CONTINUED ON SHEET 20

FIG. 24

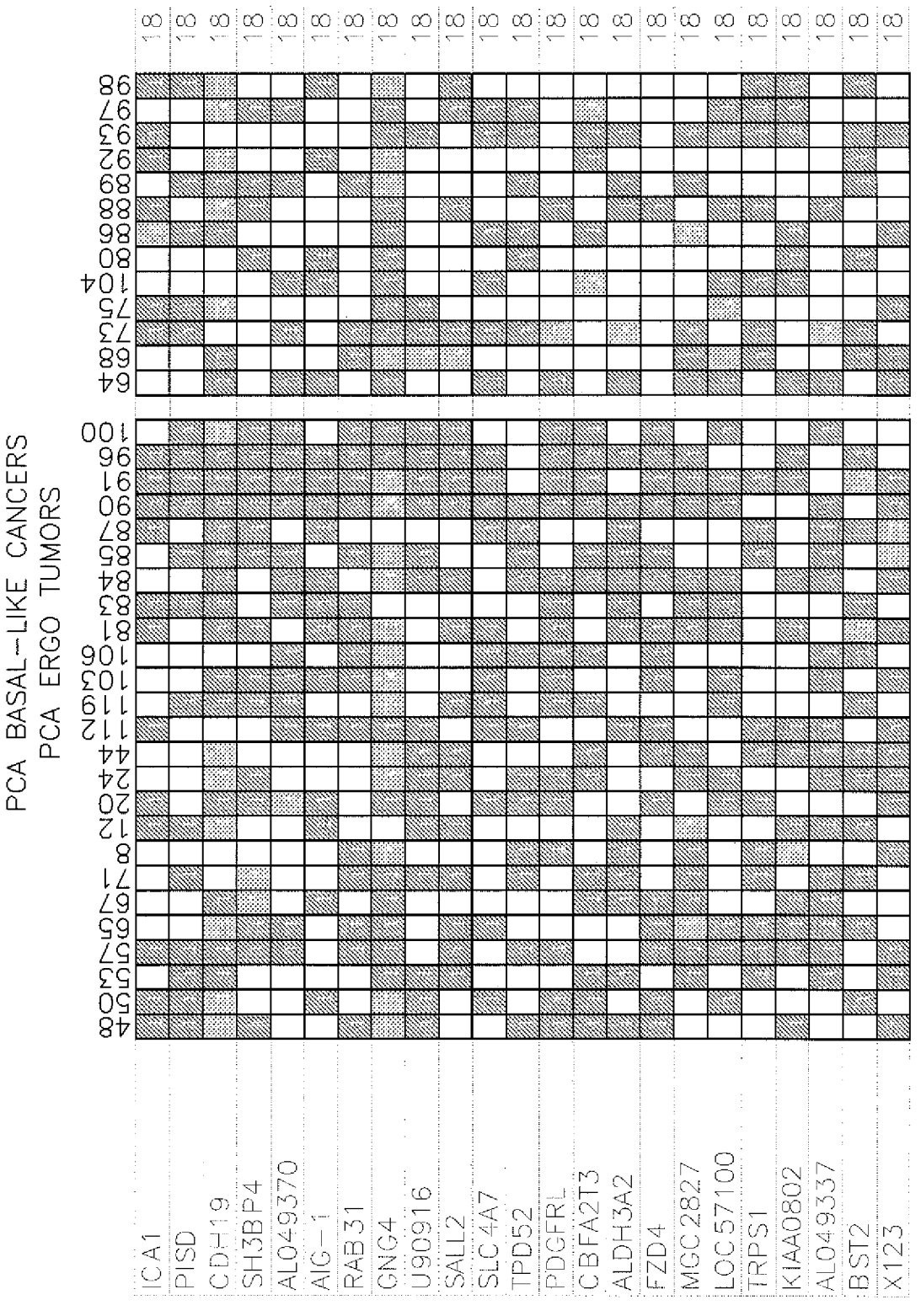

PCA BASAL-LIKE CANCERS
PCA ERGO TUMORS
ICA1
PISD
CDH19
SH3BP4
AL049370
AIG-1
RAB31
GNG4
U90916
SALL2
SLC4A7
TPD52
PDGFRL
CBFA2T3
ALDH3A2
FZD4
MGC2827
LOC57100
TRPS1
KIAA0802
AL049337
BST2
X123
CONTINUED ON SHEET 21

FIG. 24

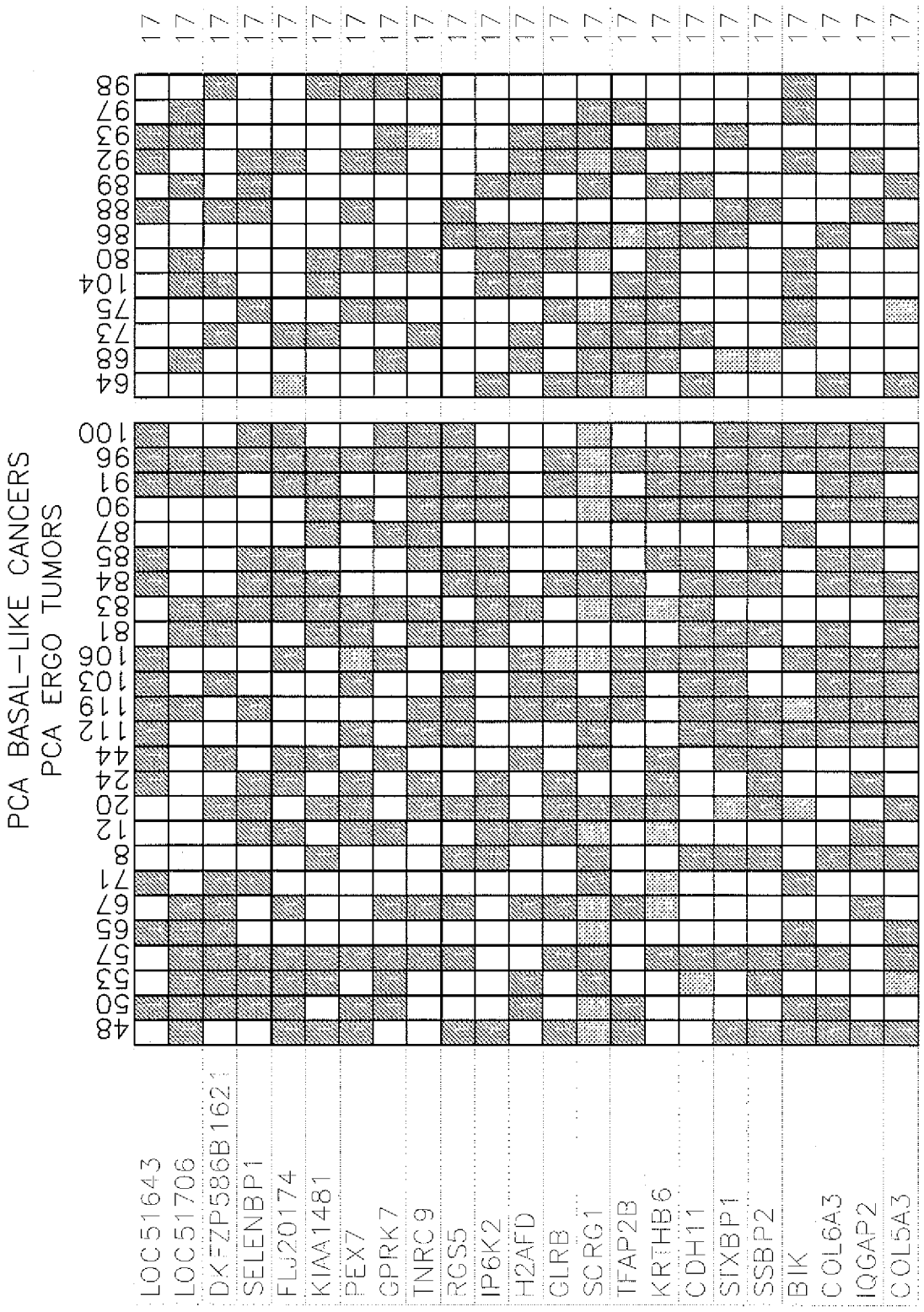

PCA BASAL-LIKE CANCERS
PCA ERGO TUMORS
LOC51643
LOC51706
DKFZP586B1621
SELENBP1
FLJ20174
KIAA1481
PEX7
GPRK7
TNRC9
RGS5
IP6K2
H2AFD
GLRB
SCRG1
TFAP2B
KRTHB6
CDH11
SYXBP1
SSBP2
BIK
COL6A3
IQGAP2
COL5A3
CONTINUED ON SHEET 22

FIG. 24

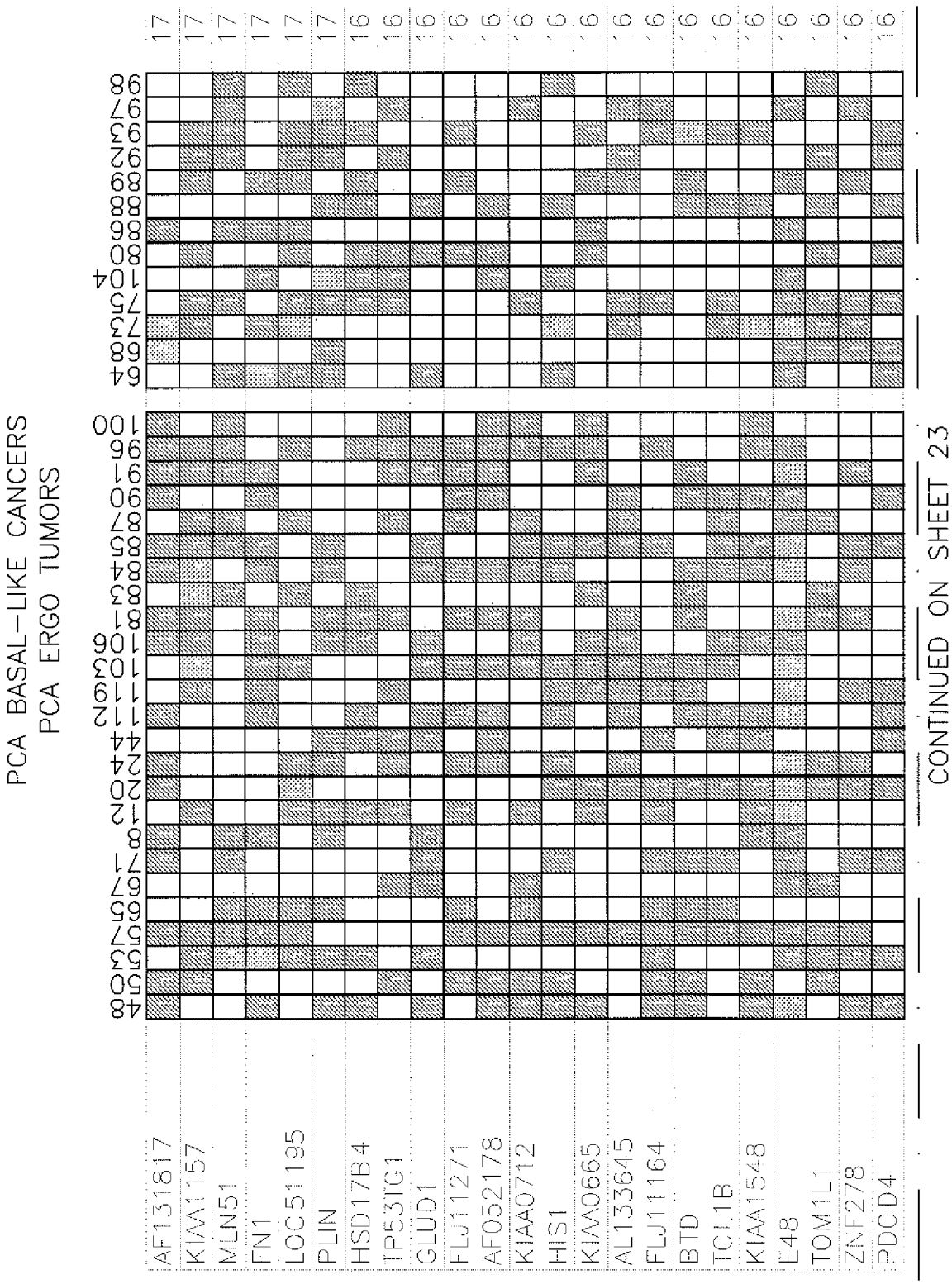

PCA BASAL-LIKE CANCERS
PCA ERGO TUMORS
AF131817
KIAA1157
MLN51
FN1
LOC51195
PLIN
HSD17B4
IP53IC1
GLUD1
FLJ11271
AF052178
KIAA0712
HIS1
KIAA0665
AL133645
FLJ11164
BTD
TCL1B
KIAA1548
E48
TOM1L1
ZNF278
PDCD4
CONTINUED ON SHEET 23

FIG. 24

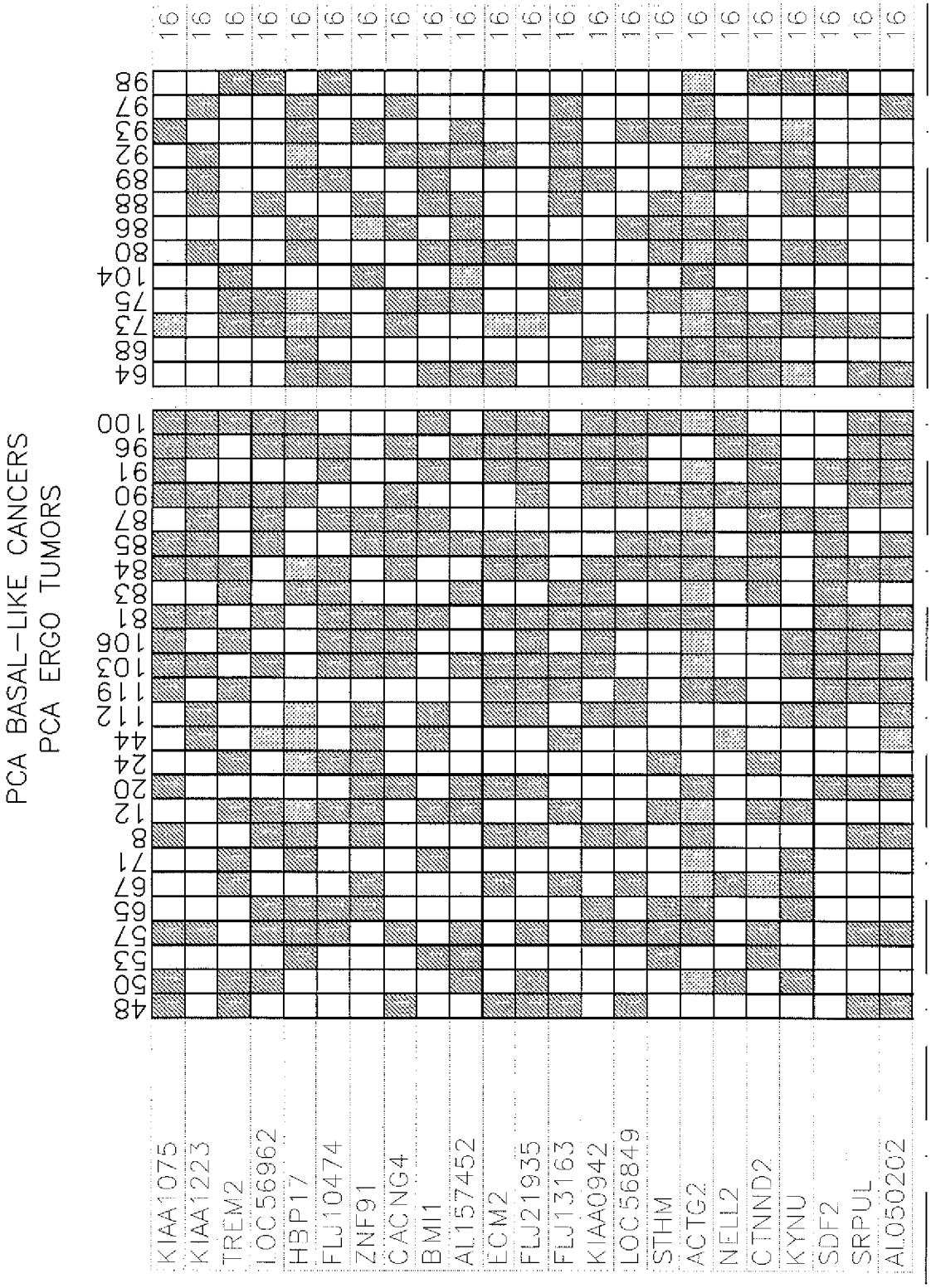

PCA BASAL-LIKE CANCERS
PCA ERGO TUMORS
KIAA1075
KIAA1223
TREM2
LOC56962
HBP17
FLJ10474
ZNF91
CACNG4
BMI1
AL157452
ECM2
FLJ21935
FLJ13163
KIAA0942
LOC56849
STHM
ACTG2
NELL2
CTNND2
KYNU
SDF2
SRPUL
AL050202
CONTINUED ON SHEET 24

FIG. 24

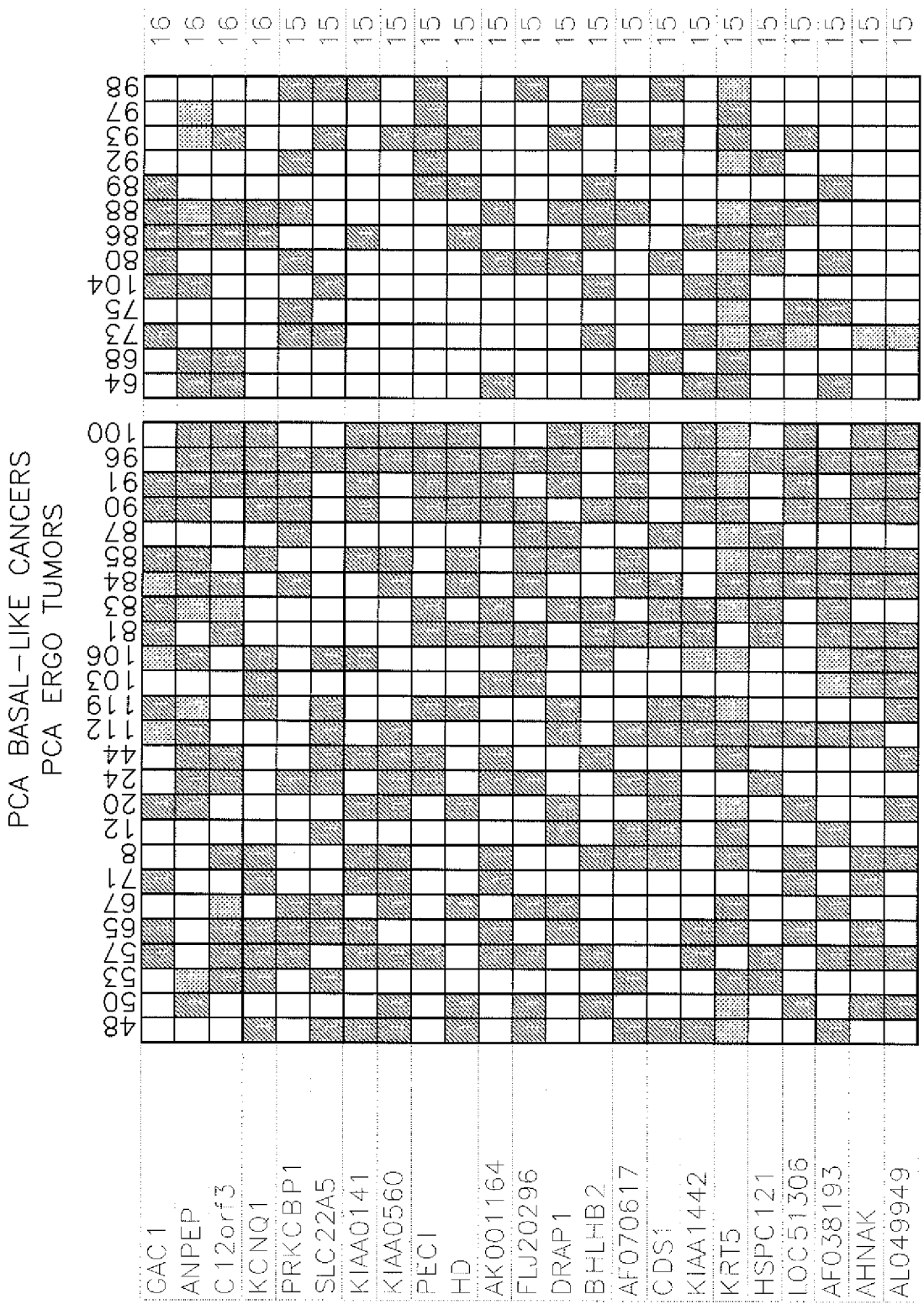

PCA BASAL-LIKE CANCERS
PCA ERGO TUMORS
GAC1
ANPEP
C12orf3
KCNQ1
PRKCBP1
SLC22A5
KIAA0141
KIAA0560
PECI
HD
AK001164
FLJ20296
DRAP1
BHLHB2
AF070617
CDS1
KIAA1442
KRT5
HSPC121
IOC51306
AF038193
AHNAK
AL049949
CONTINUED ON SHEET 25

FIG. 24

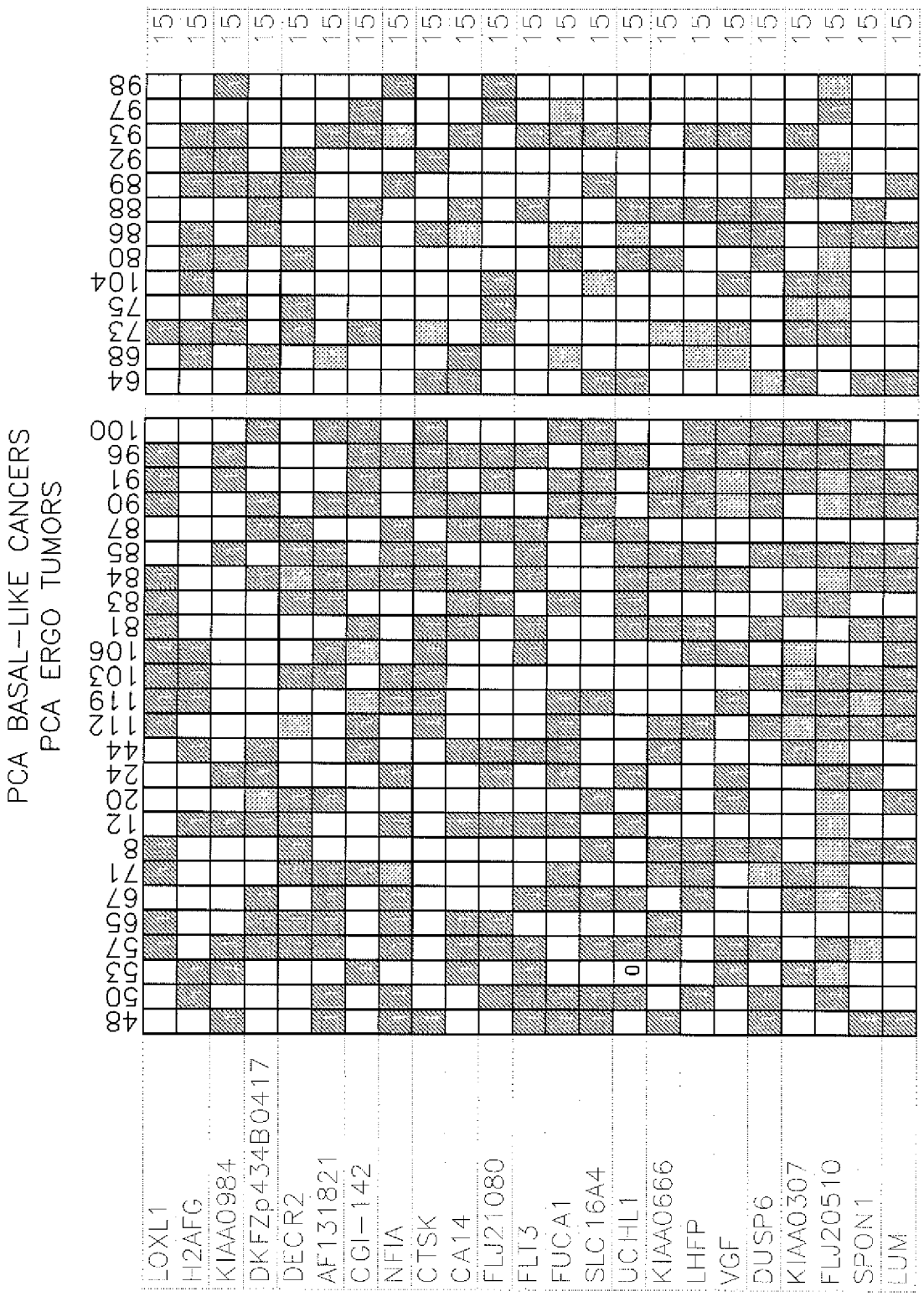

PCA BASAL-LIKE CANCERS
PCA ERGO TUMORS
LOXL1
H2AFG
KIAA0984
DKFZp434B0417
DECR2
AF131821
CGI-142
NFIA
CTSK
CA14
FLJ21080
FLI3
FUCA1
SLC16A4
UCHL1
KIAA0666
LHFP
VGF
DUSP6
KIAA0307
FLJ20510
SPON1
LUM
CONTINUED ON SHEET 26

FIG. 24

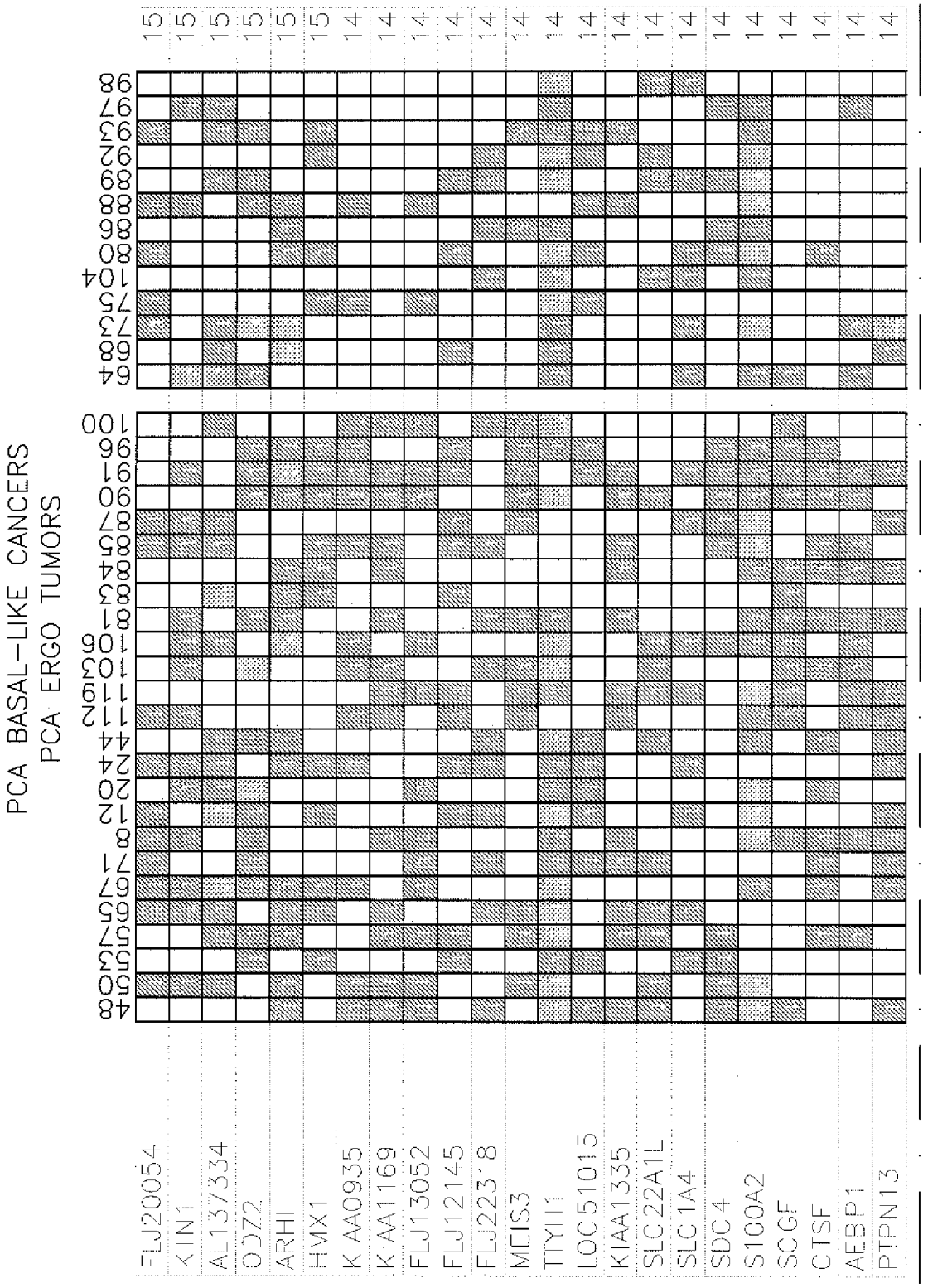

PCA BASAL-LIKE CANCERS
PCA ERGO TUMORS
FLJ20054
KIN1
AL137334
ODZ2
ARHI
HMX1
KIAA0935
KIAA1169
FLJ13052
FLJ12145
FLJ22318
MEIS3
TTYH1
LOC51015
KIAA1335
SLC22A1L
SLC1A4
SDC4
S100A2
SCGF
CTSF
AEBP1
PTPN13
CONTINUED ON SHEET 27

FIG. 24

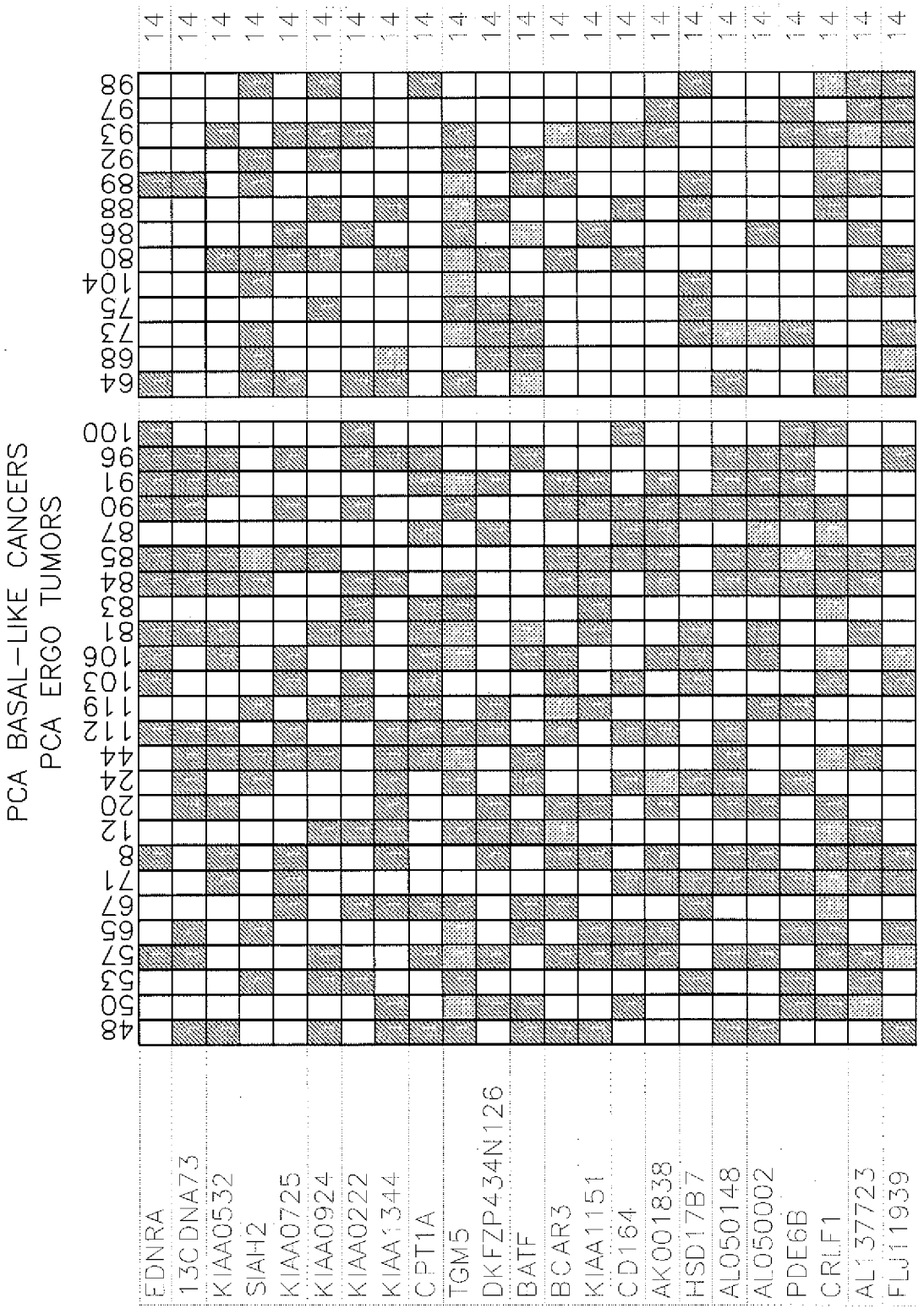

PCA BASAL-LIKE CANCERS
PCA ERGO TUMORS
EDNRA
13CDNA73
KIAA0532
SIAH2
KIAA0725
KIAA0924
KIAA0222
KIAA1344
CPT1A
TGM5
DKFZP434N126
BATF
BCAR3
KIAA1151
CD164
AK001838
HSD17B7
AL050148
AL050002
PDE6B
CRLF1
AL137723
FLJ11939
CONTINUED ON SHEET 28

FIG. 24

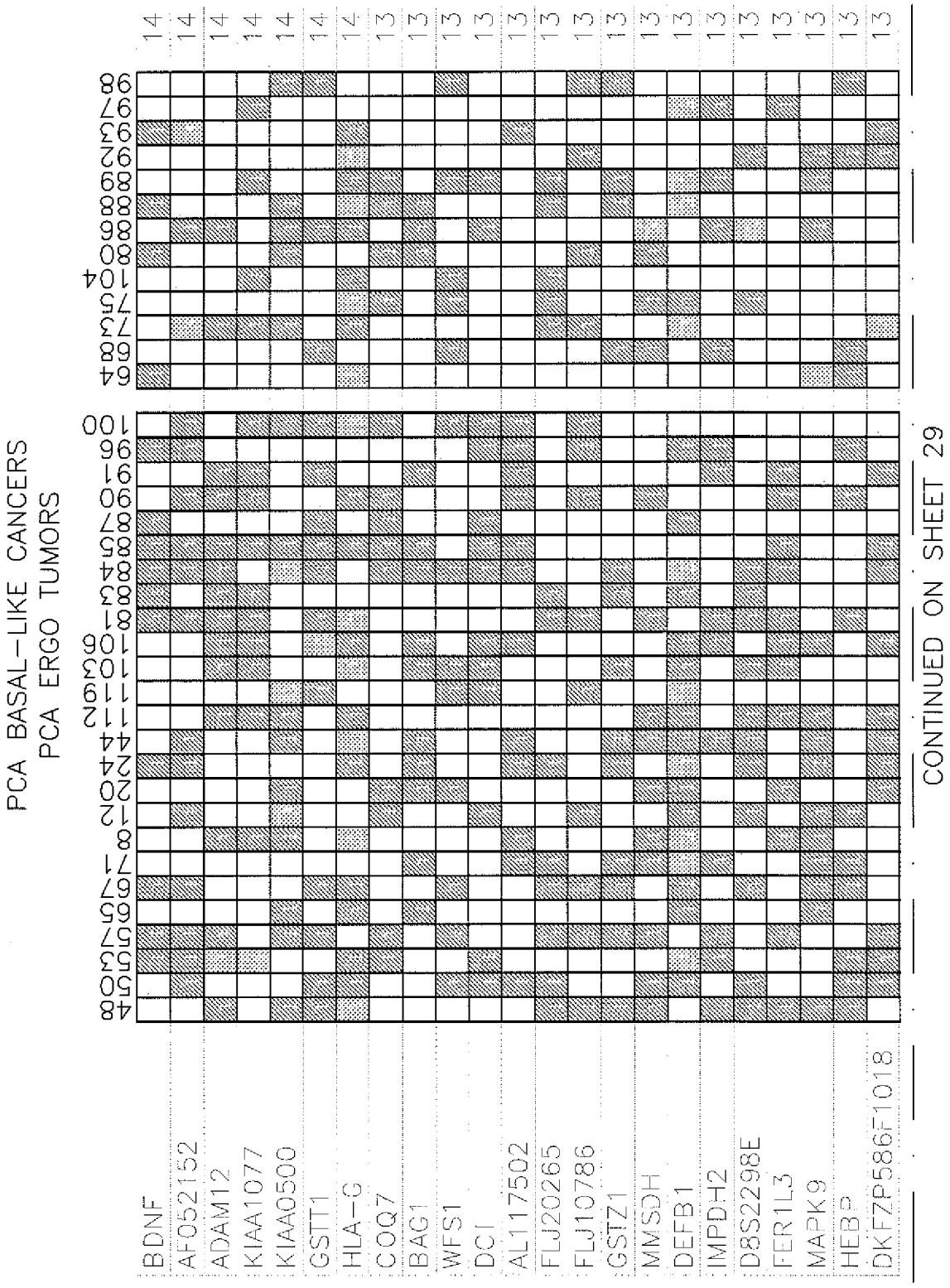

PCA BASAL-LIKE CANCERS
PCA ERGO TUMORS
BDNF
AF052152
ADAM12
KIAA1077
KIAA0500
GSTT1
HLA-G
COQ7
BAG1
WFS1
DCI
AL117502
FLJ20265
FLJ10786
GSTZ1
MMSDH
DEFB1
IMPDH2
D3S2298E
FER1L3
MAPK9
HEB
DKFZP586F1018
CONTINUED ON SHEET 29

FIG. 24

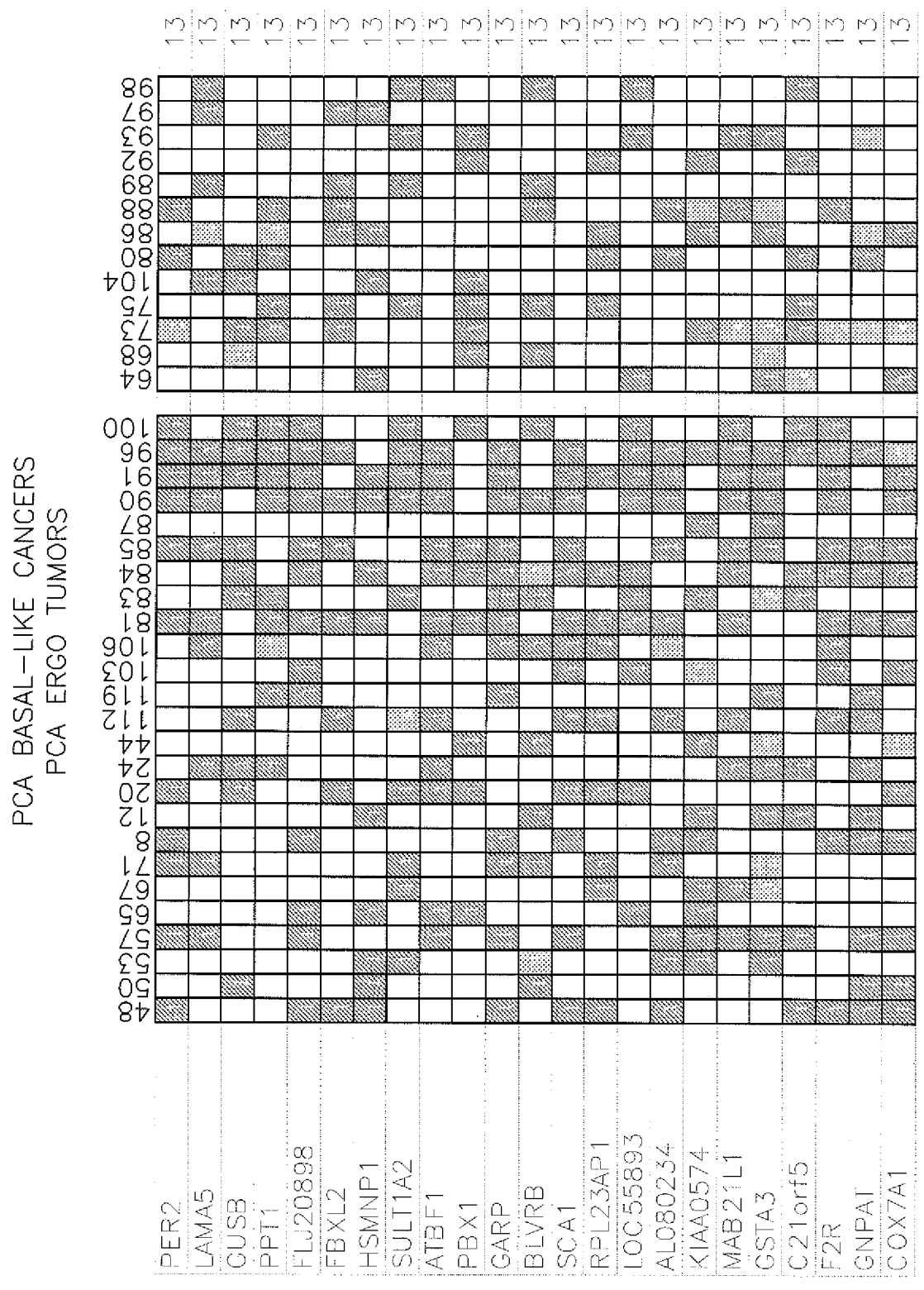

PCA BASAL-LIKE CANCERS
PCA ERGO TUMORS
PER2
LAMA5
CUSB
PPT1
HLJ20898
FBXL2
HSMNP1
SULT1A2
ATBF1
PBX1
GARP
BLVRB
SCA1
RPL23AP1
LOC55893
AL080234
KIAA0574
MAB21L1
GSTA3
C21orf5
F2R
GNPAI
COX7A1
CONTINUED ON SHEET 30

FIG. 24

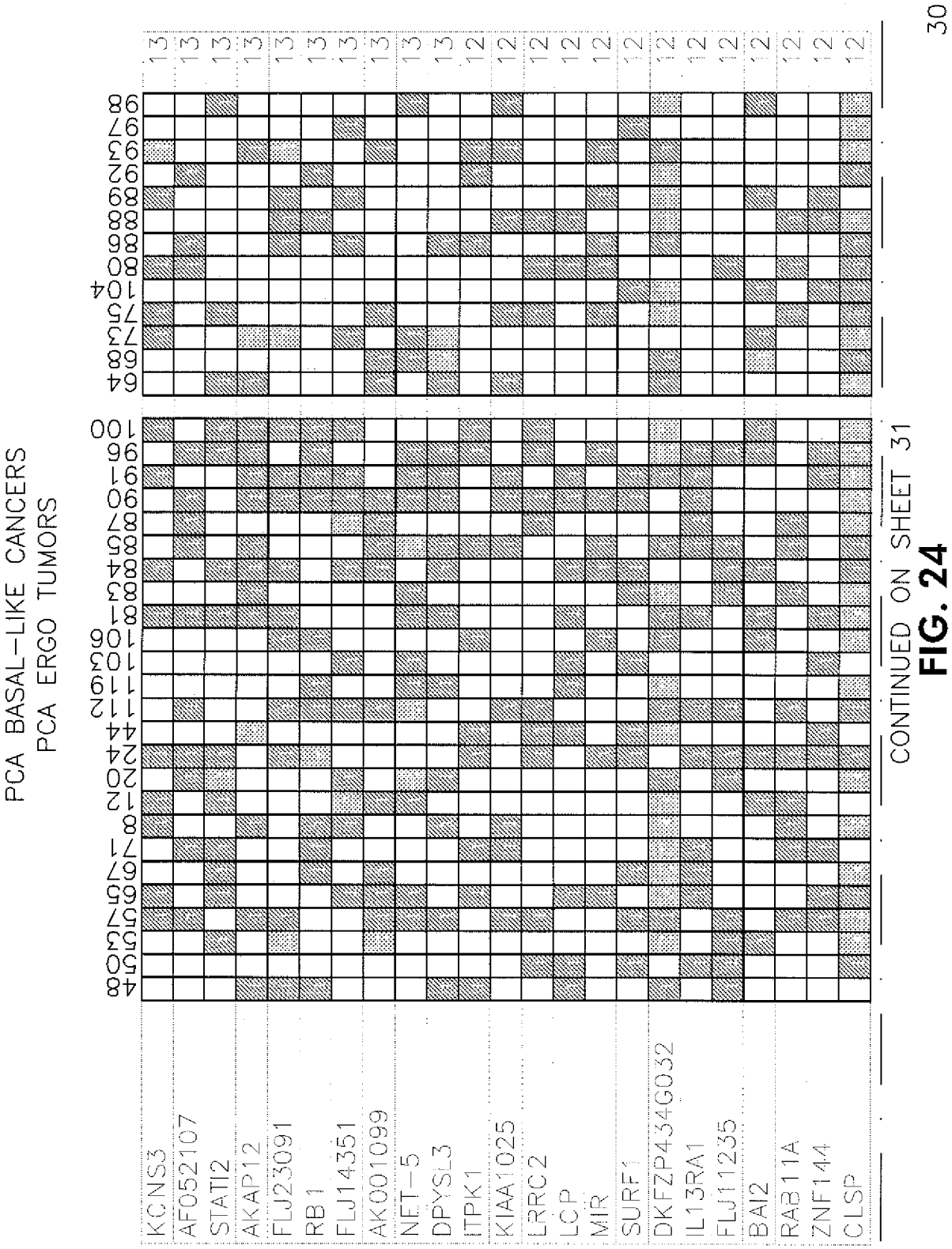

PCA BASAL-LIKE CANCERS
PCA ERGO TUMORS
KCNS3
AF052107
STAT12
AKAP12
FLJ23091
RB1
FLJ14351
AK001099
NET-5
DPYSL3
ITPK1
KIAA1025
LRRC2
LCP
MIR
SURF1
DKFZP434G032
IL13RA1
FLJ11235
BAI2
RAB11A
ZNF144
CLSP
CONTINUED ON SHEET 31

FIG. 24

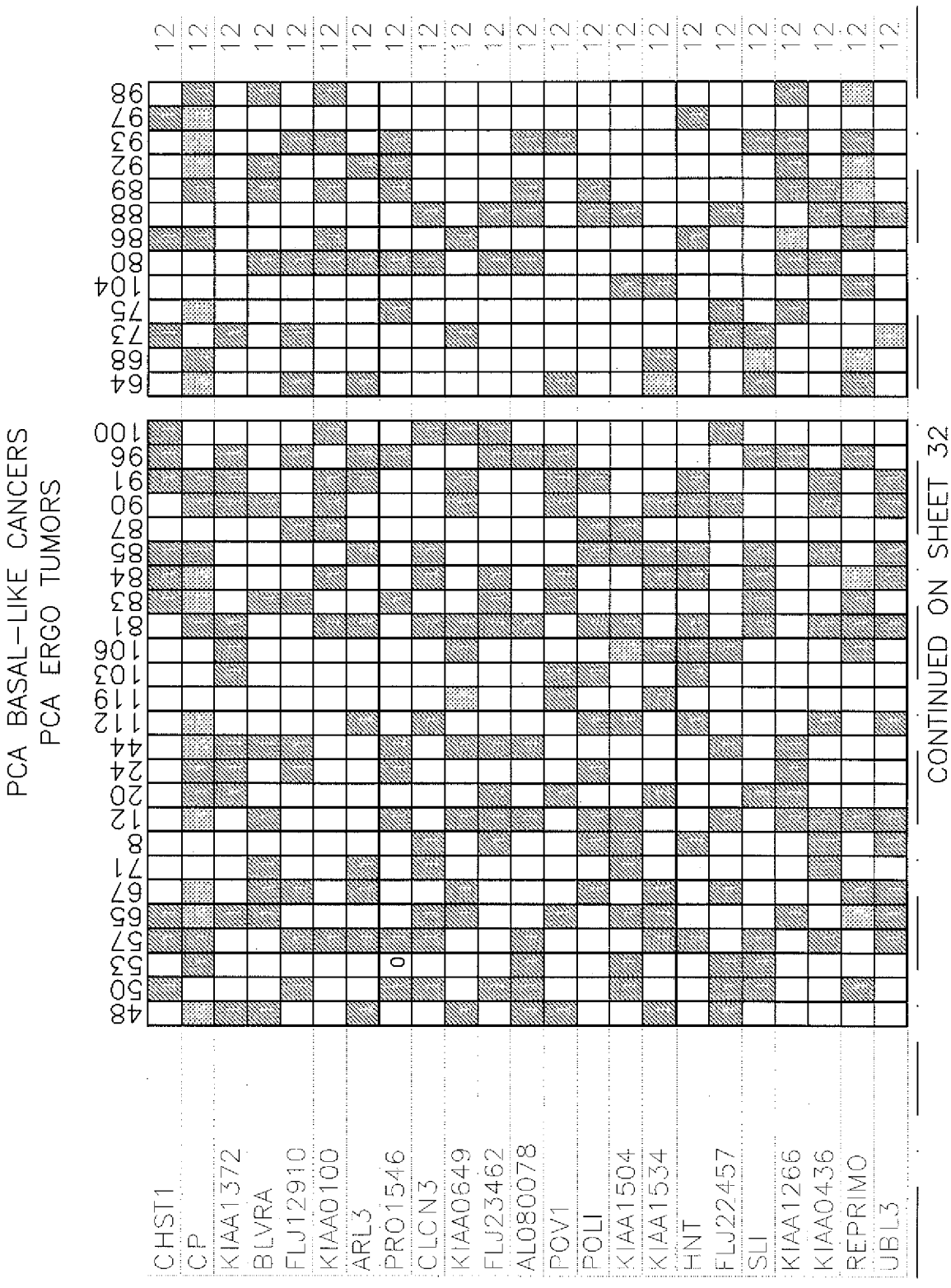

PCA BASAL-LIKE CANCERS
PCA ERGO TUMORS
CHST1
CP
KIAA1372
BLVRA
FLJ12910
KIAA0100
ARL3
PRO1546
CLCN3
KIAA0649
FLJ23462
AL080078
POV1
POLI
KIAA1504
KIAA1534
HNT
FLJ22457
SLI
KIAA1266
KIAA0436
REPRIMO
UBL3
CONTINUED ON SHEET 32

FIG. 24

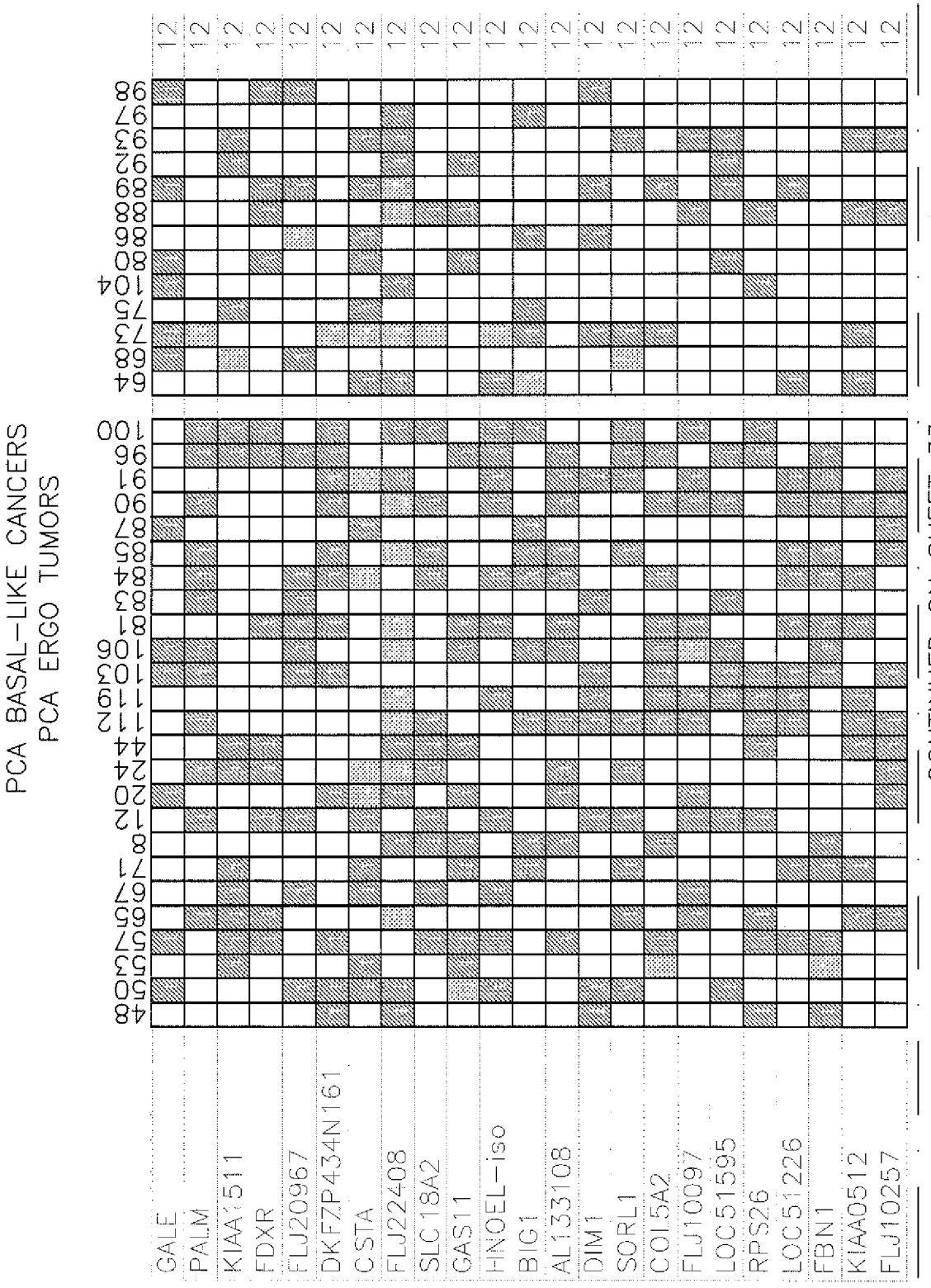

PCA BASAL-LIKE CANCERS
PCA ERGO TUMORS
GALE
PALM
KIAA1511
FDXR
FLJ20967
DKFZP434N161
CSTA
FLJ22408
SLC18A2
GAS11
HNOEL-iso
BIG1
AL133108
DIM1
SORL1
COL5A2
FLJ10097
LOC51595
RPS26
LOC51226
FBN1
KIAA0512
FLJ10257
CONTINUED ON SHEET 33

FIG. 24

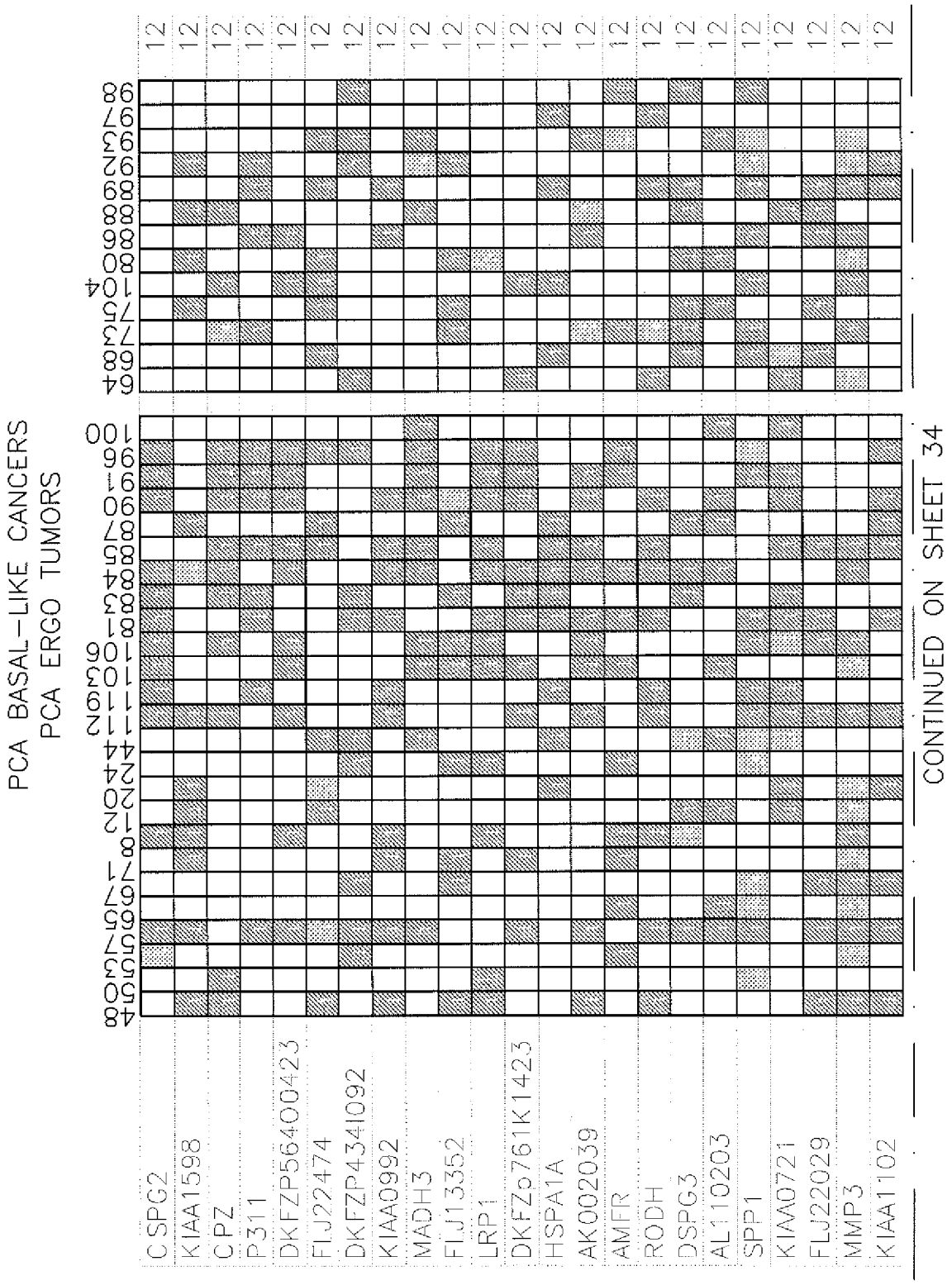

PCA BASAL-LIKE CANCERS
PCA ERGO TUMORS
CSPG2
KIAA1598
CPZ
P311
DKFZP564O0423
FLJ22474
DKFZP434I092
KIAA0992
MADH3
FLJ13352
LRP1
DKFZp761K1423
HSPA1A
AK002039
AMFR
RODH
DSPG3
AL110203
SPP1
KIAA0721
FLJ22029
MMP3
KIAA1102
CONTINUED ON SHEET 34

FIG. 24

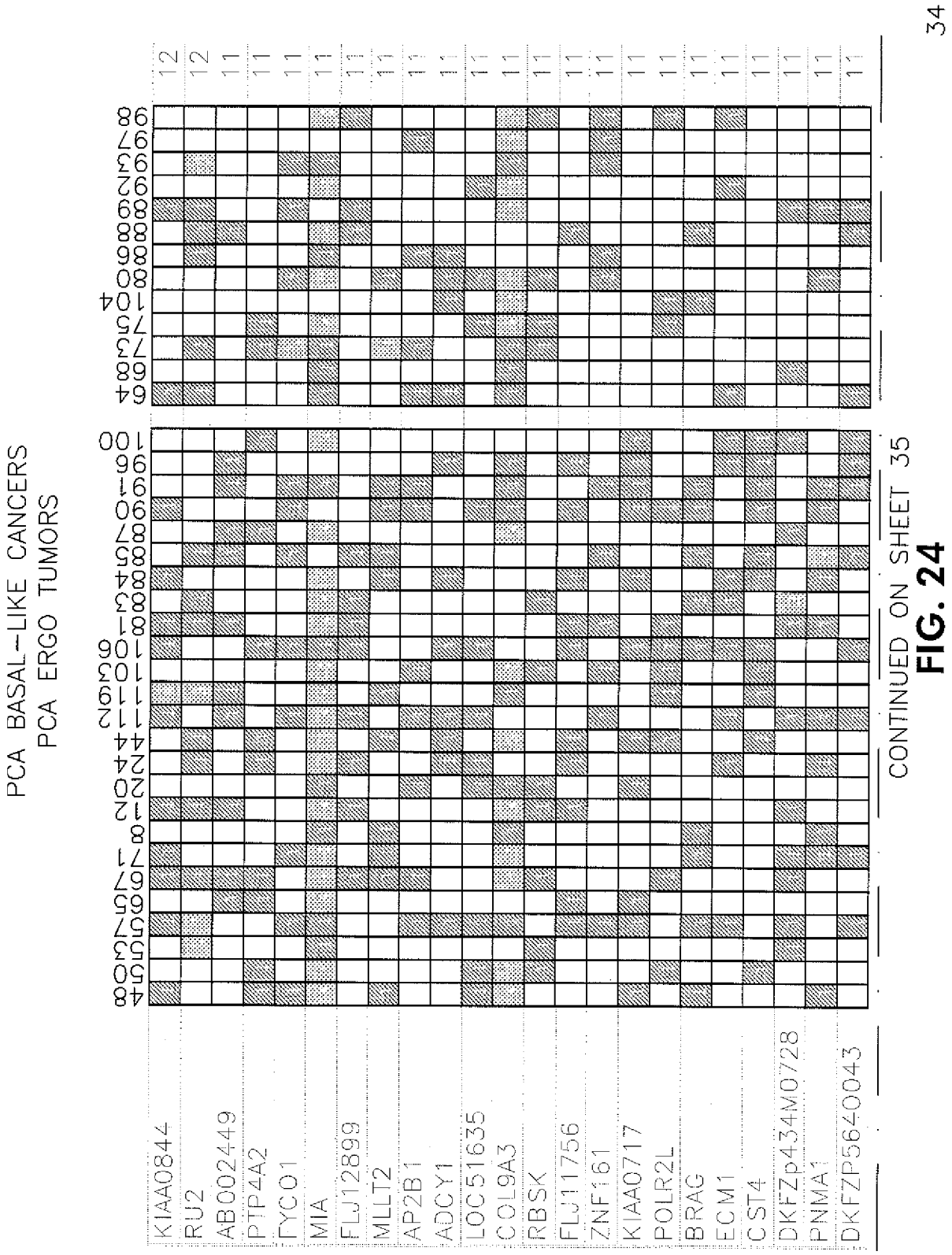

PCA BASAL-LIKE CANCERS
PCA ERGO TUMORS
KIAA0844
RU2
AB002449
PTP4A2
FYC01
MIA
FLJ12899
MLLT2
AP2B1
ADCY1
LOC51635
COL9A3
RBSK
FLJ11756
ZNF161
KIAA0717
POLR2L
BRAG
ECM1
CST4
DKFZp434M0728
PNMA1
DKFZP564O043
CONTINUED ON SHEET 35

FIG. 24

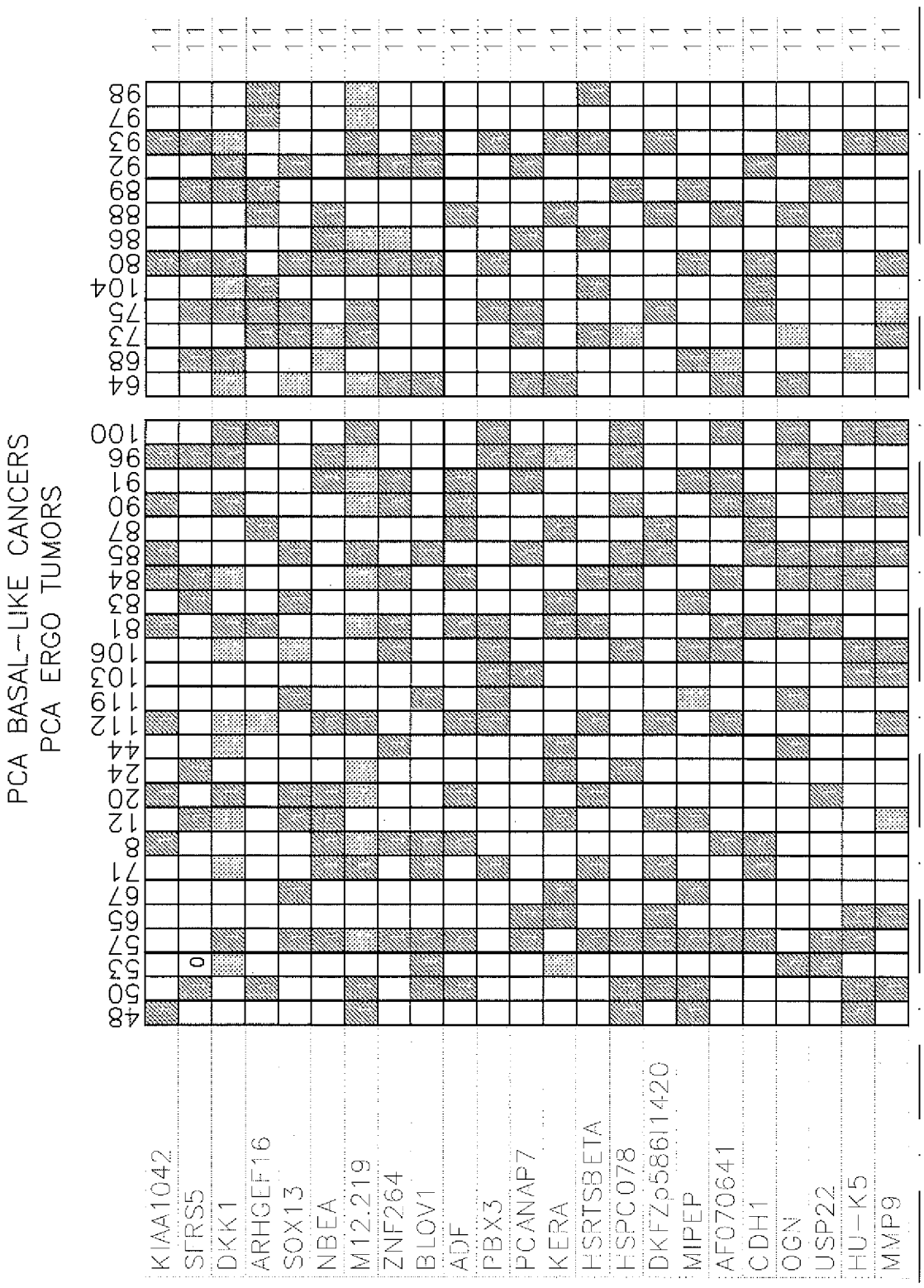

PCA BASAL-LIKE CANCERS
PCA ERGO TUMORS
KIAA1042
SFRS5
DKK1
ARHGEF16
SOX13
NBEA
M12.219
ZNF264
BLOV1
ADF
PBX3
PCANAP7
KERA
HSRTSBETA
HSPC078
DKFZp586I1420
MIPEP
AF070641
CDH1
OGN
USP22
HU-K5
MVP9
CONTINUED ON SHEET 36

FIG. 24

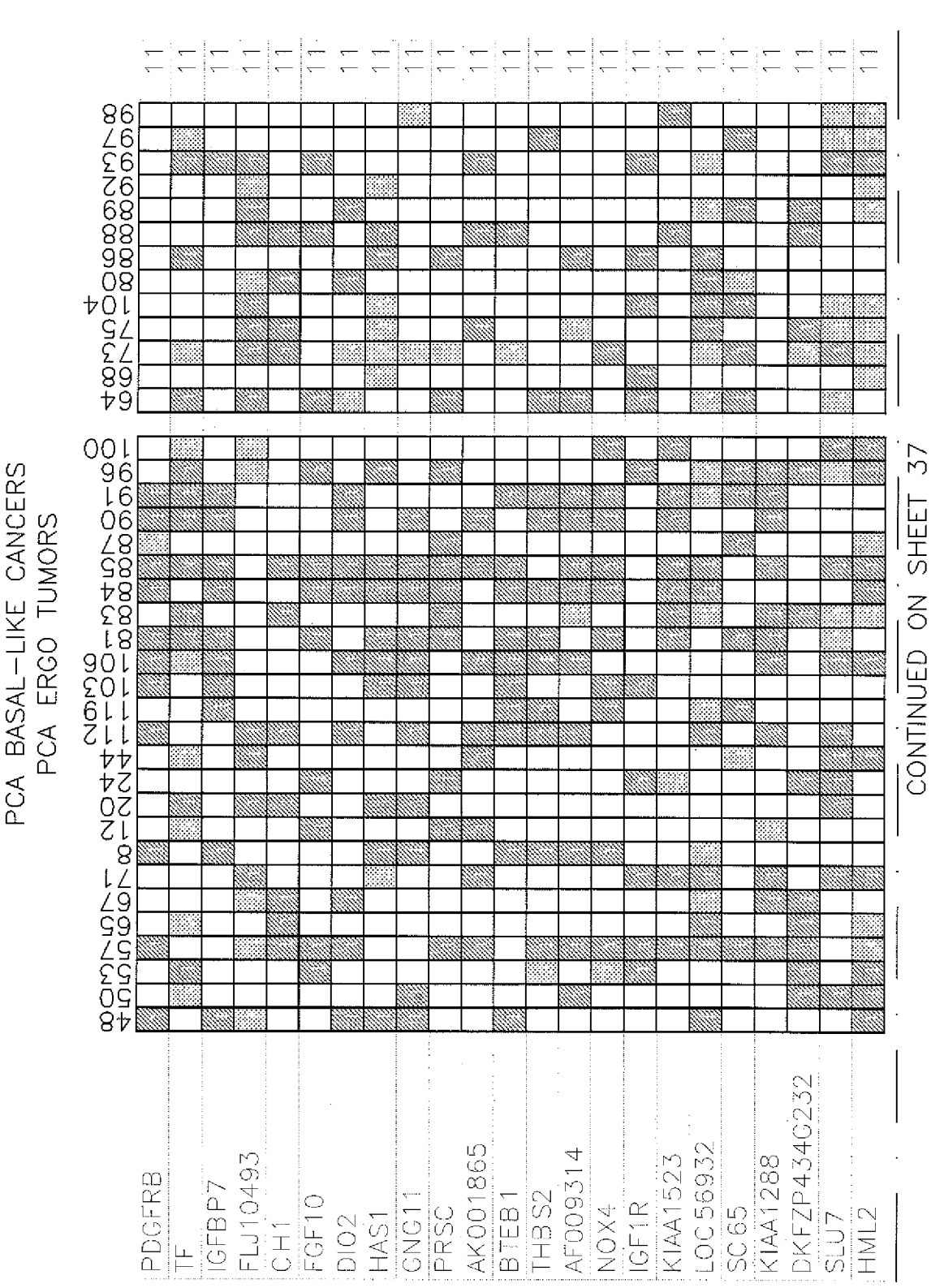

PCA BASAL-LIKE CANCERS
PCA ERGO TUMORS
PDGFRB
TF
IGFBP7
FLJ10493
CH1
FGF10
DIO2
HAS1
GNG11
PRSC
AK001865
BTEB1
THBS2
AF009314
NOX4
IGF1R
KIAA1523
LOC56932
SC65
KIAA1288
DKFZP434C232
SLU7
HML2
CONTINUED ON SHEET 37

FIG. 24

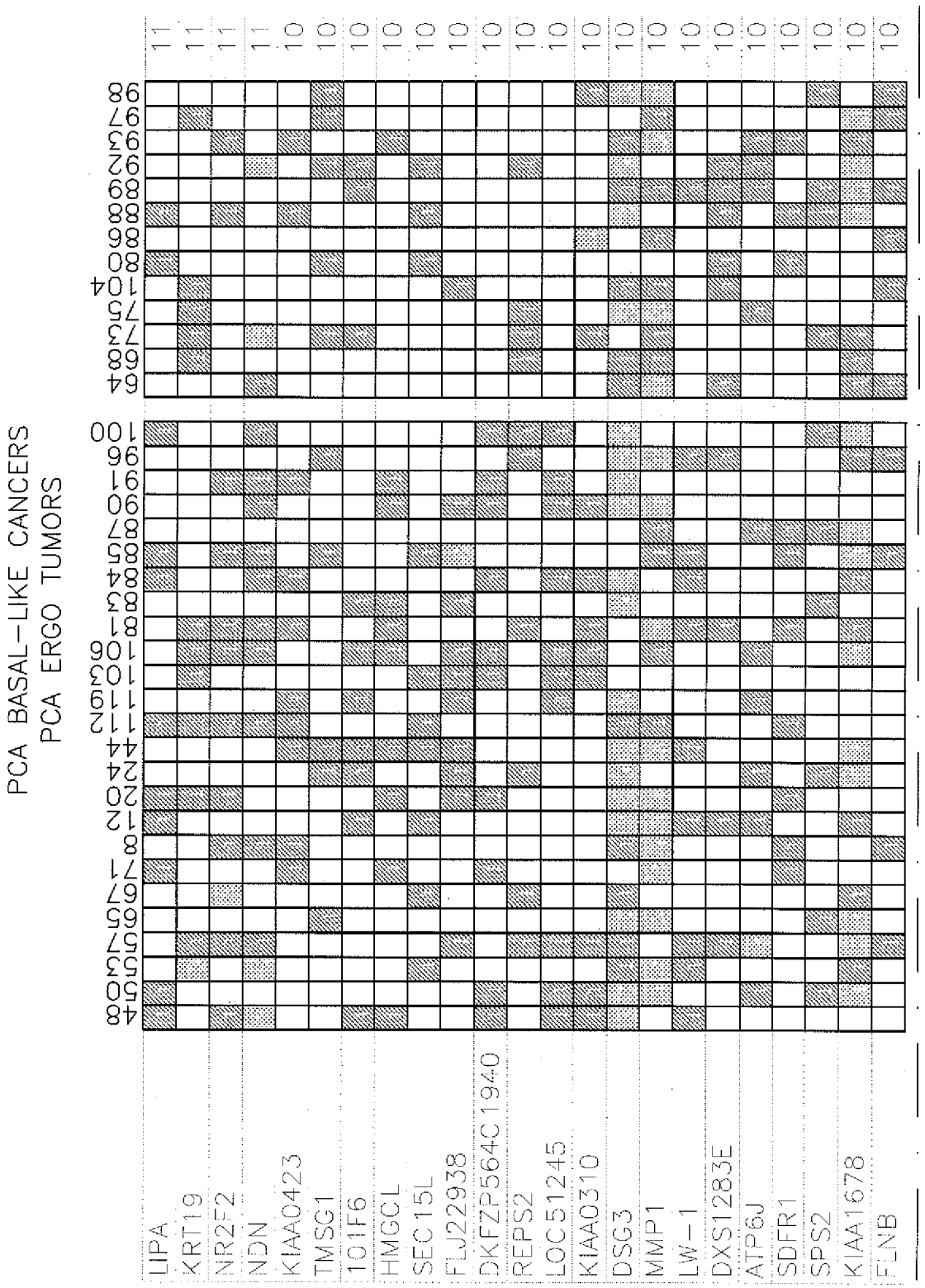

PCA BASAL-LIKE CANCERS
PCA ERGO TUMORS
LIPA
KRT19
NR2F2
NDN
KIAA0423
TMSG1
101F6
HMGCL
SEC15L
FLJ22938
DKFZP564C1940
REPS2
LOC51245
KIAA0310
DSG3
MMP1
LW-1
DXS1283E
ATP6J
SDFR1
SPS2
KIAA1678
FLNB
CONTINUED ON SHEET 38

FIG. 24

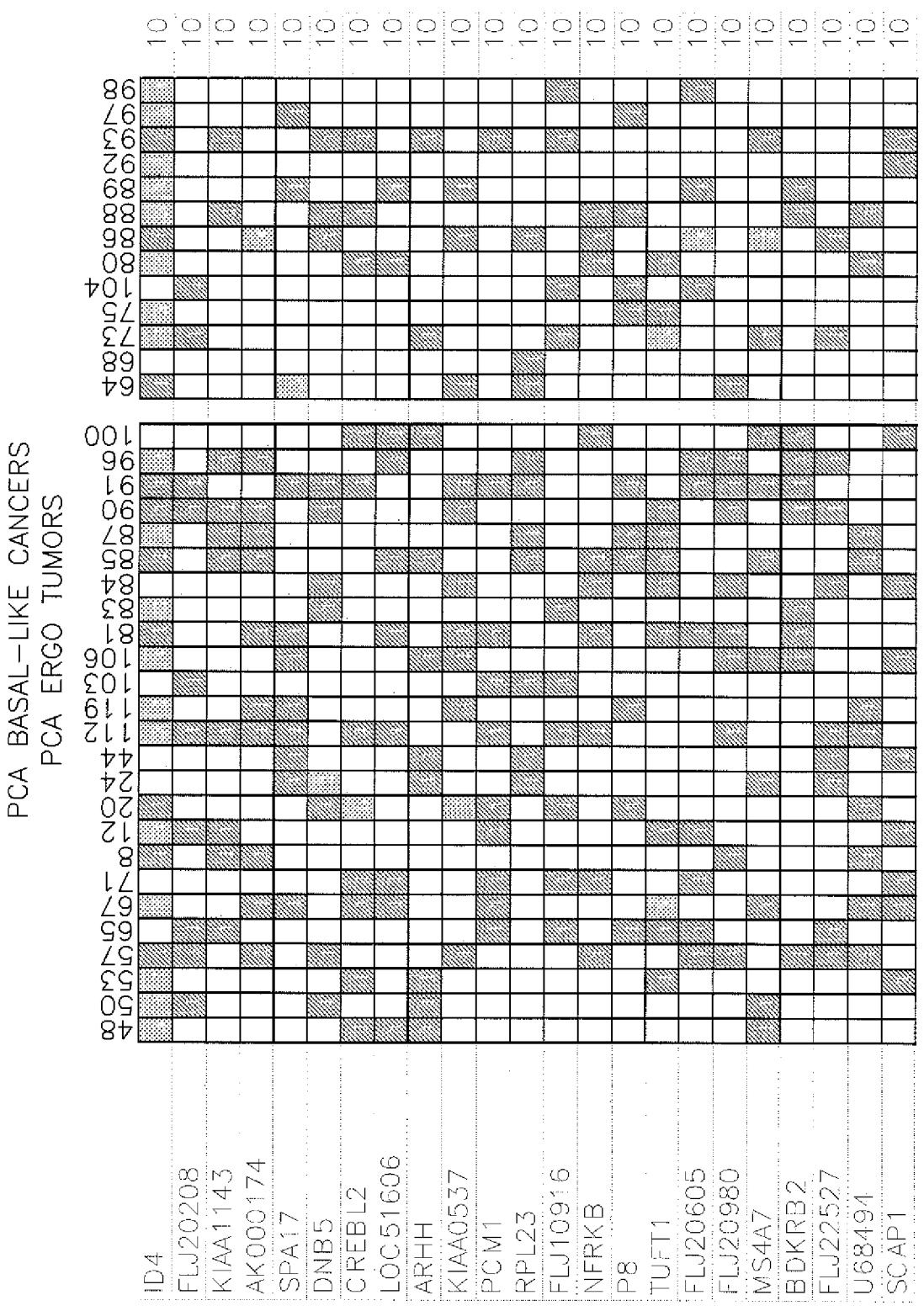

PCA BASAL-LIKE CANCERS
PCA ERGO TUMORS
ID4
FLJ20208
KIAA1143
AK000174
SPA17
DNB5
CREBL2
LOC51606
ARHH
KIAA0537
PCM1
RPL23
FLJ10916
NFRKB
P8
TUFT1
FLJ20605
FLJ20980
MS4A7
BDKRB2
FLJ22527
U68491
SCAP1
CONTINUED ON SHEET 39

FIG. 24

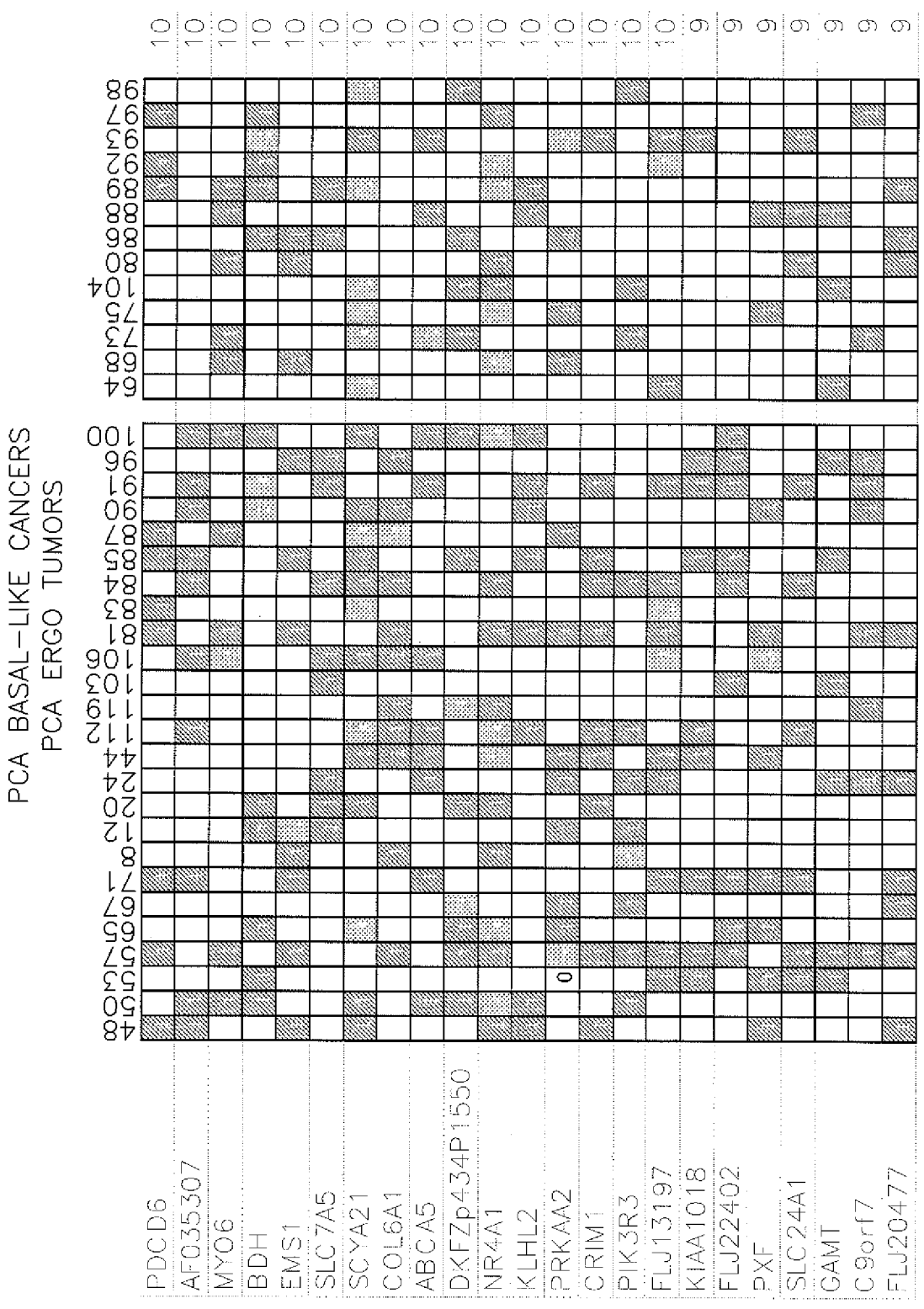

PCA BASAL-LIKE CANCERS
PCA ERGO TUMORS
PDCD6
AF035307
MYO6
BDH
EMS1
SLC7A5
SCYA21
COL6A1
ABCA5
DKFZp434P1550
NR4A1
KLHL2
PRKAA2
CRIM1
PIK3R3
FLJ13197
KIAA1018
FLJ22402
PXF
SLC24A1
GAMT
C9orf7
FLJ20477
CONTINUED ON SHEET 40

FIG. 24

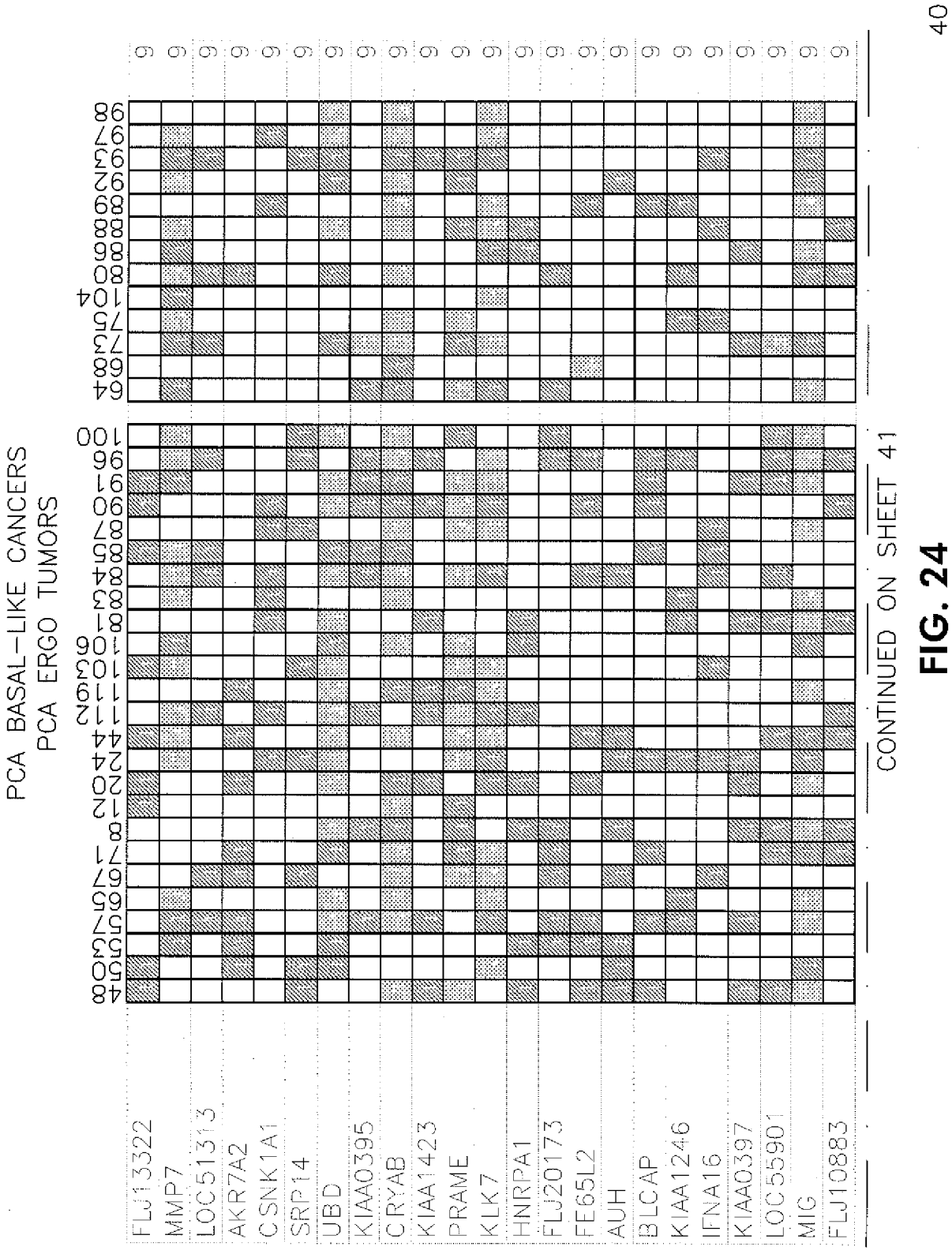

PCA BASAL-LIKE CANCERS
PCA ERGO TUMORS
FLJ13322
MMP7
LOC51313
AKR7A2
CSNK1A1
SRP14
UBD
KIAA0395
CRYAB
KIAA1423
PRAME
KLK7
HNRPA1
FLJ20173
FE65L2
AUH
BLCAP
KIAA1246
IFNA16
KIAA0397
LOC55901
MIG
FLJ10883
CONTINUED ON SHEET 41

FIG. 24

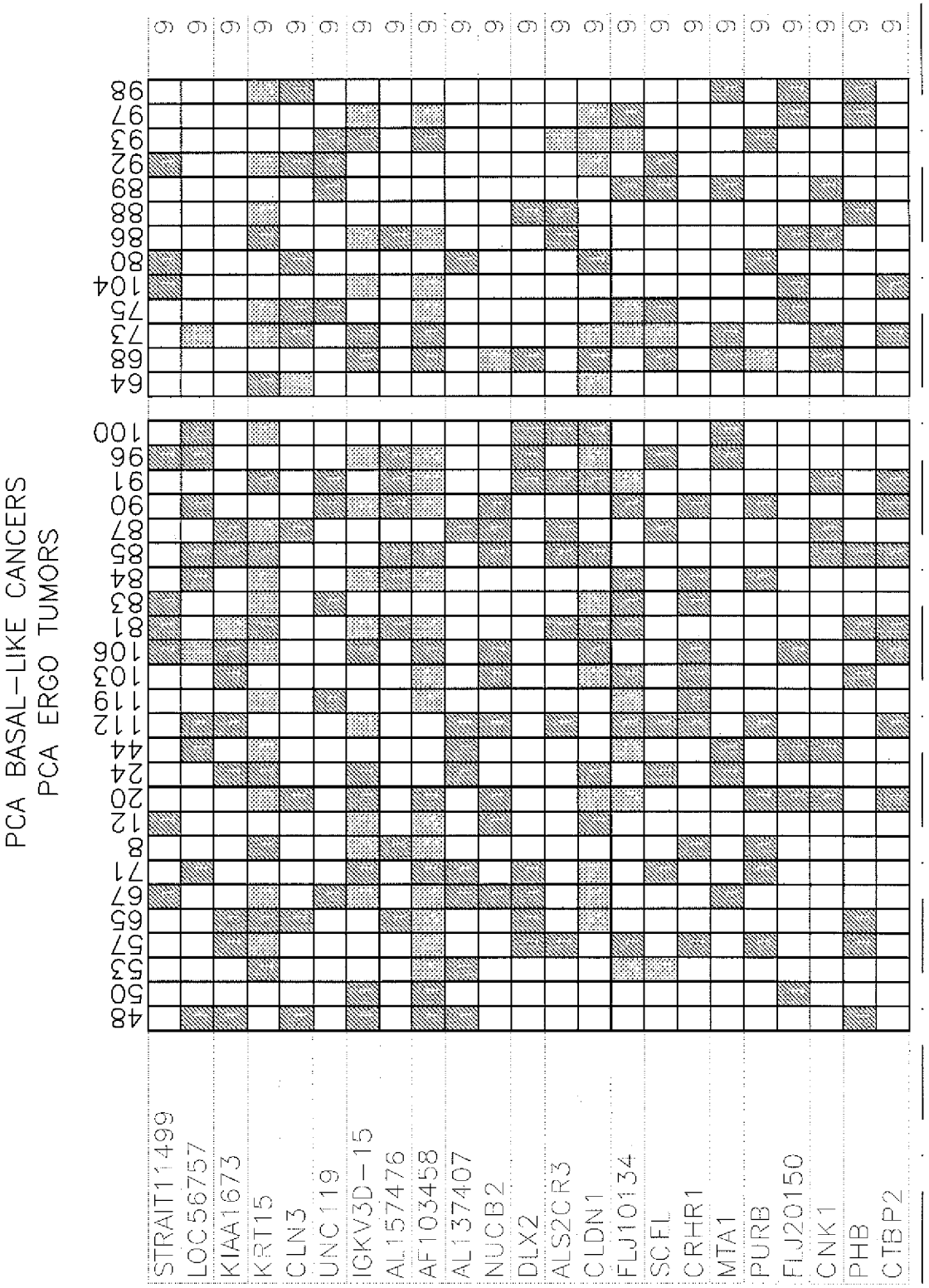

PCA BASAL-LIKE CANCERS
PCA ERGO TUMORS
STRAIT11499
LOC56757
KIAA1673
KRT15
CLN3
UNC119
IGKV3D-15
AL157476
AF103458
AL137407
NUCB2
DLX2
ALS2CR3
CLDN1
FLJ10134
SCFL
CRHR1
MTA1
PURB
FLJ20150
CNK1
PHB
CTBP2
CONTINUED ON SHEET 42

FIG. 24

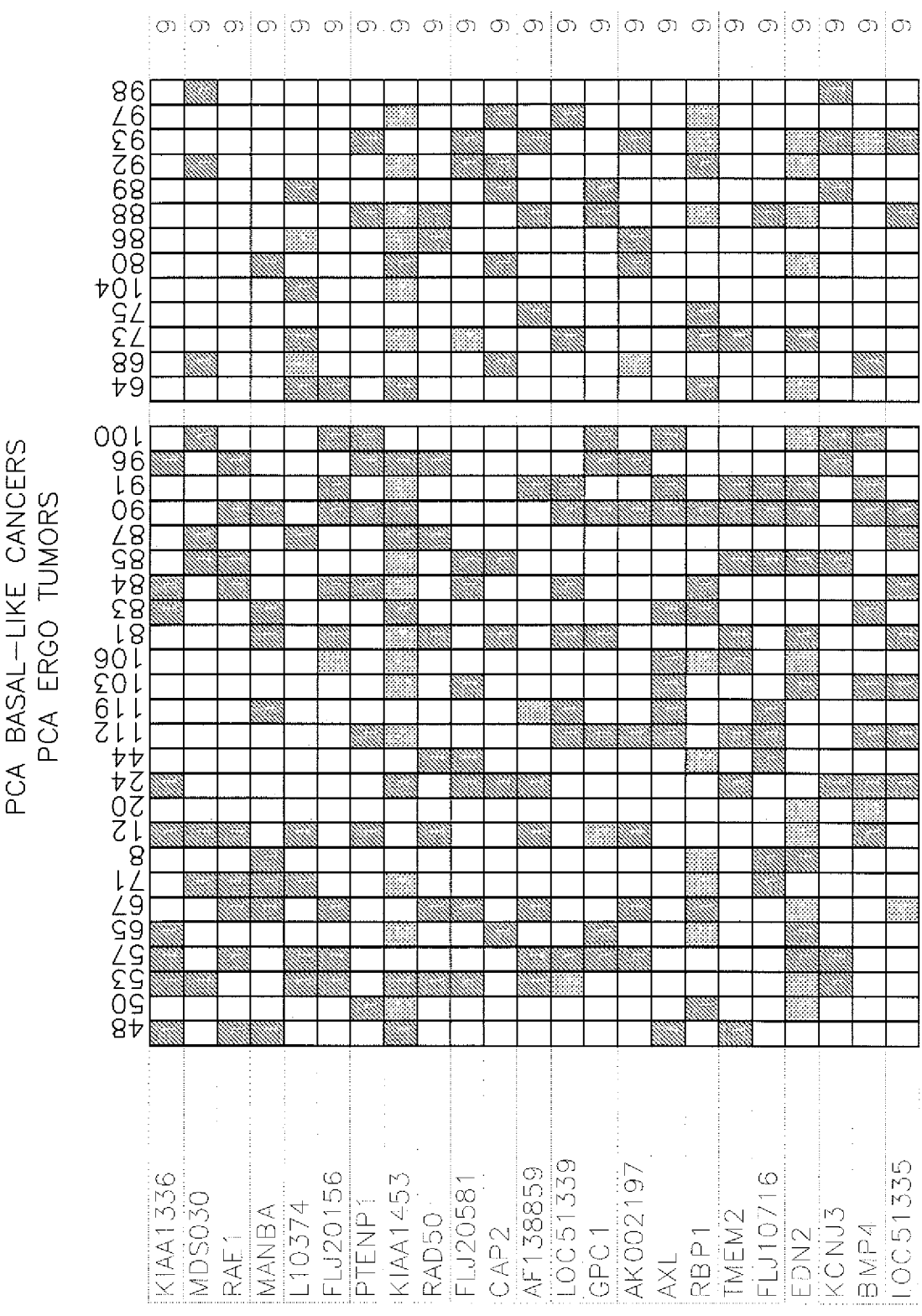

PCA BASAL-LIKE CANCERS
PCA ERGO TUMORS
KIAA1336
MDS030
RAF1
MANBA
L10374
FLJ20156
PTENP1
KIAA1453
RAD50
FLJ20581
CAP2
AF138859
LOC51339
GPC1
AK002197
AXL
RBP1
TMEM2
FLJ10716
EDN2
KCNJ3
BMP4
LOC51335
CONTINUED ON SHEET 43

FIG. 24

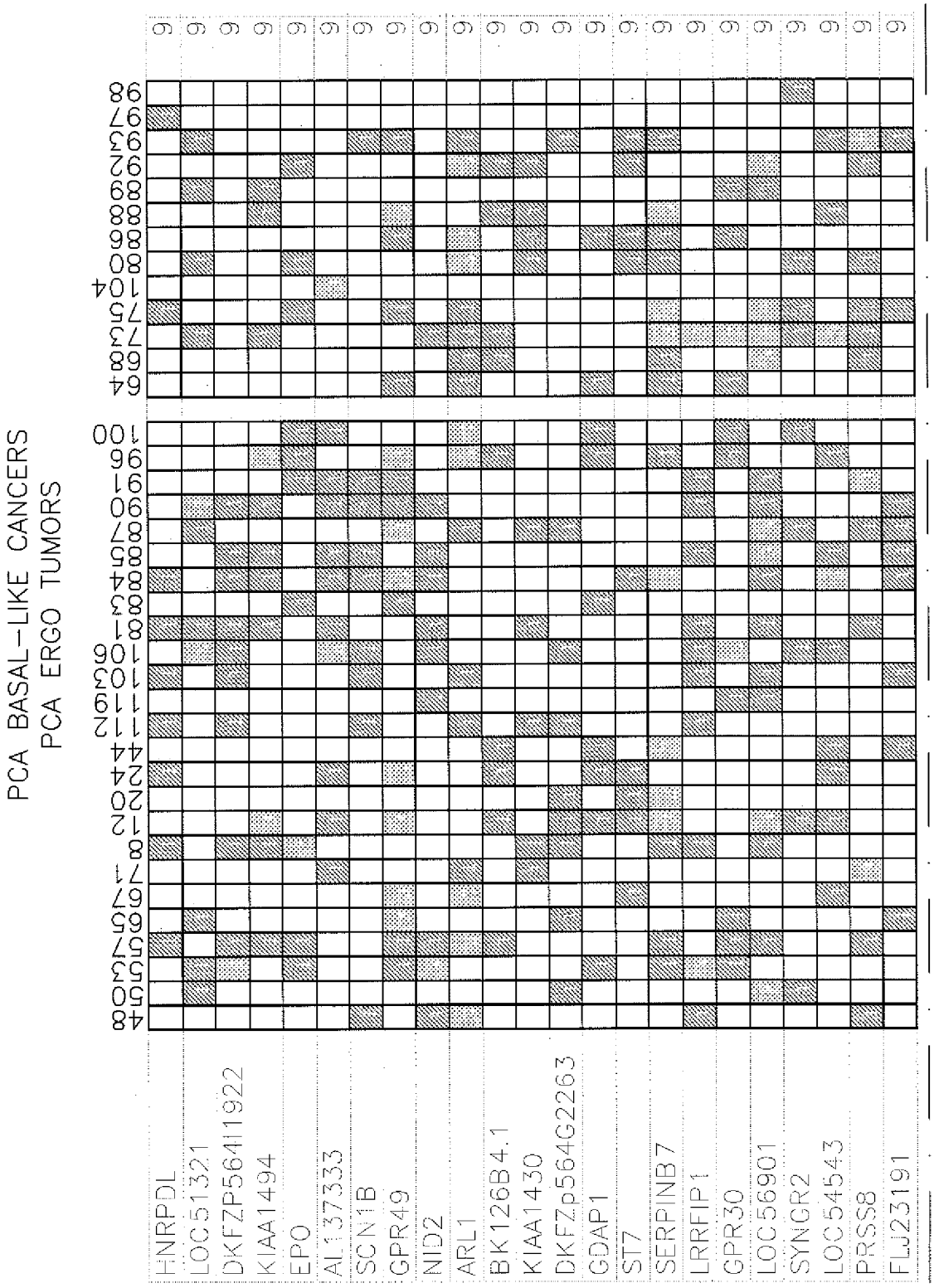

PCA BASAL-LIKE CANCERS
PCA ERGO TUMORS
HNRPDL
LOC51321
DKFZP564I1922
KIAA1494
EPO
AL137333
SCN1B
GPR49
NID2
ARL1
BK126B4.1
KIAA1430
DKFZp564G2263
GDAP1
ST7
SERPINB7
LRRFIP1
GPR30
LOC56901
SYNGR2
LOC54543
PRSS8
FLJ23191
CONTINUED ON SHEET 44

FIG. 24

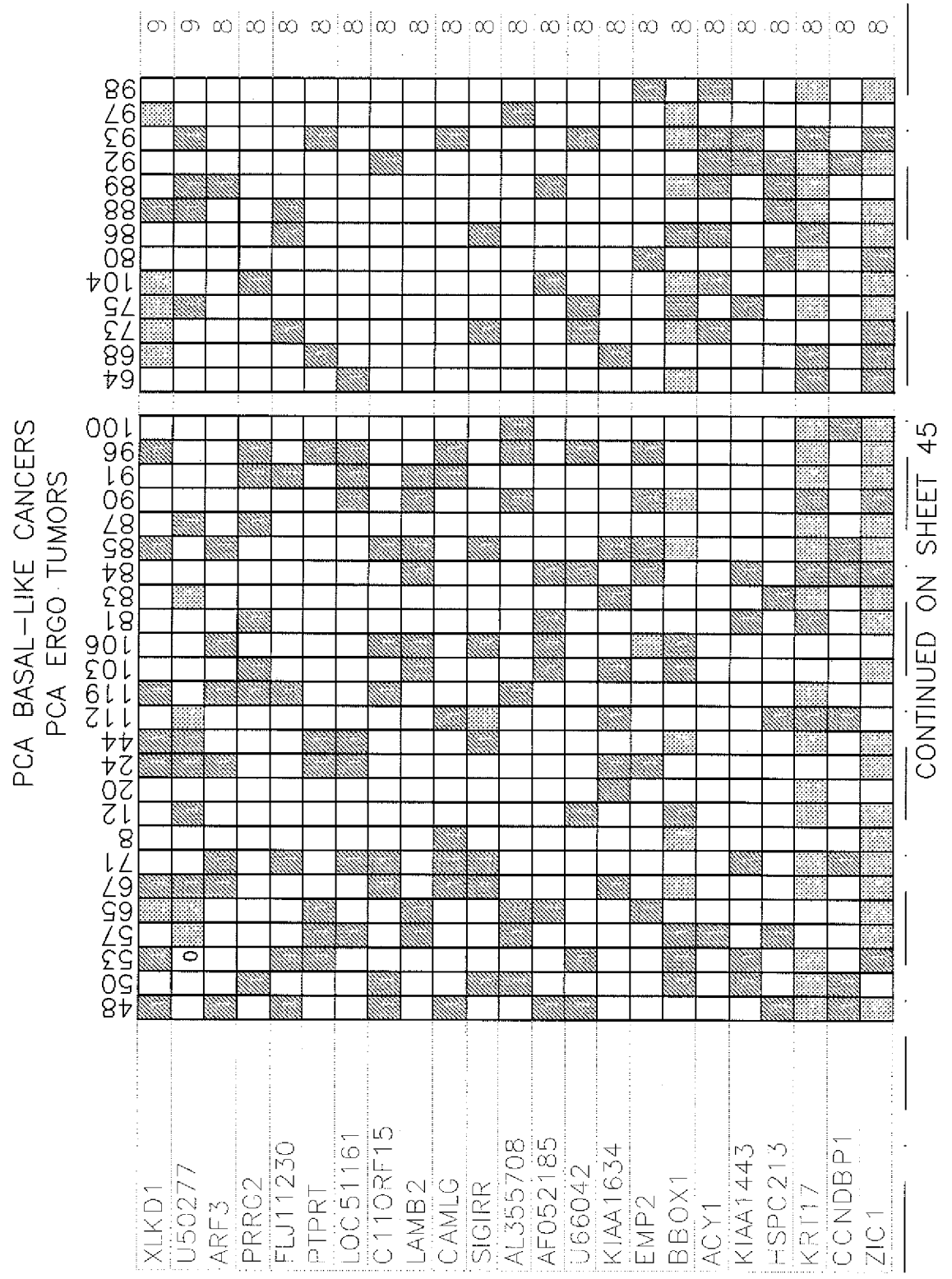

PCA BASAL-LIKE CANCERS
PCA ERGO TUMORS
XLKD1
U50277
ARF3
PRRG2
FLJ11230
PTPRT
LOC51161
C11ORF15
LAMB2
CAMLG
SIGIRR
AL355708
AF052185
U66042
KIAA1634
EMP2
BBOX1
ACY1
KIAA1443
FSPC213
KRT17
CCNDBP1
ZIC1
CONTINUED ON SHEET 45

FIG. 24

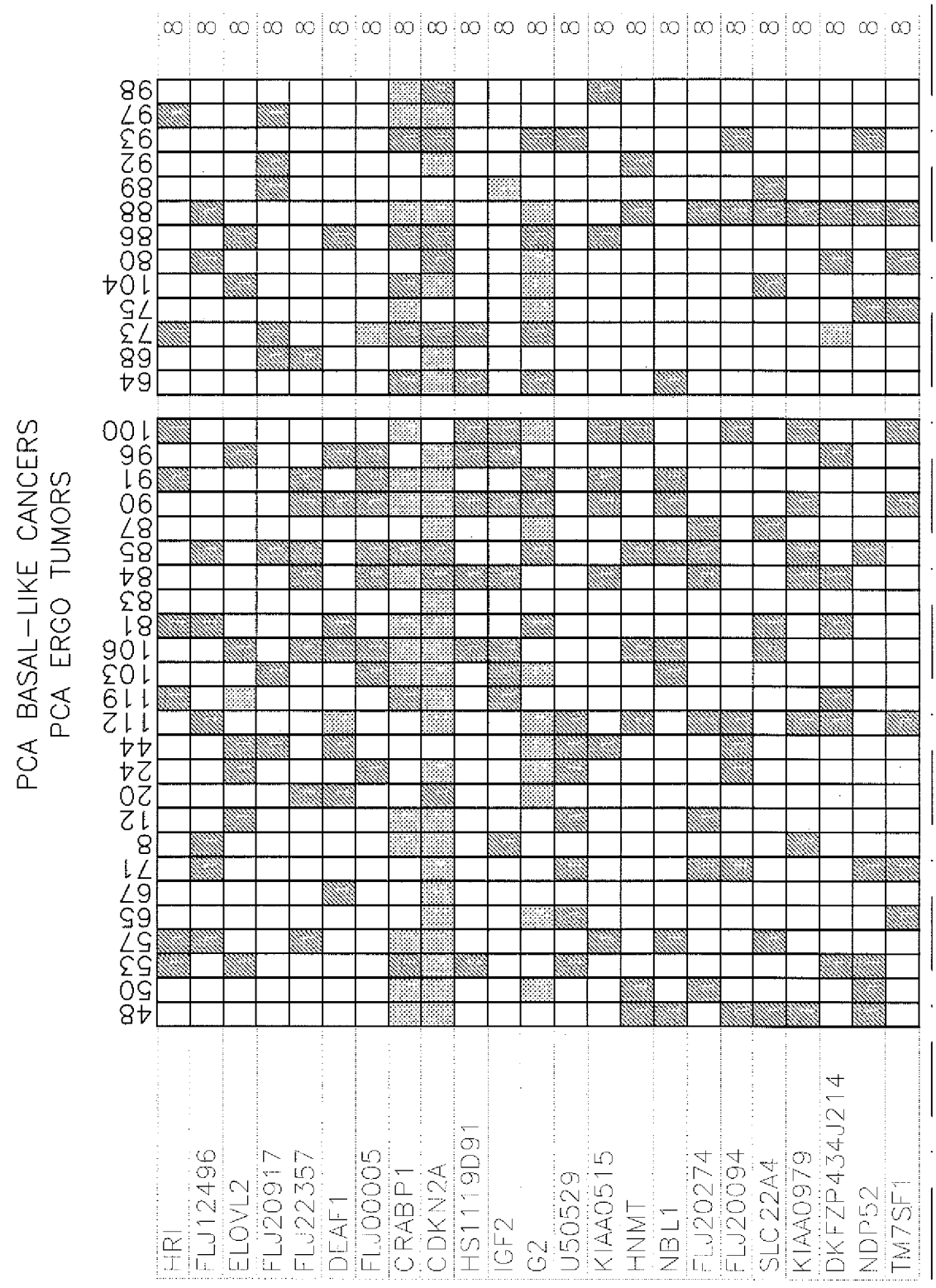

PCA BASAL-LIKE CANCERS
PCA ERGO TUMORS
HRI
FLJ12496
ELOVL2
FLJ20917
FLJ22357
DEAF1
FLJ00005
CRABP1
CDKN2A
HS1119D91
IGF2
G2
U50529
KIAA0515
HNMT
NBL1
FLJ20274
FLJ20094
SLC22A4
KIAA0979
DKFZP434J214
NDP52
TM7SF1
CONTINUED ON SHEET 46

FIG. 24

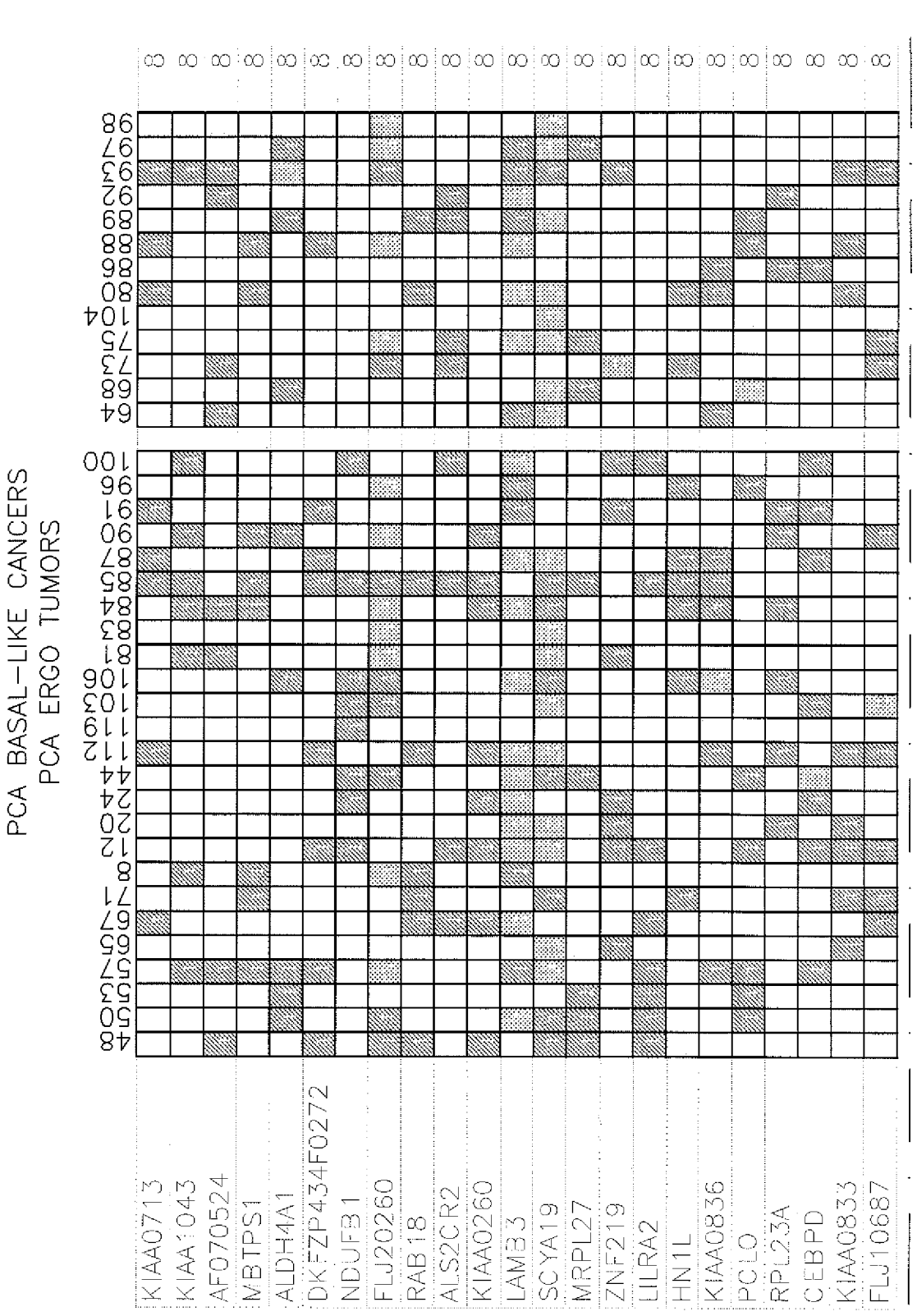

PCA BASAL-LIKE CANCERS
PCA ERGO TUMORS
KIAA0713
KIAA1043
AF070524
MBTPS1
ALDH4A1
DKFZP434F0272
NDUFB1
FLJ20260
RAB18
ALS2CR2
KIAA0260
LAMB3
SCYA19
MRPL27
ZNF219
LILRA2
HN1L
KIAA0836
PCLO
RPL23A
CEBPD
KIAA0833
FLJ10687
CONTINUED ON SHEET 47

FIG. 24

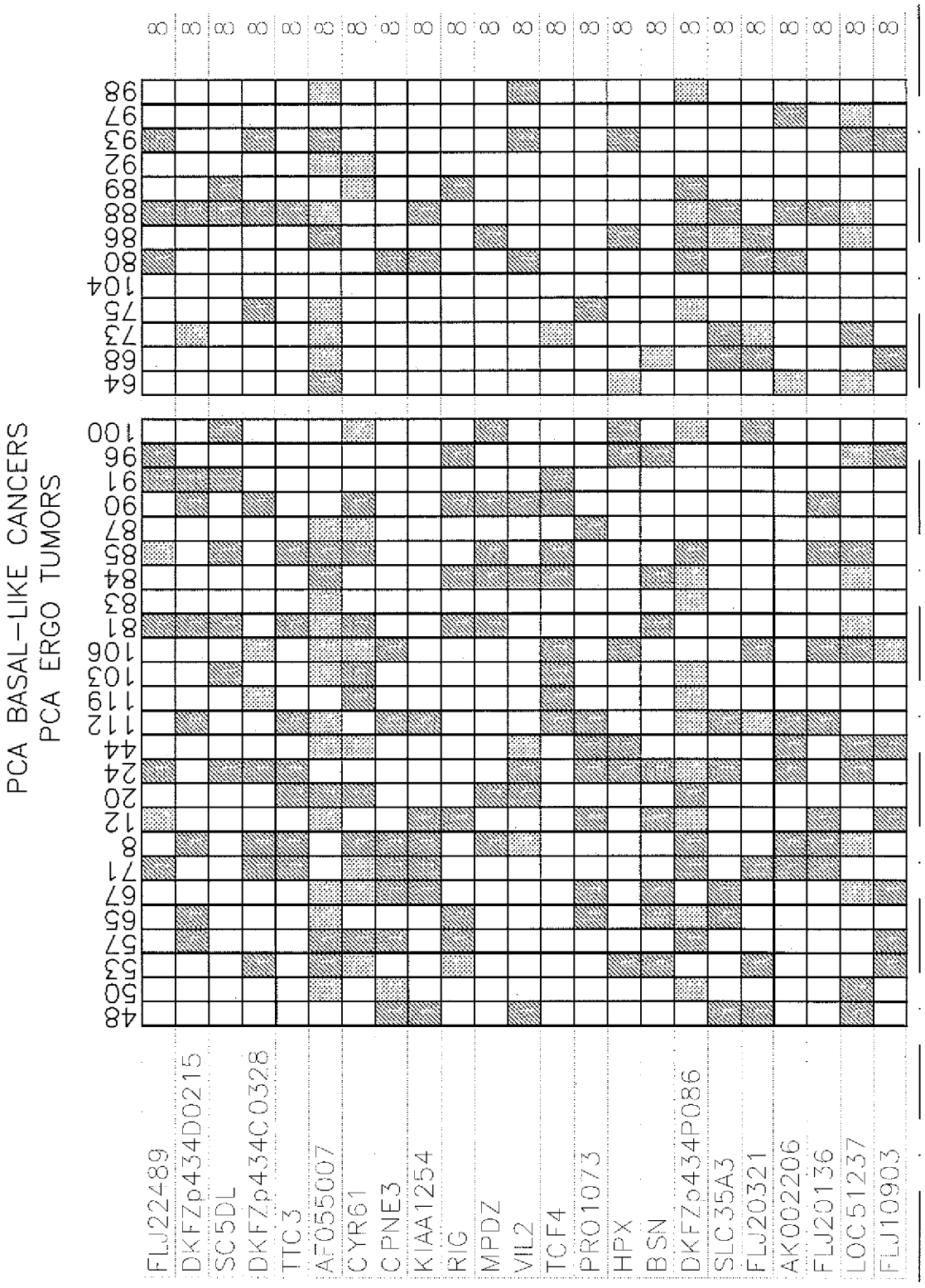

PCA BASAL-LIKE CANCERS
PCA ERGO TUMORS
FLJ22489
DKFZp434D0215
SC5DL
DKFZp434C0328
TTC3
AF055007
CYR61
CPNE3
KIAA1254
RIG
MPDZ
VIL2
TCF4
PRO1073
HPX
BSN
DKFZp434P086
SLC35A3
FLJ20321
AK002206
FLJ20136
LOC51237
FLJ10903
CONTINUED ON SHEET 48

FIG. 24

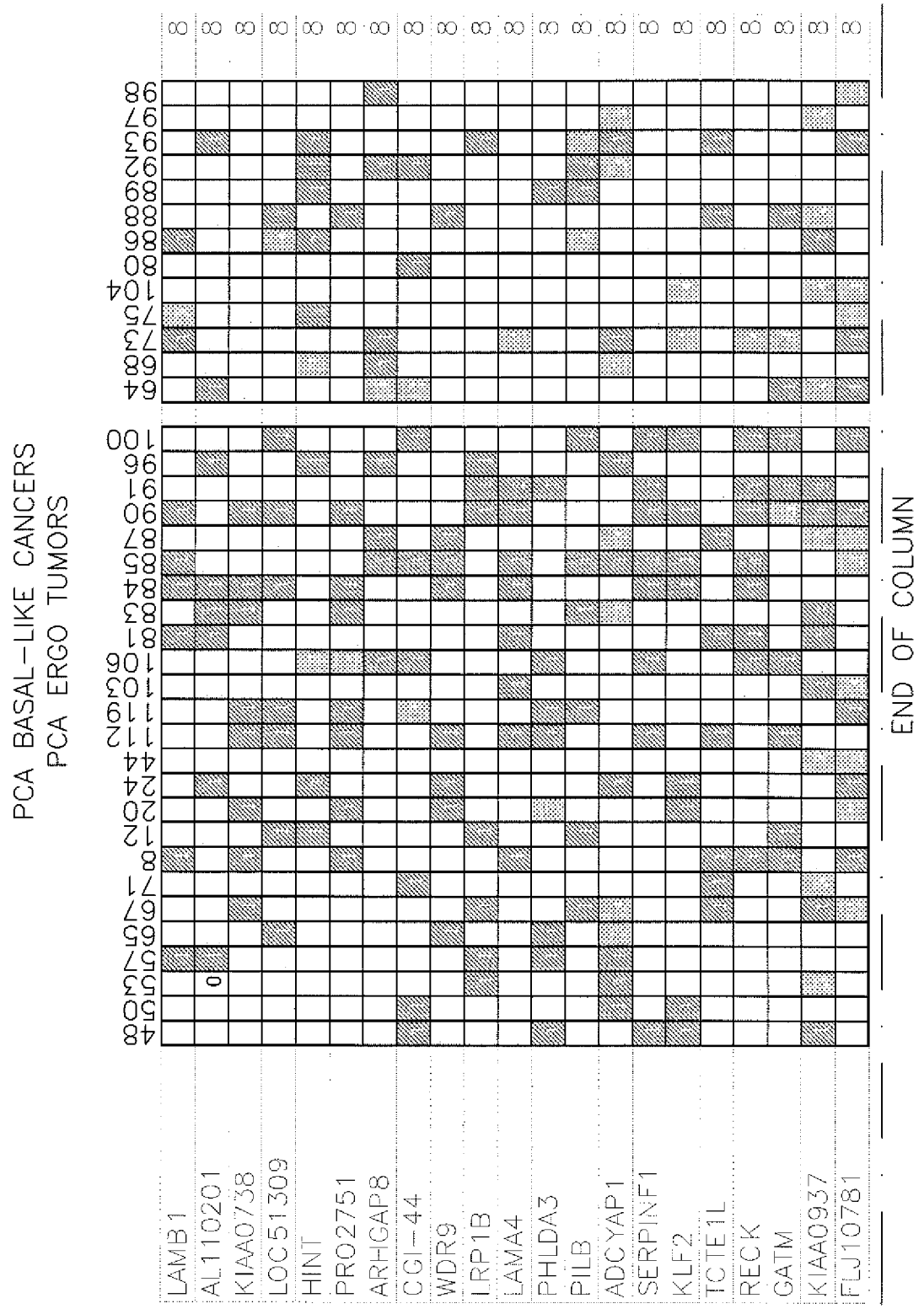

PCA BASAL-LIKE CANCERS
PCA ERGO TUMORS
LAMB1
AL110201
KIAA0738
LOC51309
HINT
PRO2751
ARHGAP8
CGI-44
WDR9
IRP1B
LAMA4
PHLDA3
PILB
ADCYAP1
SERPINF1
KLF2
TCTE1L
RECK
GATM
KIAA0937
FLJ10781
END OF COLUMN

FIG. 24

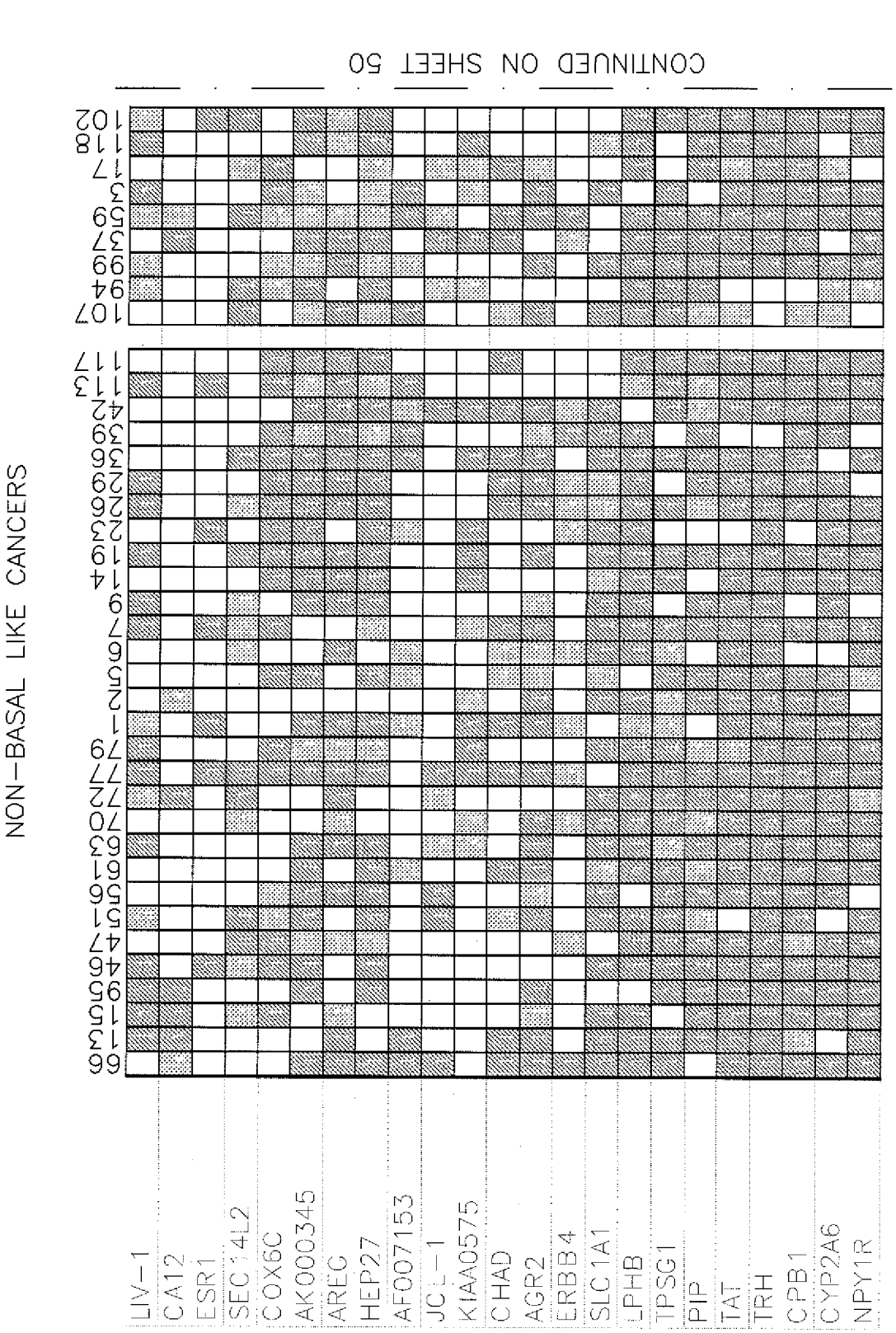

NON-BASAL LIKE CANCERS
CONTINUED ON SHEET 50
LIV-1
CA12
ESR1
SEC14L2
COX6C
AK000345
AREG
HEP27
AF007153
JCL-1
KIAA0575
CHAD
AGR2
ERBB4
SLC1A1
LPHB
TPSG1
PIP
TAT
TRH
CPB1
CYP2A6
NPY1R

FIG. 24

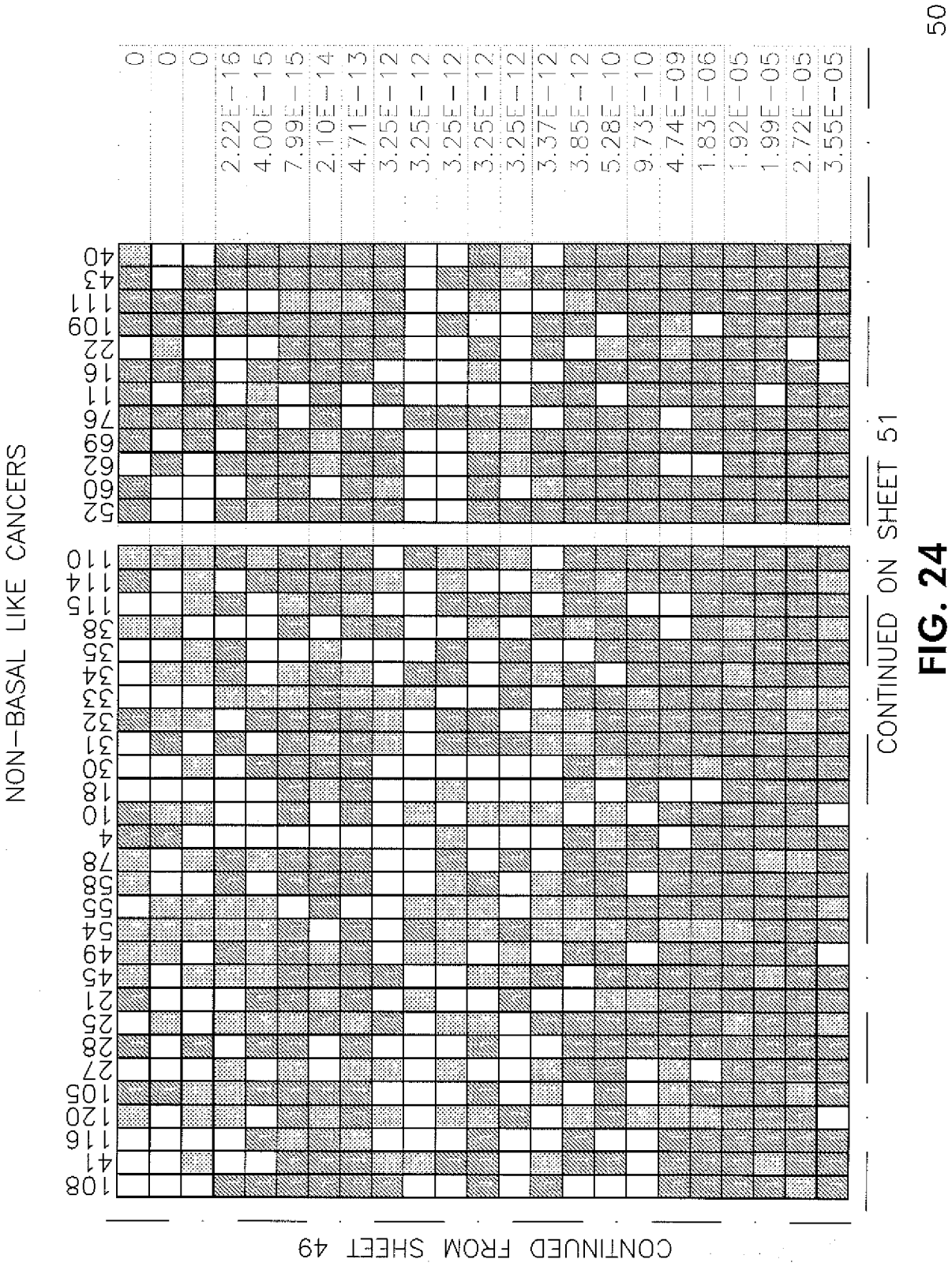

CONTINUED FROM SHEET 49
NON-BASAL LIKE CANCERS
0
0
0
2.22E-16
4.00E-15
7.99E-15
2.10E-14
4.71E-13
3.25E-12
3.25E-12
3.25E-12
3.25E-12
3.25E-12
3.37E-12
3.85E-12
5.28E-10
9.73E-10
4.74E-09
1.83E-06
1.92E-05
1.99E-05
2.72E-05
3.55E-05
CONTINUED ON SHEET 51

FIG. 24

50

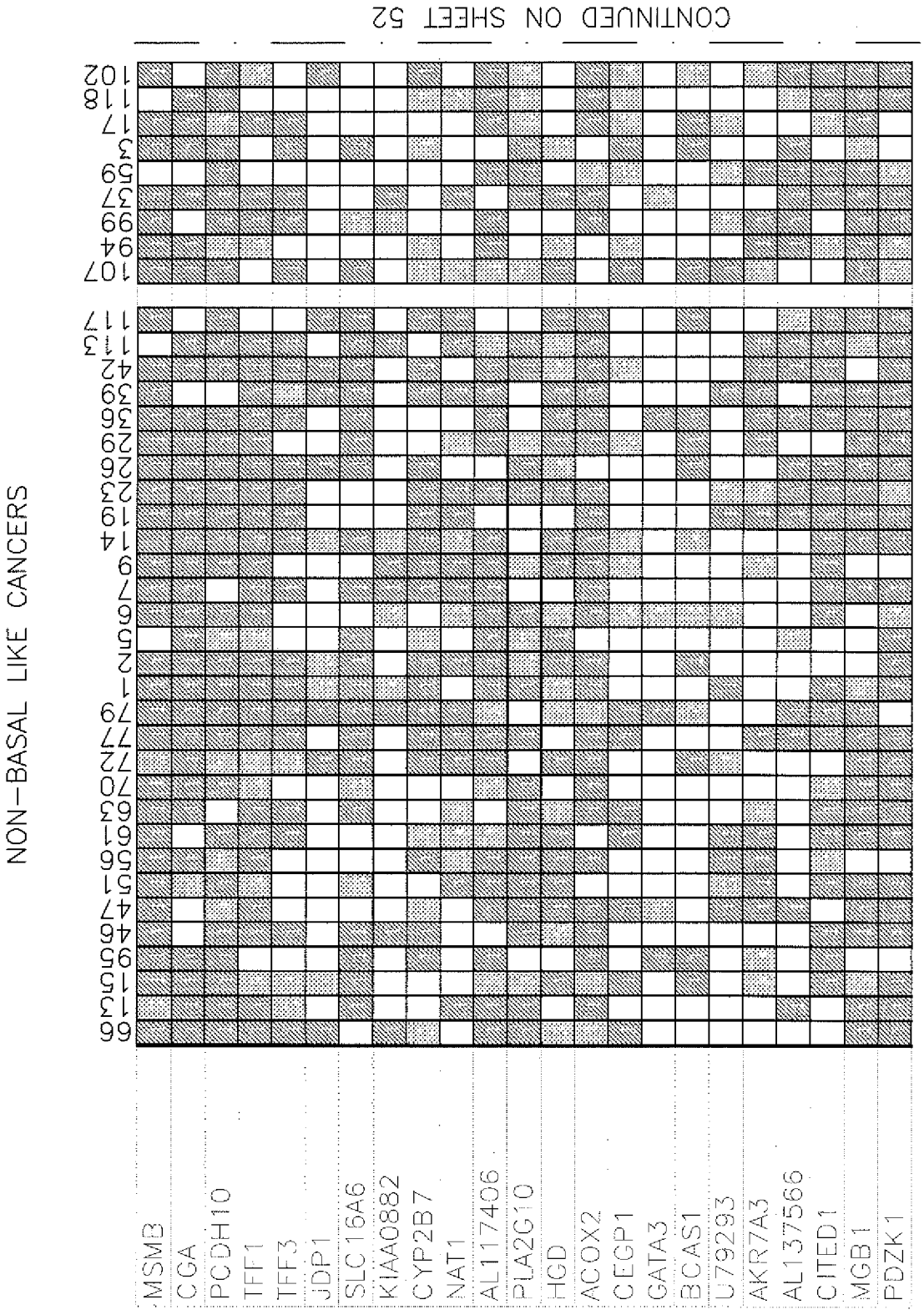

CONTINUED ON SHEET 52
NON-BASAL LIKE CANCERS
MSMB
CGA
PCDH10
TFF1
TFF3
JDP1
SLC16A6
KIAA0882
CYP2B7
NAT1
AL117406
PLA2G10
HGD
ACOX2
CEGP1
GATA3
BCAS1
U79293
AKR7A3
AL137566
CITED1
MGB1
PDZK1

FIG. 24

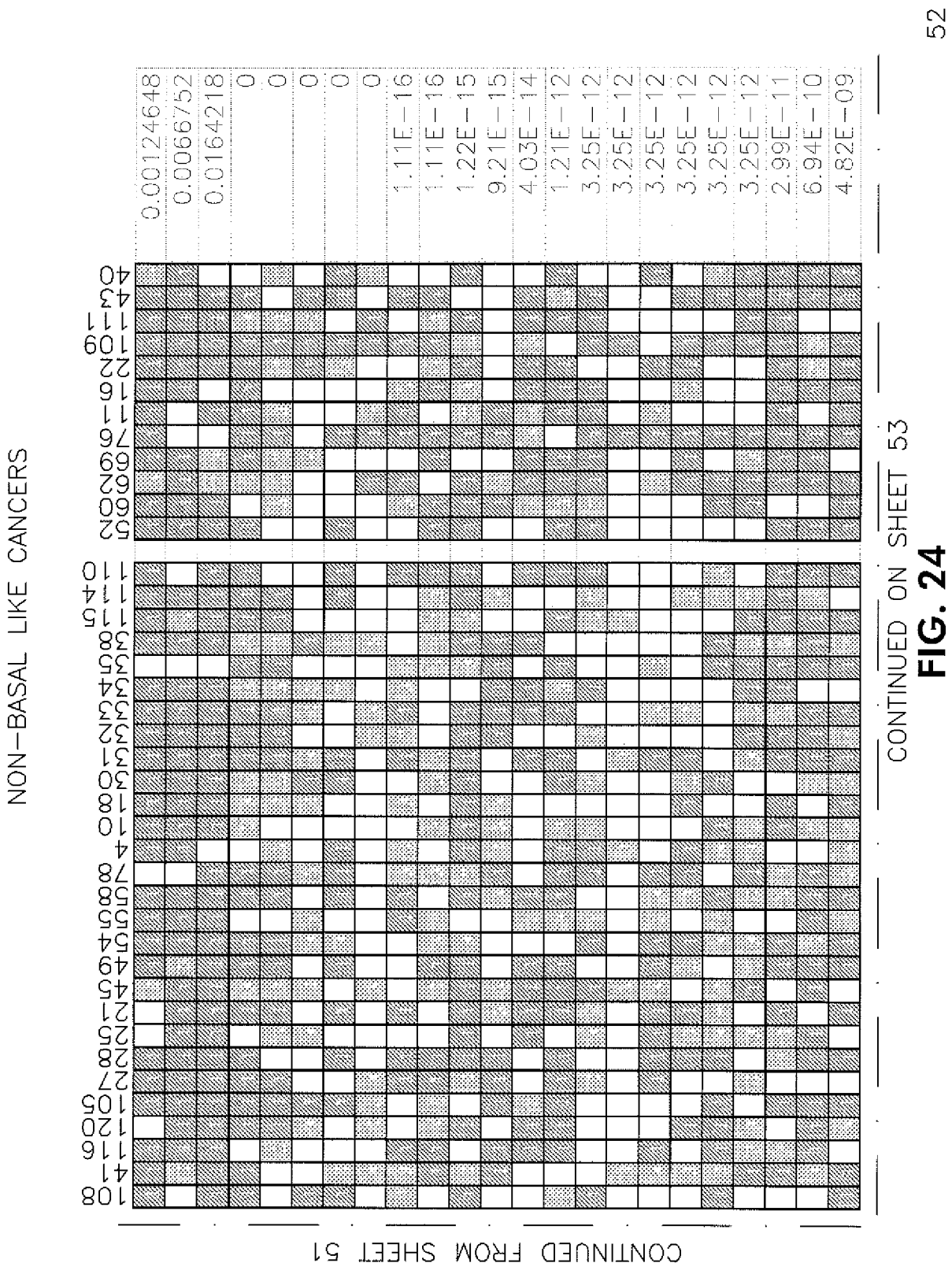

NON-BASAL LIKE CANCERS
CONTINUED FROM SHEET 51
CONTINUED ON SHEET 53
52
0.00124648
0.0066752
0.0164218
0
0
0
0
0
1.11E-16
1.11E-16
1.22E-15
9.21E-15
4.03E-14
1.21E-12
3.25E-12
3.25E-12
3.25E-12
3.25E-12
3.25E-12
3.25E-12
3.25E-12
2.99E-11
6.94E-10
4.82E-09

FIG. 24

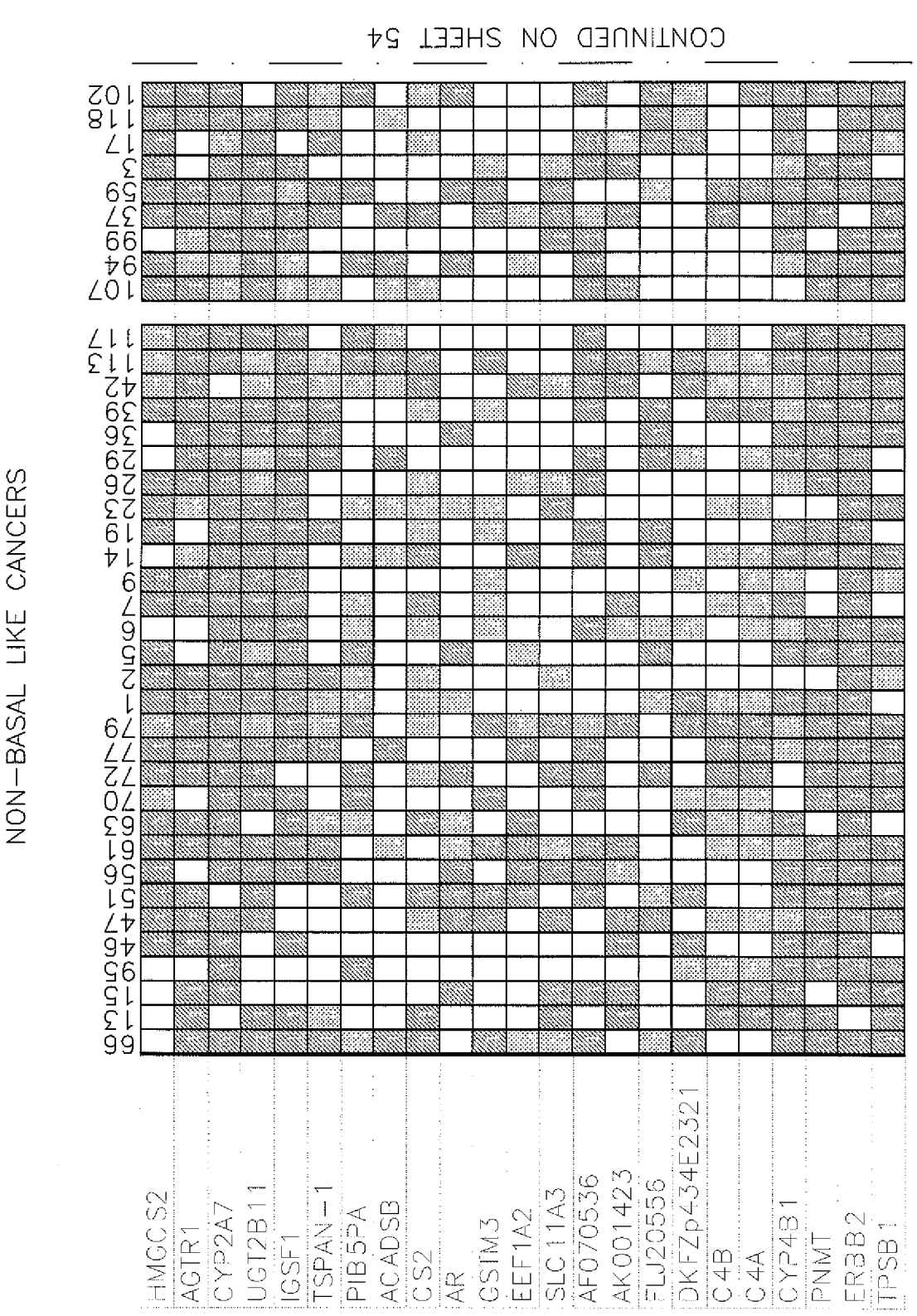

NON-BASAL LIKE CANCERS
CONTINUED ON SHEET 54
HMGCS2
AGTR1
CYP2A7
UGT2B11
IGSF1
TSPAN-1
PIB5PA
ACADSB
CS2
AR
GSTM3
EEF1A2
SLC11A3
AF070536
AK001423
FLJ20556
DKFZp434E2321
C4B
C4A
CYP4B1
PNMT
ER3B2
TPSB1

FIG. 24

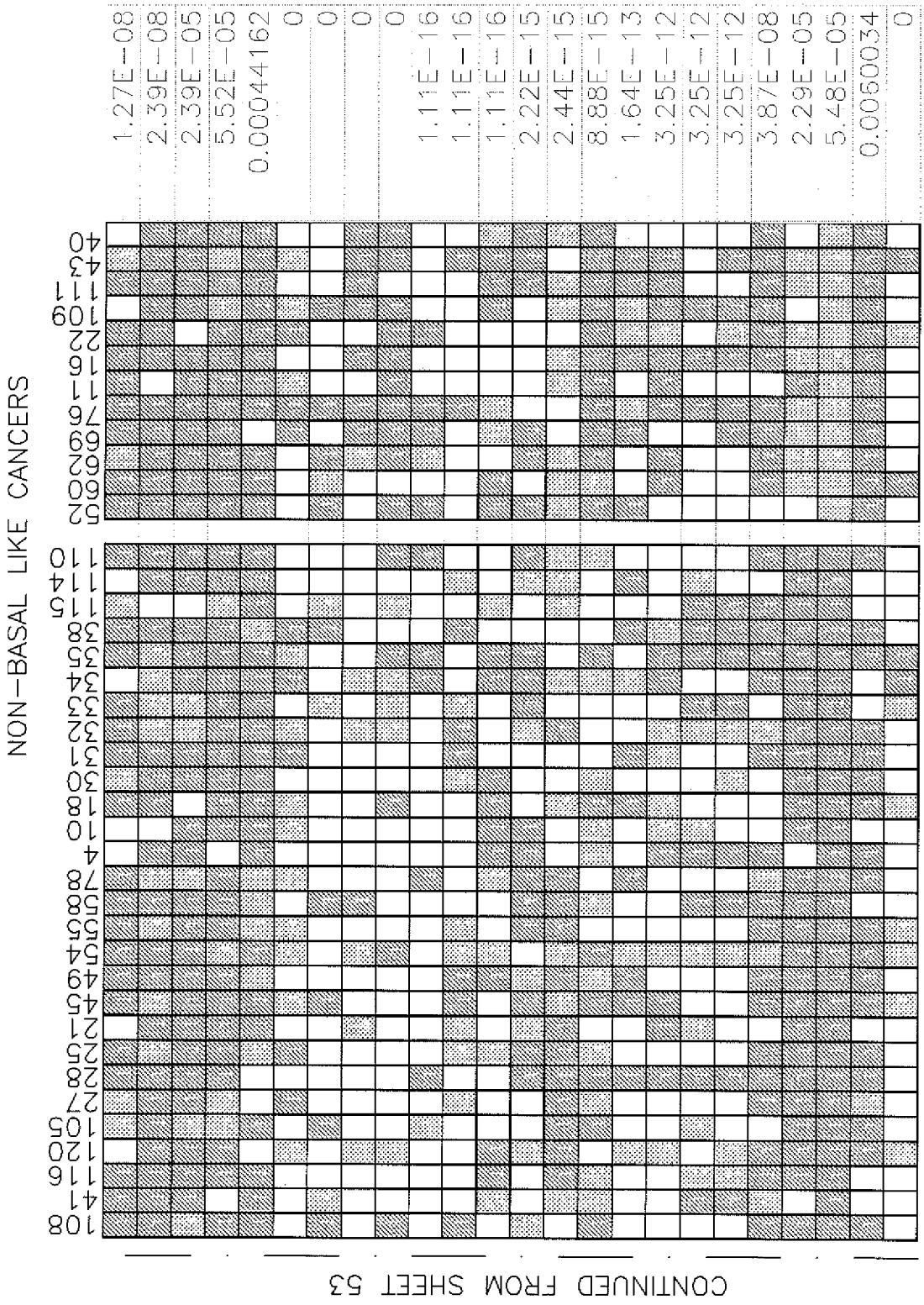

CONTINUED FROM SHEET 53
NON-BASAL LIKE CANCERS
1.27E-08
2.39E-08
2.39E-05
5.52E-05
0.00044162
0
0
0
0
1.11E-16
1.11E-16
1.11E-16
2.22E-15
2.44E-15
8.88E-15
1.64E-13
3.25E-12
3.25E-12
3.25E-12
3.87E-08
2.29E-05
5.48E-05
0.00060034
0
CONTINUED ON SHEET 55

FIG. 24

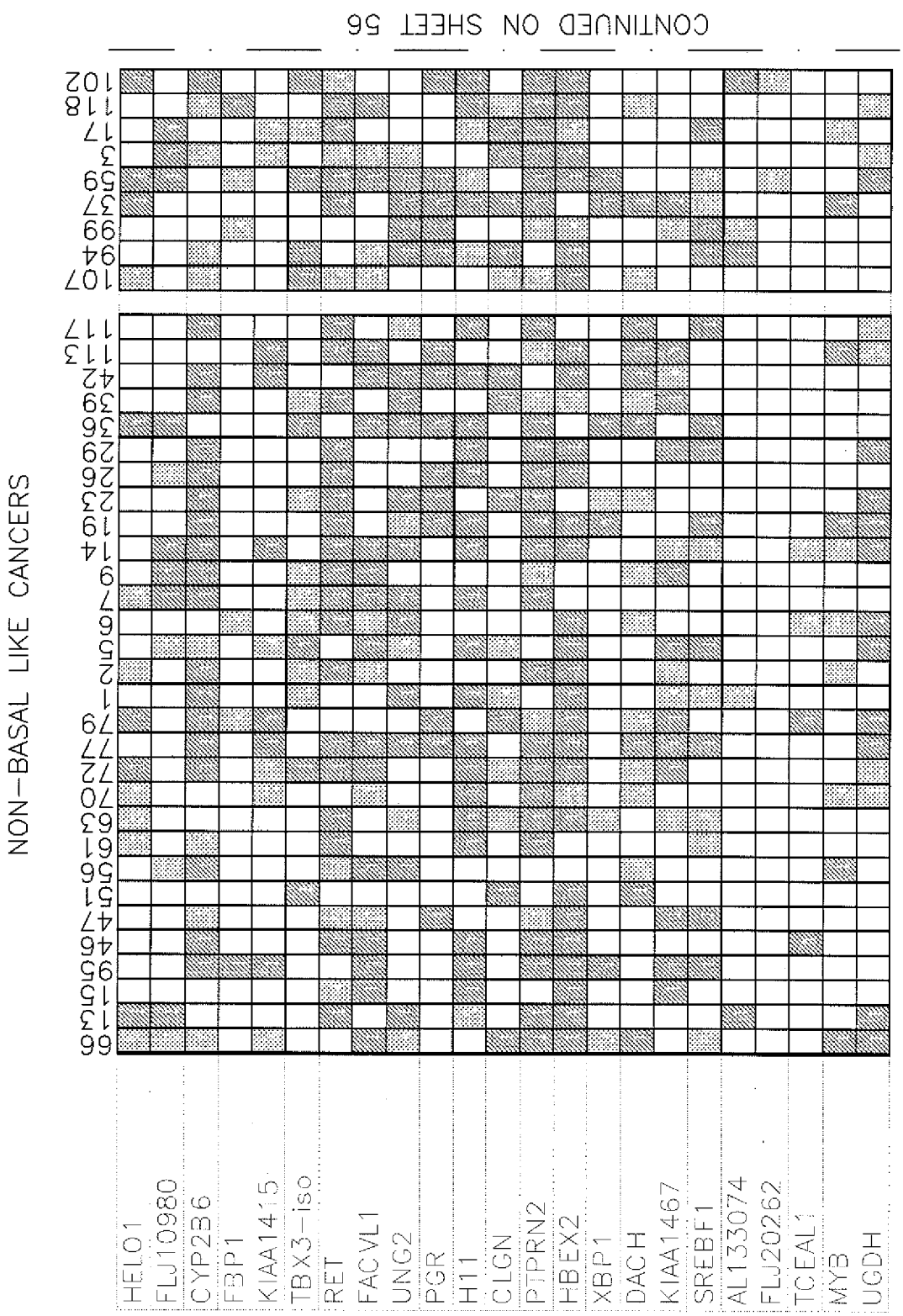

CONTINUED ON SHEET 56
NON-BASAL LIKE CANCERS
HELO1
FLJ10980
CYP236
FBP1
KIAA1415
TBX3-iso
RET
FACVL1
UNG2
PGR
H11
CLGN
PTPRN2
HBEX2
XBP1
DACH
KIAA1467
SREBF1
AL133074
FLJ20262
TCEAL1
MYB
UGDH

FIG. 24

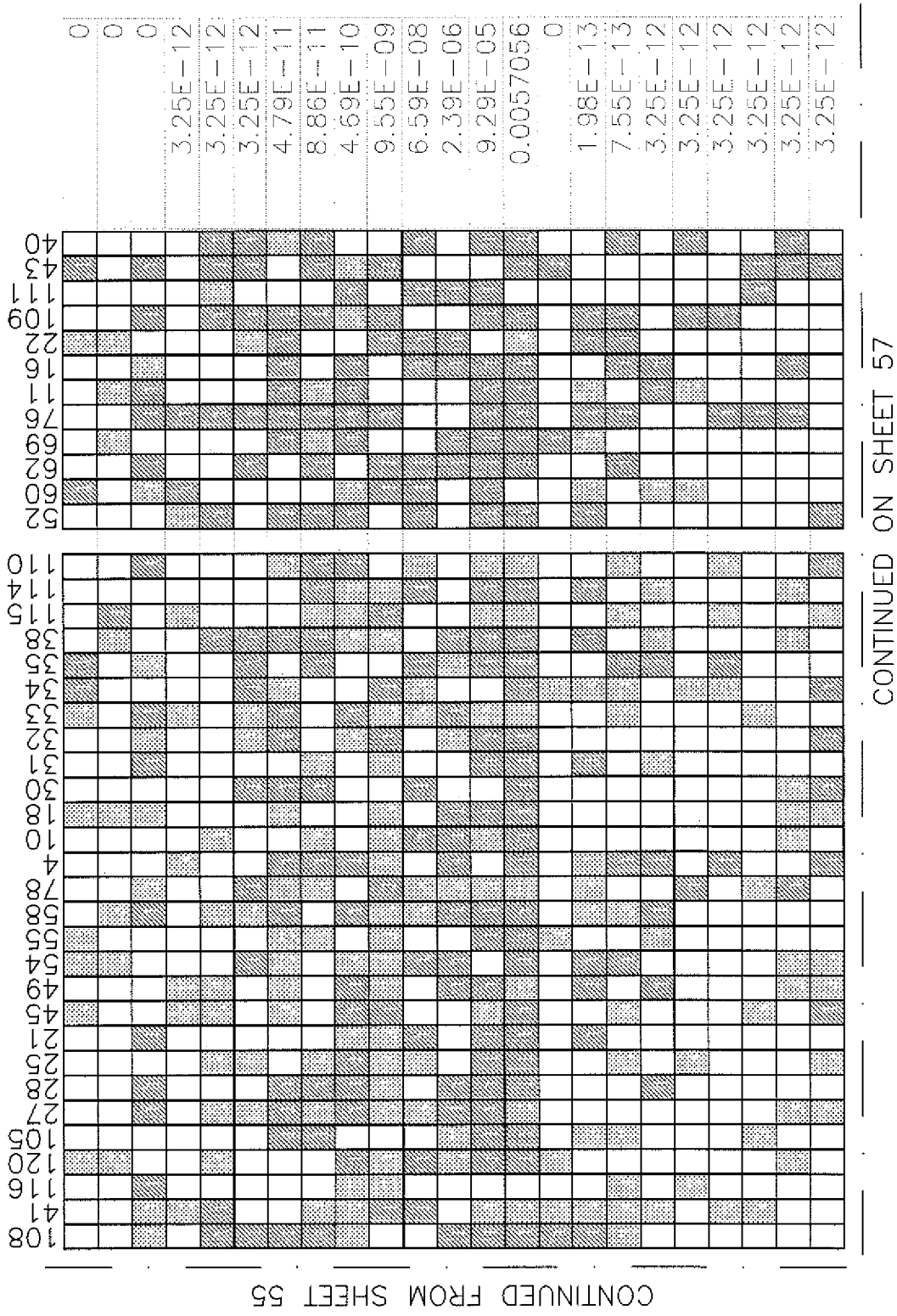

CONTINUED FROM SHEET 55
CONTINUED ON SHEET 57
0
0
0
3.25E−12
3.25E−12
3.25E−12
4.79E−11
8.86E−11
4.69E−10
9.55E−09
6.59E−08
2.39E−06
9.29E−05
0.0057056
0
1.98E−13
7.55E−13
3.25E−12
3.25E−12
3.25E−12
3.25E−12
3.25E−12
3.25E−12

FIG. 24

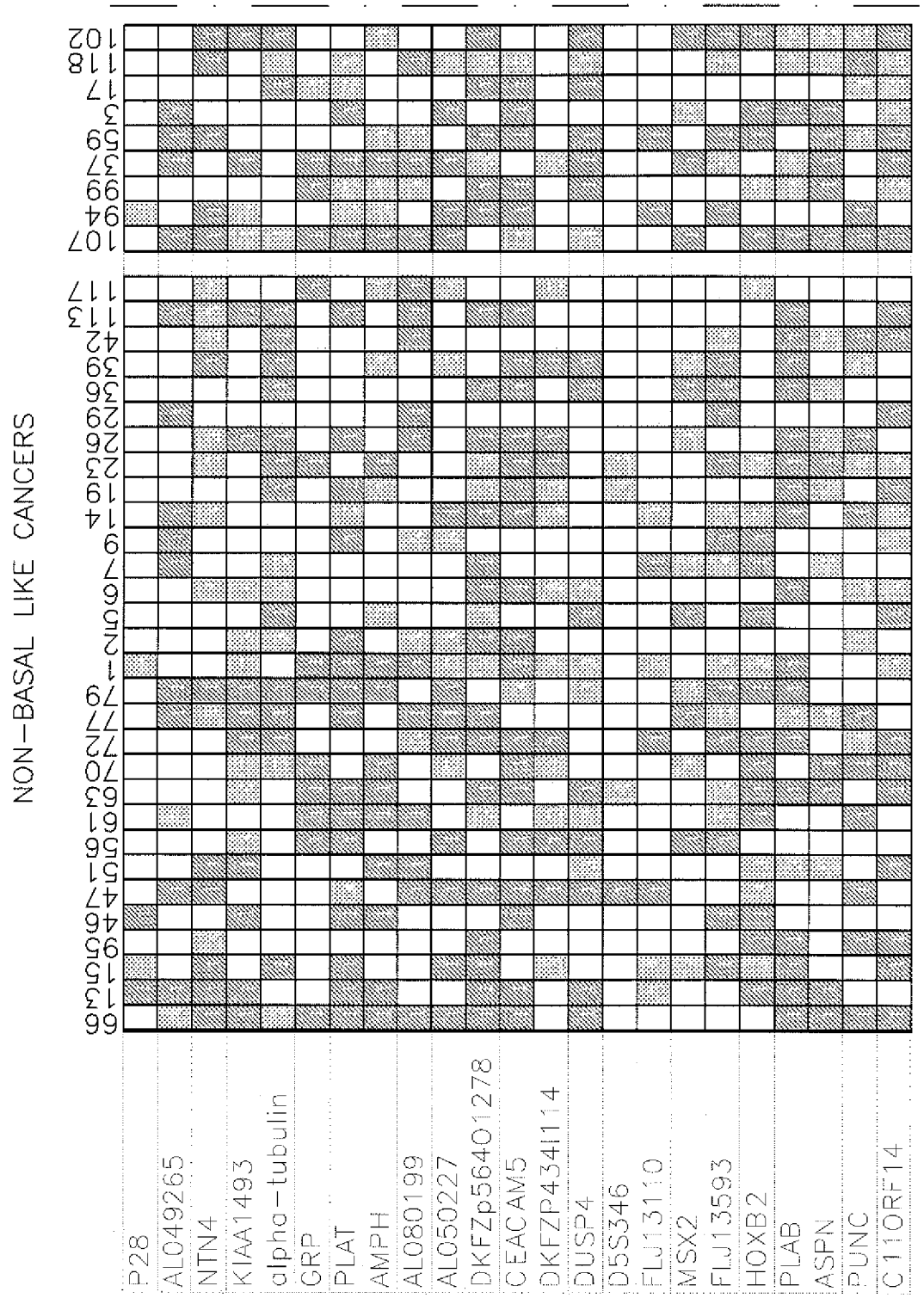

NON-BASAL LIKE CANCERS
CONTINUED ON SHEET 58
P28
AL049265
NTN4
KIAA1493
alpha-tubulin
GRP
PLAT
AMPH
AL080199
AL050227
DKFZp564O1278
CEACAM5
DKFZP434I114
DUSP4
D5S346
FLJ13110
MSX2
FLJ13593
HOXB2
PLAB
ASPN
PUNC
C11ORF14

FIG. 24

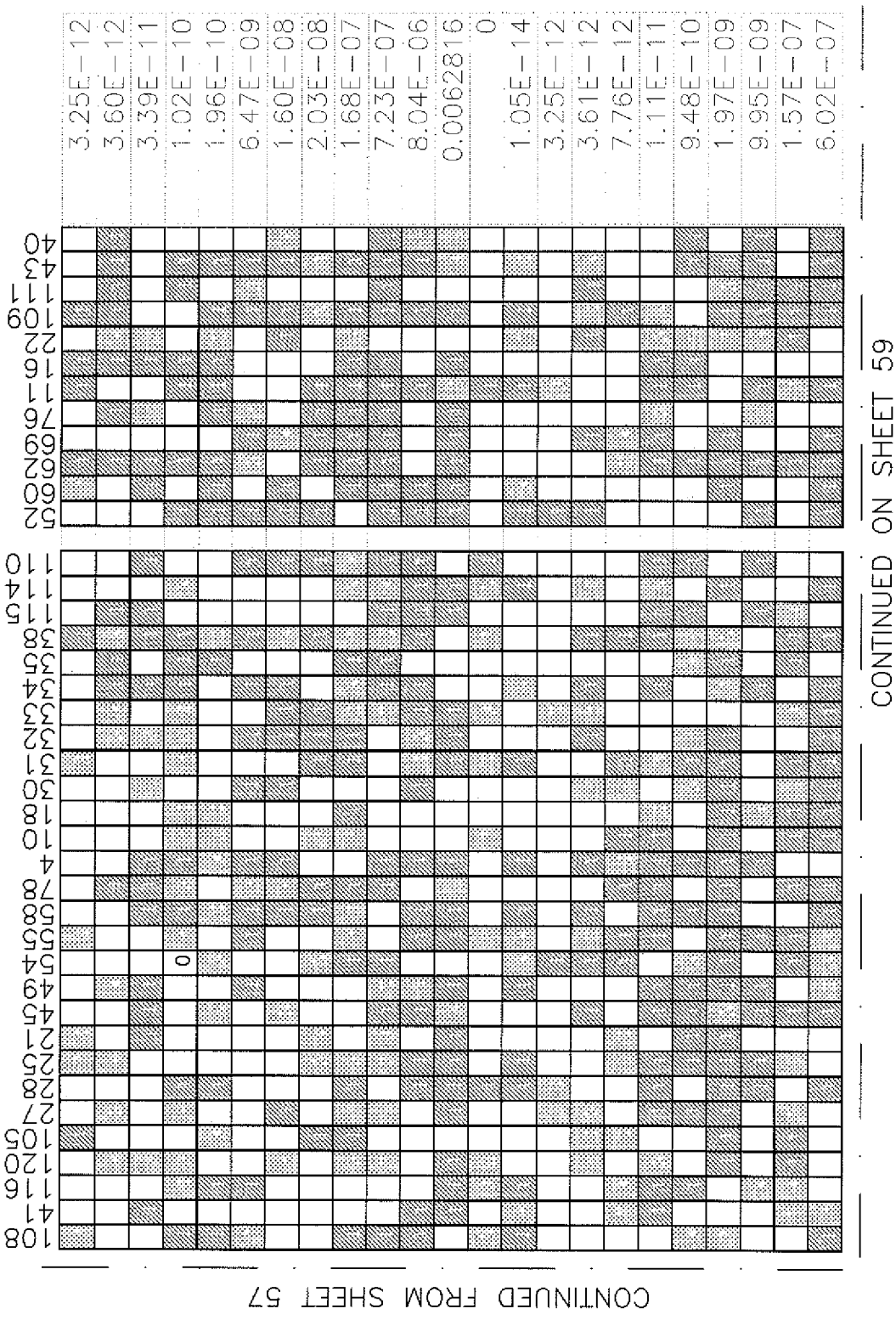

CONTINUED FROM SHEET 57
CONTINUED ON SHEET 59
3.25E-12
3.60E-12
3.39E-11
1.02E-10
1.96E-10
6.47E-09
1.60E-08
2.03E-08
1.68E-07
7.23E-07
8.04E-06
0.0062816
0
1.05E-14
3.25E-12
3.61E-12
7.76E-12
1.11E-11
9.48E-10
1.97E-09
9.95E-09
1.57E-07
6.02E-07

FIG. 24

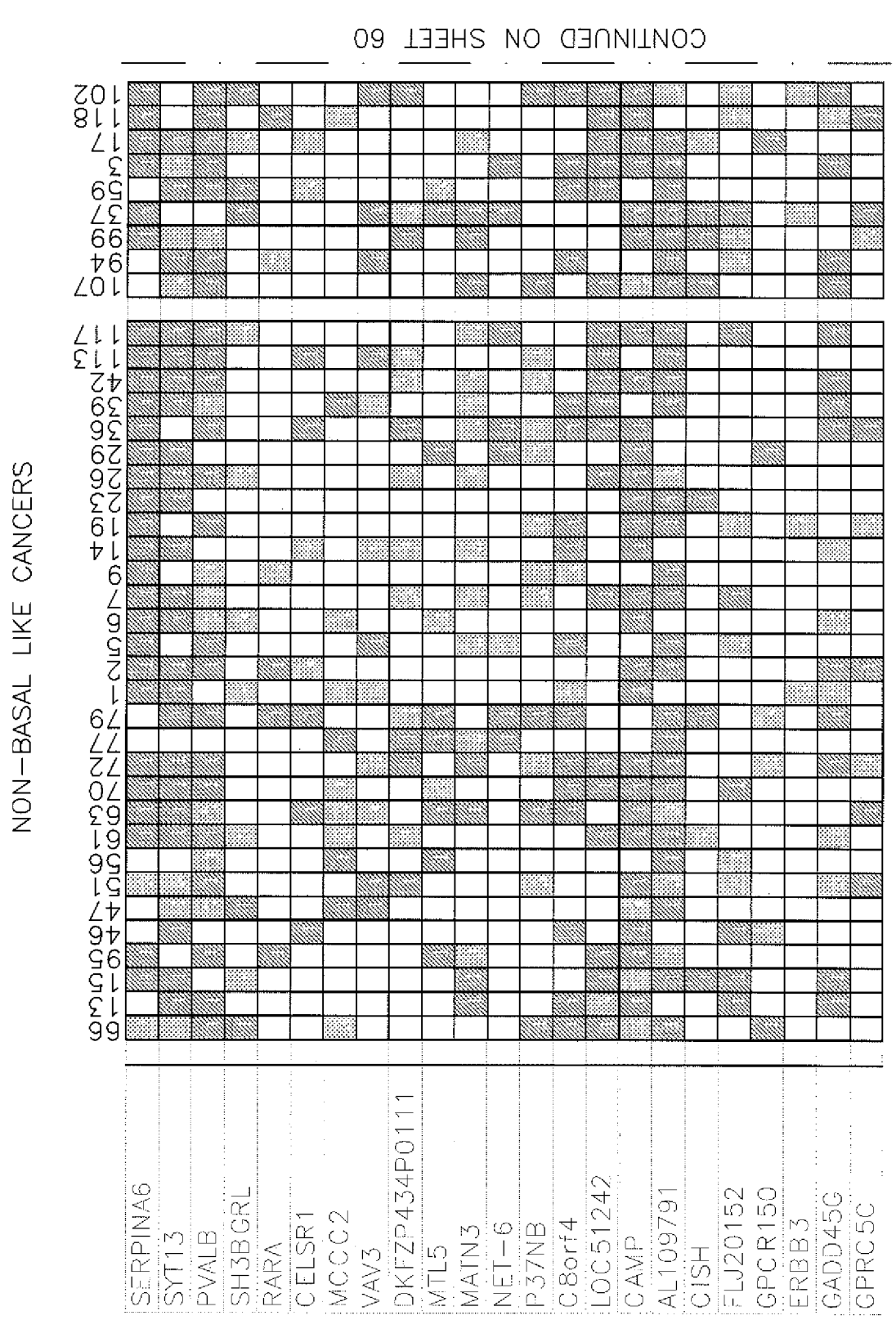

CONTINUED ON SHEET 60
NON-BASAL LIKE CANCERS
SERPINA6
SYT13
PVALB
SH3BGRL
RARA
CELSR1
MCCC2
VAV3
DKFZP434P0111
MTL5
MAIN3
NET-6
P37NB
C8orf4
LOC51242
CAMP
AL109791
CISH
FLJ20152
GPCR150
ERBB3
GADD45G
GPRC5C

FIG. 24

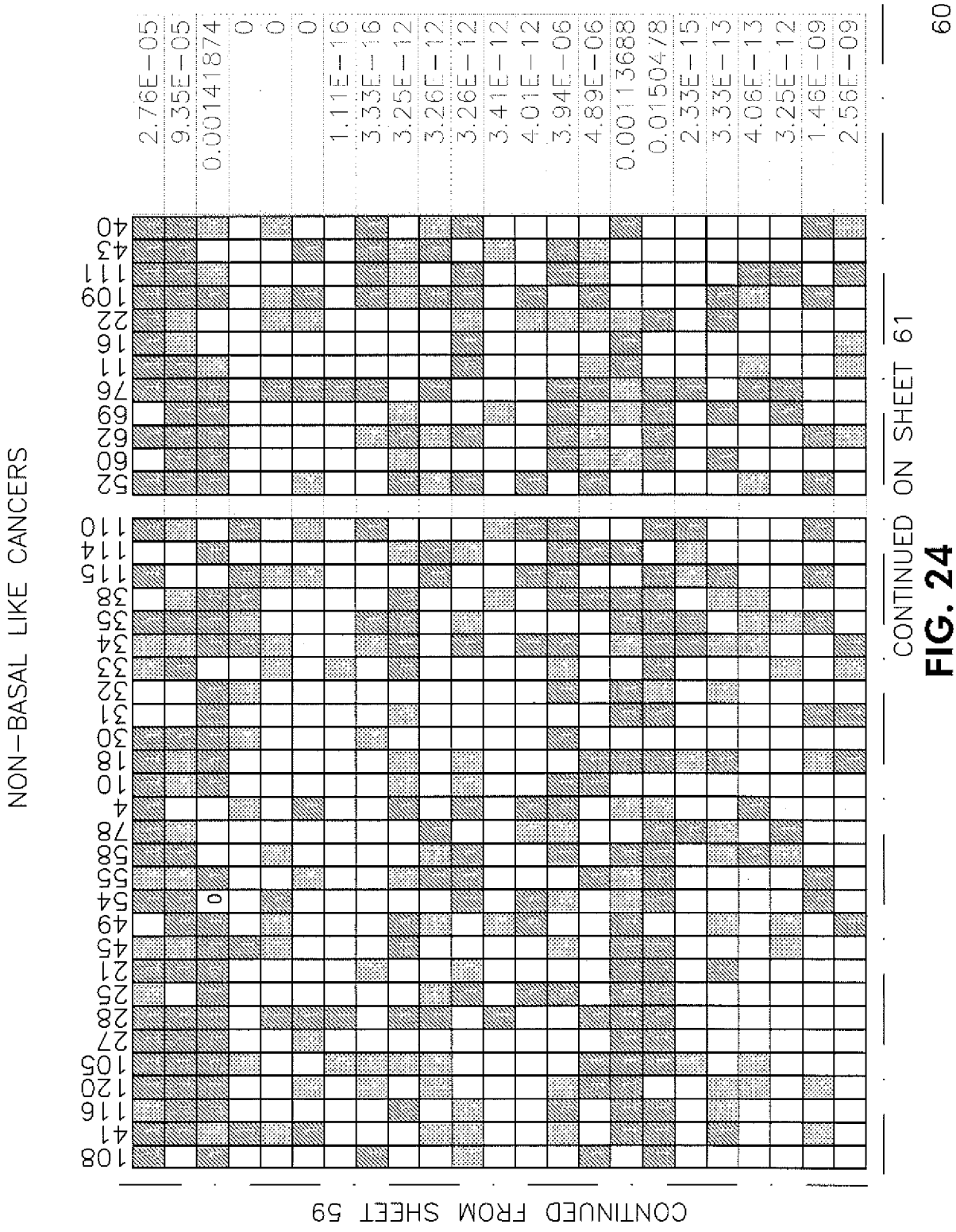

NON-BASAL LIKE CANCERS
CONTINUED FROM SHEET 59
CONTINUED ON SHEET 61
2.76E-05
9.35E-05
0.00141874
0
0
0
1.11E-16
3.33E-16
3.25E-12
3.26E-12
3.26E-12
3.41E-12
4.01E-12
3.94E-06
4.89E-06
0.00113688
0.0150478
2.33E-15
3.33E-13
4.06E-13
3.25E-12
1.46E-09
2.56E-09

FIG. 24

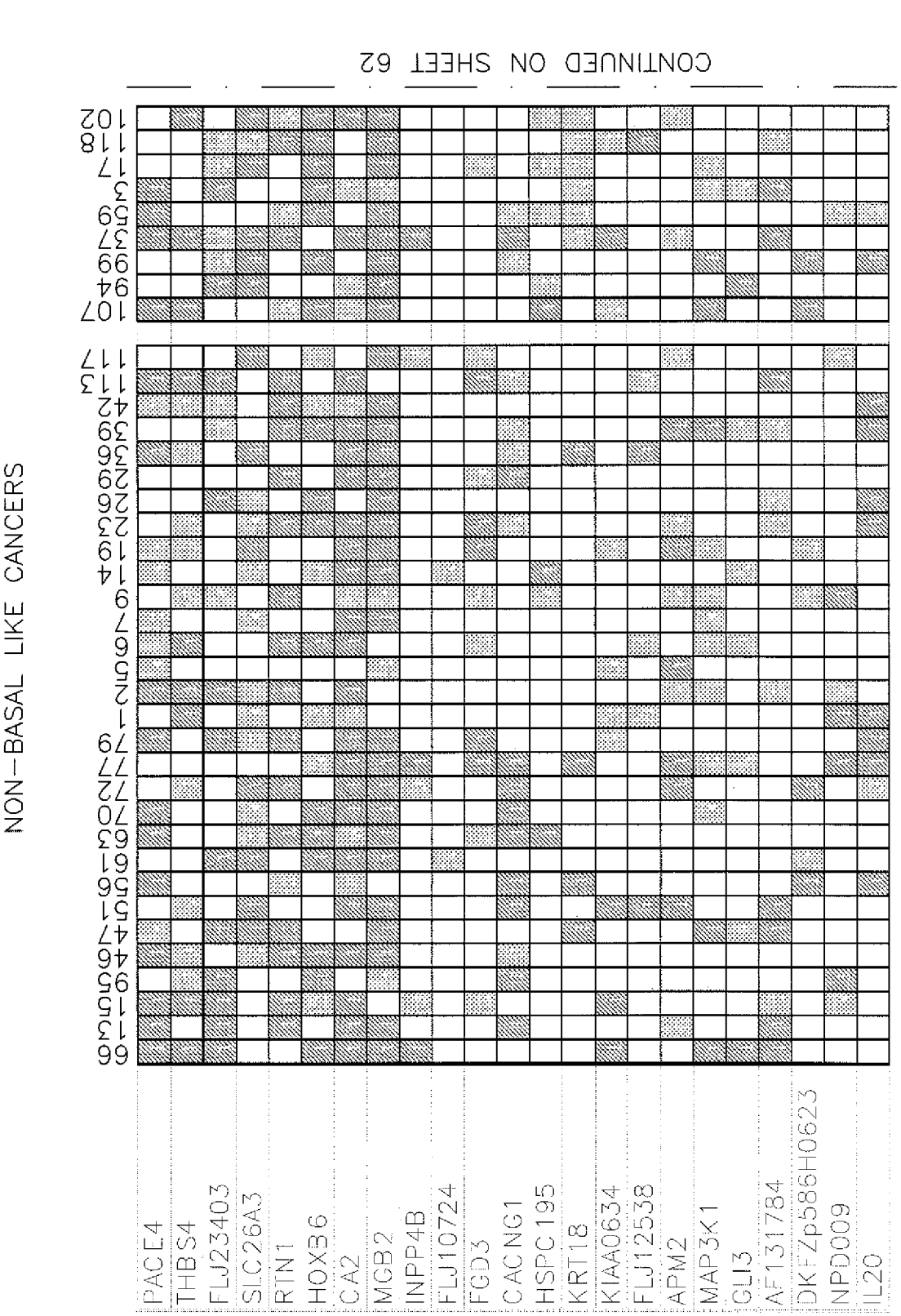

NON-BASAL LIKE CANCERS
CONTINUED ON SHEET 62
PACE4
THBS4
FLJ23403
SLC26A3
RTN1
HOXB6
CA2
MGB2
INPP4B
FLJ10724
FGD3
CACNG1
HSPC195
KRT18
KIAA0634
FLJ12538
APM2
MAP3K1
GLI3
AF131784
DKFZp586H0623
NPD009
IL20

FIG. 24

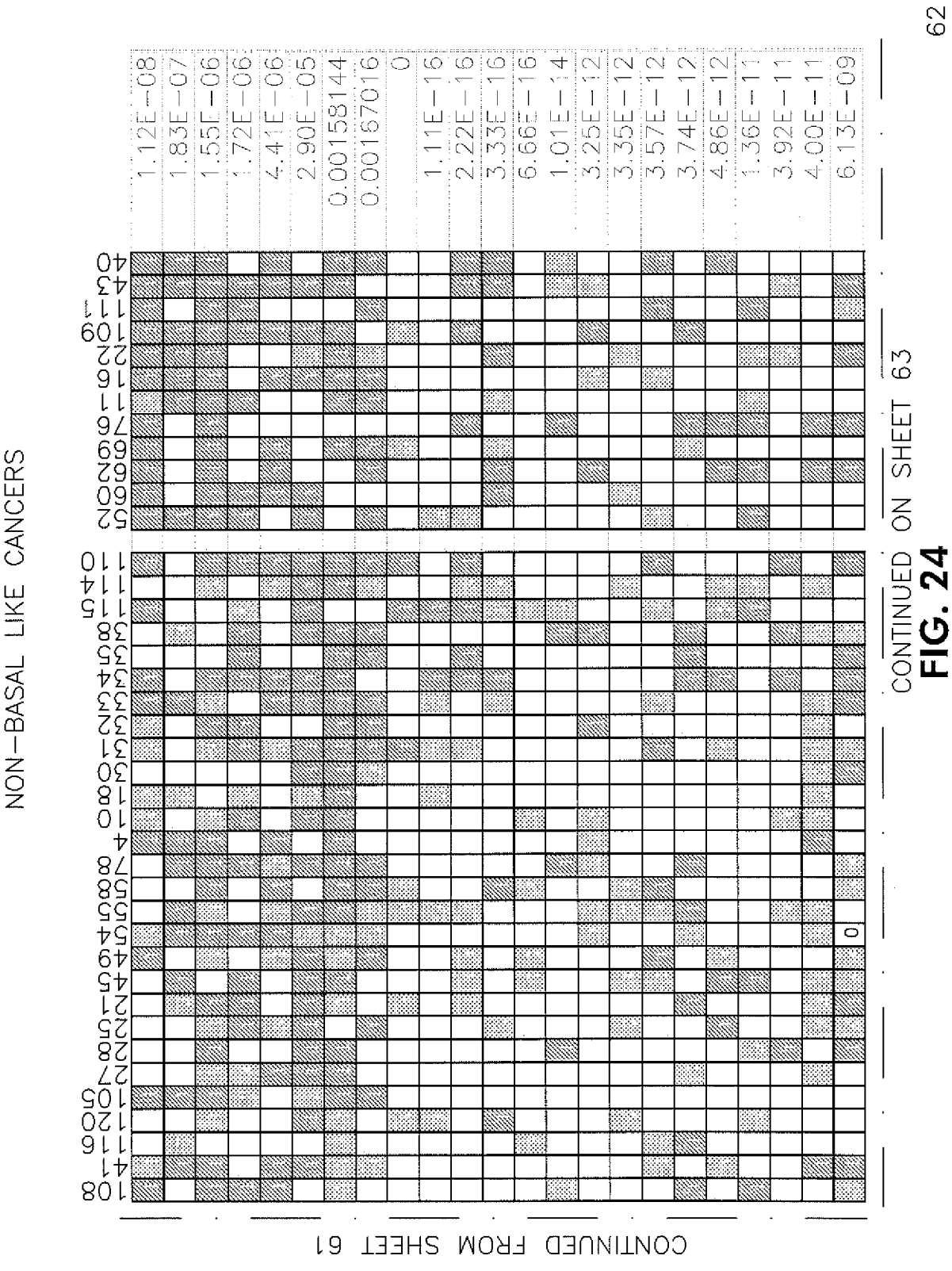

NON-BASAL LIKE CANCERS
CONTINUED FROM SHEET 61
CONTINUED ON SHEET 63
62
1.12E-08
1.83E-07
1.55E-06
1.72E-06
4.41E-06
2.90E-05
0.00158144
0.00167016
0
1.11E-16
2.22E-16
3.33E-16
6.66E-16
1.01E-14
3.25E-12
3.35E-12
3.57E-12
3.74E-12
4.86E-12
1.36E-11
3.92E-11
4.00E-11
6.13E-09

FIG. 24

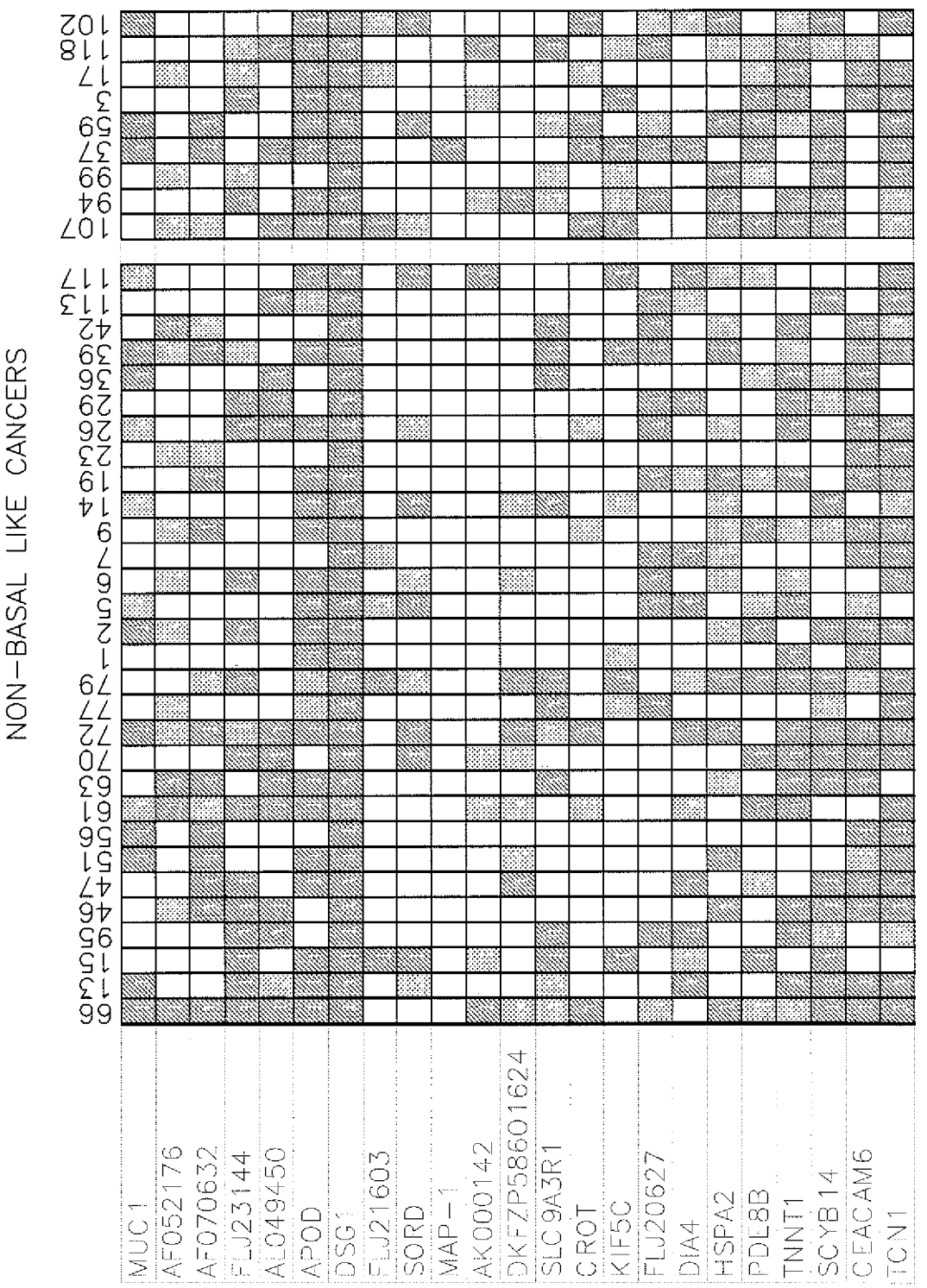

NON-BASAL LIKE CANCERS
MUC1
AF052176
AF070632
FLJ23144
AL049450
APOD
DSG1
FLJ21603
SORD
MAP-1
AK000142
DKFZP586O1624
SLC9A3R1
CROT
KIF5C
FLJ20627
DIA4
HSPA2
PDL8B
TNNT1
SCYB14
CEACAM6
TCN1
CONTINUED ON SHEET 64

FIG. 24

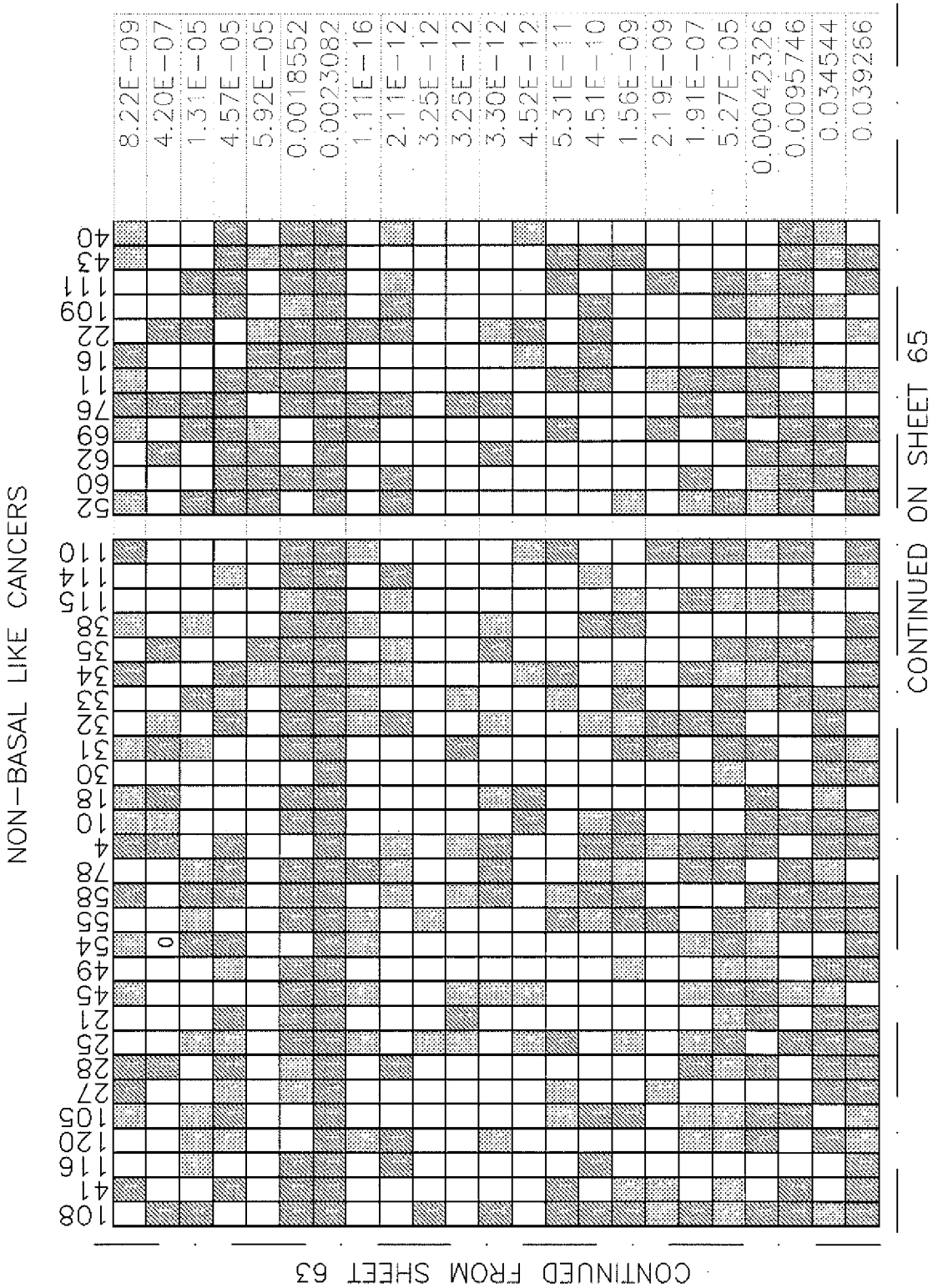

CONTINUED FROM SHEET 63
NON-BASAL LIKE CANCERS
108 41 116 120 105 27 228 225 215 245 49 54 55 58 78 4 10 18 30 31 32 33 34 35 38 115 114 110
52 60 62 69 76 11 16 22 109 111 43 40
8.22E-09
4.20E-07
1.31E-05
4.57E-05
5.92E-05
0.0018552
0.0023082
1.11E-16
2.11E-12
3.25E-12
3.25E-12
3.30E-12
4.52E-12
5.31E-11
4.51E-10
1.56E-09
2.19E-09
1.91E-07
5.27E-05
0.00042326
0.00095746
0.034544
0.039266
CONTINUED ON SHEET 65

FIG. 24

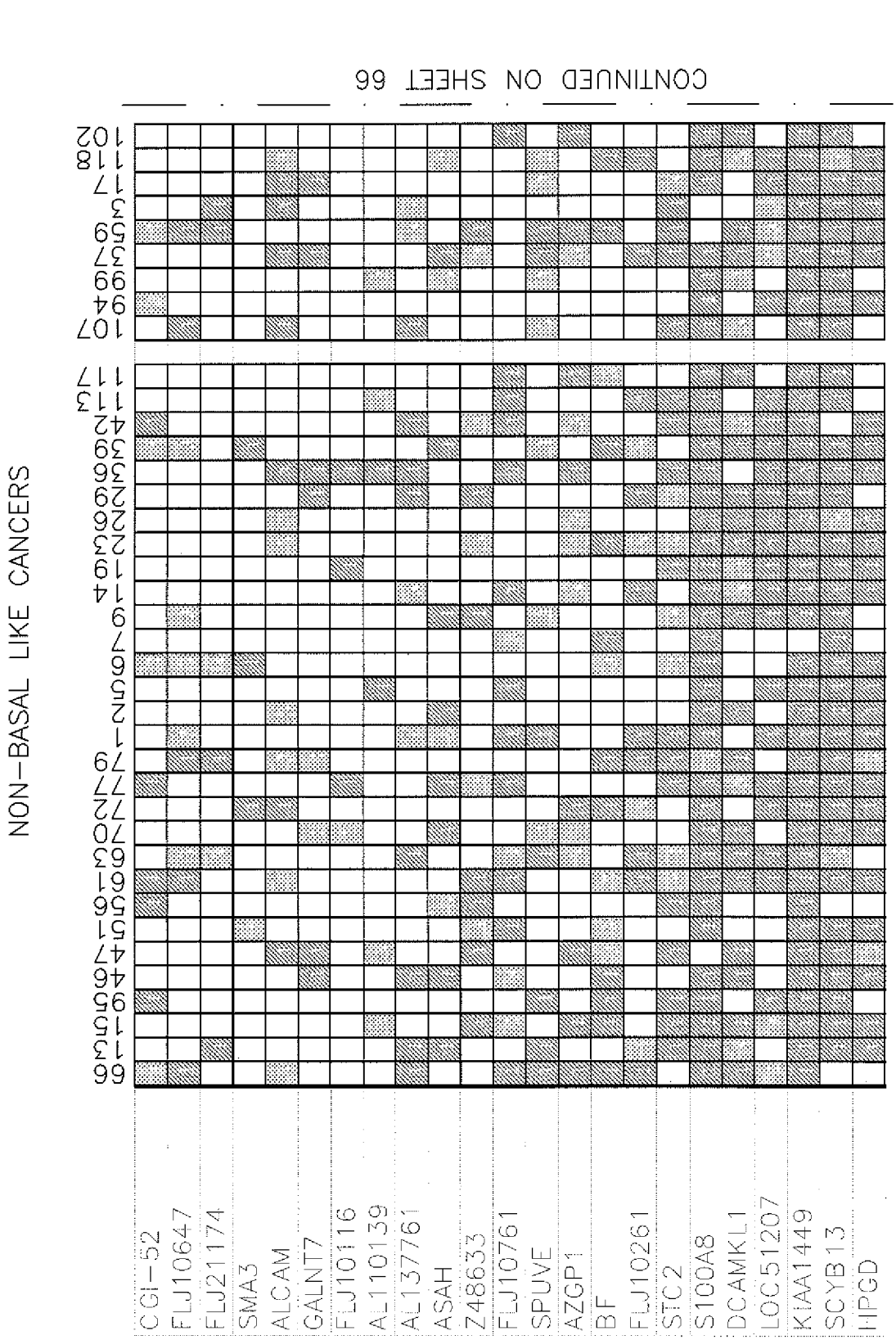

NON-BASAL LIKE CANCERS
CGI-52
FLJ10647
FLJ21174
SMA3
ALCAM
GALNT7
FLJ10116
AL110139
AL137761
ASAH
Z48633
FLJ10761
SPUVE
AZGP1
BF
FLJ10261
STC2
S100A8
DCAMKL1
LOC51207
KIAA1449
SCYB13
HPGD
66 13 15 95 46 47 51 56 61 63 70 72 77 79 1 2 5 6 7 9 14 19 23 26 29 36 39 42 11 3 17
107 94 99 57 59 3 17 18 102
CONTINUED ON SHEET 66

FIG. 24

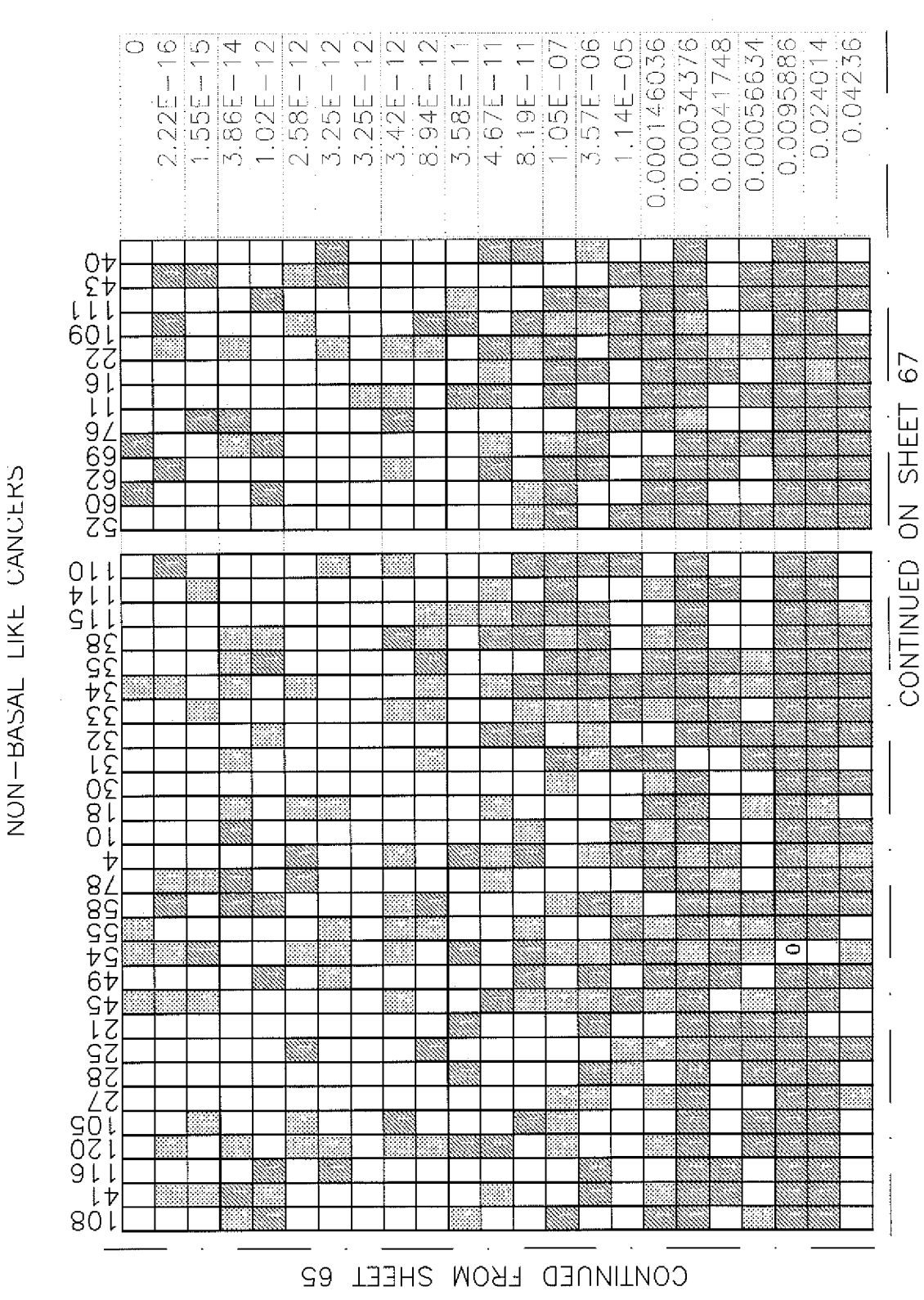

NON-BASAL LIKE CANCERS
CONTINUED FROM SHEET 65
CONTINUED ON SHEET 67
0
2.22E-16
1.55E-15
3.86E-14
1.02E-12
2.58E-12
3.25E-12
3.25E-12
3.42E-12
8.94E-12
3.58E-11
4.67E-11
8.19E-11
1.05E-07
3.57E-06
1.14E-05
0.000146036
0.000034376
0.000041748
0.000056634
0.0095886
0.024014
0.04236

FIG. 24

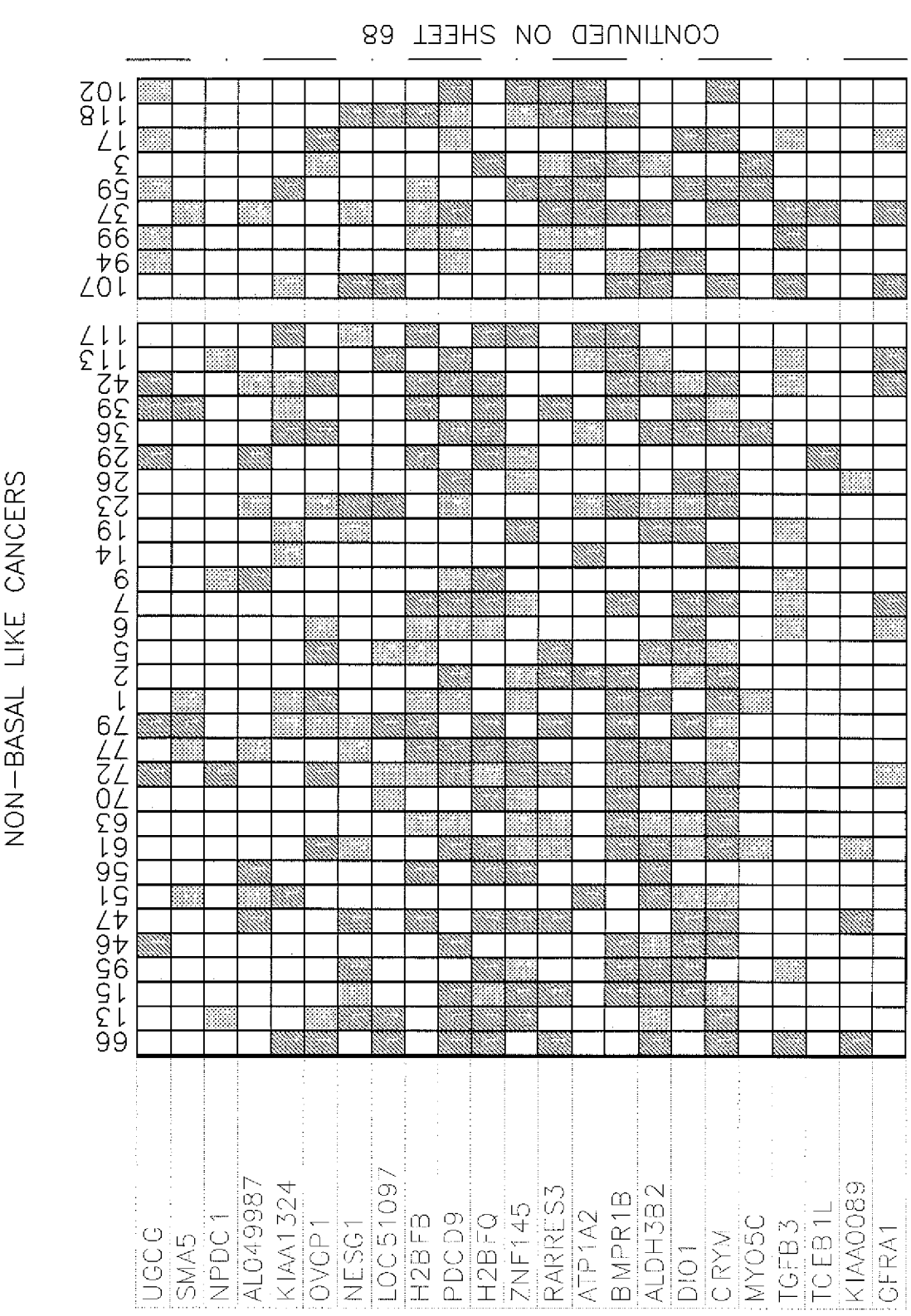

NON-BASAL LIKE CANCERS
UGCG
SMA5
NPDC1
AL049987
KIAA1324
OVCP1
NESG1
LOC51097
H2BFB
PDCD9
H2BFQ
ZNF145
RARRES3
ATP1A2
BMPR1B
ALDH3B2
DIO1
CRYM
MYO5C
TGFB3
TCEB1L
KIAA0089
CFRA1
CONTINUED ON SHEET 68

FIG. 24

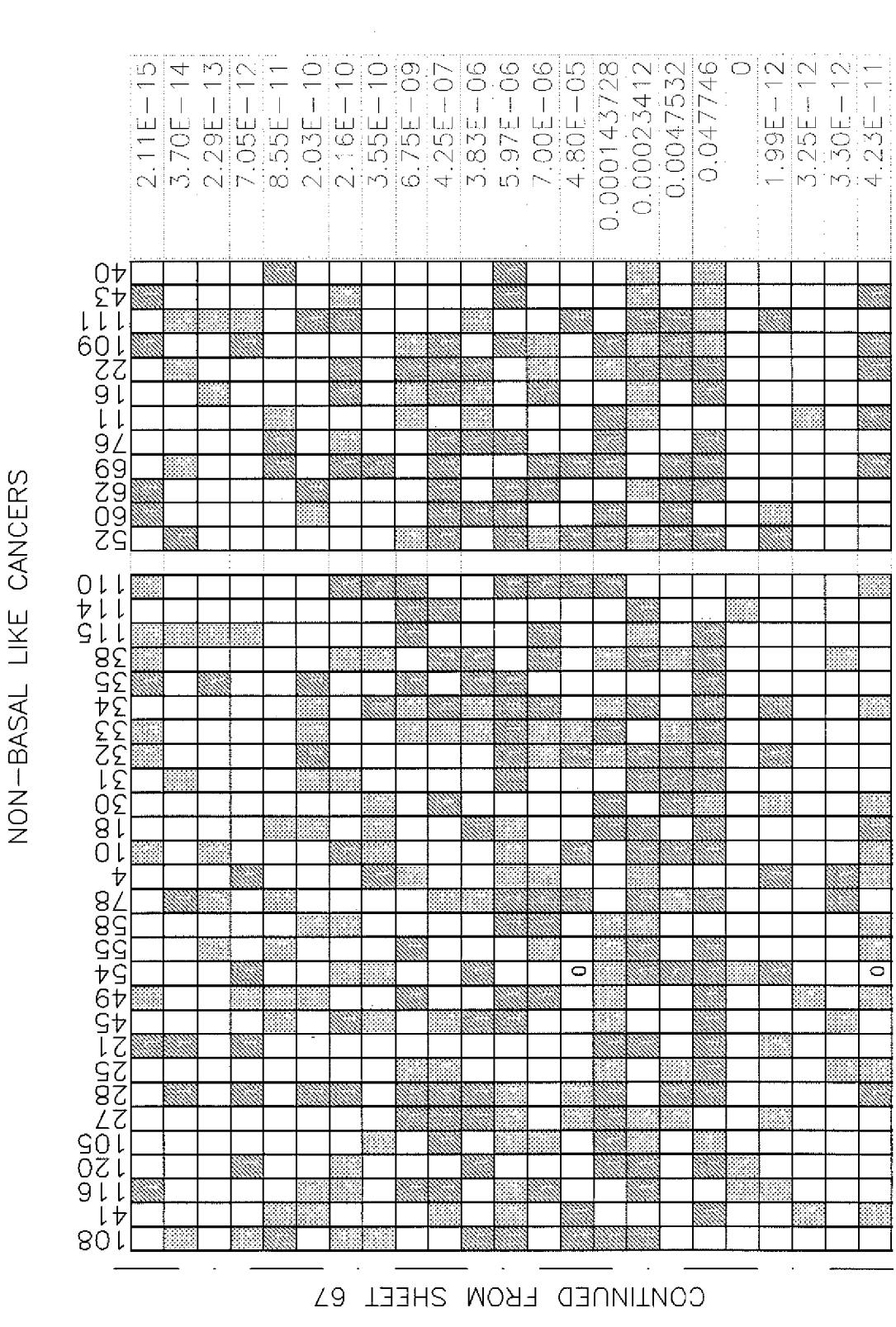

NON-BASAL LIKE CANCERS
CONTINUED FROM SHEET 67
CONTINUED ON SHEET 69
2.11E-15
3.70E-14
2.29E-13
7.05E-12
8.55E-11
2.03E-10
2.16E-10
3.55E-10
6.75E-09
4.25E-07
3.83E-06
5.97E-06
7.00E-06
4.80E-05
0.000143728
0.00023412
0.0047532
0.047746
0
1.99E-12
3.25E-12
3.30E-12
4.23E-11

FIG. 24

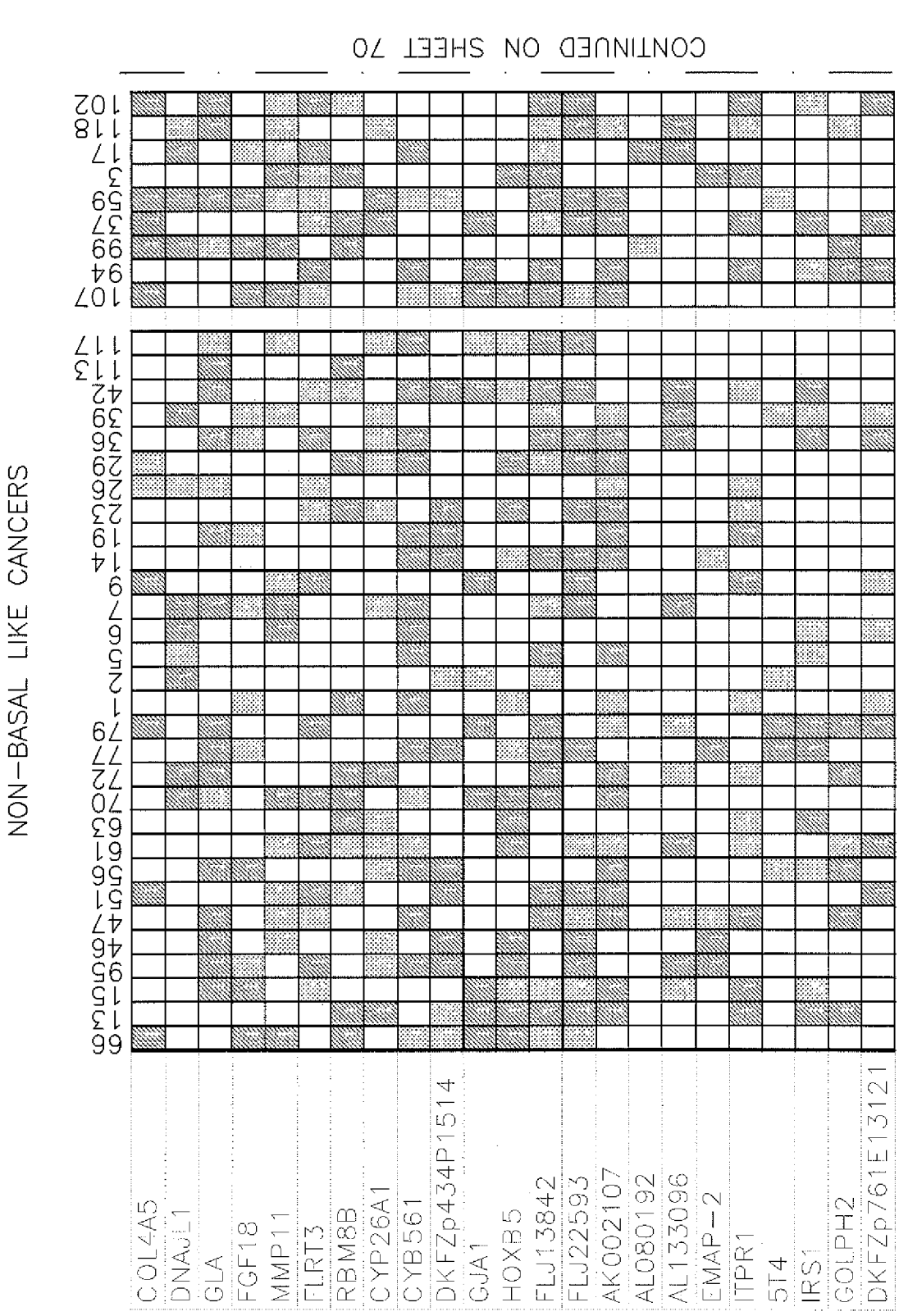

CONTINUED ON SHEET 70
NON-BASAL LIKE CANCERS
COL4A5
DNAJL1
GLA
FGF18
MMP11
FLRT3
RBM8B
CYP26A1
CYB561
DKFZp434P1514
GJA1
HOXB5
FLJ13842
FLJ22593
AK002107
AL080192
AL133096
EMAP-2
ITPR1
5T4
IRS1
GOLPH2
DKFZp761E13121

FIG. 24

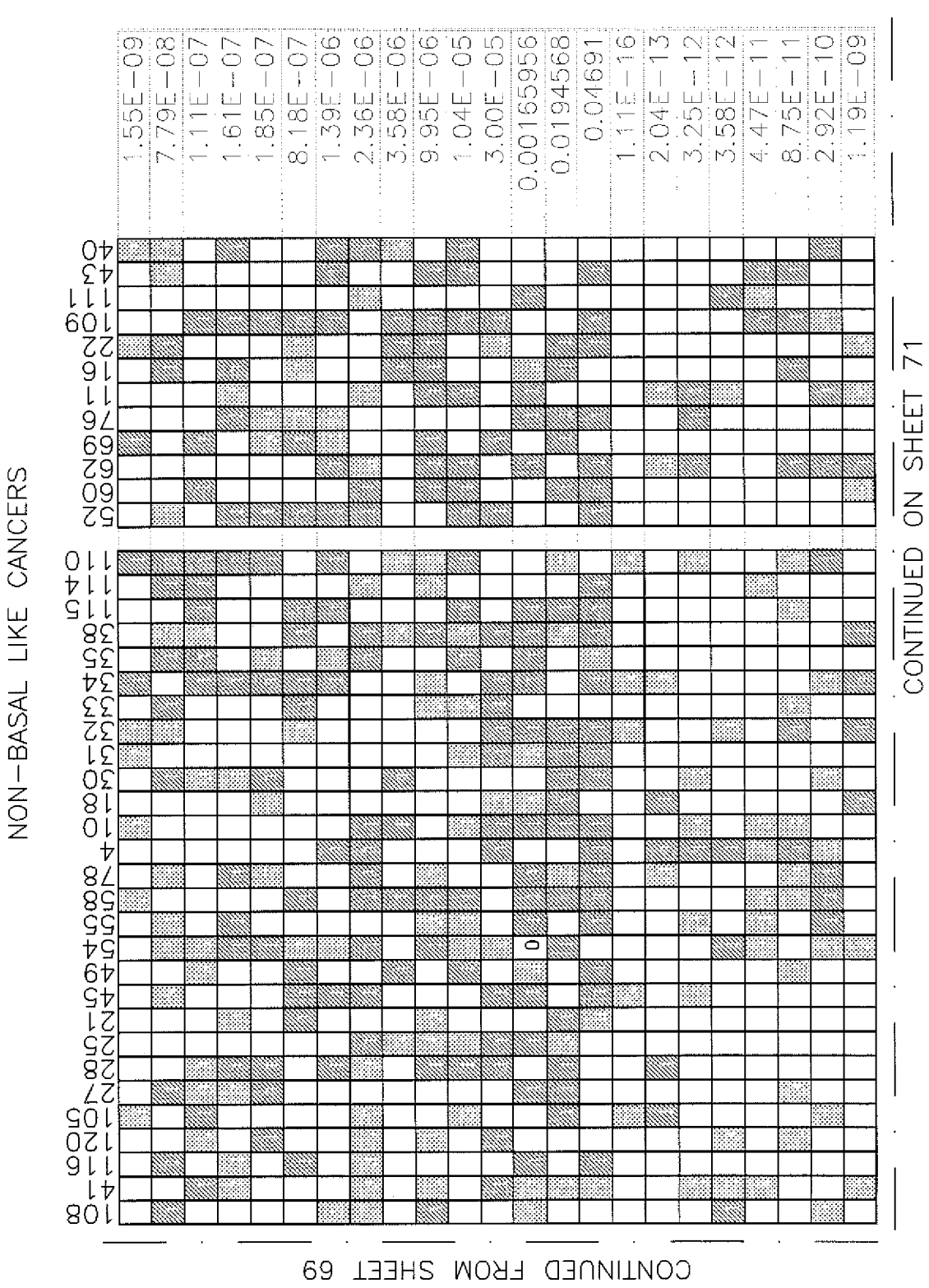

CONTINUED FROM SHEET 69
NON-BASAL LIKE CANCERS
1.55E-09
7.79E-08
1.11E-07
1.61E-07
1.85E-07
8.18E-07
1.39E-06
2.36E-06
3.58E-06
9.95E-06
1.04E-05
3.00E-05
0.00165956
0.0194568
0.04691
1.11E-16
2.04E-13
3.25E-12
3.58E-12
4.47E-11
8.75E-11
2.92E-10
1.19E-09
CONTINUED ON SHEET 71

FIG. 24

70

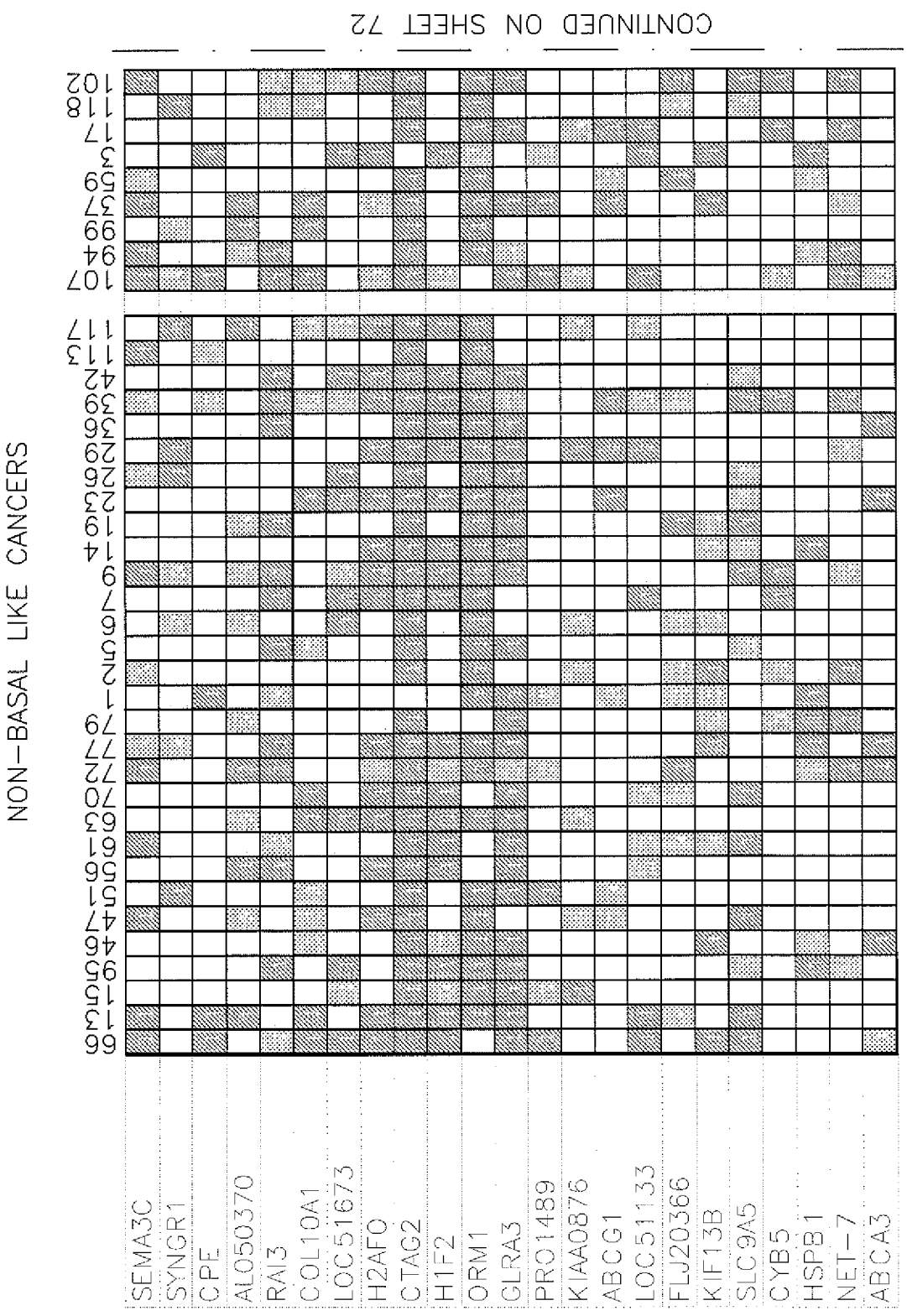
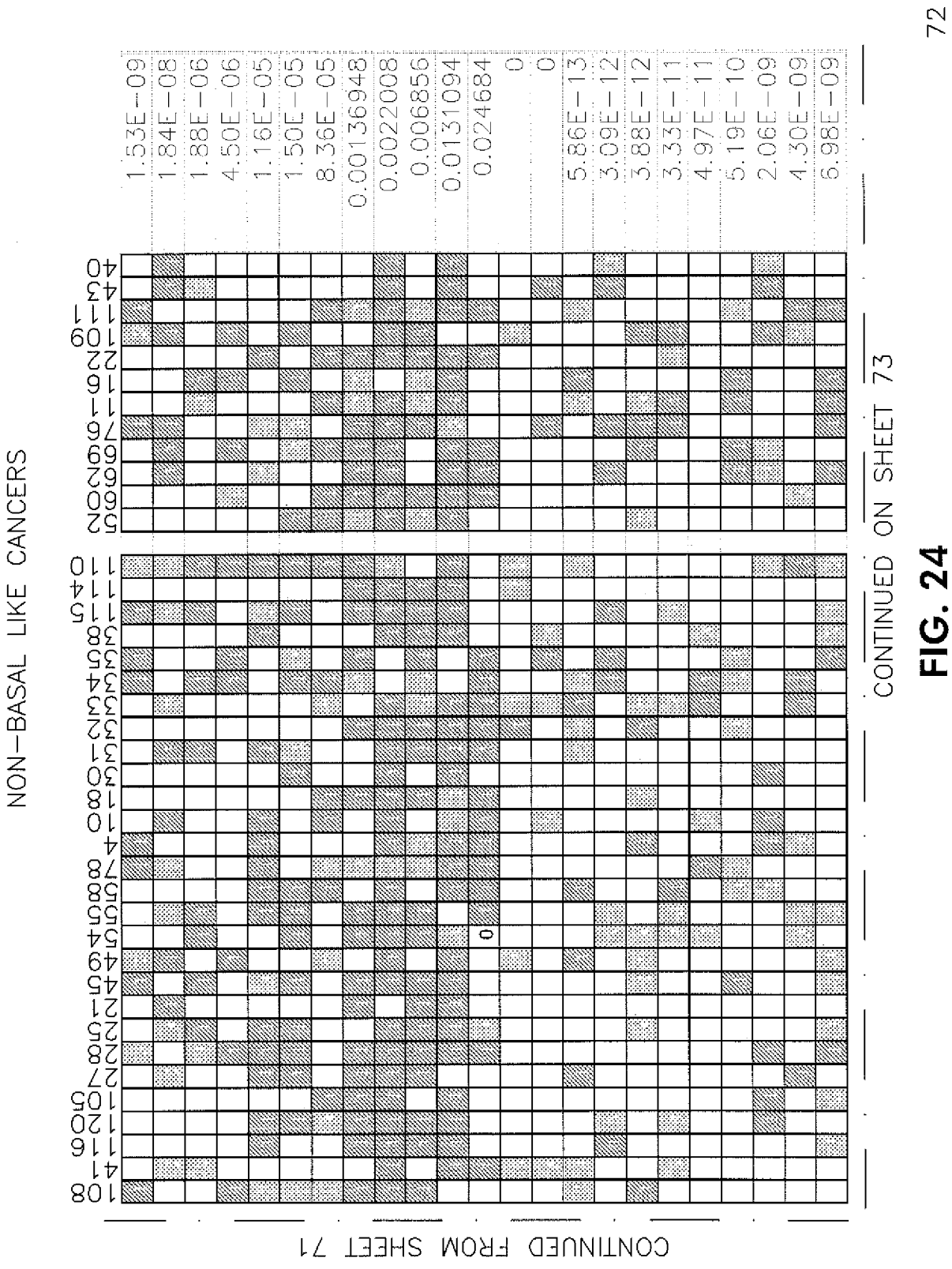

CONTINUED ON SHEET 72
NON-BASAL LIKE CANCERS
SEMA3C
SYNGR1
CPE
AL050370
RAI3
COL10A1
LOC51673
H2AFO
CTAG2
H1F2
ORM1
GLRA3
PRO1489
KIAA0876
ABCG1
LOC51133
FLJ20366
KIF13B
SLC9A5
CYB5
HSPB1
NET-7
ABCA3

FIG. 24


CONTINUED FROM SHEET 71
NON-BASAL LIKE CANCERS
1.53E-09
1.84E-08
1.88E-06
4.50E-06
1.16E-05
1.50E-05
8.36E-05
0.00136948
0.0022008
0.006856
0.0131094
0.024684
0
0
5.86E-13
3.09E-12
3.88E-12
3.33E-11
4.97E-11
5.19E-10
2.06E-09
4.30E-09
6.98E-09
CONTINUED ON SHEET 73

72

FIG. 24

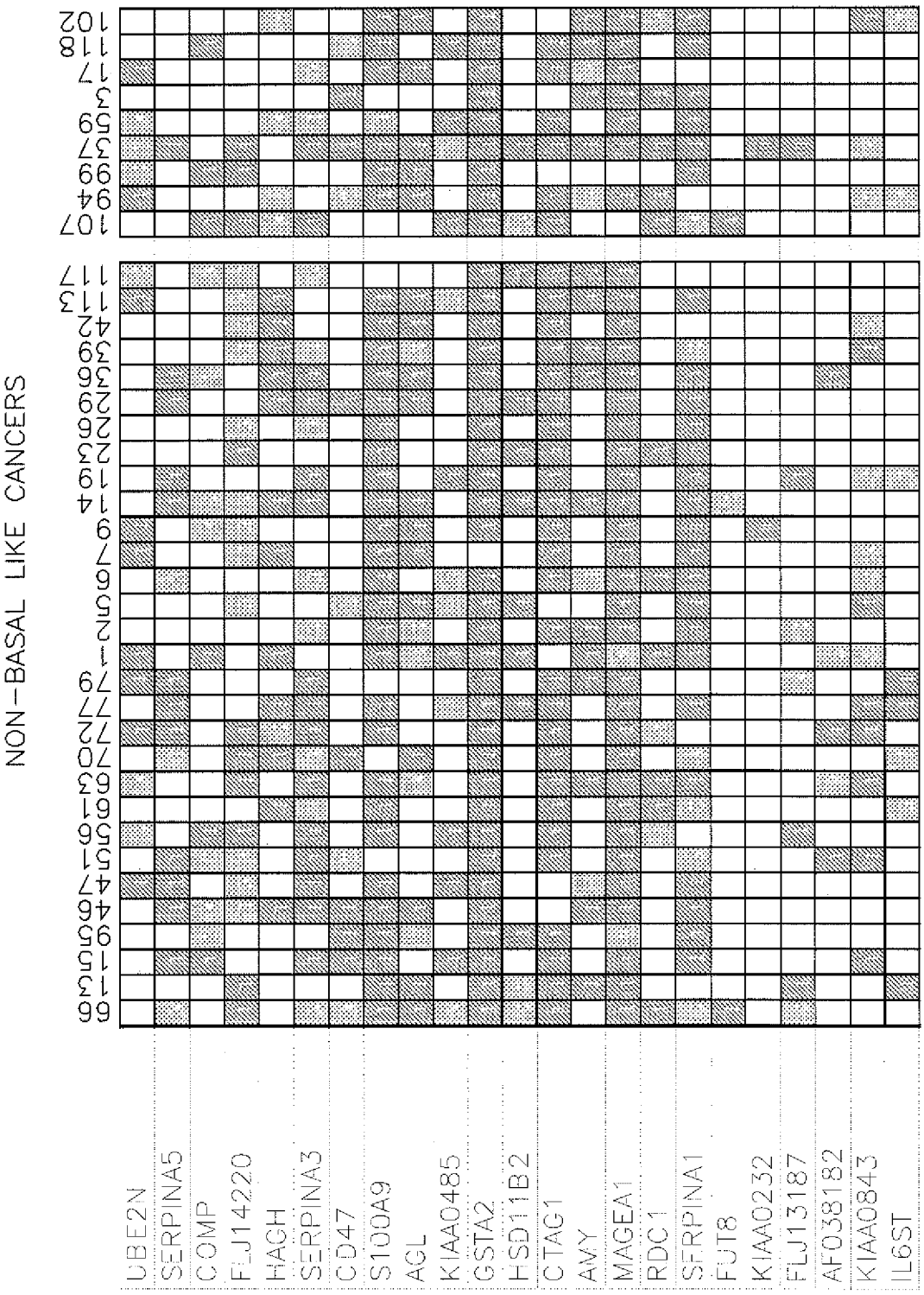

NON-BASAL LIKE CANCERS
CONTINUED ON SHEET 74
UBE2N
SERPINA5
COMP
FLJ14220
HAGH
SERPINA3
CD47
S100A9
AGL
KIAA0485
GSTA2
HSD11B2
CTAG1
AVY
MAGEA1
RDC1
SFRPINA1
FJT8
KIAA0232
FLJ13187
AF038182
KIAA0843
IL6ST

FIG. 24

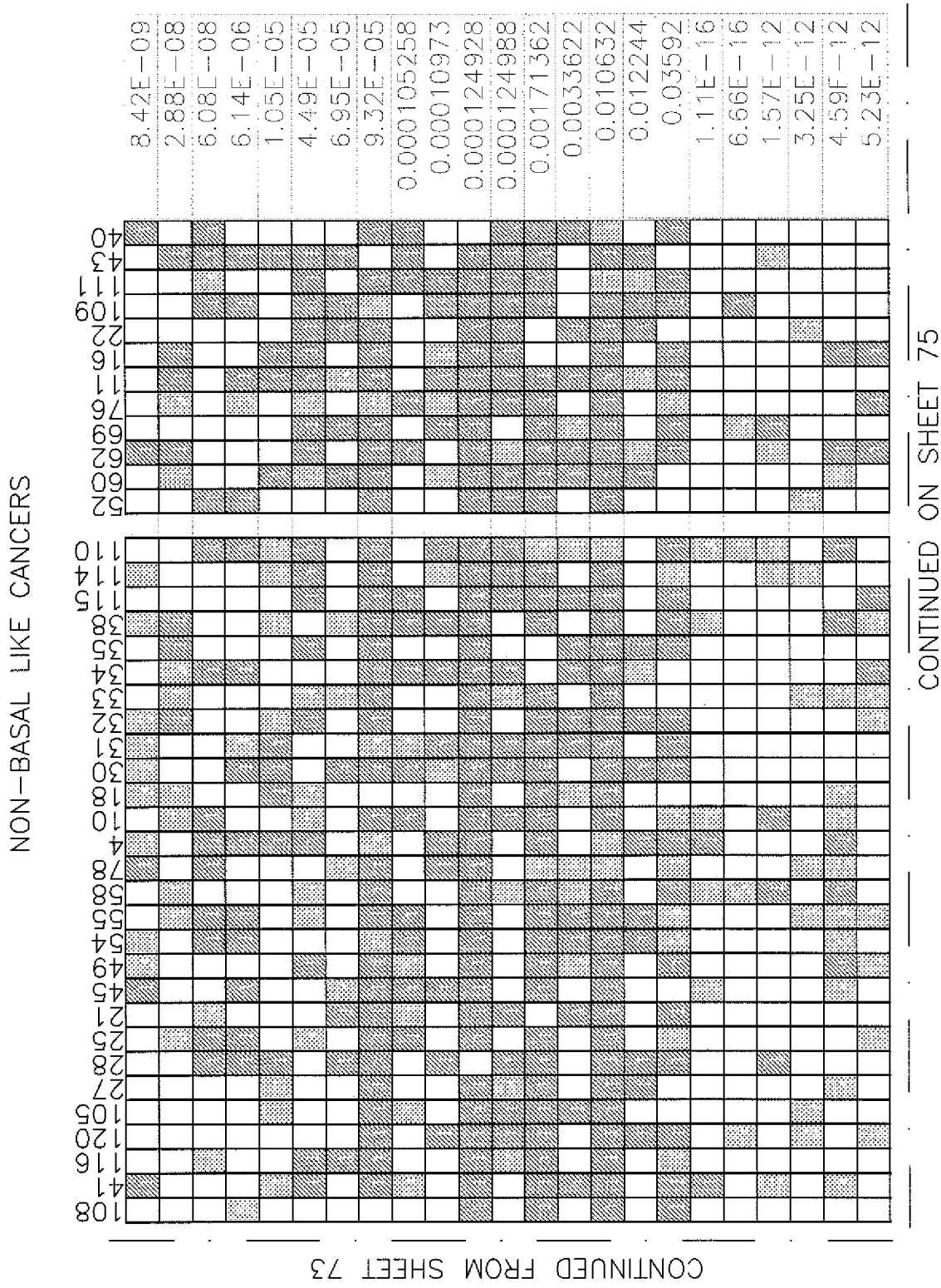

CONTINUED FROM SHEET 73
NON-BASAL LIKE CANCERS
CONTINUED ON SHEET 75
8.42E-09
2.88E-08
6.08E-08
6.14E-06
1.05E-05
4.49E-05
6.95E-05
9.32E-05
0.000105258
0.00010973
0.000124928
0.000124988
0.00171362
0.0033622
0.010632
0.012244
0.03592
1.11E-16
6.66E-16
1.57E-12
3.25E-12
4.59E-12
5.23E-12

FIG. 24

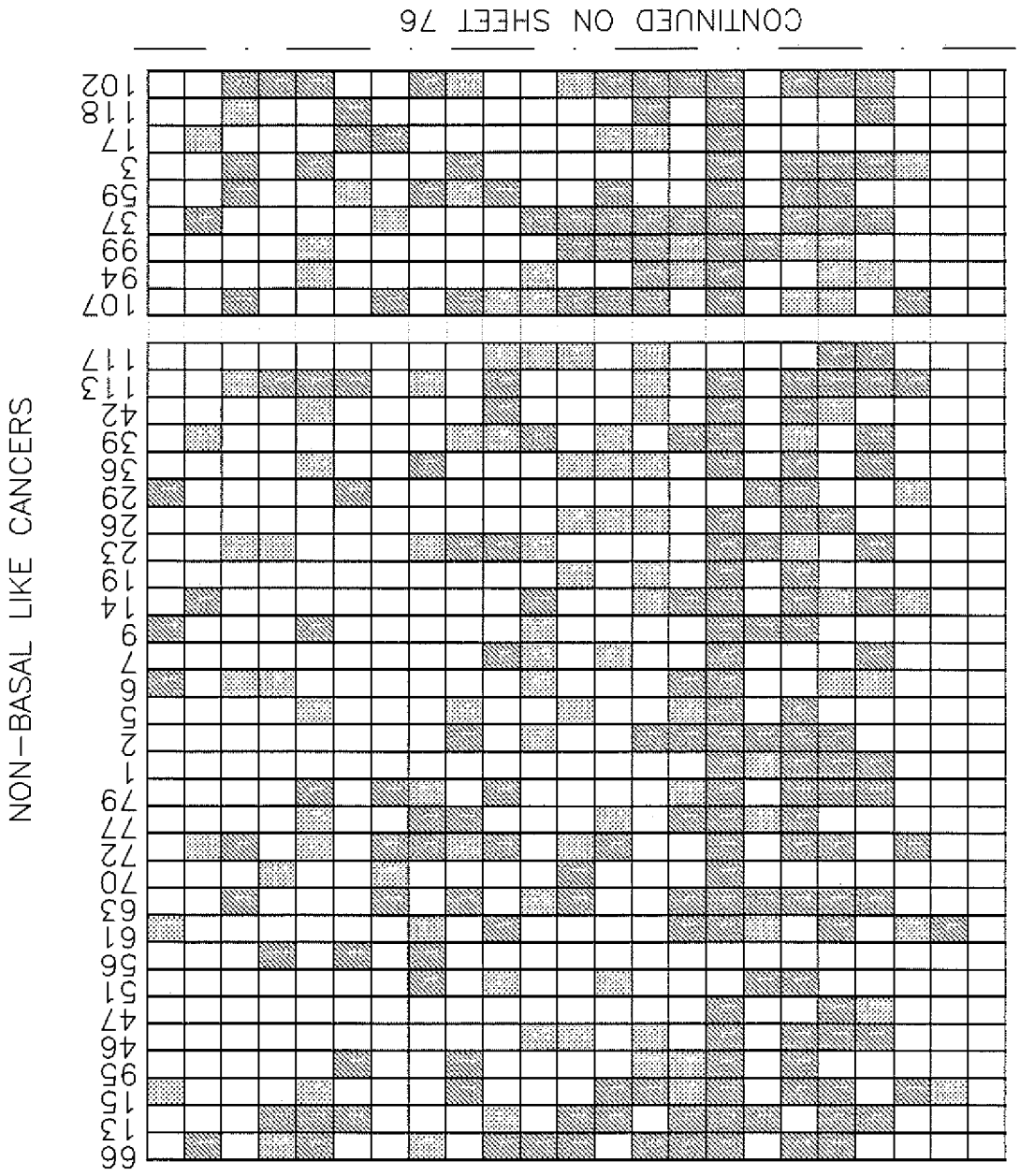


FIG. 24

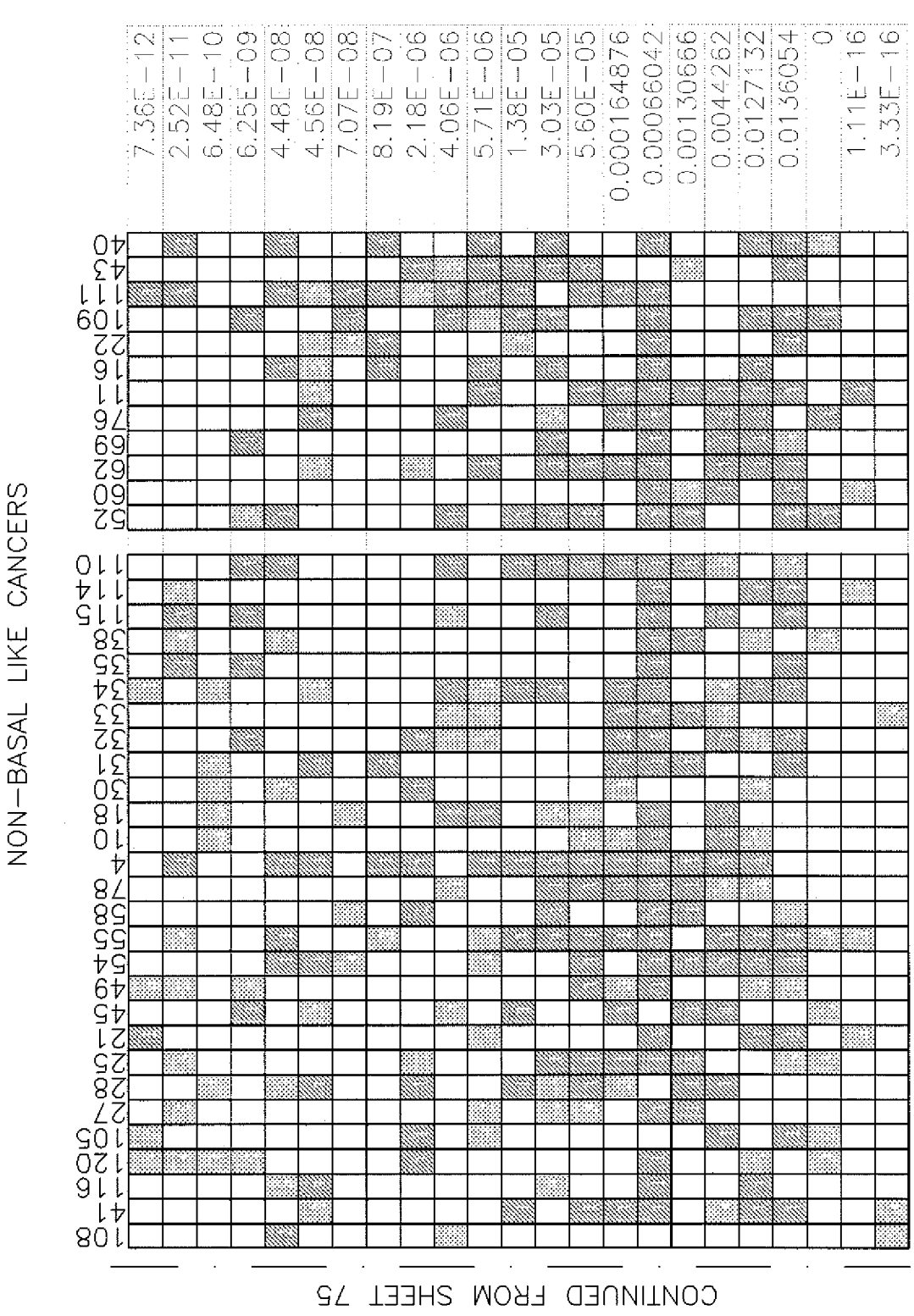

CONTINUED FROM SHEET 75
NON-BASAL LIKE CANCERS
CONTINUED ON SHEET 77

FIG. 24

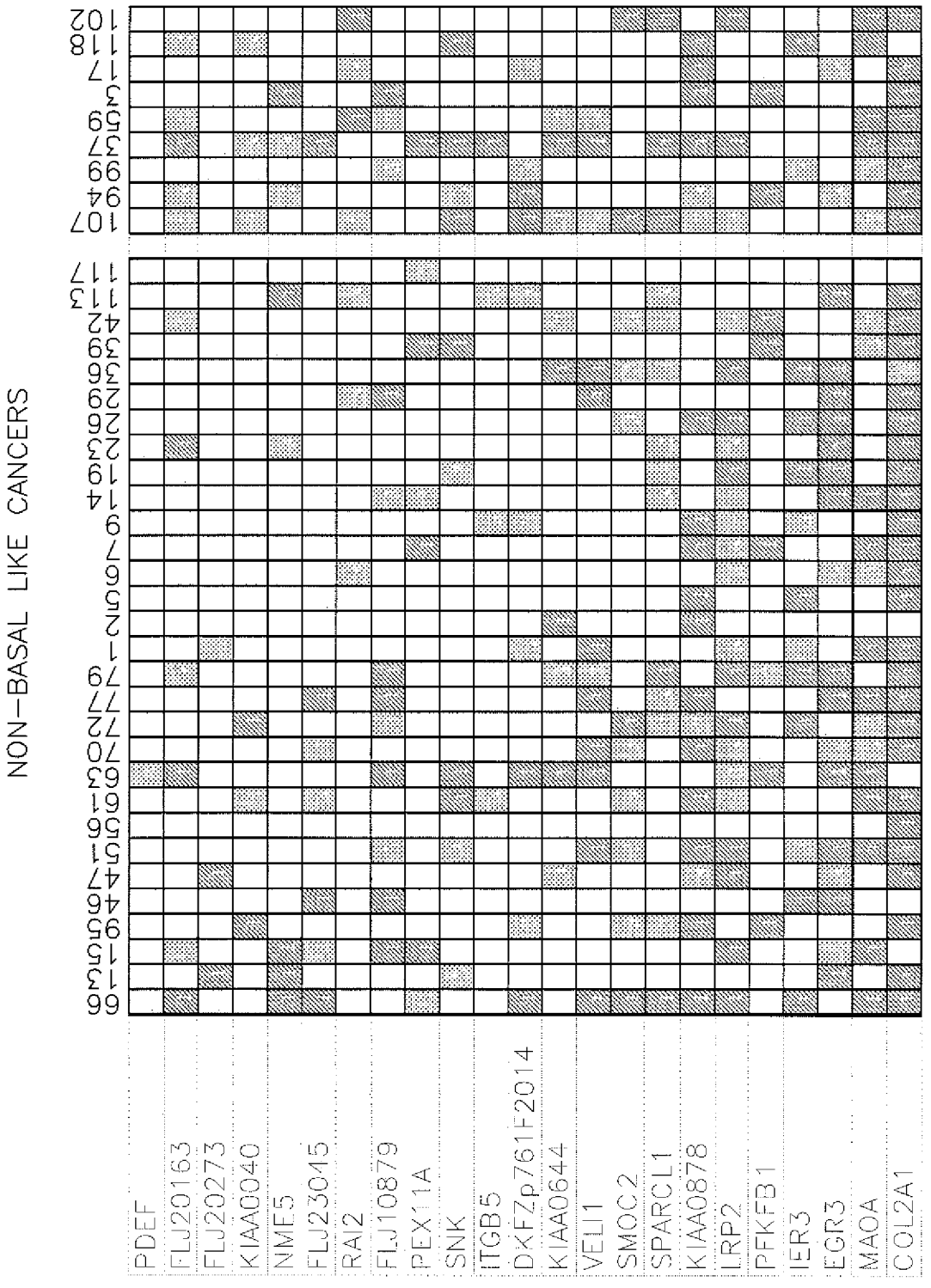

CONTINUED ON SHEET 78
NON-BASAL LIKE CANCERS
PDEF
FLJ20163
FLJ20273
KIAA0040
NME5
FLJ23045
RAI2
FLJ10879
PEX11A
SNK
ITGB5
DKFZp761F2014
KIAA0644
VEL11
SMOC2
SPARCL1
KIAA0878
LRP2
PFKFB1
IER3
EGR3
MAOA
COL2A1

FIG. 24

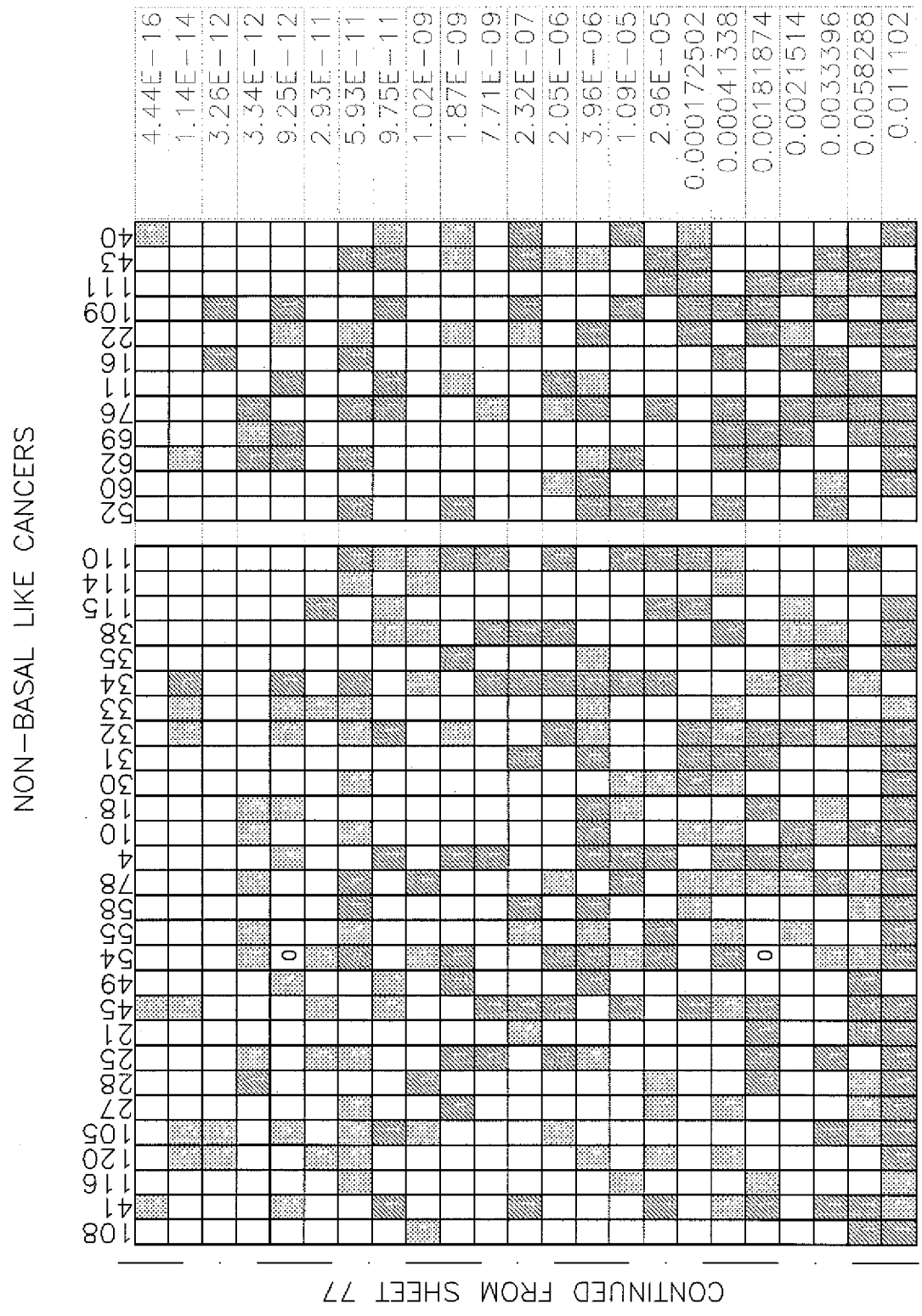

CONTINUED FROM SHEET 77
NON-BASAL LIKE CANCERS
4.44E-16
1.14E-14
3.26E-12
3.34E-12
9.25E-12
2.93E-11
5.93E-11
9.75E-11
1.02E-09
1.87E-09
7.71E-09
2.32E-07
2.05E-06
3.96E-06
1.09E-05
2.96E-05
0.000172502
0.000041338
0.00181874
0.00021514
0.00033396
0.00058288
0.011102
CONTINUED ON SHEET 79

FIG. 24

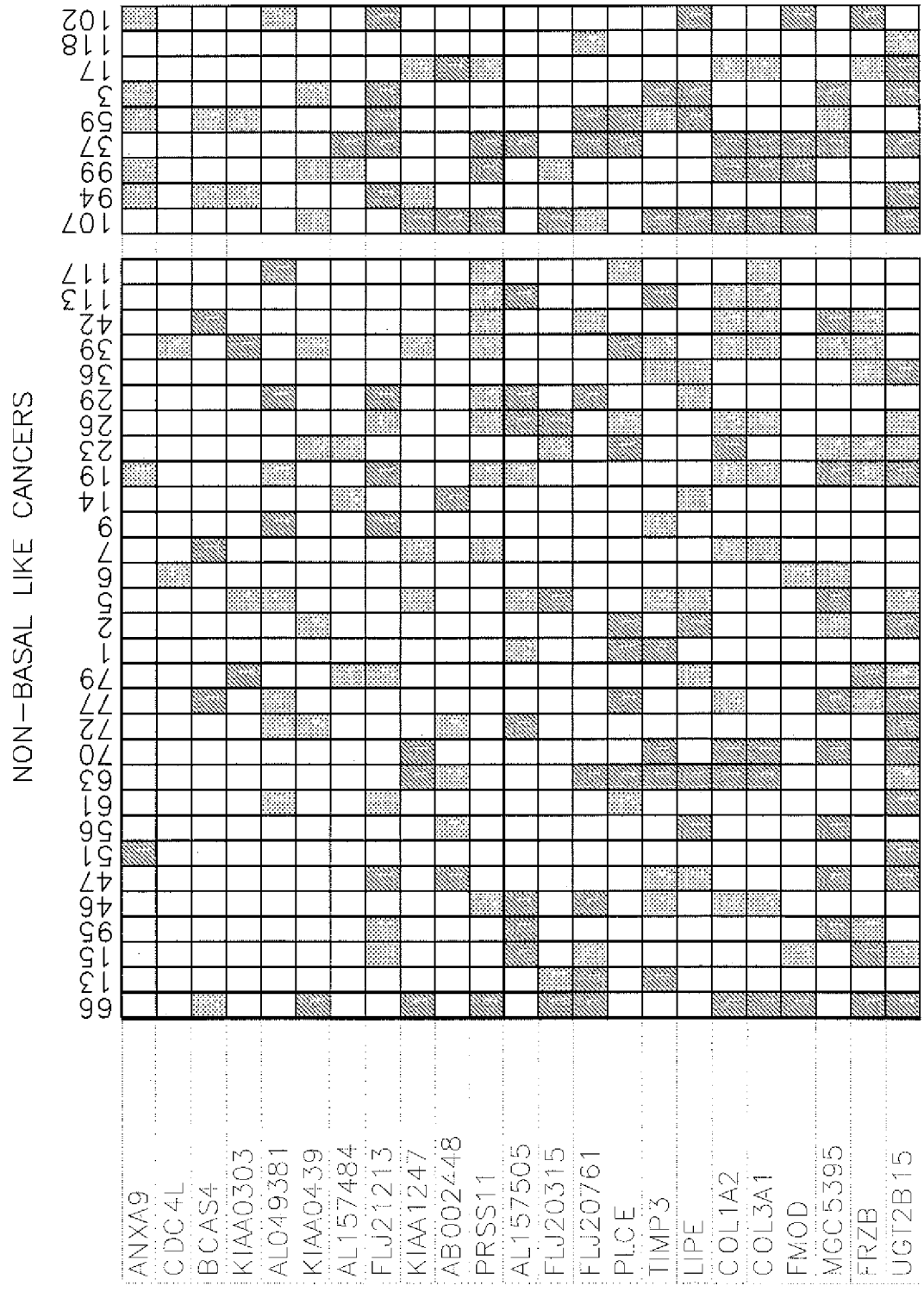

CONTINUED ON SHEET 80
NON-BASAL LIKE CANCERS
ANXA9
CDC4L
BCAS4
KIAA0303
AL049381
KIAA0439
AL157484
FLJ21213
KIAA1247
AB002448
PRSS11
AL157505
FLJ20315
FLJ20761
PLCE
TIMP3
LIPE
COL1A2
COL3A1
FMOD
MGC5395
FRZB
UGT2B15

FIG. 24

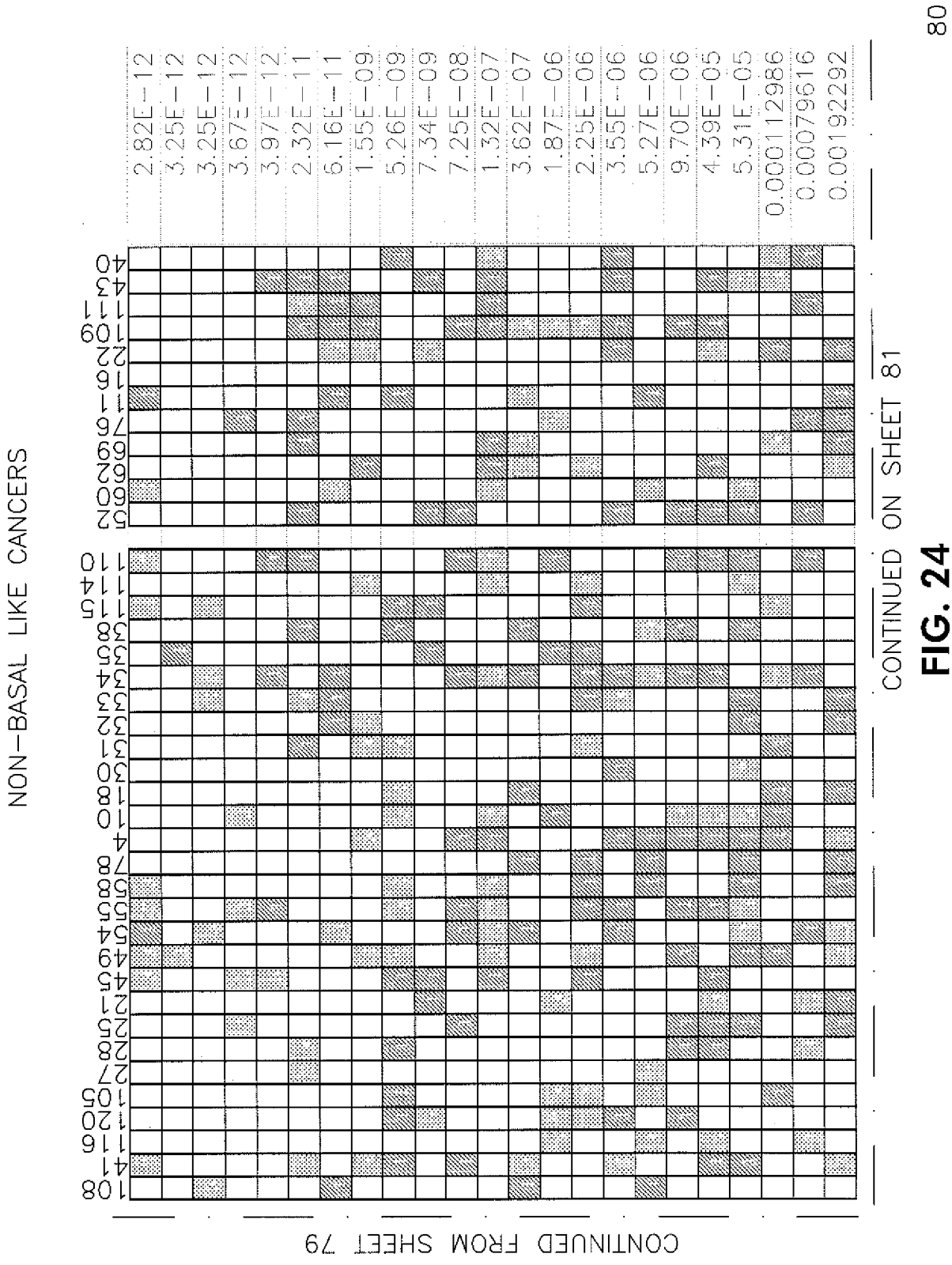

NON-BASAL LIKE CANCERS
CONTINUED FROM SHEET 79
CONTINUED ON SHEET 81
2.82E-12
3.25E-12
3.25E-12
3.67E-12
3.97E-12
2.32E-11
6.16E-11
1.55E-09
5.26E-09
7.34E-09
7.25E-08
1.32E-07
3.62E-07
1.87E-06
2.25E-06
3.55E-06
5.27E-06
9.70E-06
4.39E-05
5.31E-05
0.000112986
0.000079616
0.001192292

FIG. 24

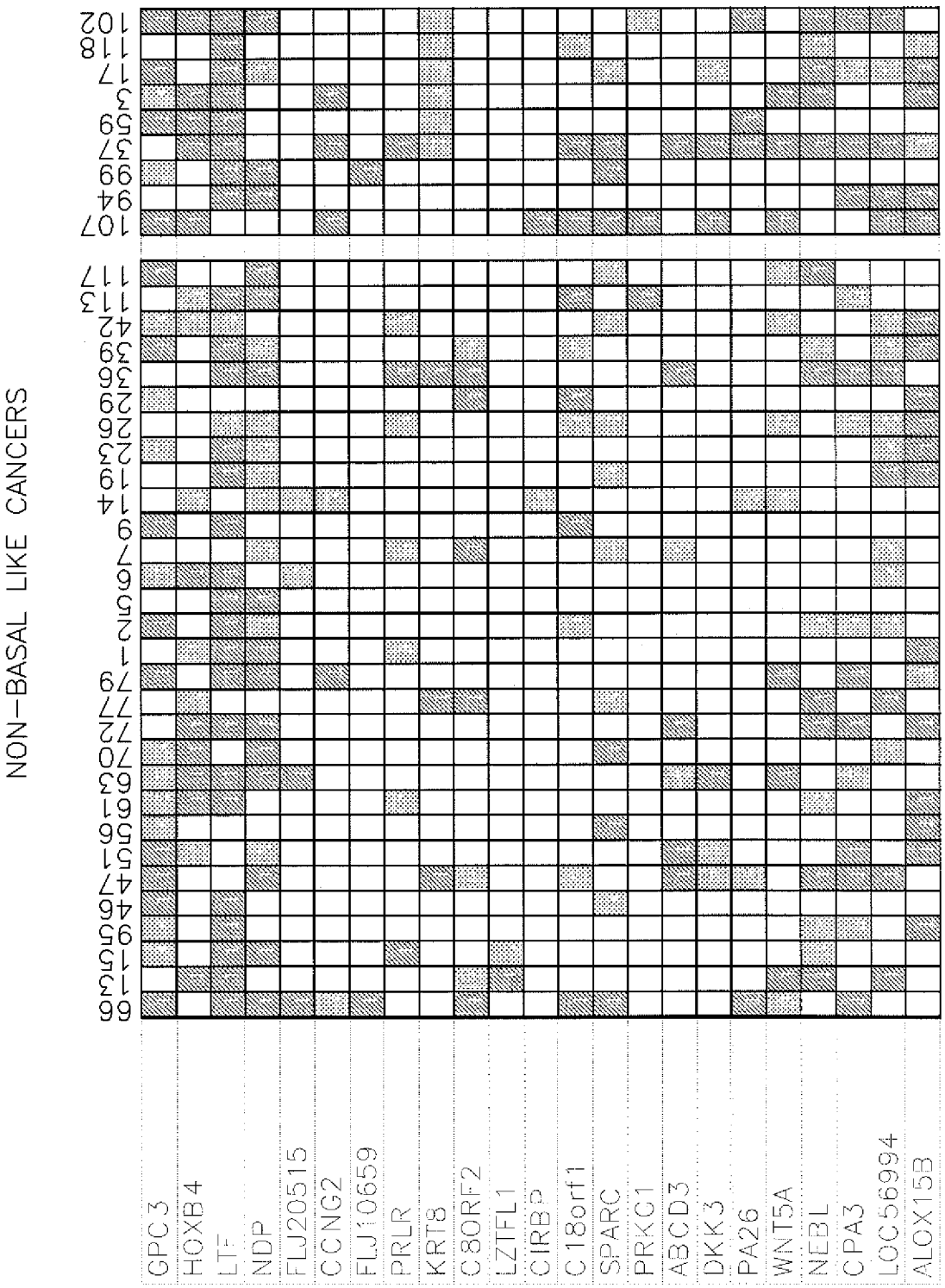

NON-BASAL LIKE CANCERS
CONTINUED ON SHEET 82
GPC3
HOXB4
LTF
NDP
FLJ20515
CCNG2
FLJ10659
PRLR
KRT8
C80RF2
LZTFL1
CIRBP
C18orf1
SPARC
PRKC1
ABCD3
DKK3
PA26
WNT5A
NEBL
CPA3
LOC56994
ALOX15B

FIG. 24

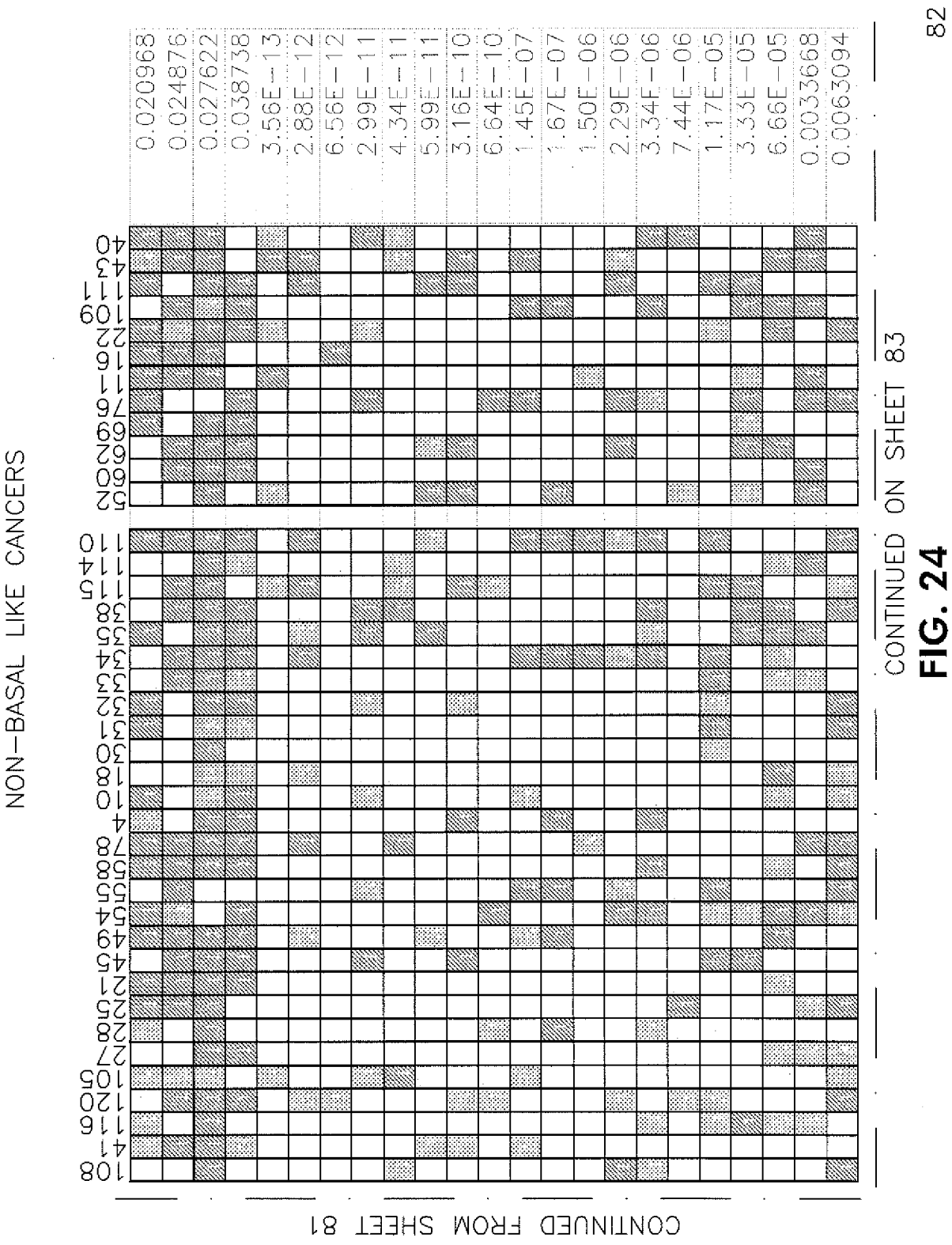

NON-BASAL LIKE CANCERS
CONTINUED FROM SHEET 81
CONTINUED ON SHEET 83
82
0.020963
0.024876
0.027622
0.038738
3.56E-13
2.88E-12
6.56E-12
2.99E-11
4.34E-11
5.99E-11
3.16E-10
6.64E-10
1.45E-07
1.67E-07
1.50E-06
2.29E-06
3.34E-06
7.44E-06
1.17E-05
3.33E-05
6.66E-05
0.0033668
0.0063094

FIG. 24

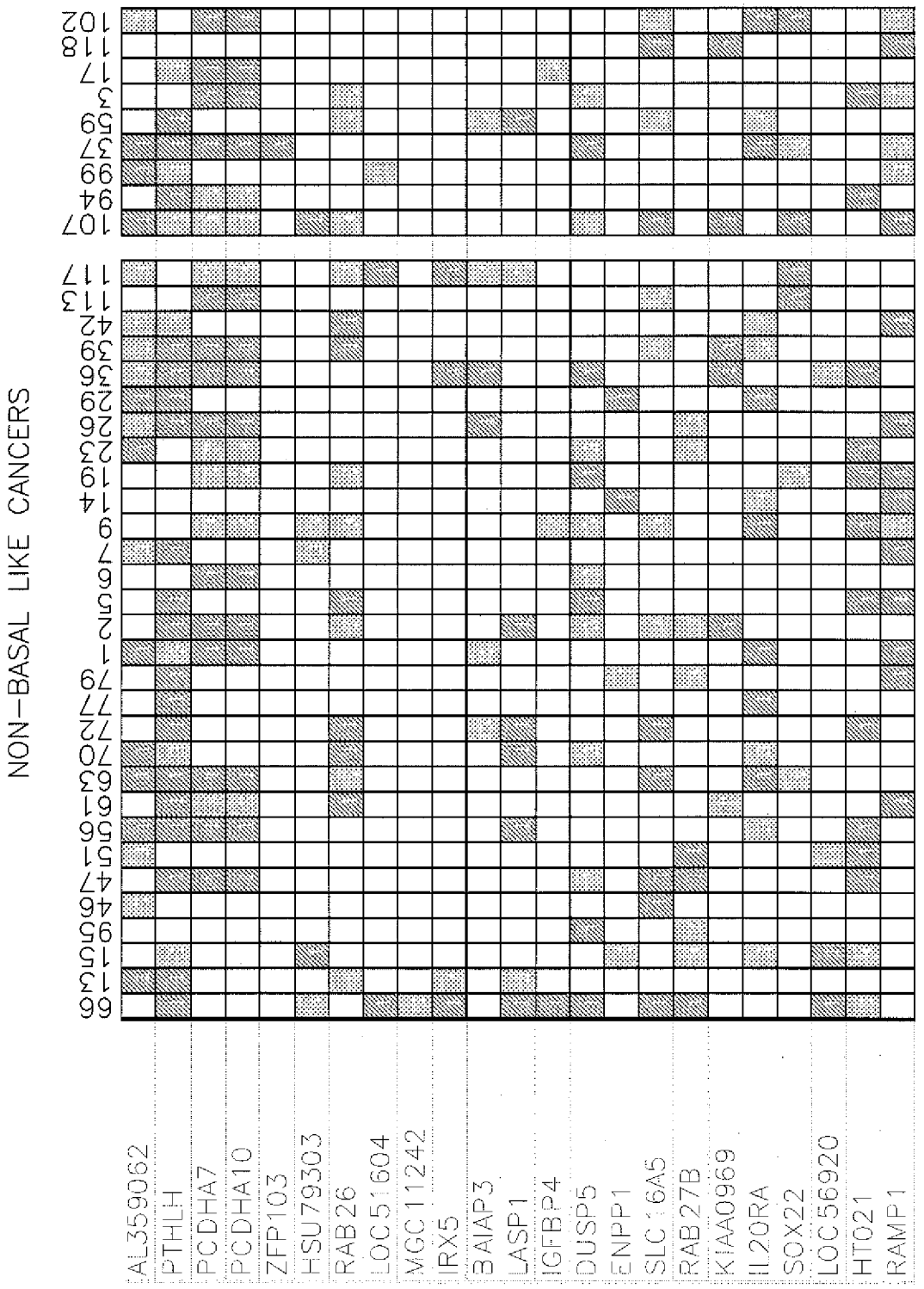
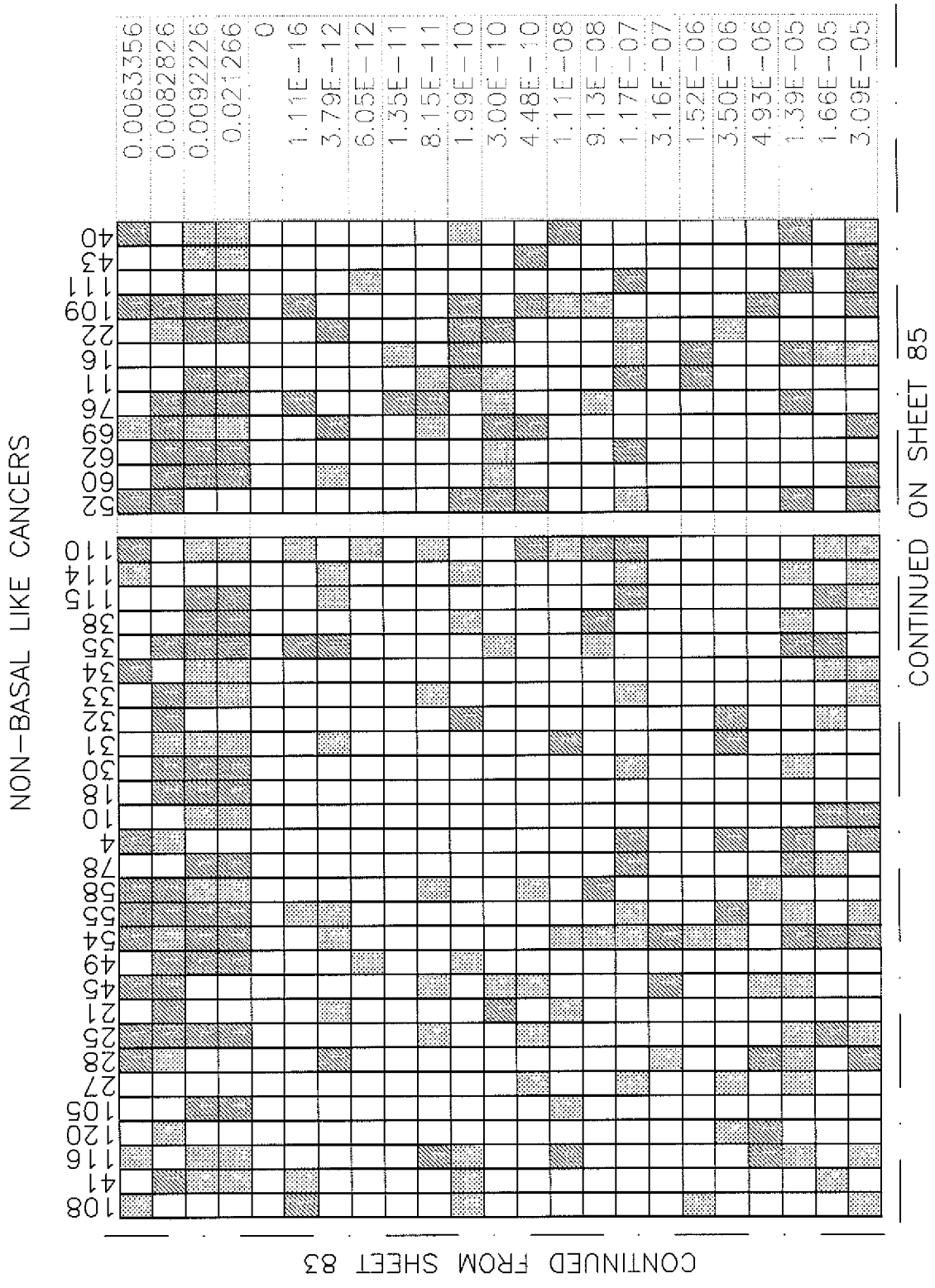

NON-BASAL LIKE CANCERS
AL359062
PTHLH
PCDHA7
PCDHA10
ZFP103
HSU79303
RAB26
LOC51604
MGC11242
IRX5
BAIAP3
LASP1
IGFBP4
DUSP5
ENPP1
SLC16A5
RAB27B
KIAA0969
IL20RA
SOX22
LOC56920
HT021
RAMP1
CONTINUED ON SHEET 84

FIG. 24


CONTINUED FROM SHEET 83
NON-BASAL LIKE CANCERS
0.0063356
0.0082826
0.0092226
0.021266
0
1.11E-16
3.79E-12
6.05E-12
1.35E-11
8.15E-11
1.99E-10
3.00E-10
4.48E-10
1.11E-08
9.13E-08
1.17E-07
3.16E-07
1.52E-06
3.50E-06
4.93E-06
1.39E-05
1.66E-05
3.09E-05
CONTINUED ON SHEET 85

84

FIG. 24

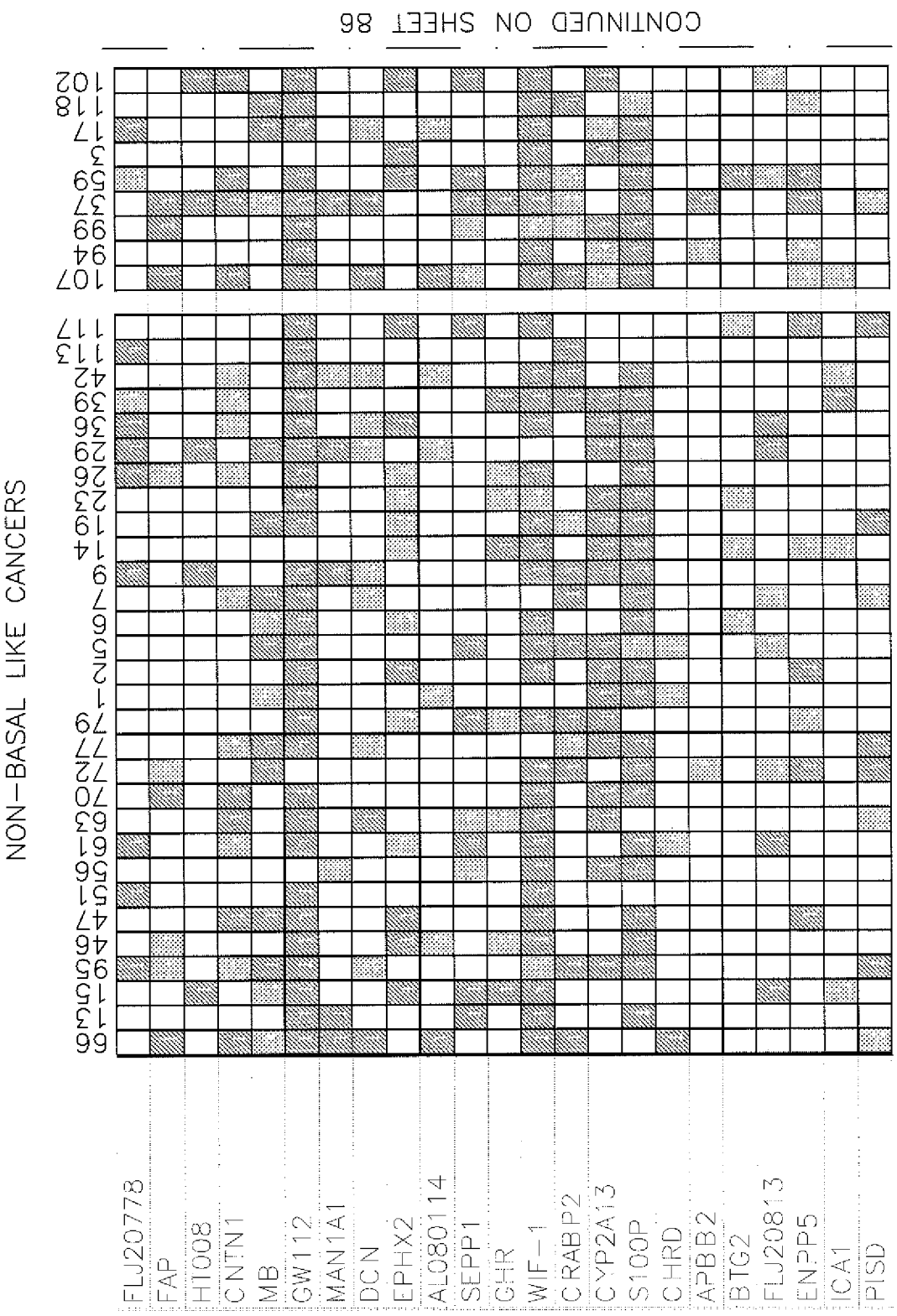

NON-BASAL LIKE CANCERS
CONTINUED ON SHEET 86
FLJ20773
FAP
HT008
CNTN1
MB
GW112
MAN1A1
DCN
EPHX2
AL080114
SEPP1
CHR
WIF-1
CRABP2
CYP2A13
S100P
CHRD
APBB2
BTG2
FLJ20813
ENPP5
ICA1
PISD

FIG. 24

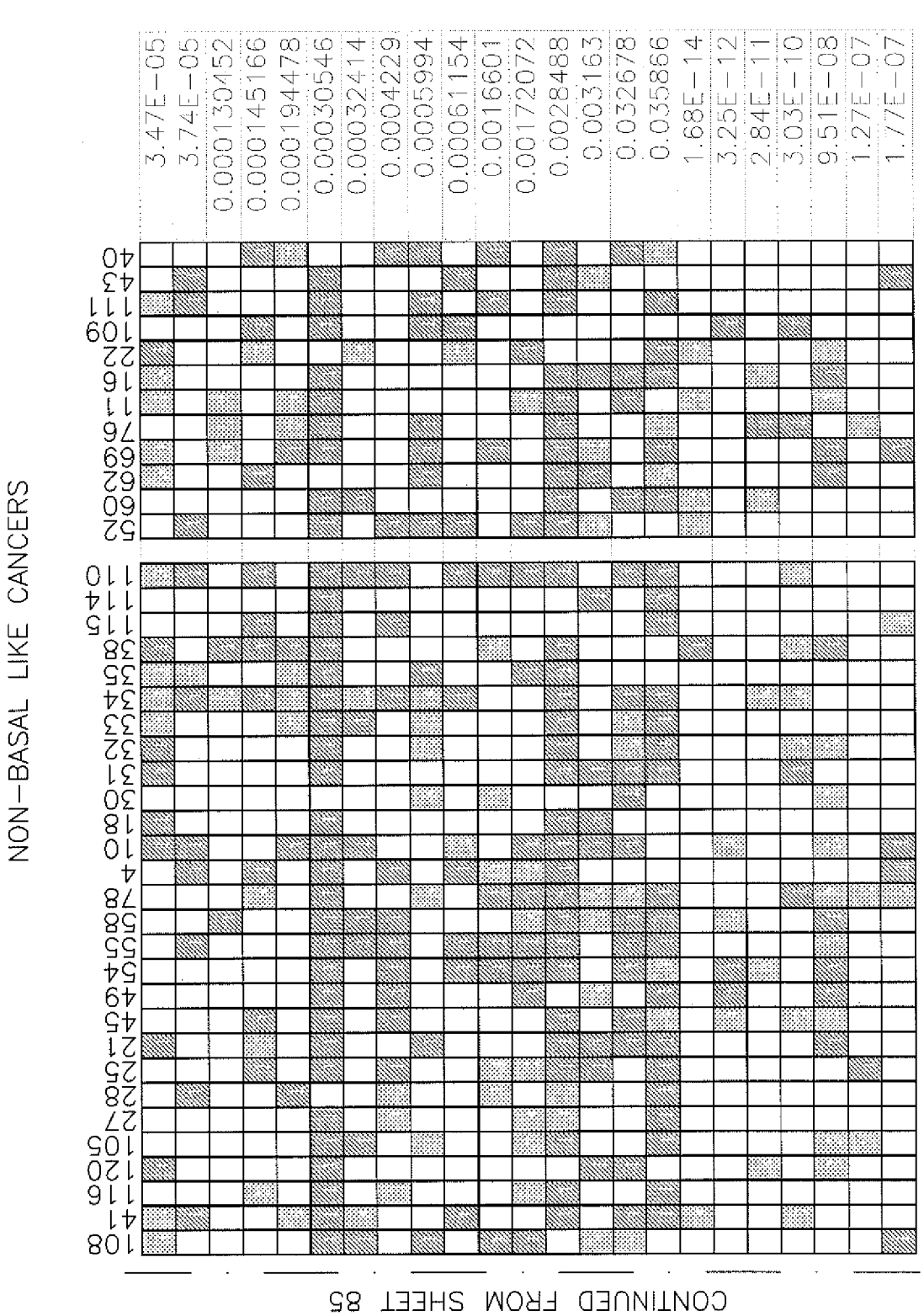

NON-BASAL LIKE CANCERS
CONTINUED FROM SHEET 85
CONTINUED ON SHEET 87
3.47E-05
3.74E-05
0.000130452
0.000145166
0.000194478
0.000305546
0.000324144
0.000422929
0.000599437
0.000611537
0.001660107
0.001720717
0.002848797
0.003163
0.032678
0.035866
1.68E-14
3.25E-12
2.84E-11
3.03E-10
9.51E-08
1.27E-07
1.77E-07

FIG. 24

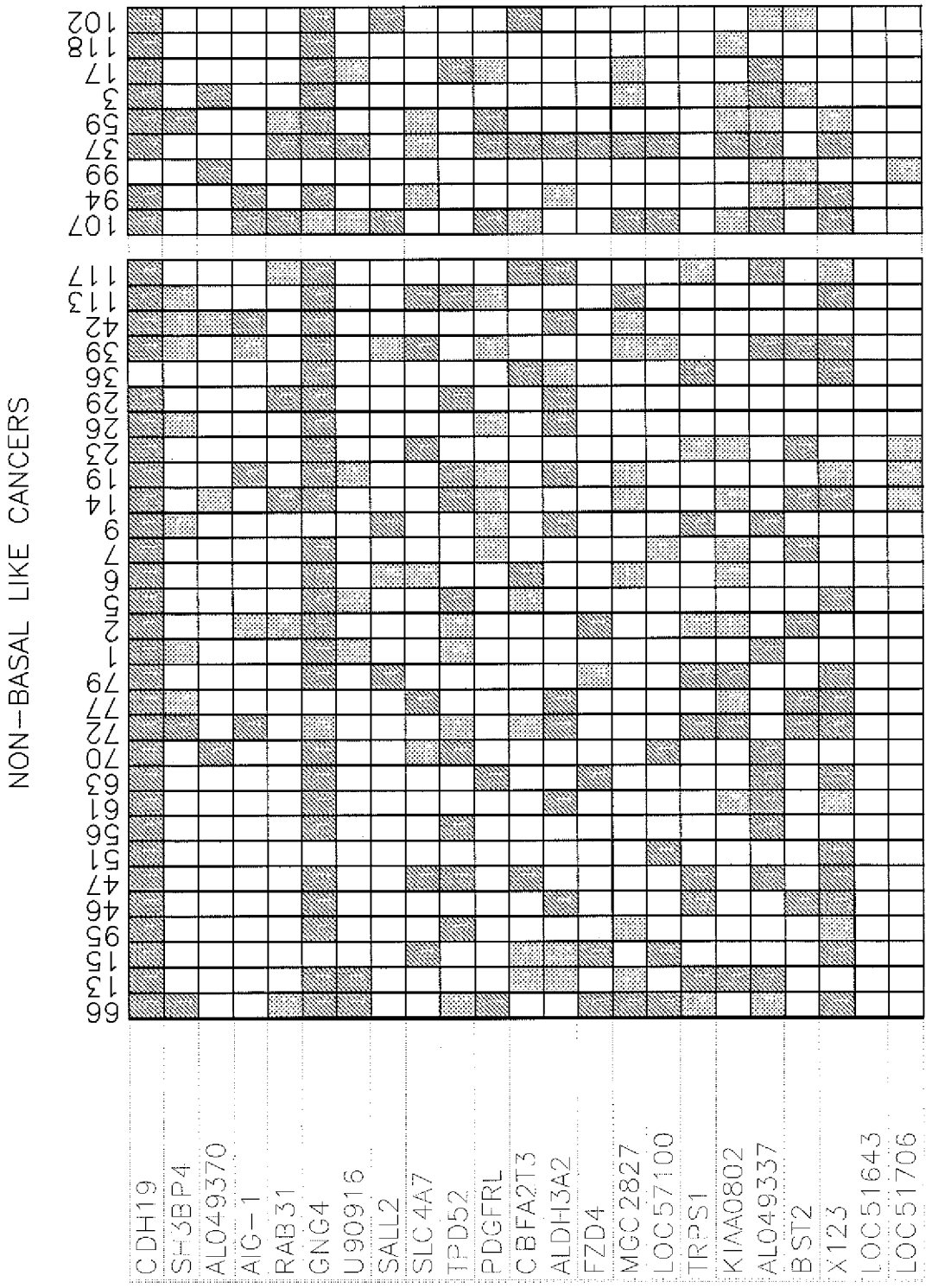

CONTINUED ON SHEET 88
NON-BASAL LIKE CANCERS
CDH19
SF3B4
AL049370
AIG-1
RAB31
GNG4
U90916
SALL2
SLC4A7
TPD52
PDGFRL
CBFA2T3
ALDH3A2
FZD4
MGC2827
LOC57100
TRPS1
KIAA0802
AL049337
BST2
X123
LOC51643
LOC51706

FIG. 24

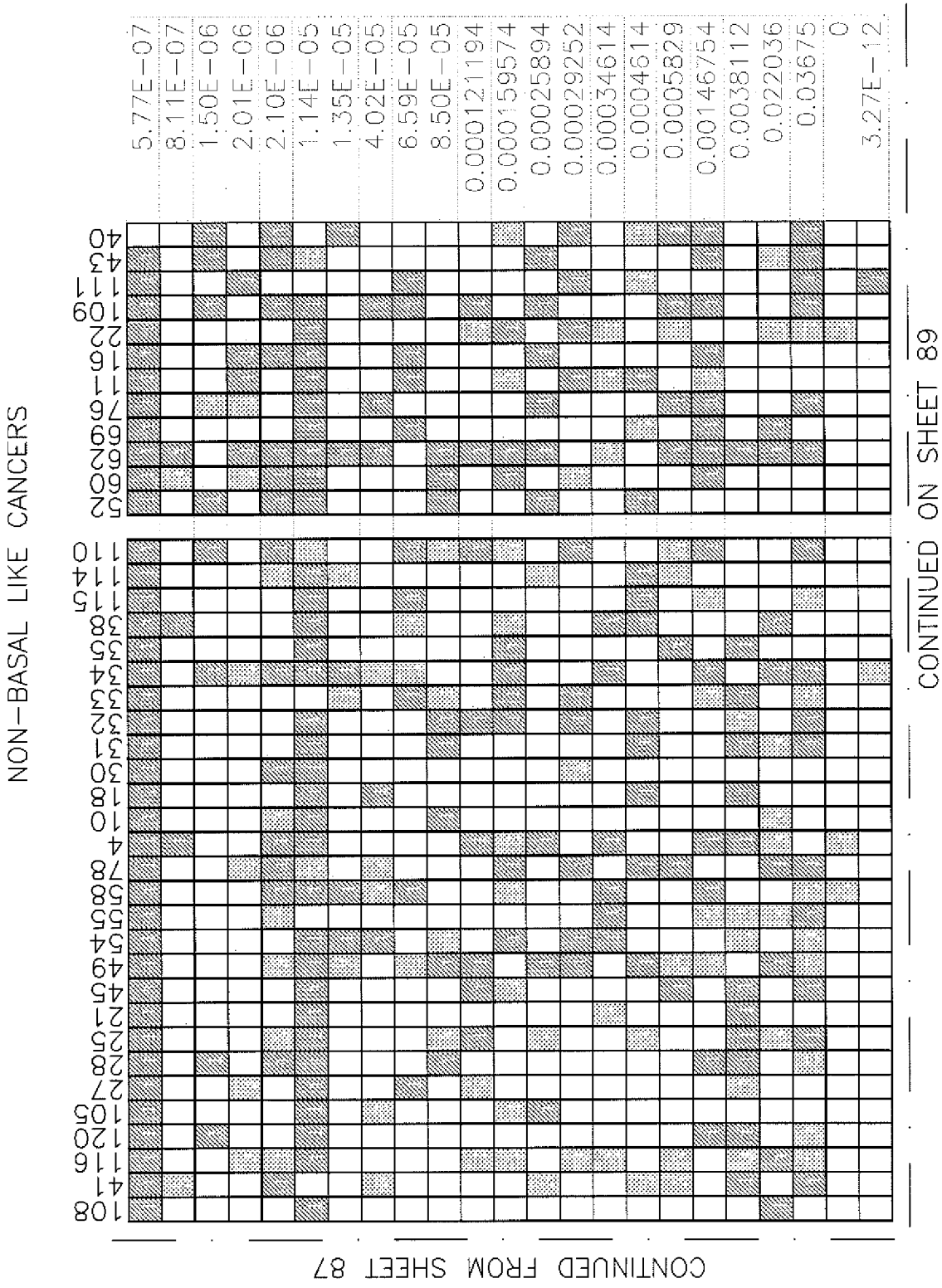

CONTINUED FROM SHEET 87
NON-BASAL LIKE CANCERS
5.77E-07
8.11E-07
1.50E-06
2.01E-06
2.10E-06
1.14E-05
1.35E-05
4.02E-05
6.59E-05
8.50E-05
0.000121194
0.000159574
0.00025894
0.00029252
0.00034614
0.0004614
0.0005829
0.00146754
0.0038112
0.022036
0.03675
0
3.27E-12
CONTINUED ON SHEET 89

FIG. 24

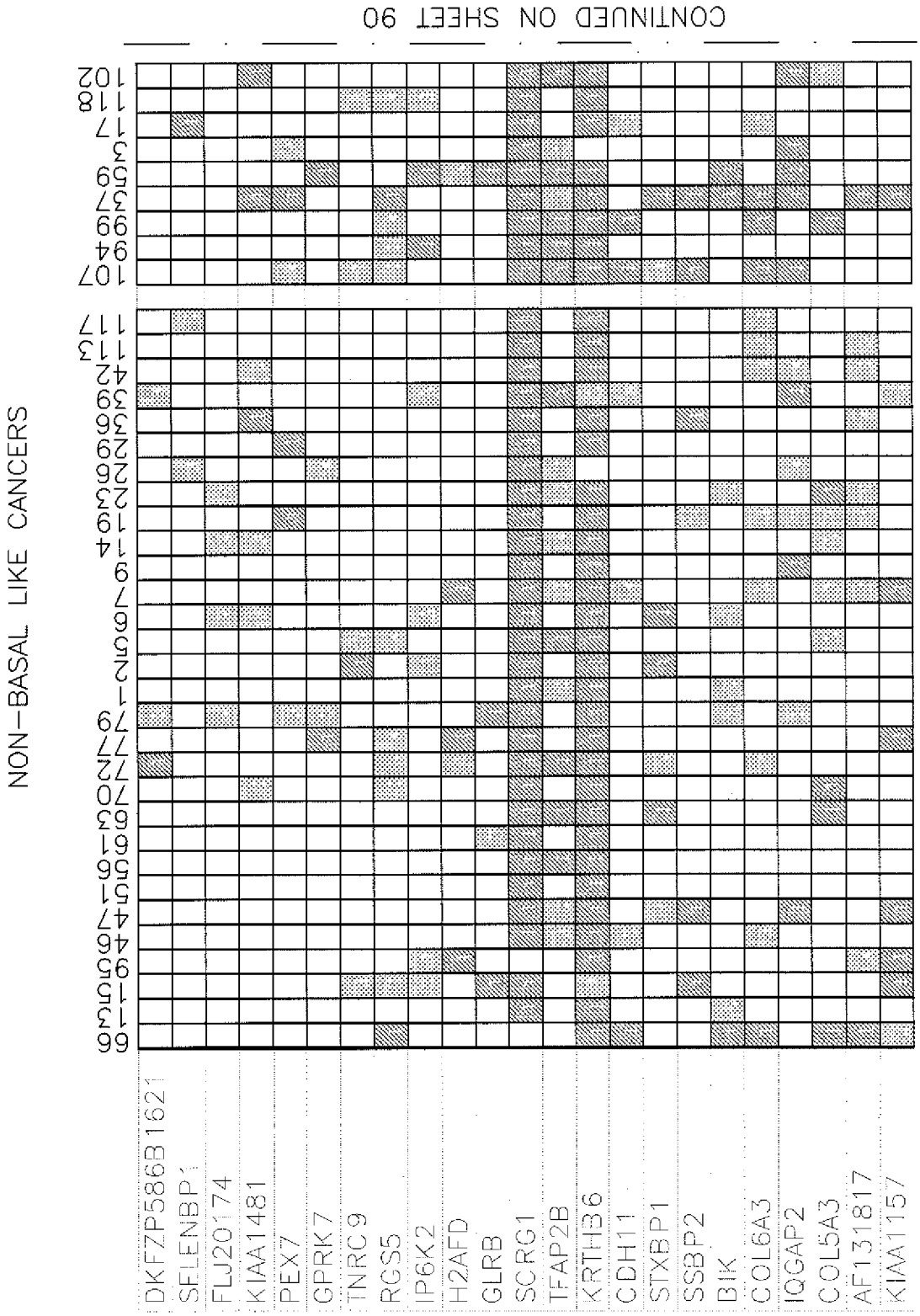

NON-BASAL LIKE CANCERS
CONTINUED ON SHEET 90
DKFZP586B1621
SFLENBP1
FLJ20174
KIAA1481
PEX7
GPRK7
TNRC9
RGS5
IP6K2
H2AFD
GLRB
SCRG1
TFAP2B
KRTHB6
CDH11
STXBP1
SSBP2
BIK
COL6A3
IQGAP2
COL5A3
AF131817
KIAA1157

FIG. 24

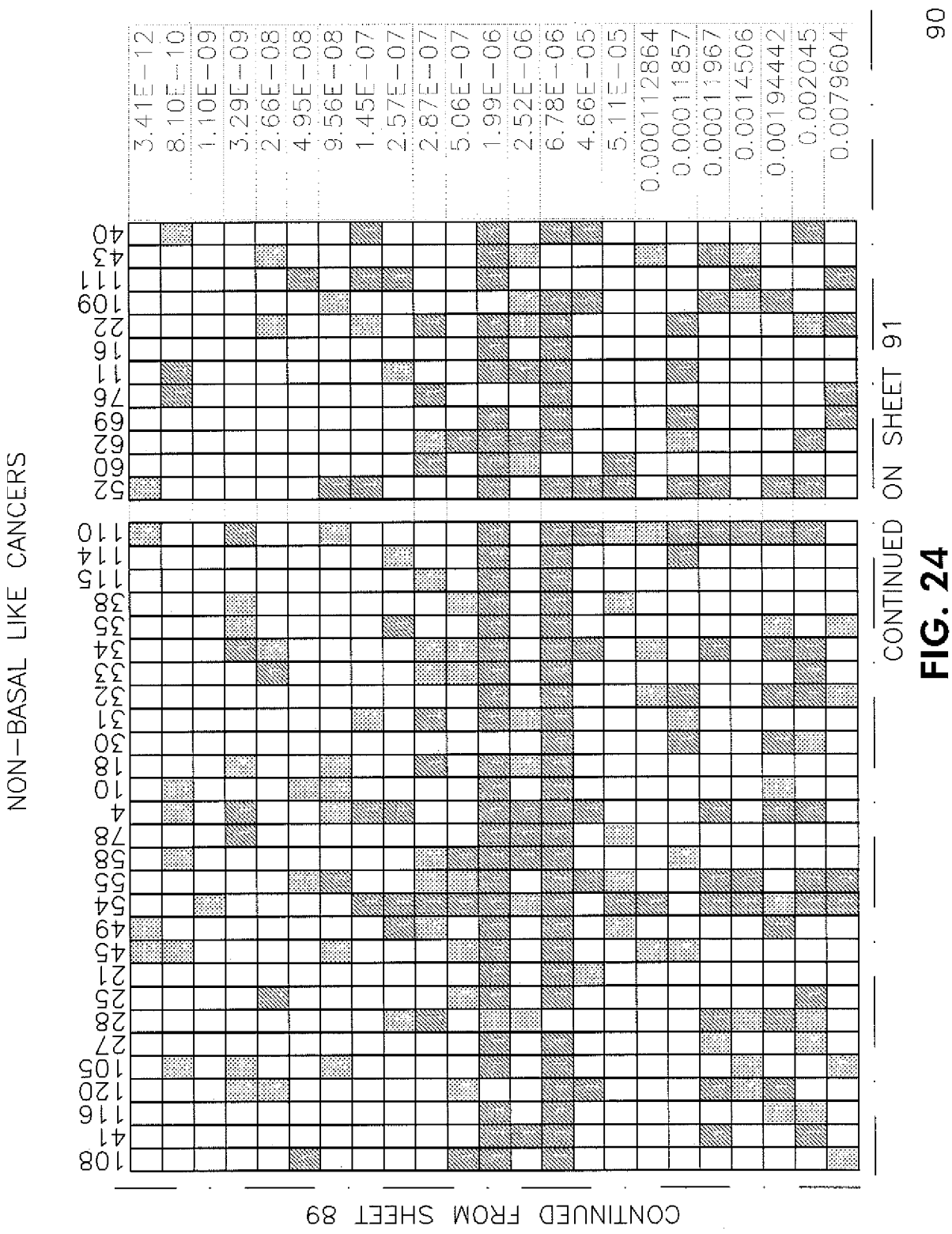

NON-BASAL LIKE CANCERS
CONTINUED FROM SHEET 89
CONTINUED ON SHEET 91
3.41E-12
8.10E-10
1.10E-09
3.29E-09
2.66E-08
4.95E-08
9.56E-08
1.45E-07
2.57E-07
2.87E-07
5.06E-07
1.99E-06
2.52E-06
6.78E-06
4.66E-05
5.11E-05
0.000112864
0.00011857
0.00011967
0.00014506
0.00194442
0.002045
0.0079604
90

FIG. 24

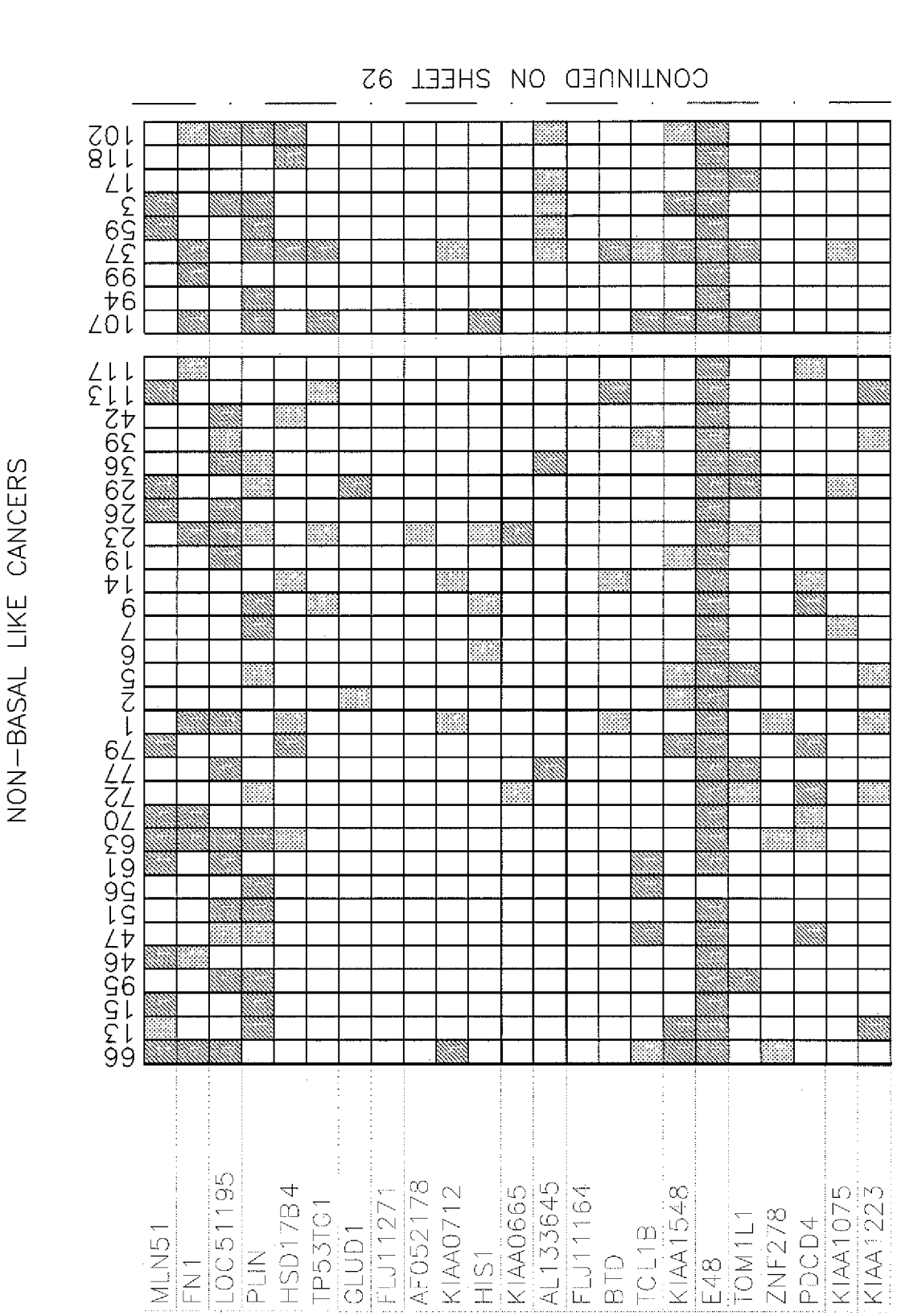

NON-BASAL LIKE CANCERS
CONTINUED ON SHEET 92
MLN51
FN1
LOC51195
PLIN
HSD17B4
TP53TC1
GLUD1
FLJ11271
AF052178
KIAA0712
HIS1
KIAA0665
AL133645
FLJ11164
BTD
TCL1B
KIAA1548
E48
TOM1L1
ZNF278
PDCD4
KIAA1075
KIAA1223

FIG. 24

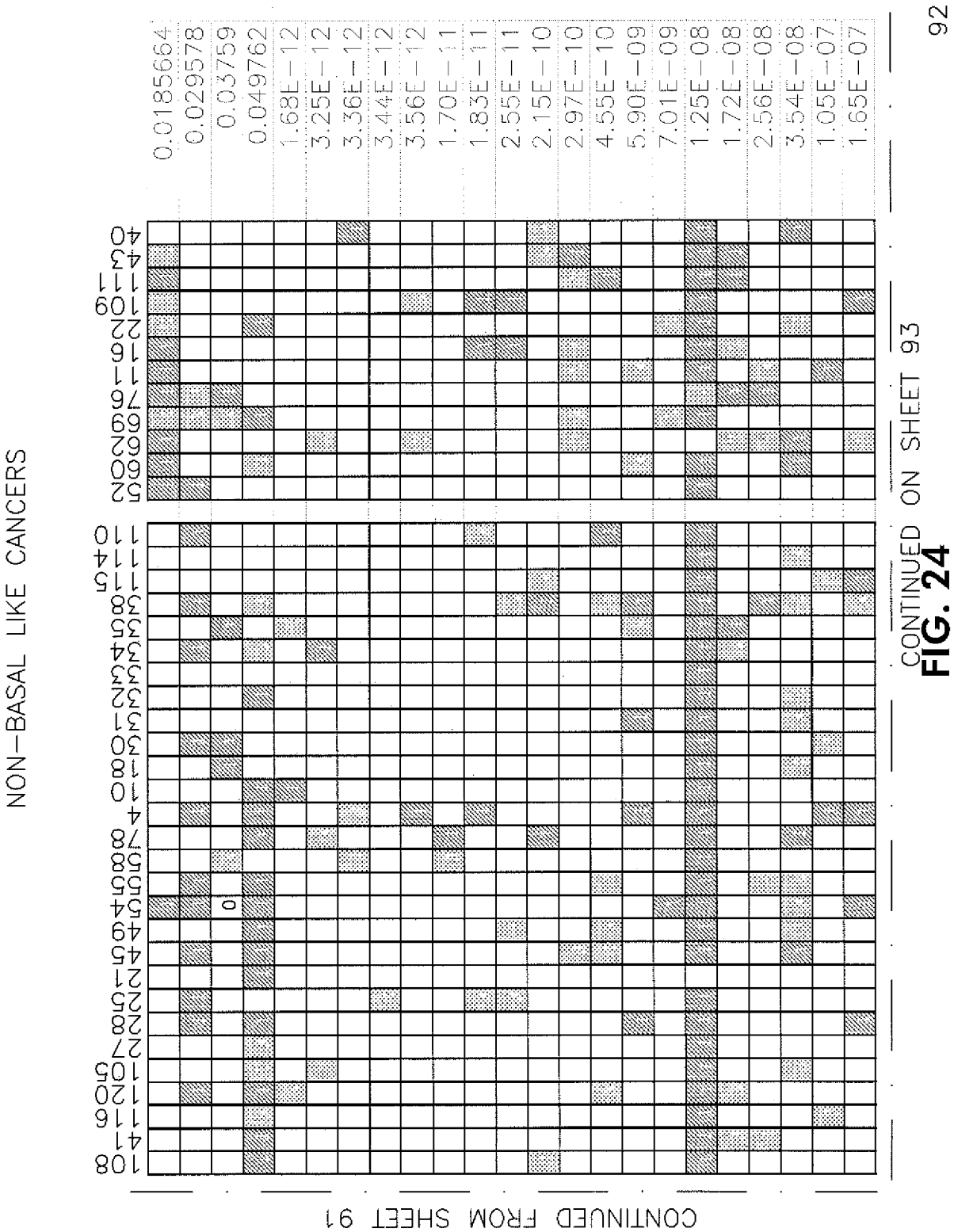

NON-BASAL LIKE CANCERS
0.0185664
0.029578
0.03759
0.049762
1.68E-12
3.25E-12
3.36E-12
3.44E-12
3.56E-12
1.70E-11
1.83E-11
2.55E-11
2.15E-10
2.97E-10
4.55E-10
5.90E-09
7.01E-09
1.25E-08
1.72E-08
2.56E-08
3.54E-08
1.05E-07
1.65E-07
CONTINUED FROM SHEET 91
CONTINUED ON SHEET 93

FIG. 24

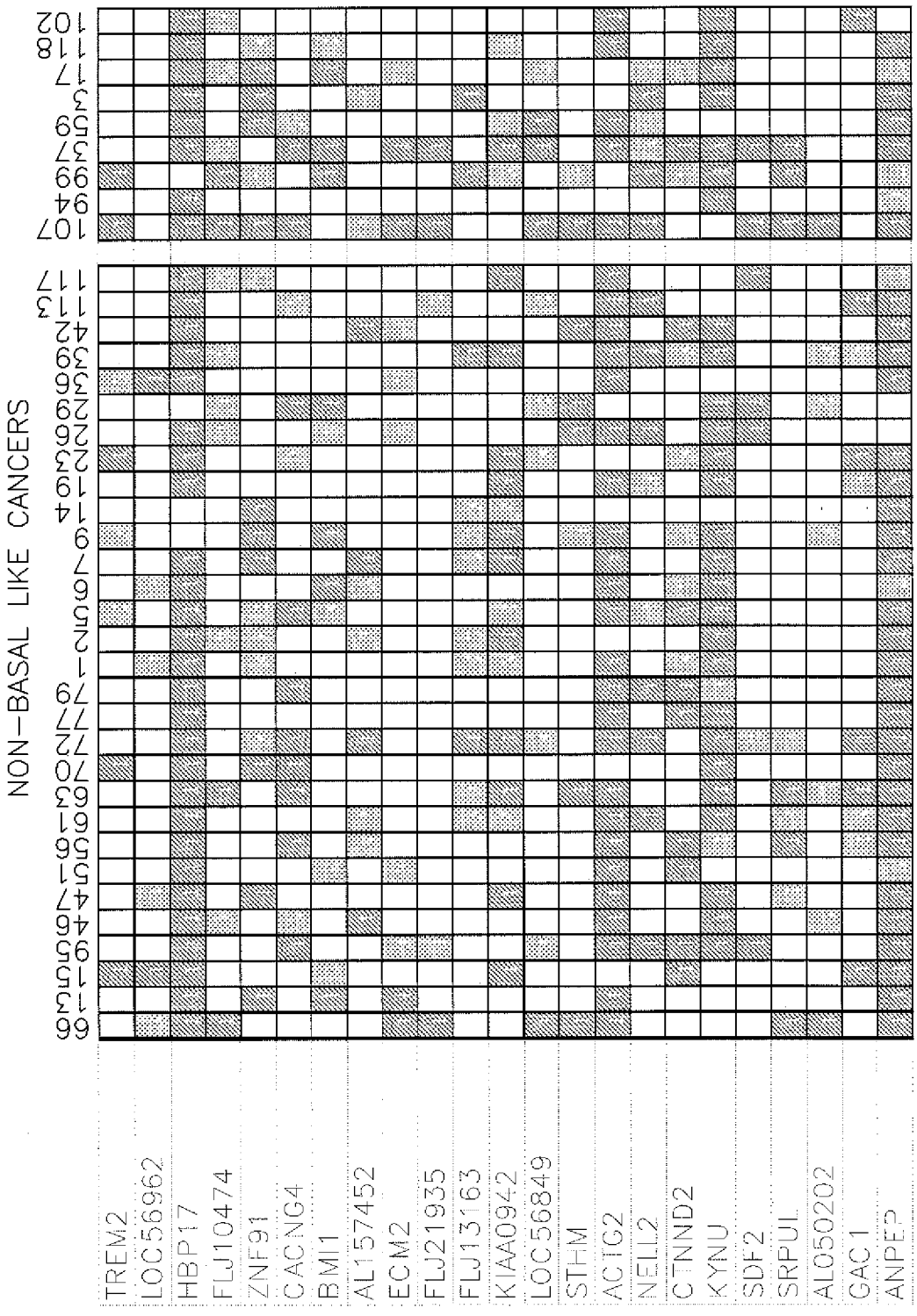

CONTINUED ON SHEET 94
NON-BASAL LIKE CANCERS
TREM2
LOC56962
HBP17
FLJ10474
ZNF91
CACNG4
BMI1
AL157452
ECM2
FLJ21935
FLJ13163
KIAA0942
LOC56849
STHM
ACTG2
NELL2
CTNND2
KYNU
SDF2
SRPUL
AL050202
GAC1
ANPEP

FIG. 24

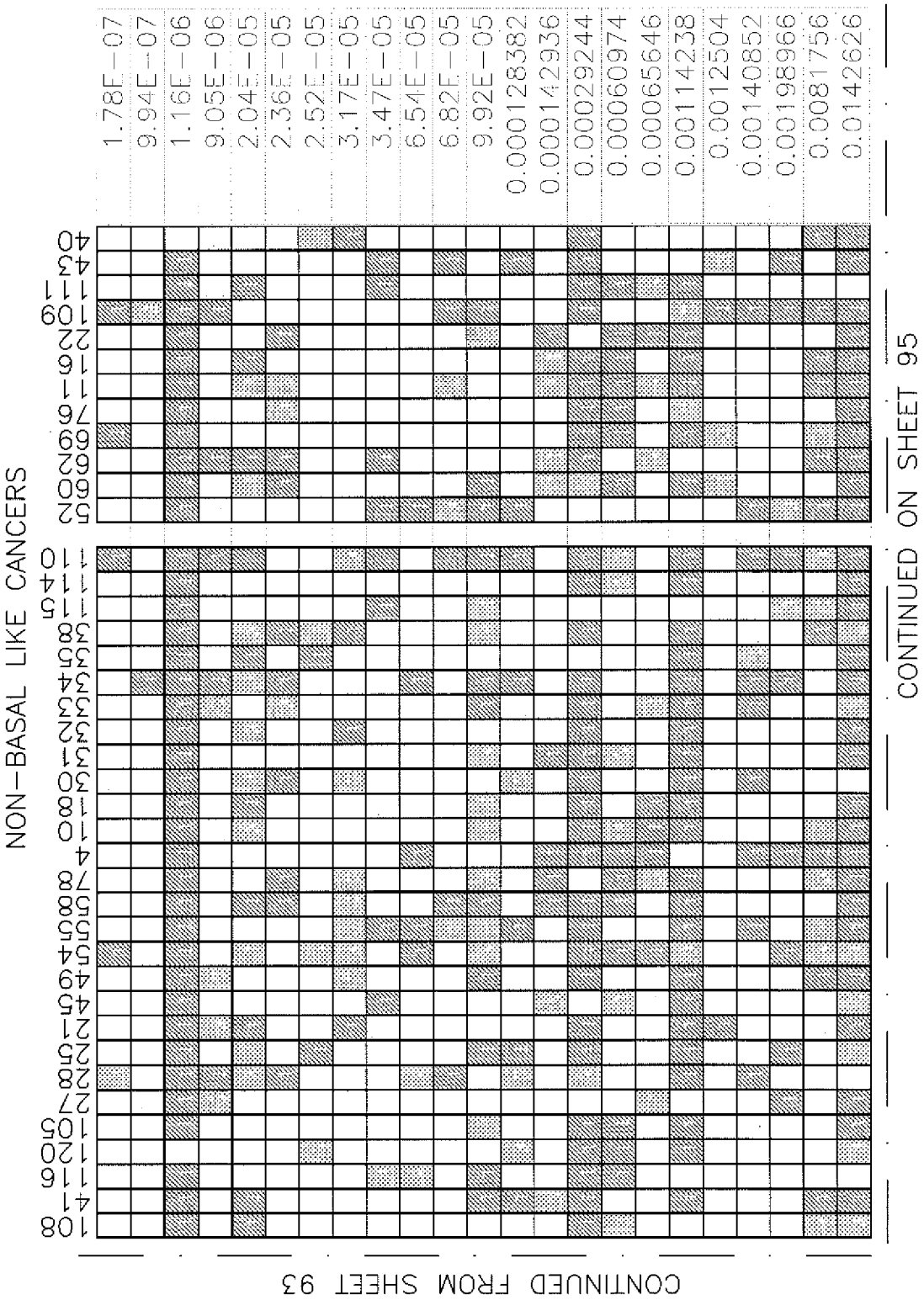

CONTINUED FROM SHEET 93
NON-BASAL LIKE CANCERS
1.78E-07
9.94E-07
1.16E-06
9.05E-06
2.04E-05
2.36E-05
2.52E-05
3.17E-05
3.47E-05
6.54E-05
6.82E-05
9.92E-05
0.000128382
0.000142936
0.00029244
0.00060974
0.00065646
0.00114238
0.00125041
0.00140852
0.00198966
0.00817561
0.0142626
CONTINUED ON SHEET 95

FIG. 24

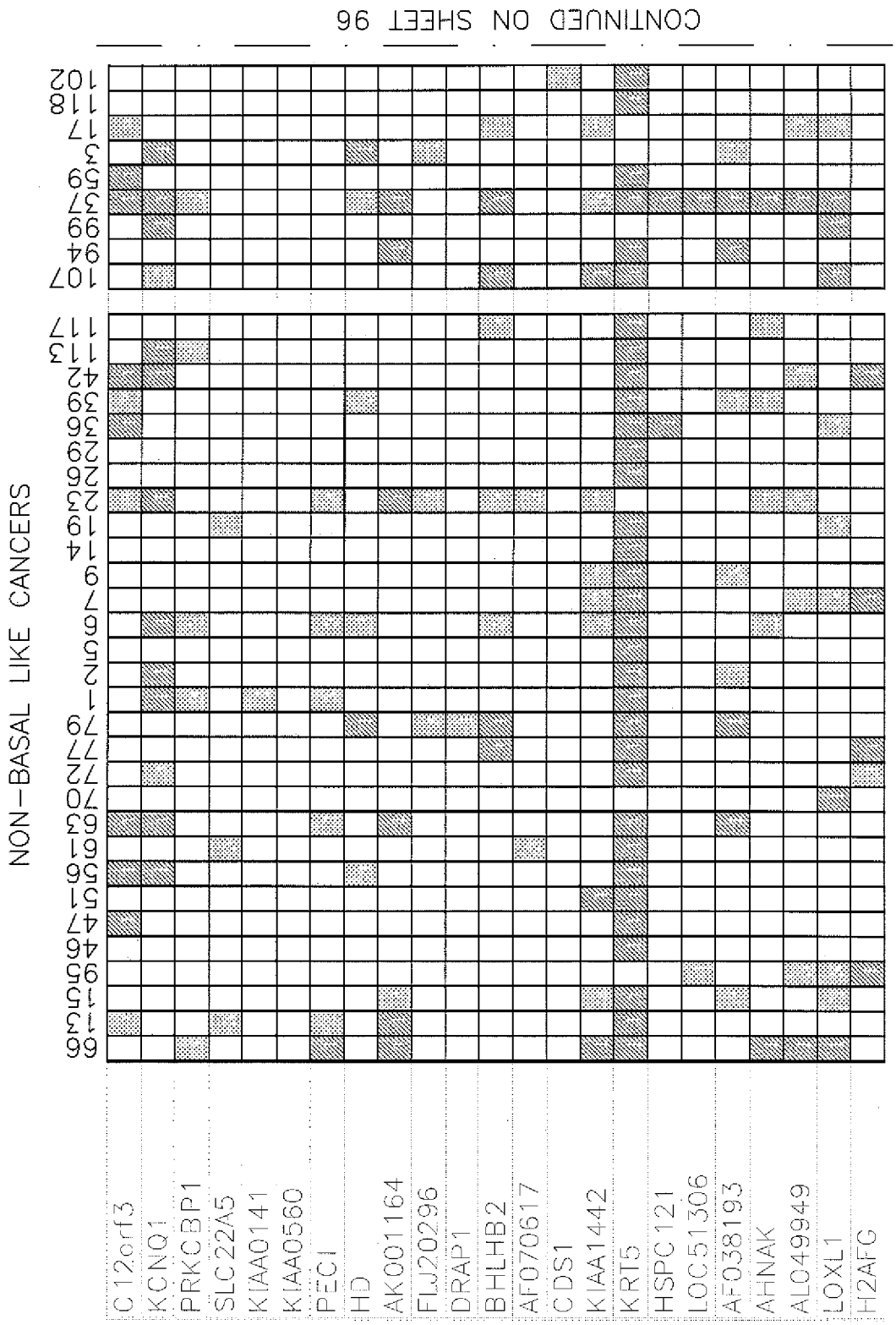

NON-BASAL LIKE CANCERS
C12orf3
KCNQ1
PRKCBP1
SLC22A5
KIAA0141
KIAA0560
PECI
HD
AK001164
FLJ20296
DRAP1
BHLHB2
AF070617
CDS1
KIAA1442
KRT5
HSPC121
LOC51306
AF038193
AHNAK
AL049949
LOXL1
H2AFC
CONTINUED ON SHEET 96

FIG. 24

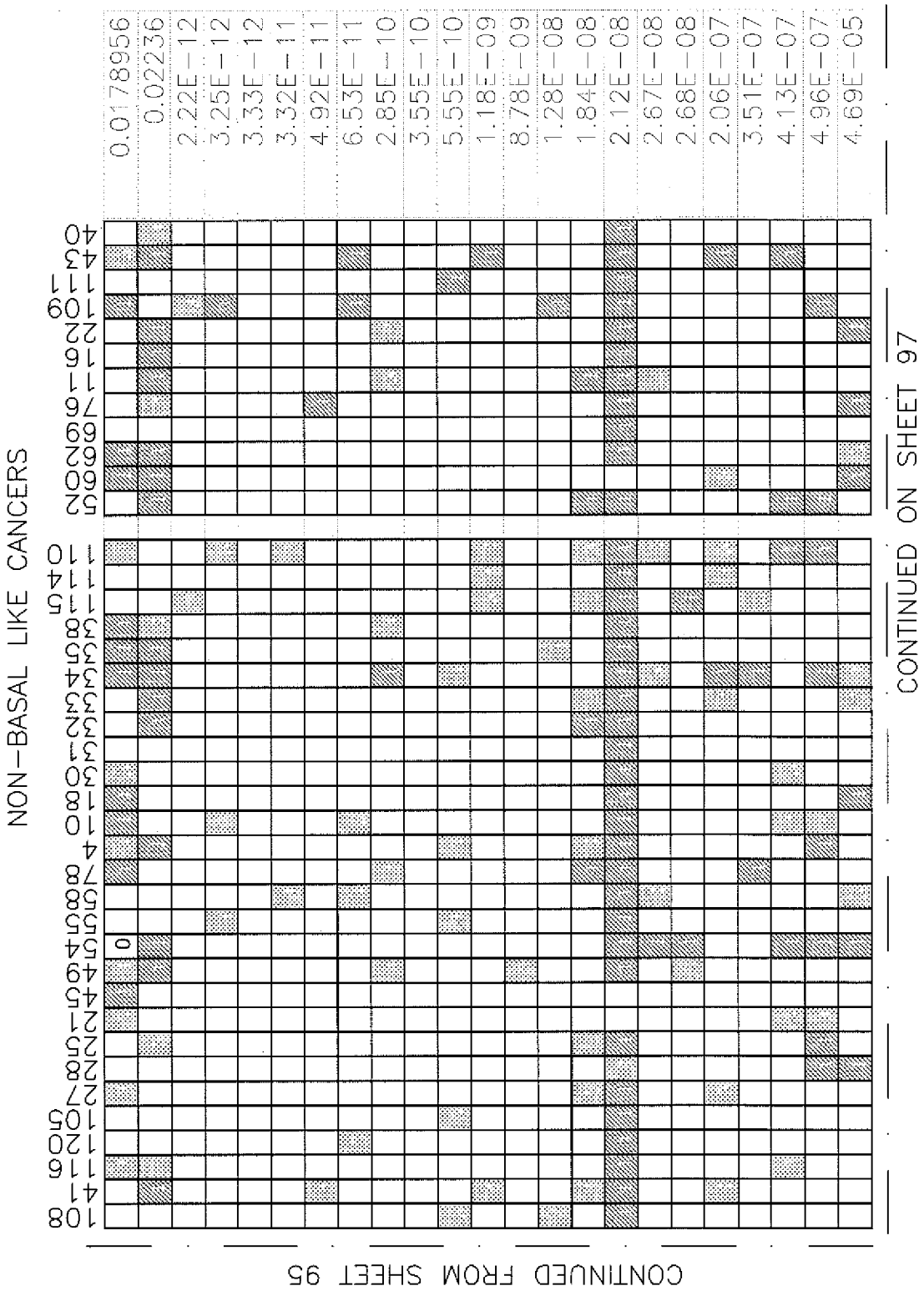

NON-BASAL LIKE CANCERS
0.0178956
0.02236
2.22E-12
3.25E-12
3.33E-12
3.32E-11
4.92E-11
6.53E-11
2.85E-10
3.55E-10
5.55E-10
1.18E-09
8.78E-09
1.28E-08
1.84E-08
2.12E-08
2.67E-08
2.68E-08
2.06E-07
3.51E-07
4.13E-07
4.96E-07
4.69E-05
CONTINUED FROM SHEET 95
CONTINUED ON SHEET 97

FIG. 24

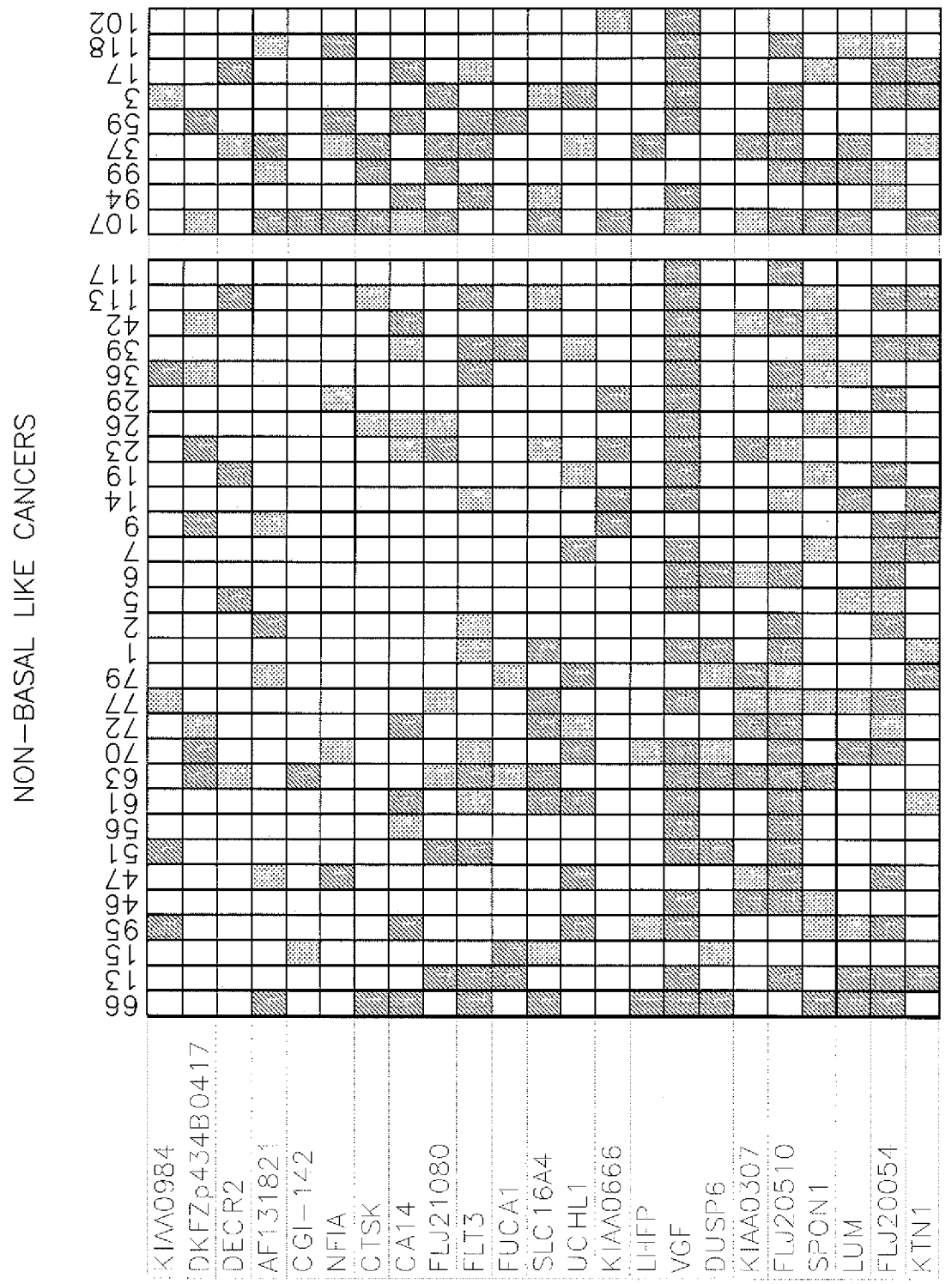

NON-BASAL LIKE CANCERS
CONTINUED ON SHEET 98
KIAA0984
DKFZp434B0417
DECR2
AF131821
CGI-142
NFIA
CTSK
CA14
FLJ21080
FLT3
FUCA1
SLC16A4
UCHL1
KIAA0666
LHFP
VGF
DUSP6
KIAA0307
FLJ20510
SPON1
LUM
FLJ20054
KTN1

FIG. 24

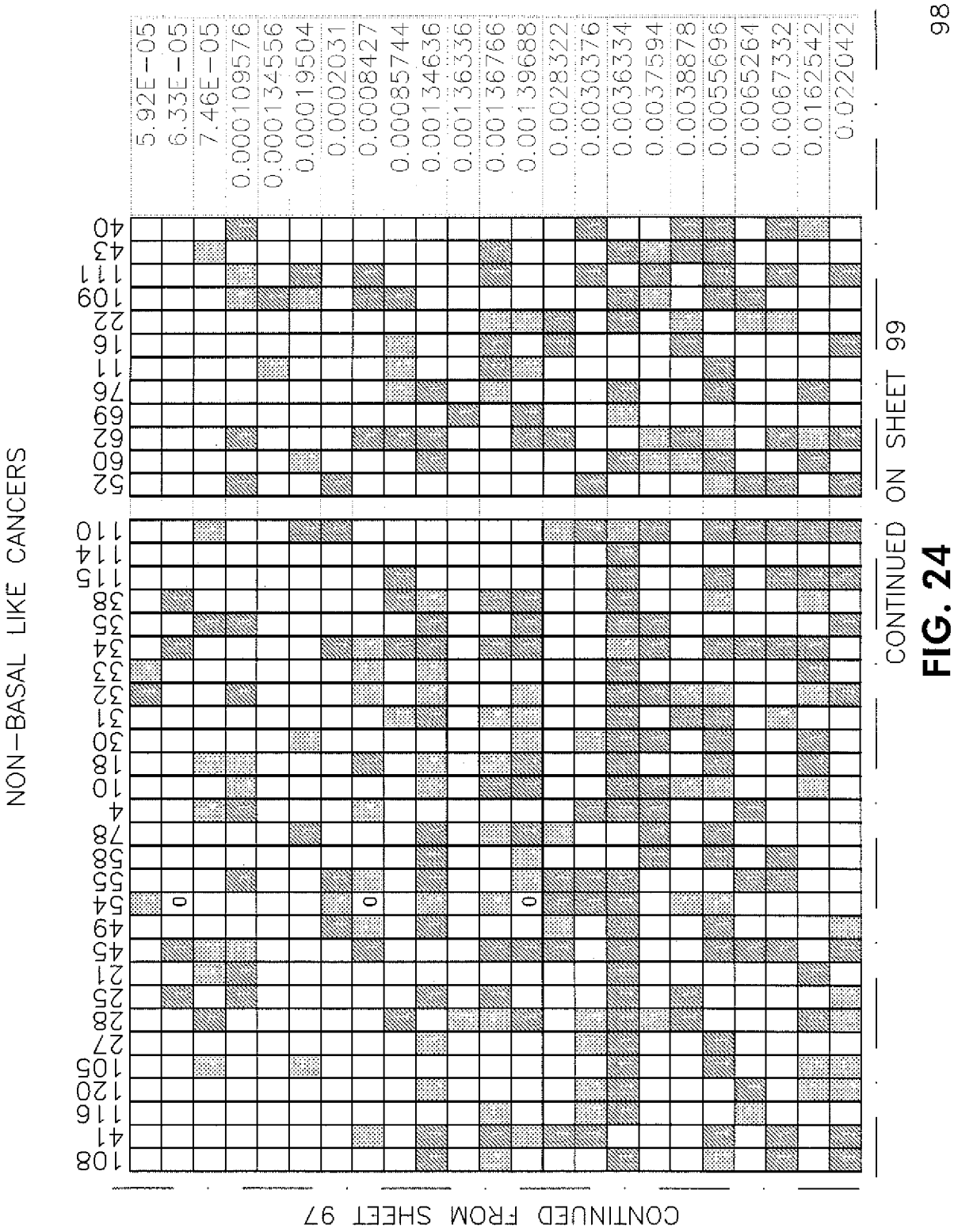

NON-BASAL LIKE CANCERS
CONTINUED FROM SHEET 97
CONTINUED ON SHEET 99
5.92E-05
6.33E-05
7.46E-05
0.00010957 6
0.00013455 6
0.00019504
0.0002031
0.0008427
0.0008574 4
0.0013463 6
0.0013633 6
0.0013676 6
0.0013968 8
0.0028322
0.0030376
0.0036334
0.0037594
0.0038878
0.0055696
0.0065264
0.0067332
0.0162542
0.022042

FIG. 24

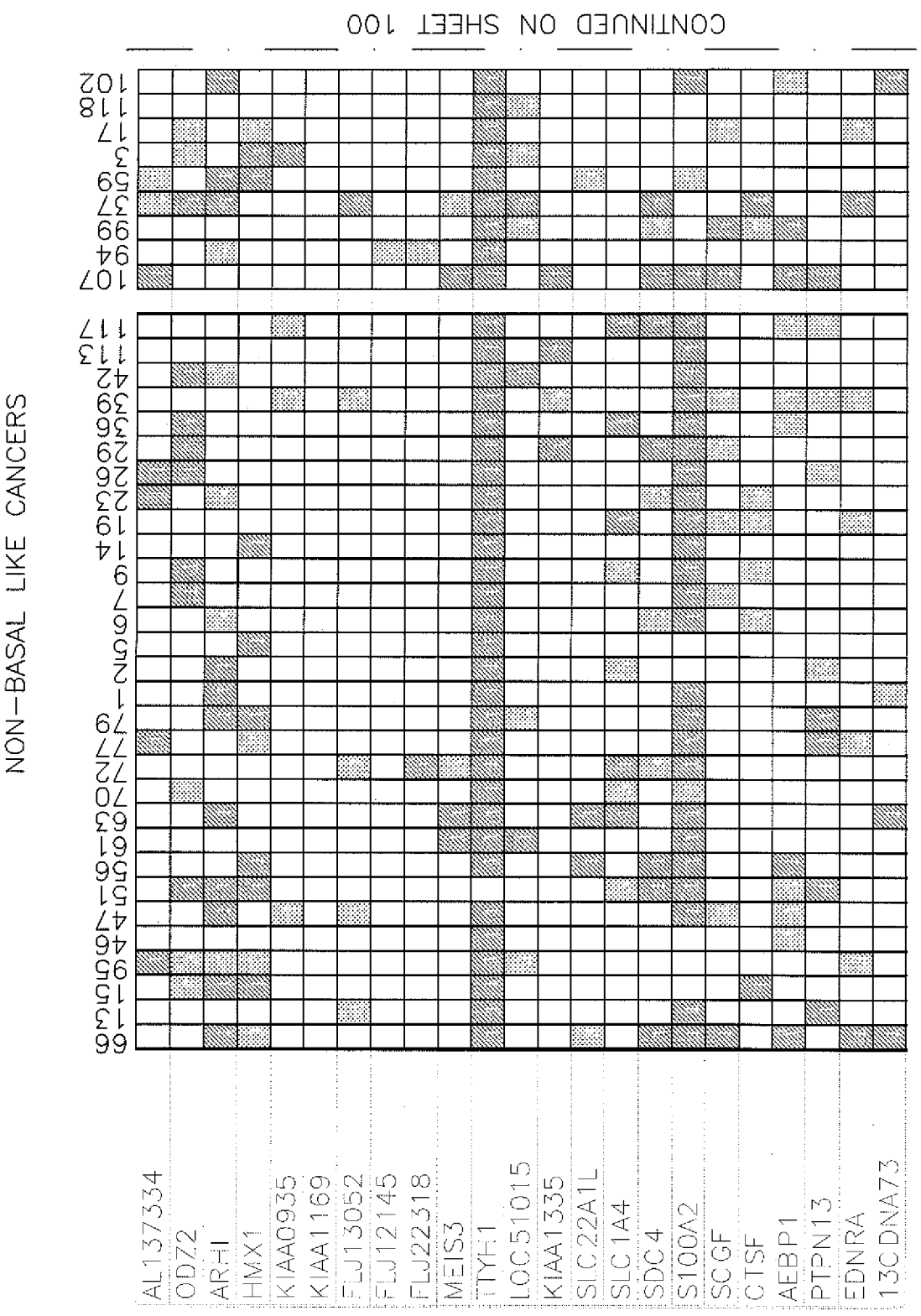

NON-BASAL LIKE CANCERS
CONTINUED ON SHEET 100
AL137334
ODZ2
ARHI
HMX1
KIAA0935
KIAA1169
FLJ13052
FLJ12145
FLJ22318
MEIS3
TYH1
LOC51015
KIAA1335
SLC22A1L
SLC1A4
SDC4
S100A2
SCGF
CTSF
AEBP1
PTPN13
EDNRA
13CDNA73

FIG. 24

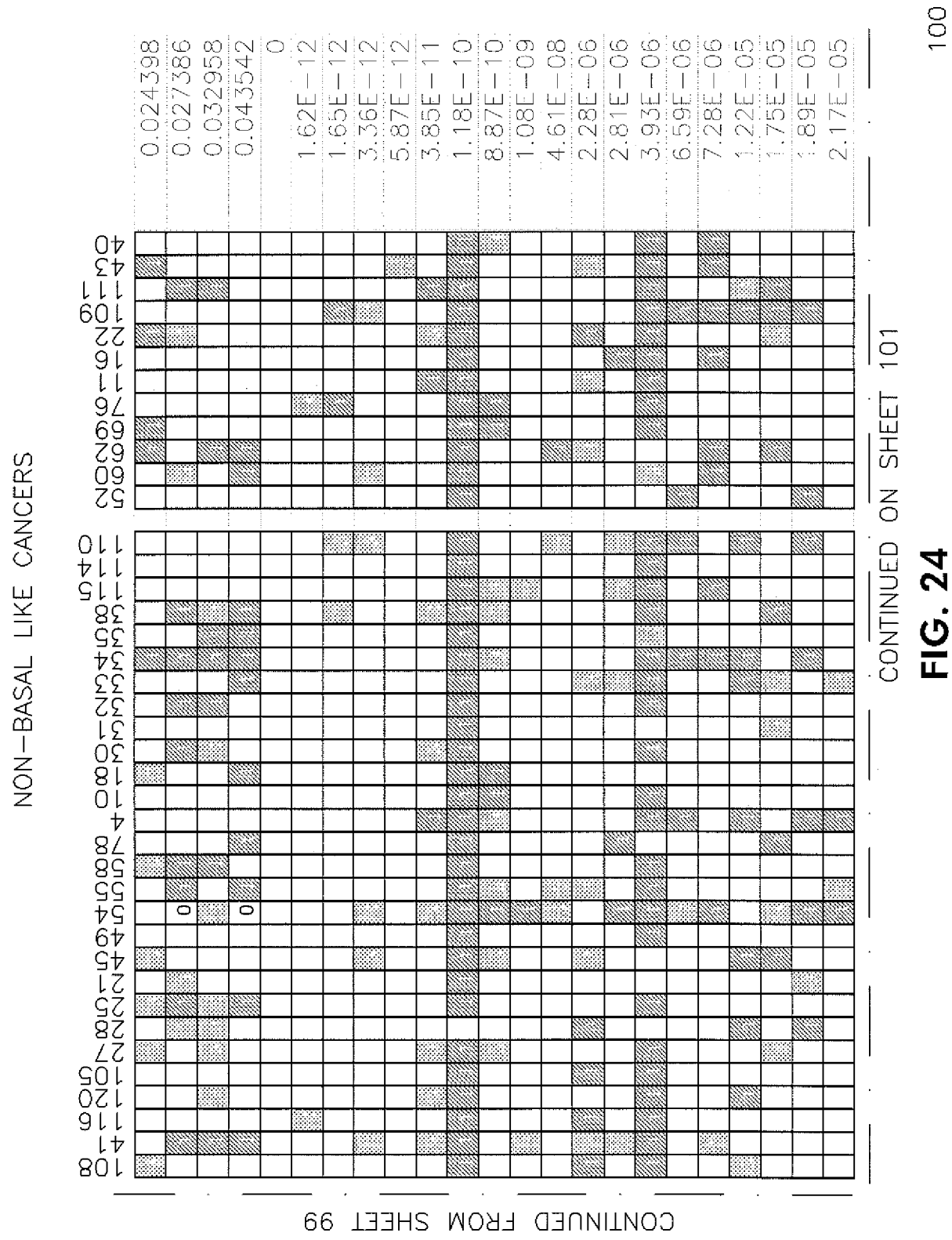

CONTINUED FROM SHEET 99
NON-BASAL LIKE CANCERS
0.024398
0.027386
0.032958
0.043542
0
1.62E-12
1.65E-12
3.36E-12
5.87E-12
3.85E-11
1.18E-10
8.87E-10
1.08E-09
4.61E-08
2.28E-06
2.81E-06
3.93E-06
6.59E-06
7.28E-06
1.22E-05
1.75E-05
1.89E-05
2.17E-05
CONTINUED ON SHEET 101

FIG. 24

100

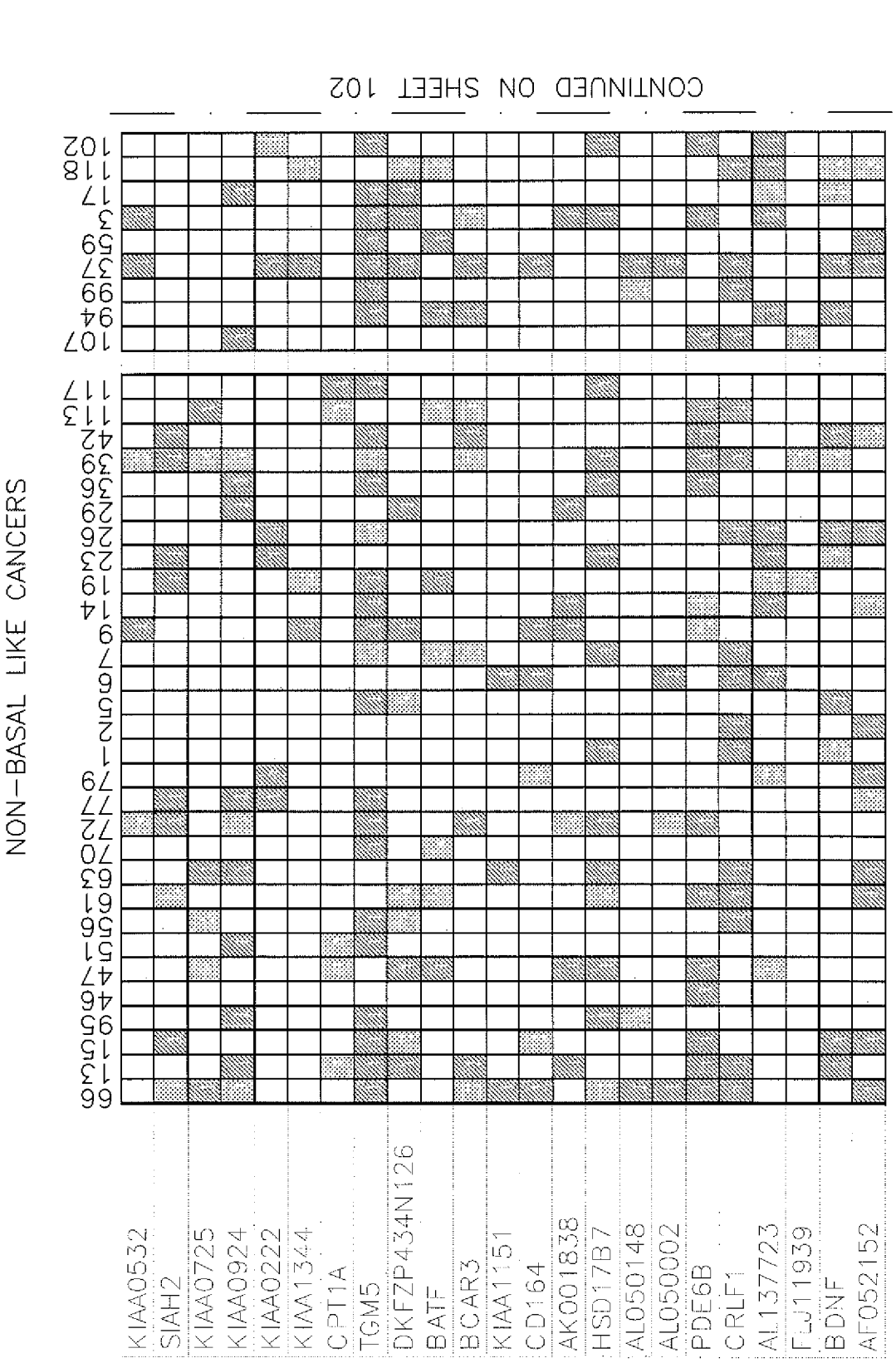

NON-BASAL LIKE CANCERS
CONTINUED ON SHEET 102
KIAA0532
SIAH2
KIAA0725
KIAA0924
KIAA0222
KIAA1344
CPT1A
TGM5
DKFZP434N126
BATF
BCAR3
KIAA1151
CD164
AK001838
HSD17B7
AL050148
AL050002
PDE6B
CRLF1
AL137723
FLJ11939
BDNF
AF052152

FIG. 24

101

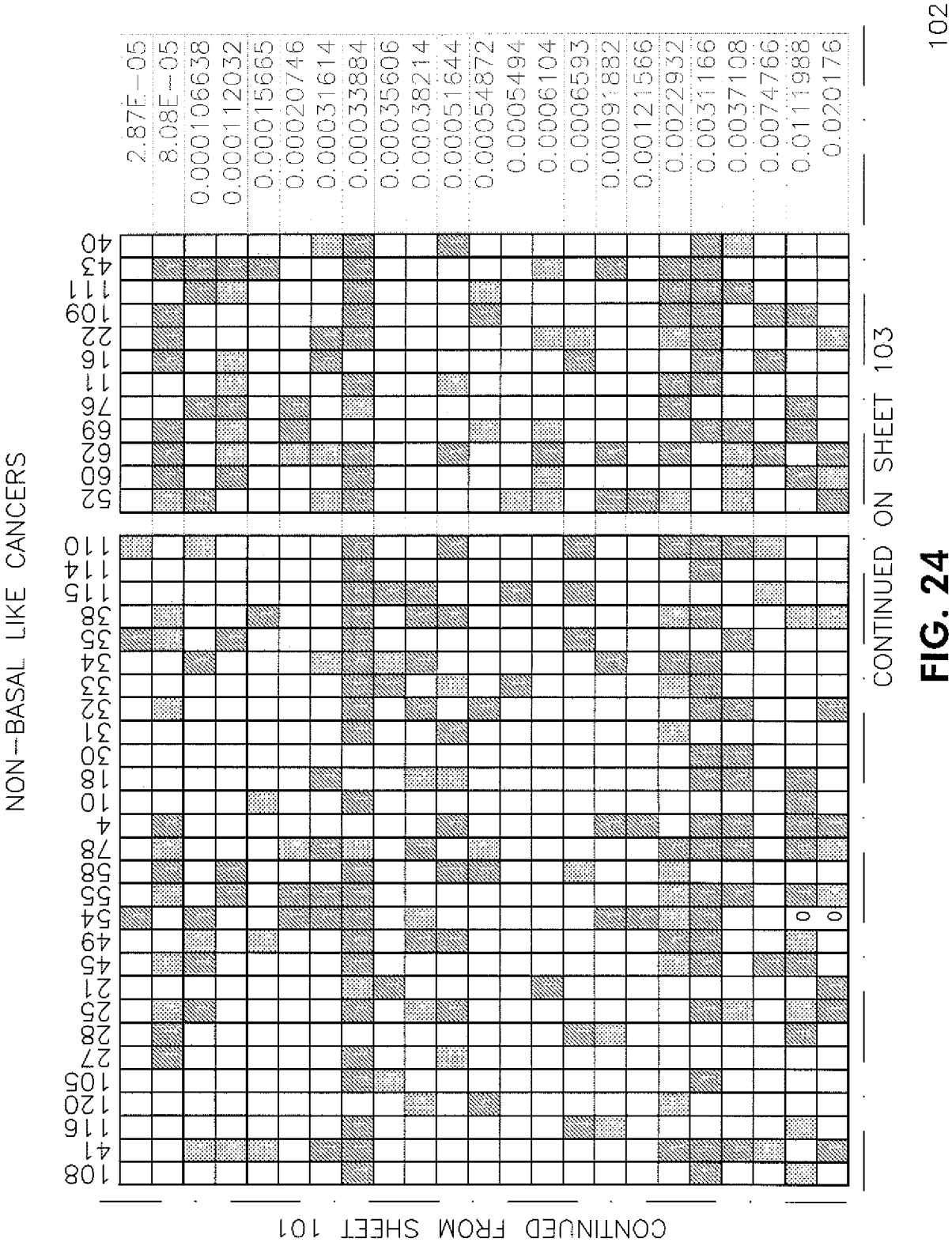

NON-BASAL LIKE CANCERS
CONTINUED FROM SHEET 101
CONTINUED ON SHEET 103
102
2.87E-05
8.08E-05
0.000106638
0.000112032
0.000115665
0.000120746
0.000131614
0.000133884
0.000135606
0.000138214
0.000151644
0.000154872
0.000205494
0.000206104
0.000206593
0.000209882
0.000121566
0.000122932
0.000131166
0.000137108
0.000174766
0.001119988
0.020176

FIG. 24

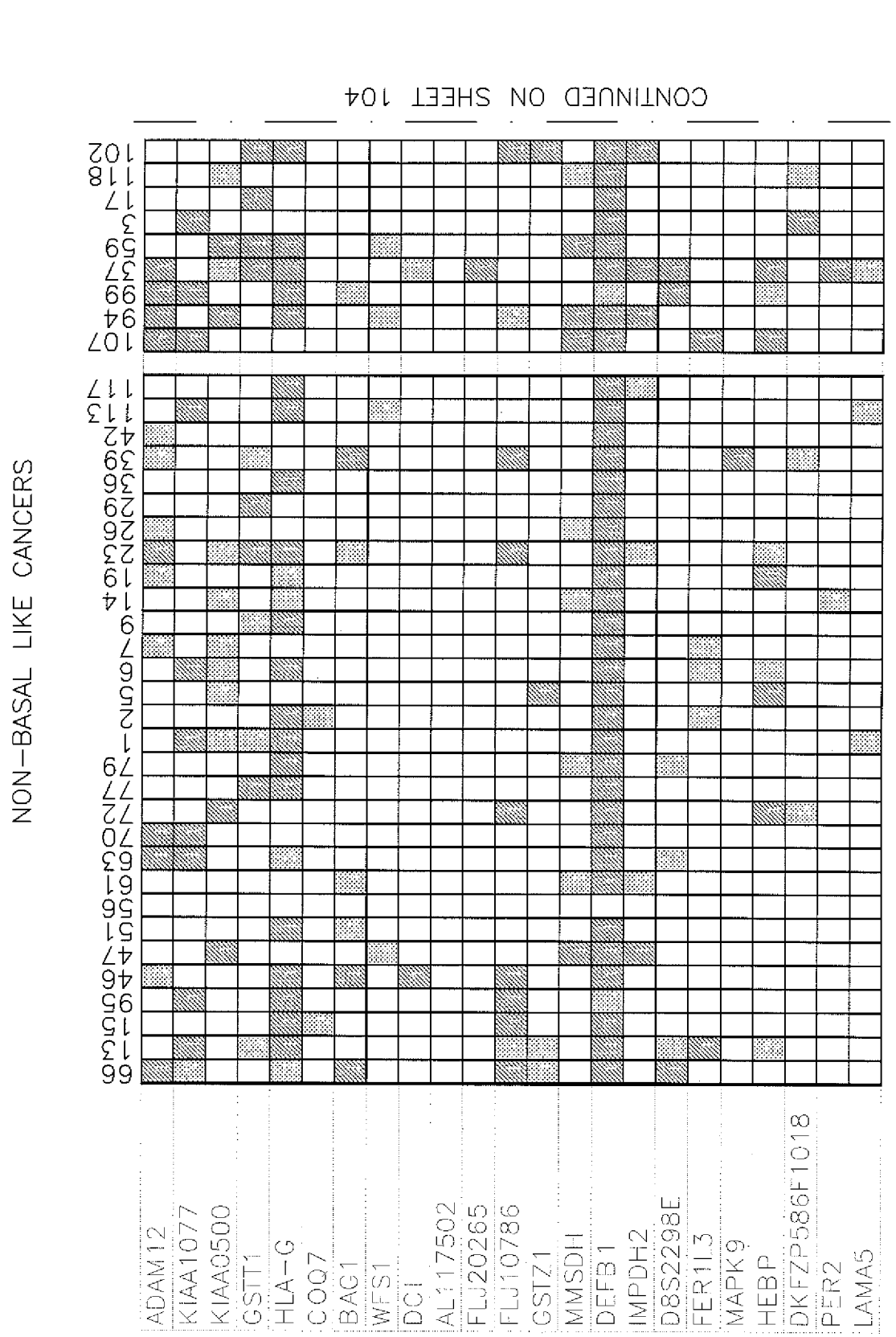

NON-BASAL LIKE CANCERS
CONTINUED ON SHEET 104
ADAM12
KIAA1077
KIAA0500
GSTT1
HLA-G
COQ7
BAG1
WFS1
DCI
AL117502
FLJ20265
FLJ10786
GSTZ1
MMSDH
DEFB1
IMPDH2
D8S2298E
FER1L3
MAPK9
HEBP
DKFZP586F1018
PER2
LAMA5

FIG. 24

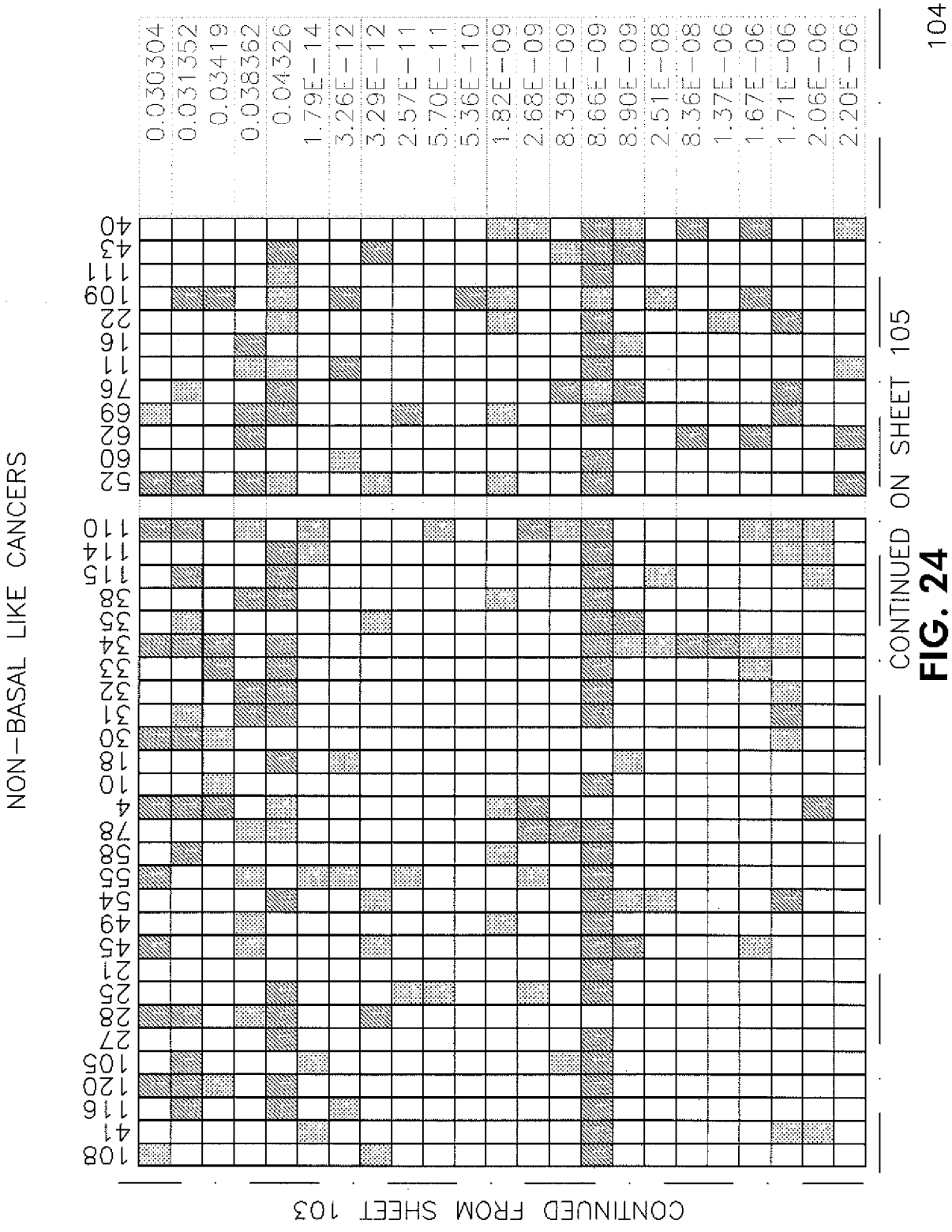
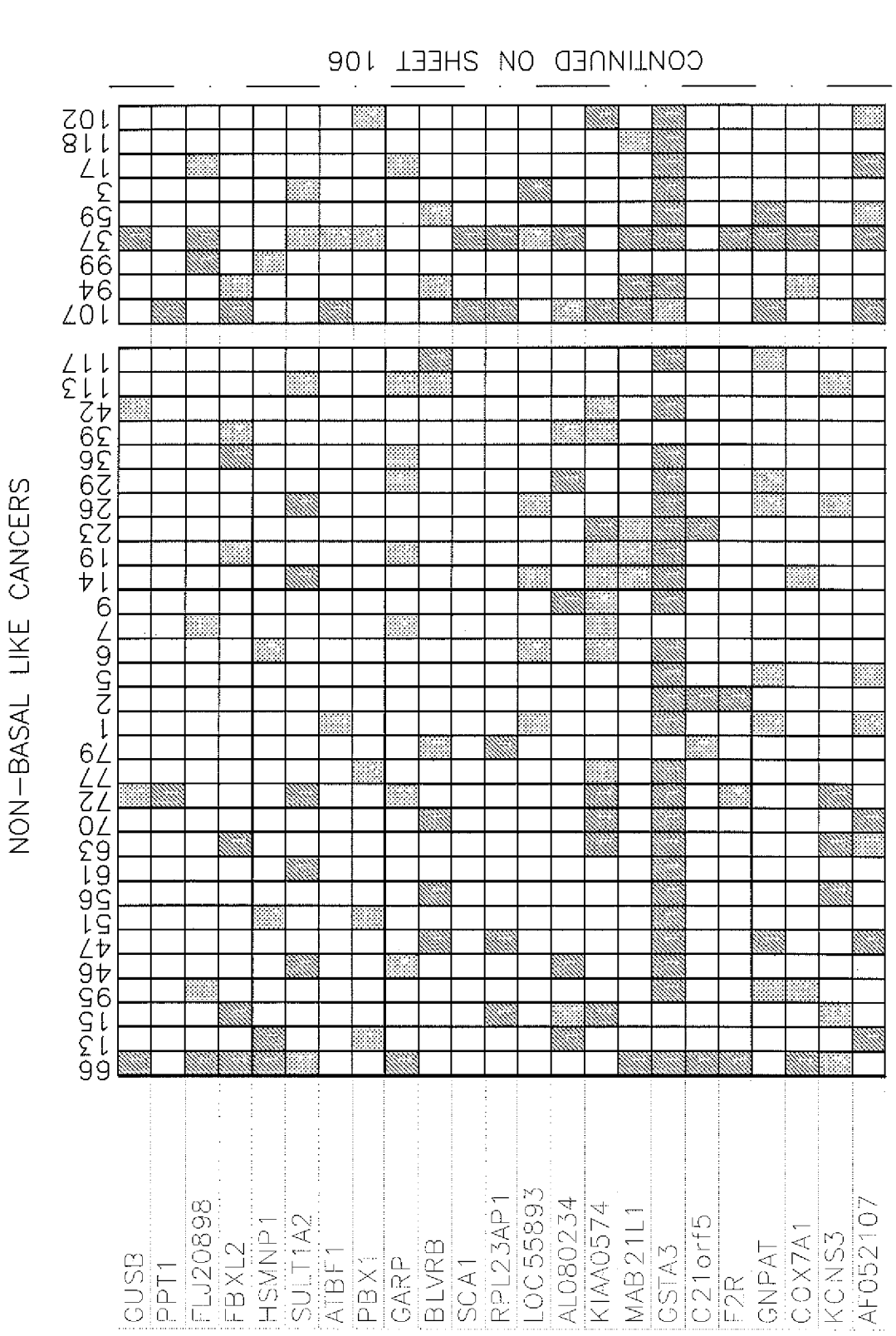

CONTINUED FROM SHEET 103
NON-BASAL LIKE CANCERS
0.030304
0.031352
0.03419
0.038362
0.04326
1.79E-14
3.26E-12
3.29E-12
2.57E-11
5.70E-11
5.36E-10
1.82E-09
2.68E-09
8.39E-09
8.66E-09
8.90E-09
2.51E-08
8.36E-08
1.37E-06
1.67E-06
1.71E-06
2.06E-06
2.20E-06
CONTINUED ON SHEET 105

FIG. 24

104


NON-BASAL LIKE CANCERS
CONTINUED ON SHEET 106
GUSB
PPT1
FLJ20898
FBXL2
HSMNP1
SULT1A2
ATBF1
PBX1
GARP
BLVRB
SCA1
RPL23AP1
LOC55893
AL080234
KIAA0574
MAB21L1
GSTA3
C21orf5
F2R
GNPAT
COX7A1
KCNS3
AF052107

105

FIG. 24

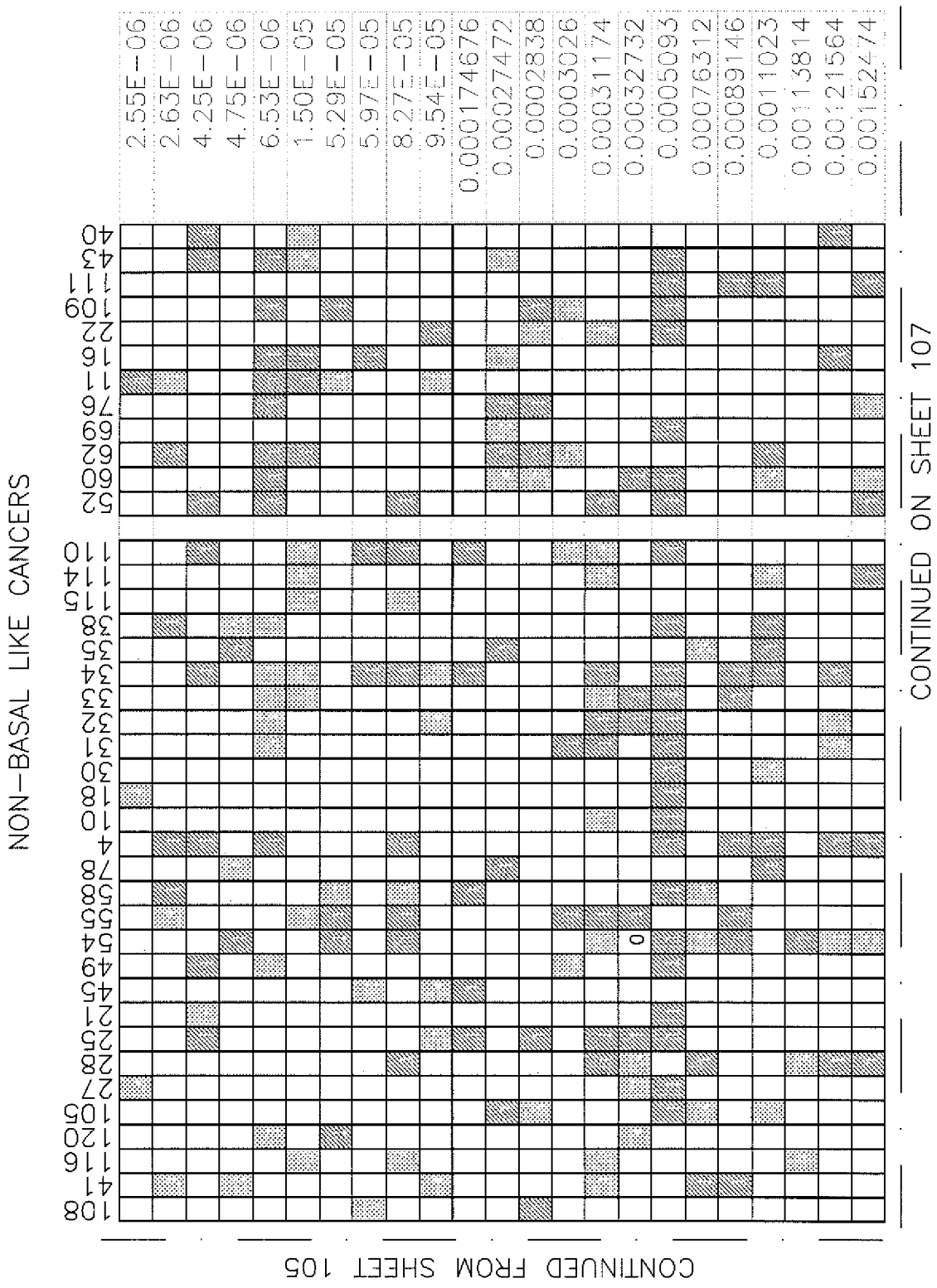

NON-BASAL LIKE CANCERS
CONTINUED FROM SHEET 105
CONTINUED ON SHEET 107
106
2.55E-06
2.63E-06
4.25E-06
4.75E-06
6.53E-06
1.50E-05
5.29E-05
5.97E-05
8.27E-05
9.54E-05
0.000174676
0.00027472
0.00028838
0.00033026
0.00031174
0.00032732
0.00035093
0.00076312
0.00089146
0.00111023
0.00113814
0.00121564
0.00152474

FIG. 24

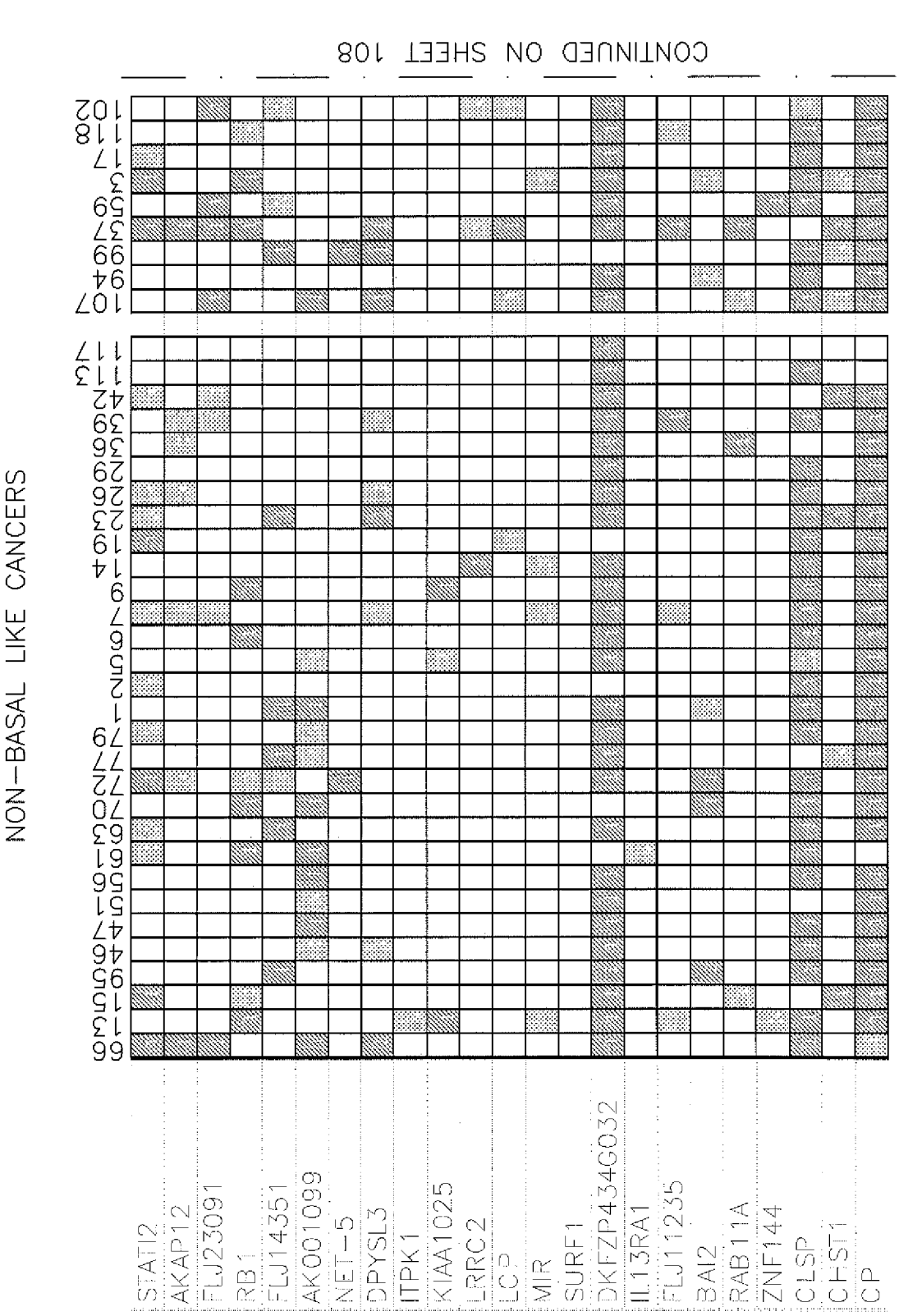

NON-BASAL LIKE CANCERS
CONTINUED ON SHEET 108
STAT2
AKAP12
FLJ23091
RB1
FLJ14351
AK001099
NET-5
DPYSL3
ITPK1
KIAA1025
LRRC2
LCP
MIR
SURF1
DKFZP434G032
IL13RA1
FLJ11235
BAI2
RAB11A
ZNF144
CLSP
CHST1
CP

FIG. 24

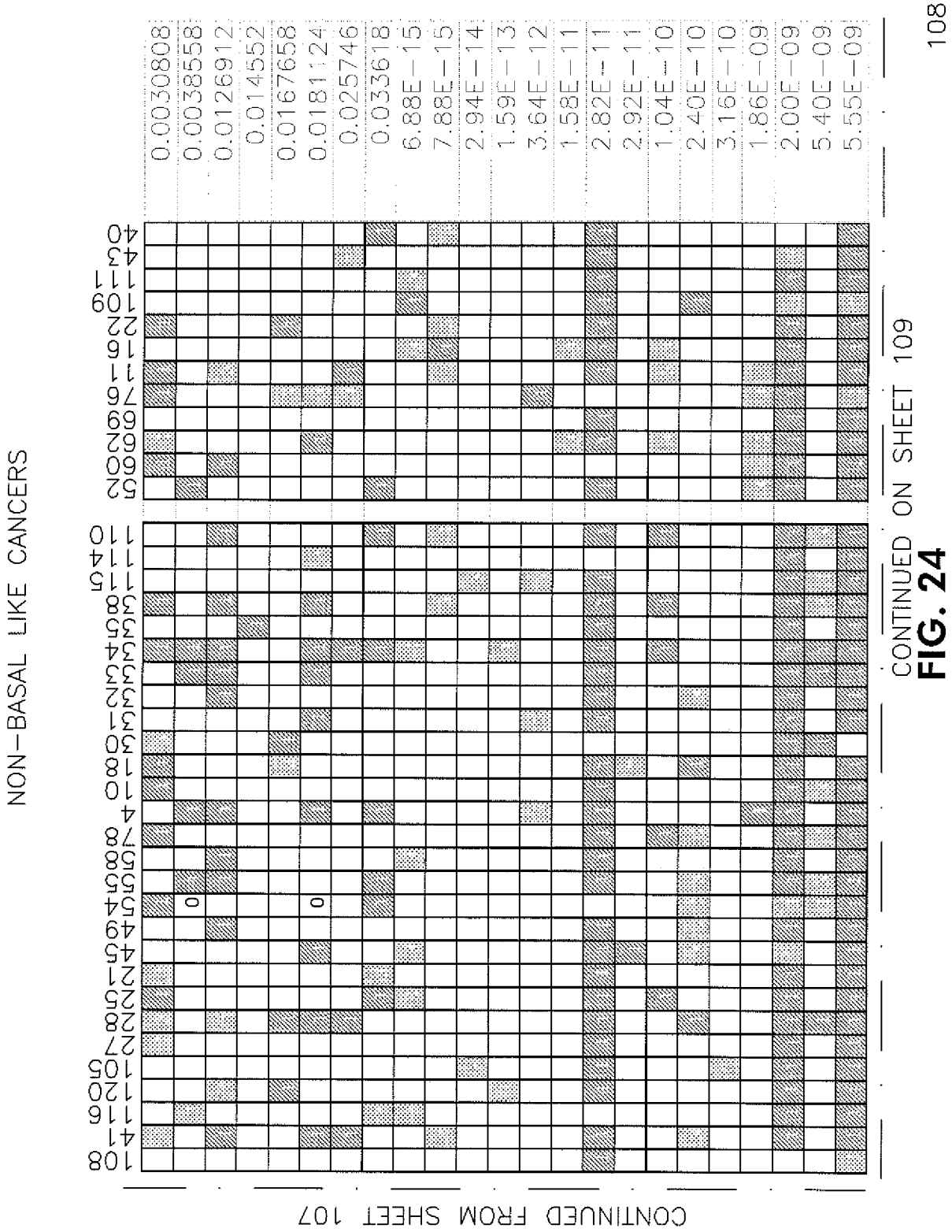

NON-BASAL LIKE CANCERS
CONTINUED FROM SHEET 107
CONTINUED ON SHEET 109
108
0.0030808
0.0038558
0.0126912
0.014552
0.0167658
0.0181124
0.025746
0.033618
6.88E-15
7.88E-15
2.94E-14
1.59E-13
3.64E-12
1.58E-11
2.82E-11
2.92E-11
1.04E-10
2.40E-10
3.16E-10
1.86E-09
2.00E-09
5.40E-09
5.55E-09

FIG. 24

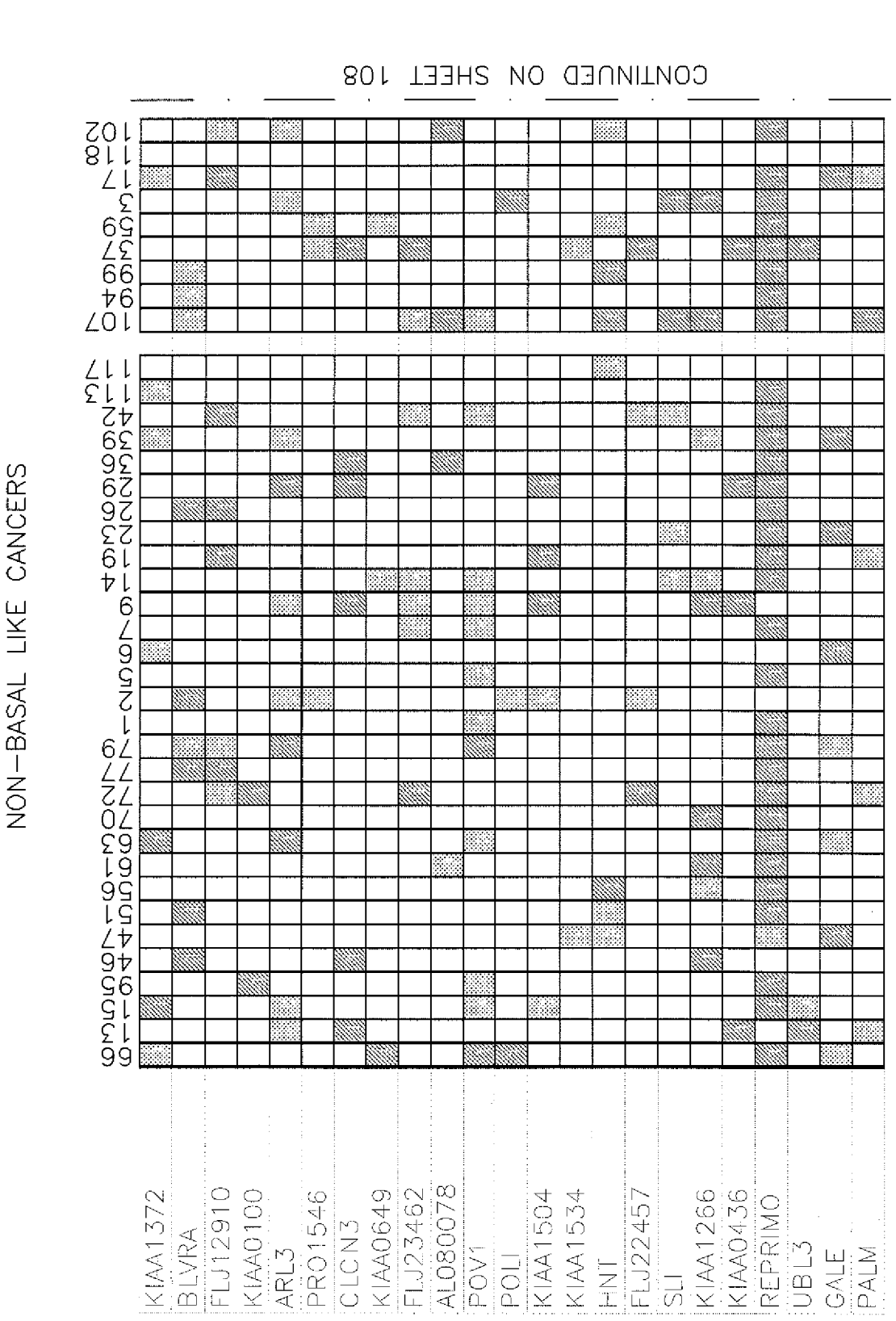

NON-BASAL LIKE CANCERS
CONTINUED ON SHEET 108
KIAA1372
BLVRA
FLJ12910
KIAA0100
ARL3
PRO1546
CLCN3
KIAA0649
FLJ23462
AL080078
POV1
POL1
KIAA1504
KIAA1534
HNT
FLJ22457
SLI
KIAA1266
KIAA0436
REPRIMO
UBL3
GALE
PALM

FIG. 24

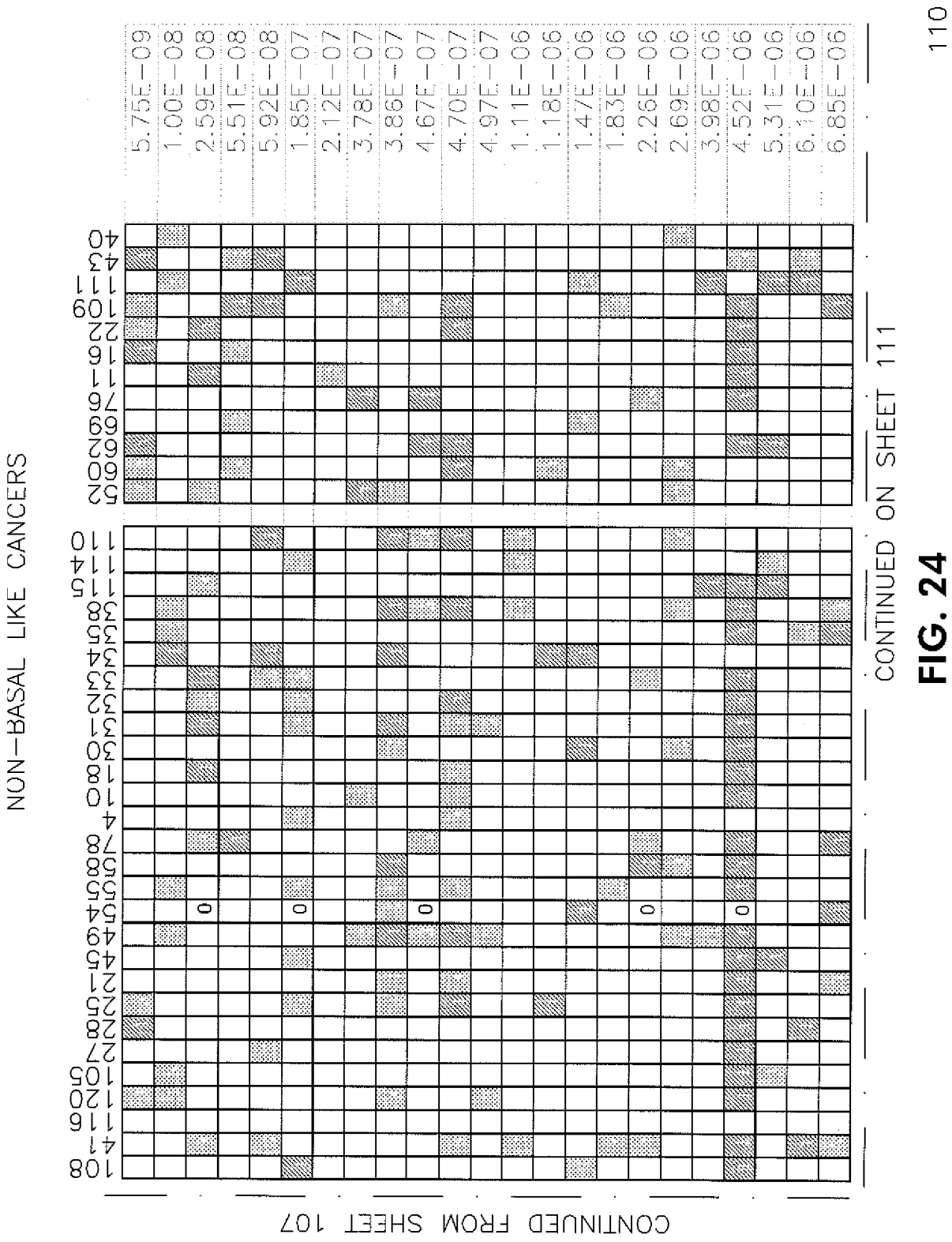

NON-BASAL LIKE CANCERS
CONTINUED FROM SHEET 107
CONTINUED ON SHEET 111
5.75E-09
1.00E-08
2.59E-08
5.51E-08
5.92E-08
1.85E-07
2.12E-07
3.78E-07
3.86E-07
1.67E-07
4.70E-07
4.97E-07
1.11E-06
1.18E-06
1.47E-06
1.83E-06
2.26E-06
2.69E-06
3.98E-06
4.52E-06
5.31E-06
6.10E-06
6.85E-06
52 60 62 69 76 11 16 22 109 111 43 40
110 114 115 38 35 34 33 32 31 30 18 10 4 78 58 55 54 49 45 21 25 28 27 105 120 116 41 108

FIG. 24

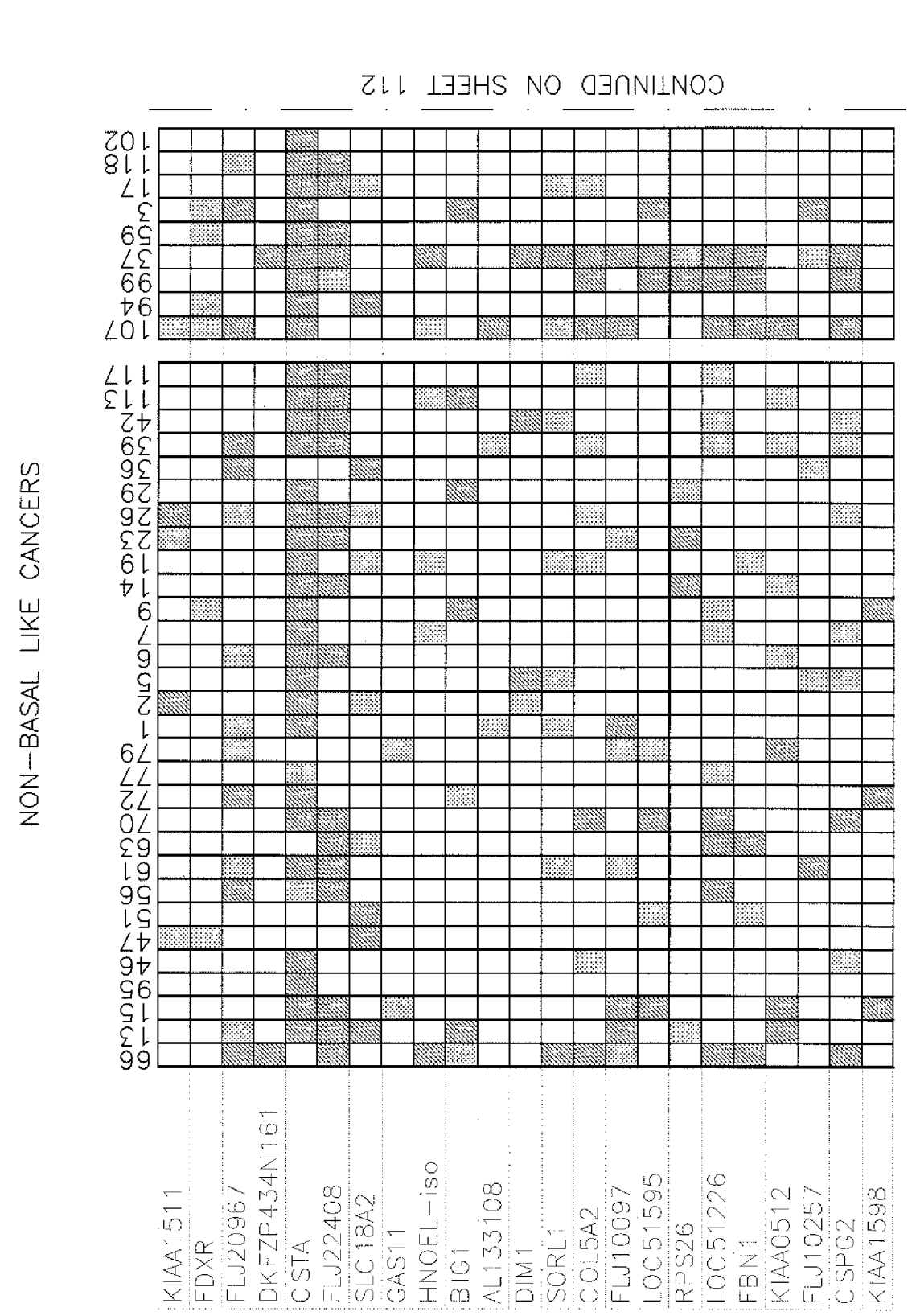
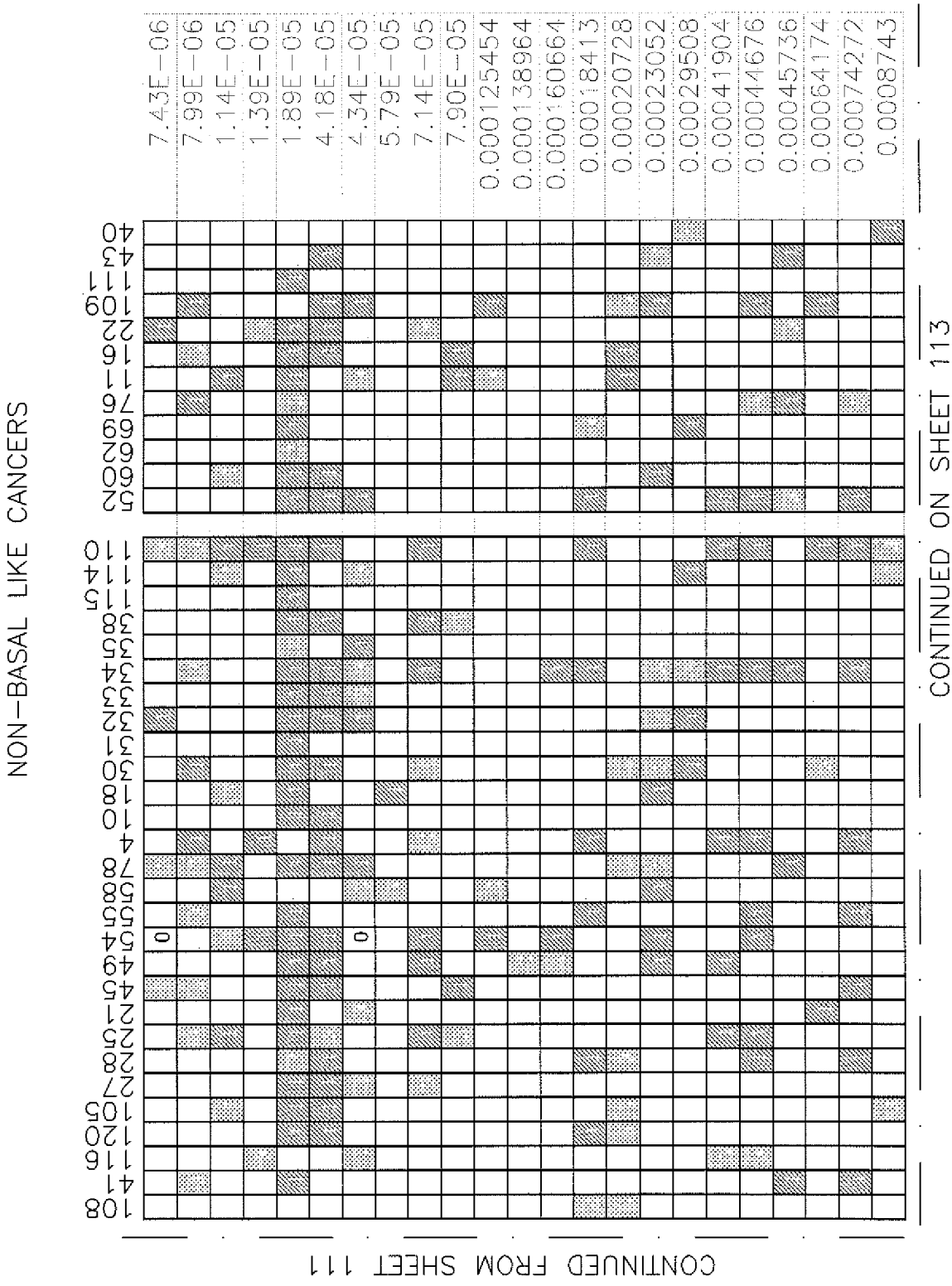

NON-BASAL LIKE CANCERS
CONTINUED ON SHEET 112
KIAA1511
FDXR
FLJ20967
DKFZP434N161
CSTA
FLJ22408
SLC18A2
GAS11
HNOEL-iso
BIG1
AL133108
DIM1
SORL1
COL5A2
FLJ10097
LOC51595
RPS26
LOC51226
FBN1
KIAA0512
FLJ10257
CSPG2
KIAA1598

FIG. 24


NON-BASAL LIKE CANCERS
CONTINUED FROM SHEET 111
CONTINUED ON SHEET 113
7.43E-06
7.99E-06
1.14E-05
1.39E-05
1.89E-05
4.18E-05
4.34E-05
5.79E-05
7.14E-05
7.90E-05
0.000125454
0.000138964
0.000160664
0.000184413
0.000207228
0.000230352
0.000295908
0.000419047
0.000446765
0.000457360
0.000641744
0.000742720
0.000874343

112

FIG. 24

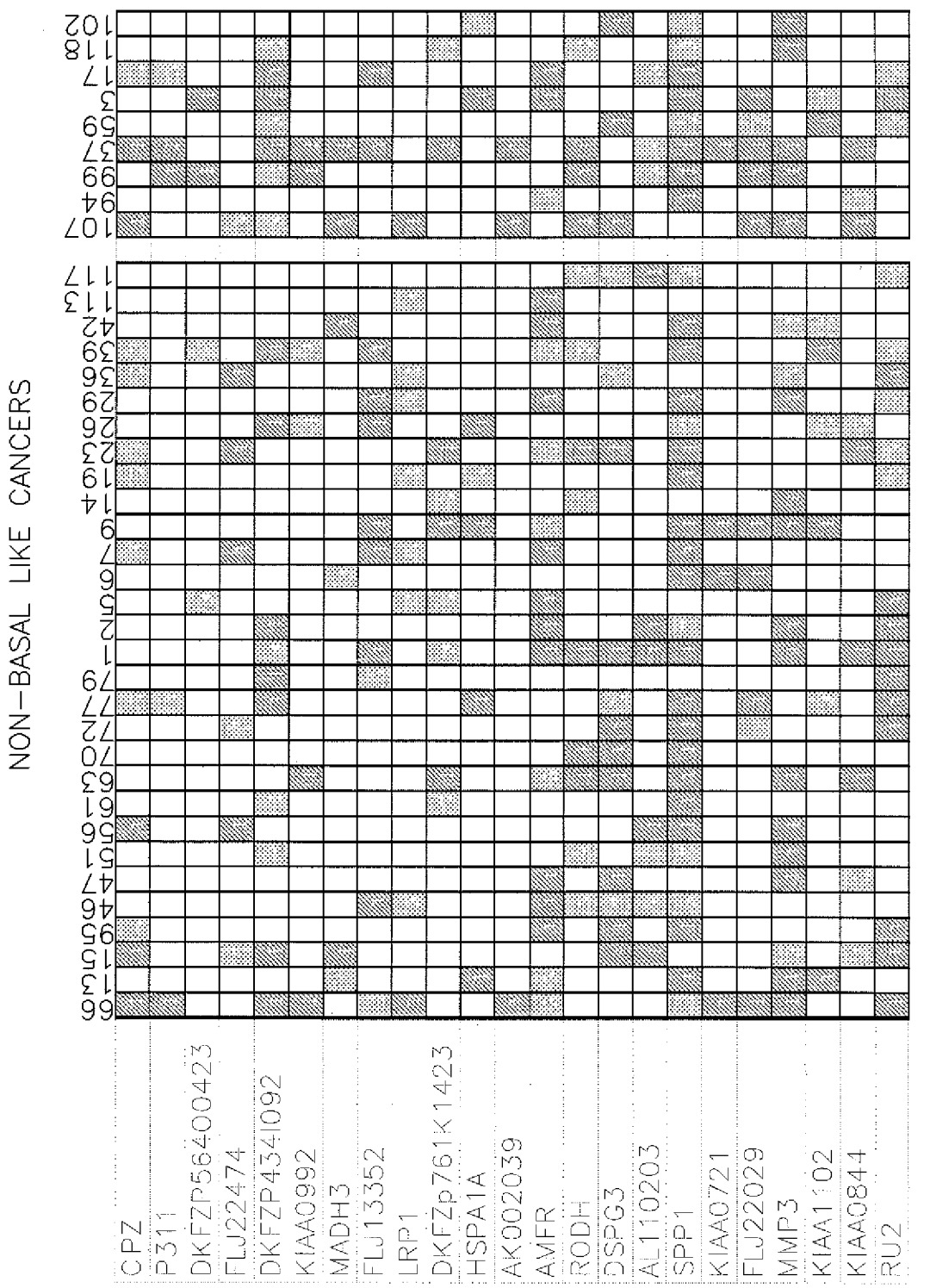

NON-BASAL LIKE CANCERS
CONTINUED ON SHEET 114
CPZ
P311
DKFZP564O0423
FLJ22474
DKFZP434I092
KIAA0992
MADH3
FLJ13352
LRP1
DKFZp761K1423
HSPA1A
AK002039
AMFR
RODH
DSPG3
AL110203
SPP1
KIAA0721
FLJ22029
MMP3
KIAA1102
KIAA0844
RU2

FIG. 24

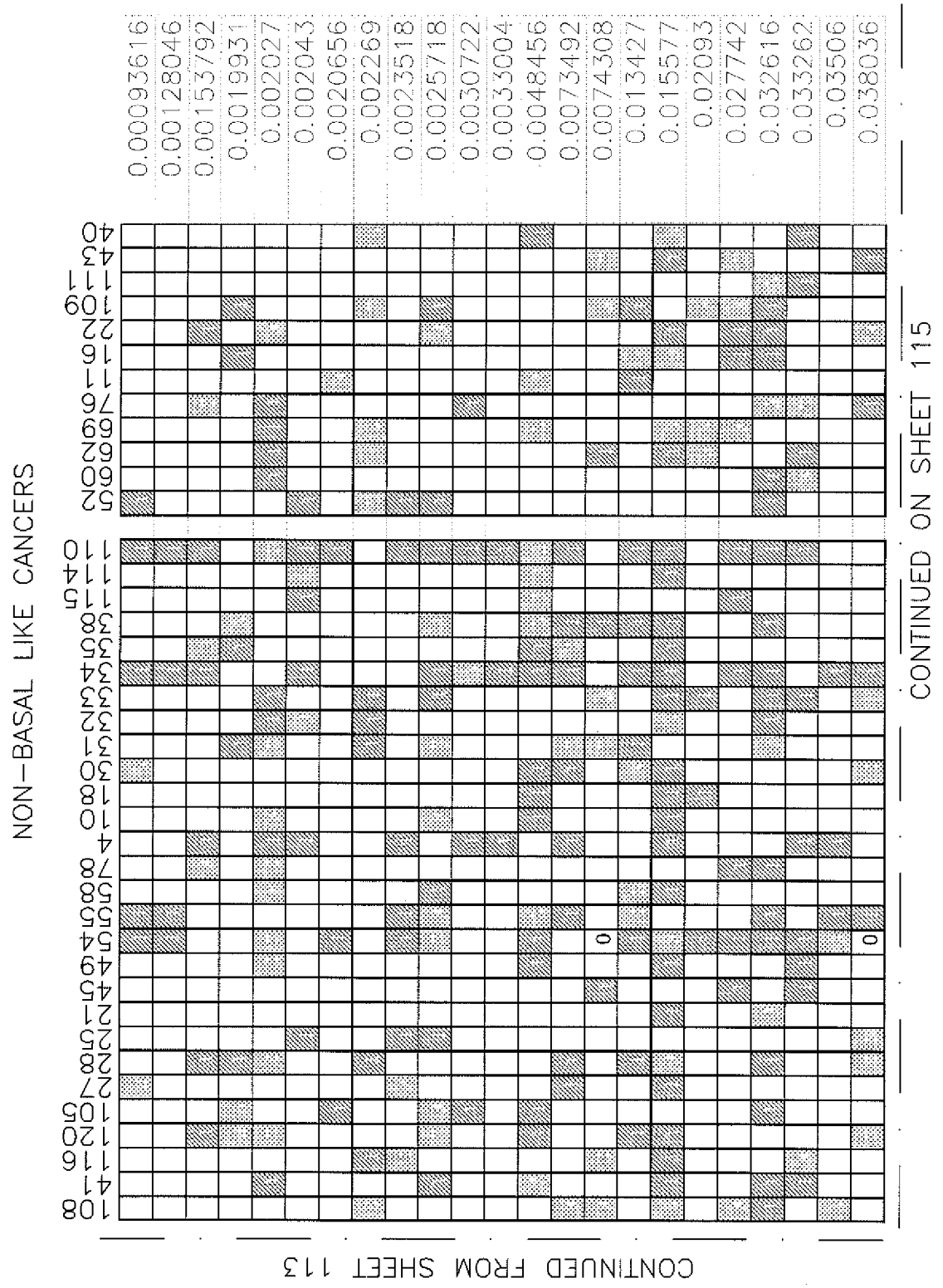

CONTINUED FROM SHEET 113
NON-BASAL LIKE CANCERS
108 41 116 120 105 27 28 25 21 45 49 54 55 58 78 10 18 30 31 32 33 34 35 38 115 114 110
52 60 62 69 76 11 16 22 109 11 43 40
0.00093616
0.00128046
0.00153792
0.0019931
0.002027
0.002043
0.0020656
0.002269
0.0023518
0.0025718
0.0030722
0.0033004
0.0048456
0.0073492
0.0074308
0.013427
0.015577
0.02093
0.027742
0.032616
0.033262
0.03506
0.038036
CONTINUED ON SHEET 115

FIG. 24

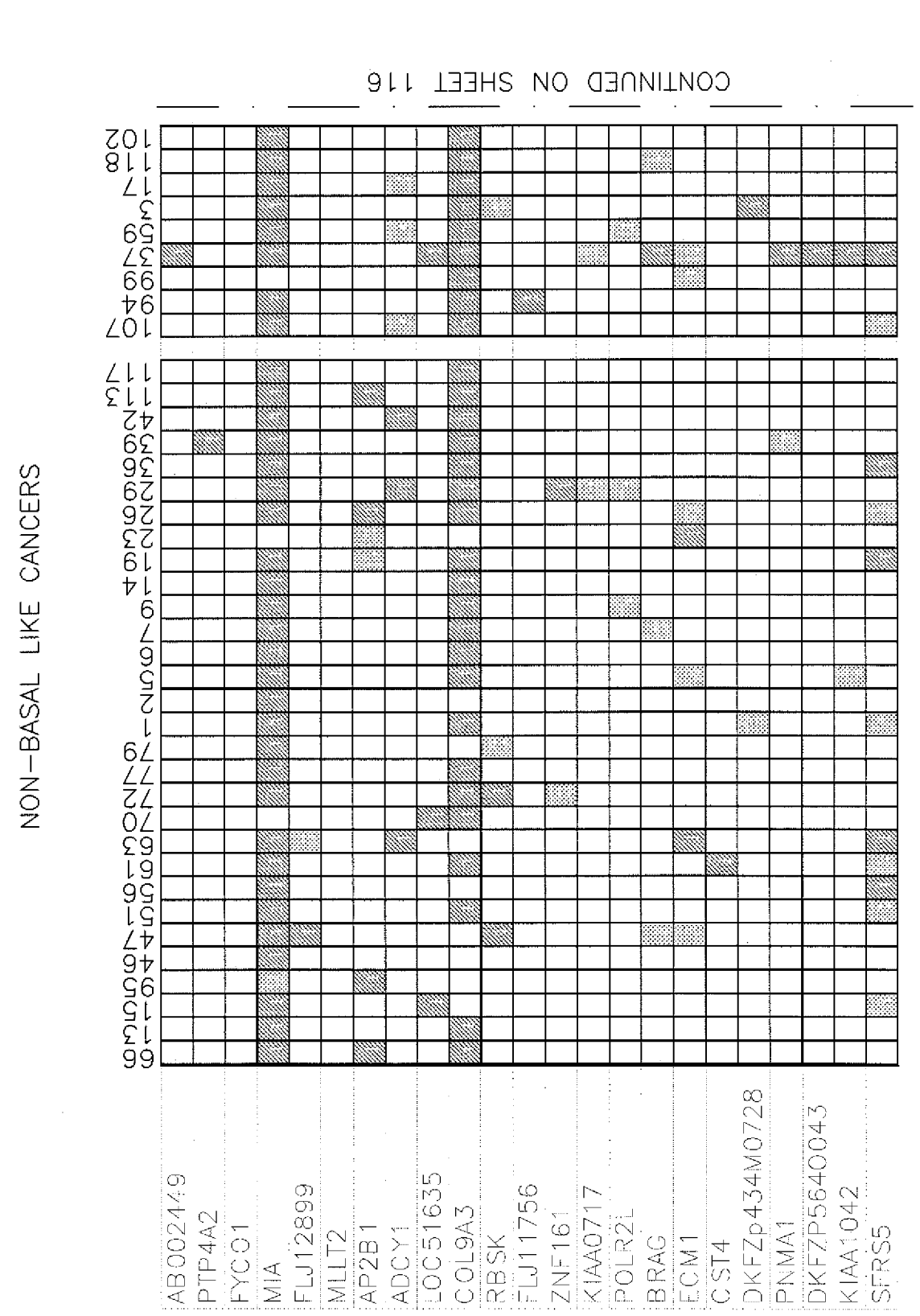

NON-BASAL LIKE CANCERS
CONTINUED ON SHEET 116
ABO02449
PTP4A2
FYCO1
MIA
FLJ12899
MLLT2
AP2B1
ADCY1
LOC51635
COL9A3
RBSK
FLJ11756
ZNF161
KIAA0717
POLR2L
BRAG
ECM1
CST4
DKFZp434M0728
PNMA1
DKFZP564O043
KIAA1042
SFRS5

FIG. 24

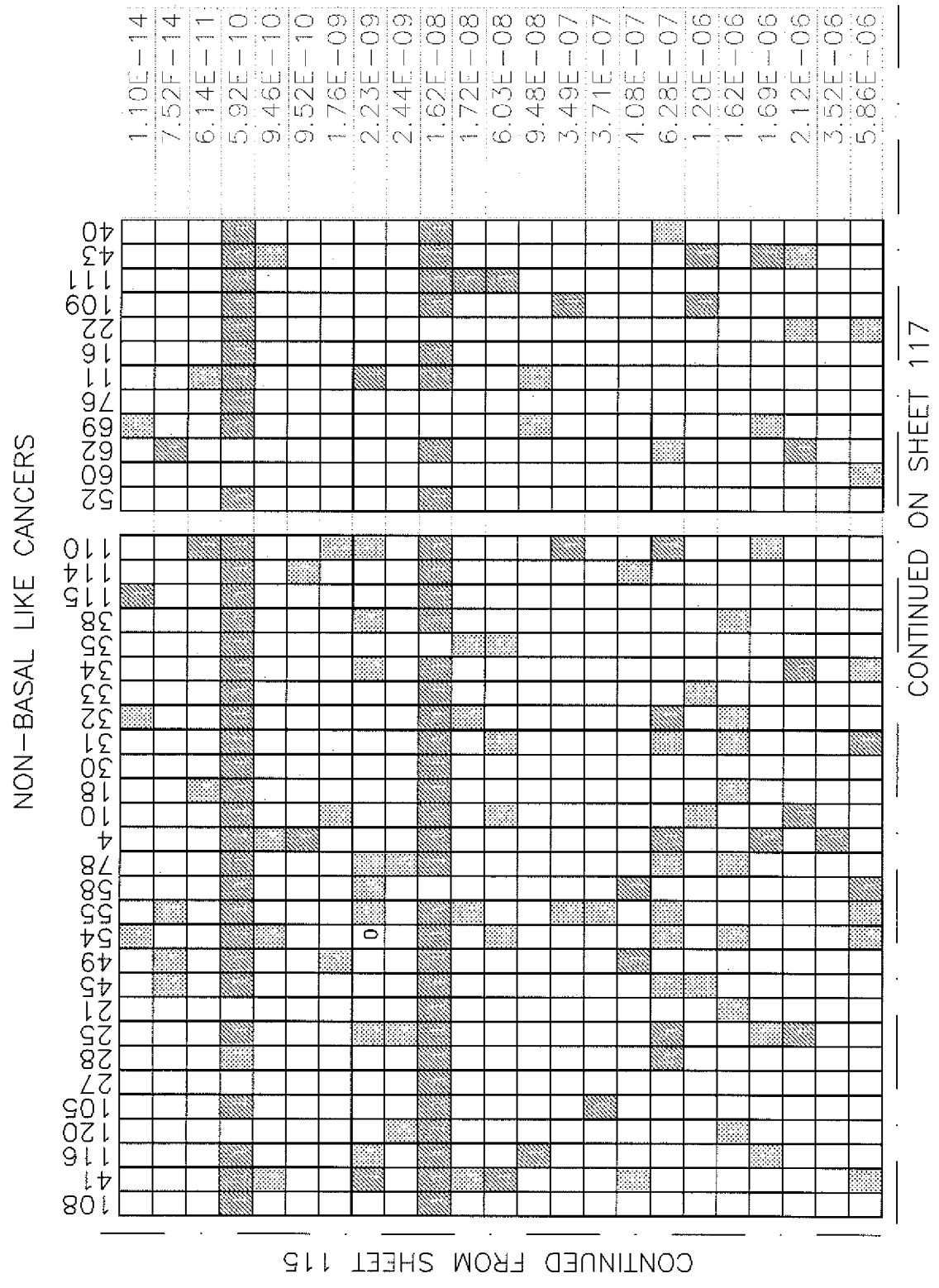

CONTINUED FROM SHEET 115
NON-BASAL LIKE CANCERS
1.10E-14
7.52E-14
6.14E-11
5.92E-10
9.46E-10
9.52E-10
1.76E-09
2.23E-09
2.44E-09
1.62E-08
1.72E-08
6.03E-08
9.48E-08
3.49E-07
3.71E-07
4.08E-07
6.28E-07
1.20E-06
1.62E-06
1.69E-06
2.12E-06
3.52E-06
5.86E-06
CONTINUED ON SHEET 117

FIG. 24

116

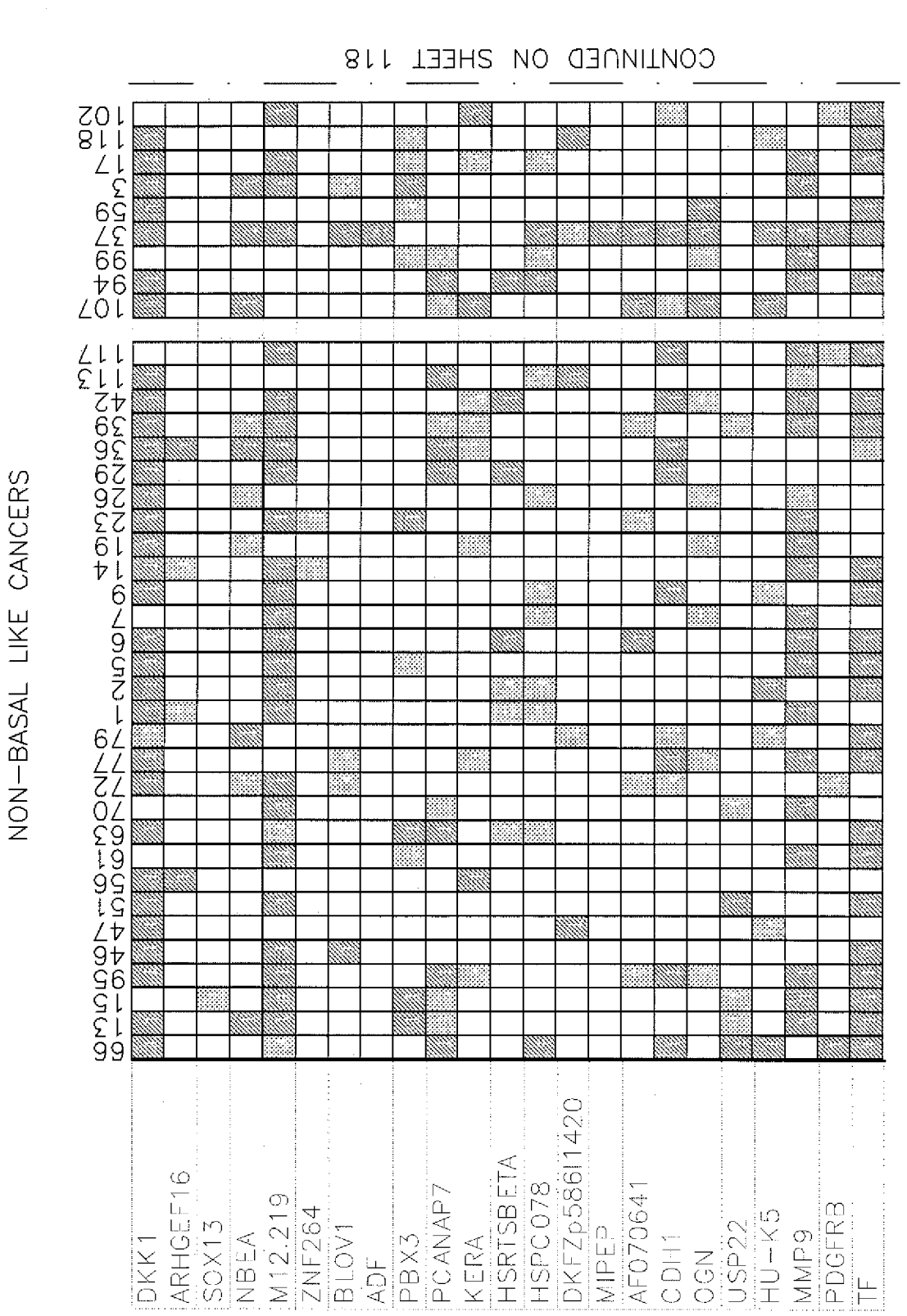

NON-BASAL LIKE CANCERS
DKK1
ARHGEF16
SOX13
NBEA
M12.219
ZNF264
BLOV1
ADF
PBX3
PCANAP7
KERA
HSRTSBETA
HSPC078
DKFZp586I1420
MIPEP
AF070641
CDH1
OGN
USP22
HU-K5
MMP9
PDGFRB
TF
CONTINUED ON SHEET 118

FIG. 24

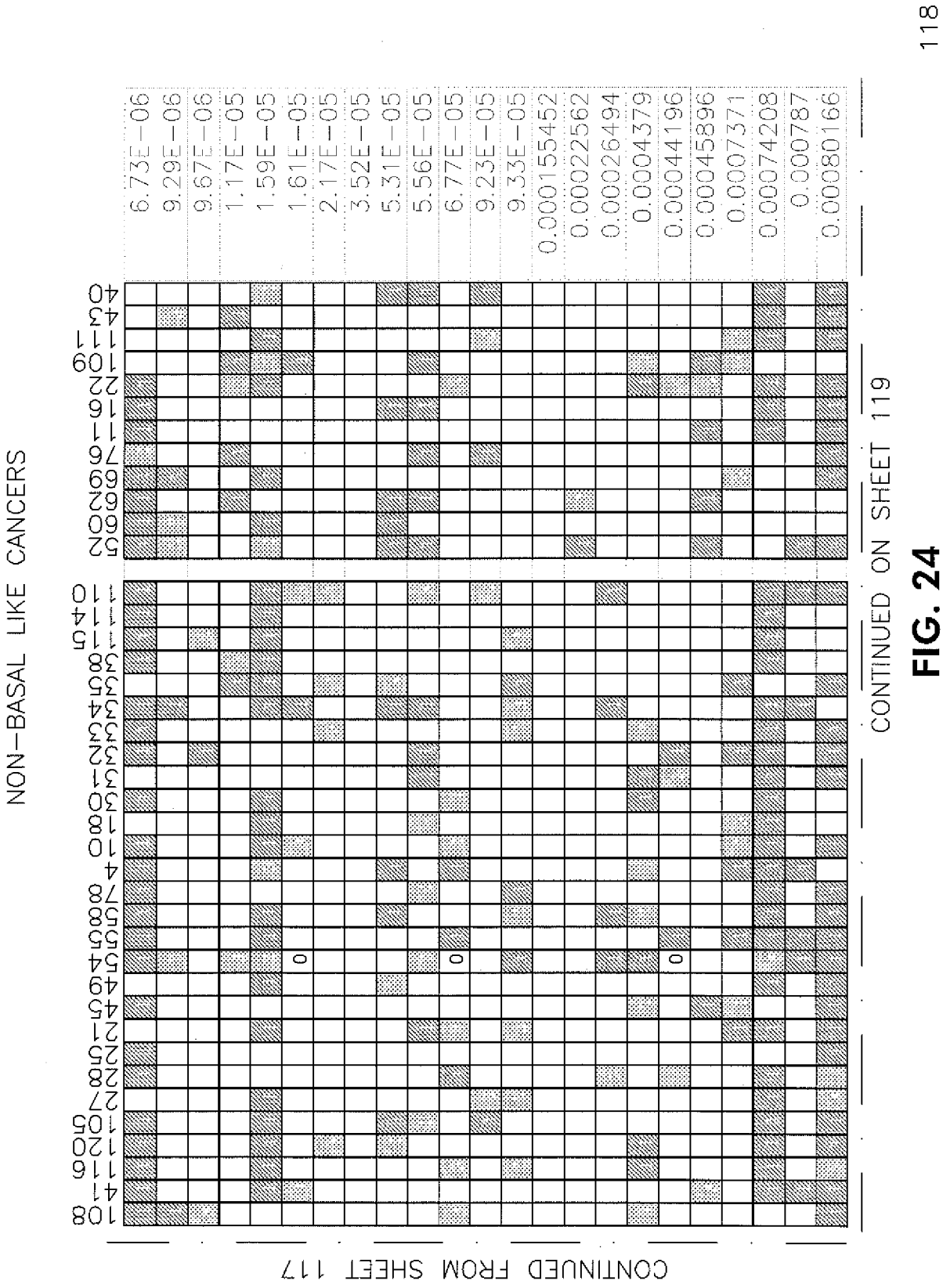

NON-BASAL LIKE CANCERS
CONTINUED FROM SHEET 117
CONTINUED ON SHEET 119
6.73E-06
9.29E-06
9.67E-06
1.17E-05
1.59E-05
1.61E-05
2.17E-05
3.52E-05
5.31E-05
5.56E-05
6.77E-05
9.23E-05
9.33E-05
0.000155452
0.000225562
0.000264494
0.000437879
0.000441196
0.000458896
0.000737371
0.000742082
0.000787
0.000801666

FIG. 24

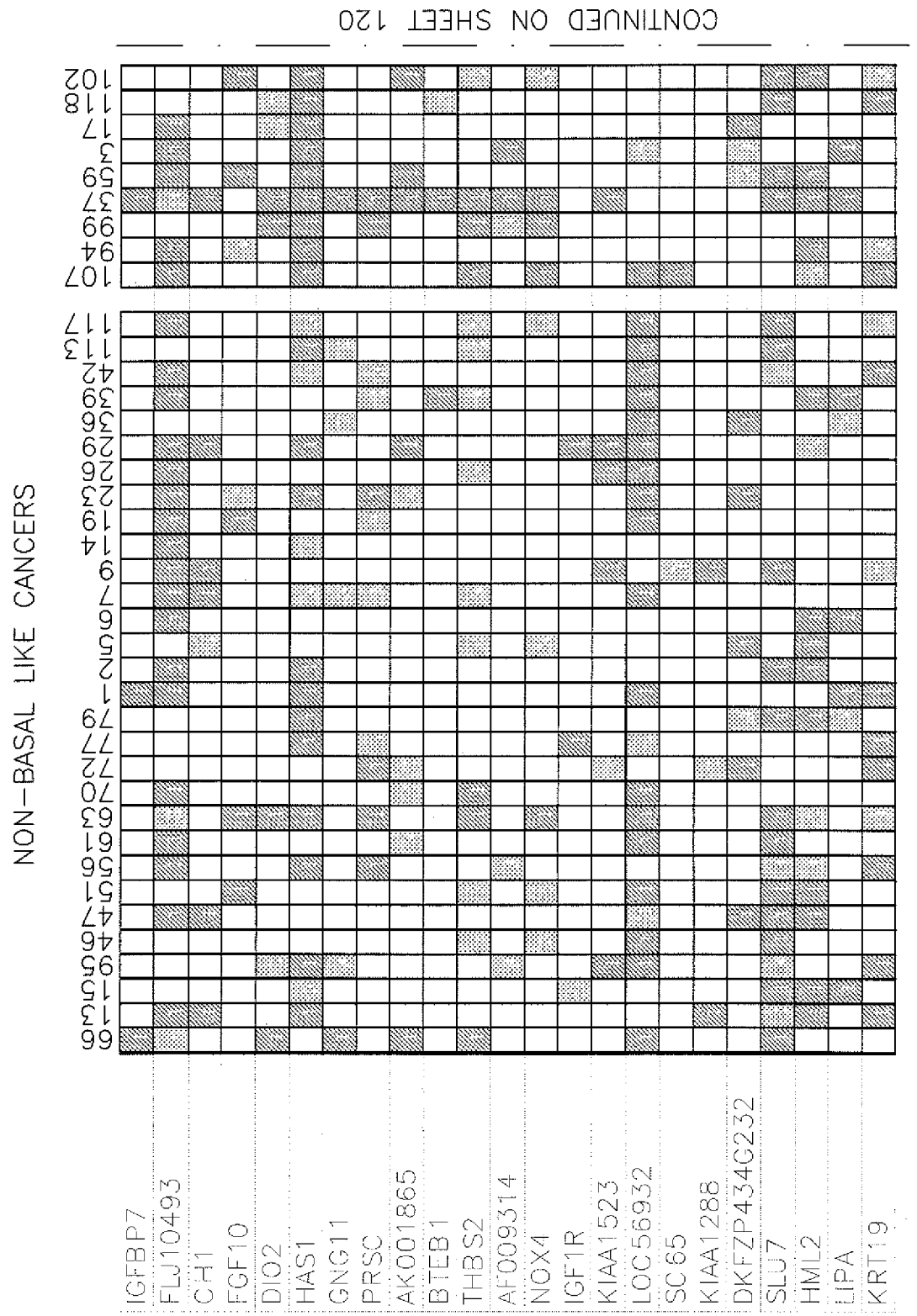
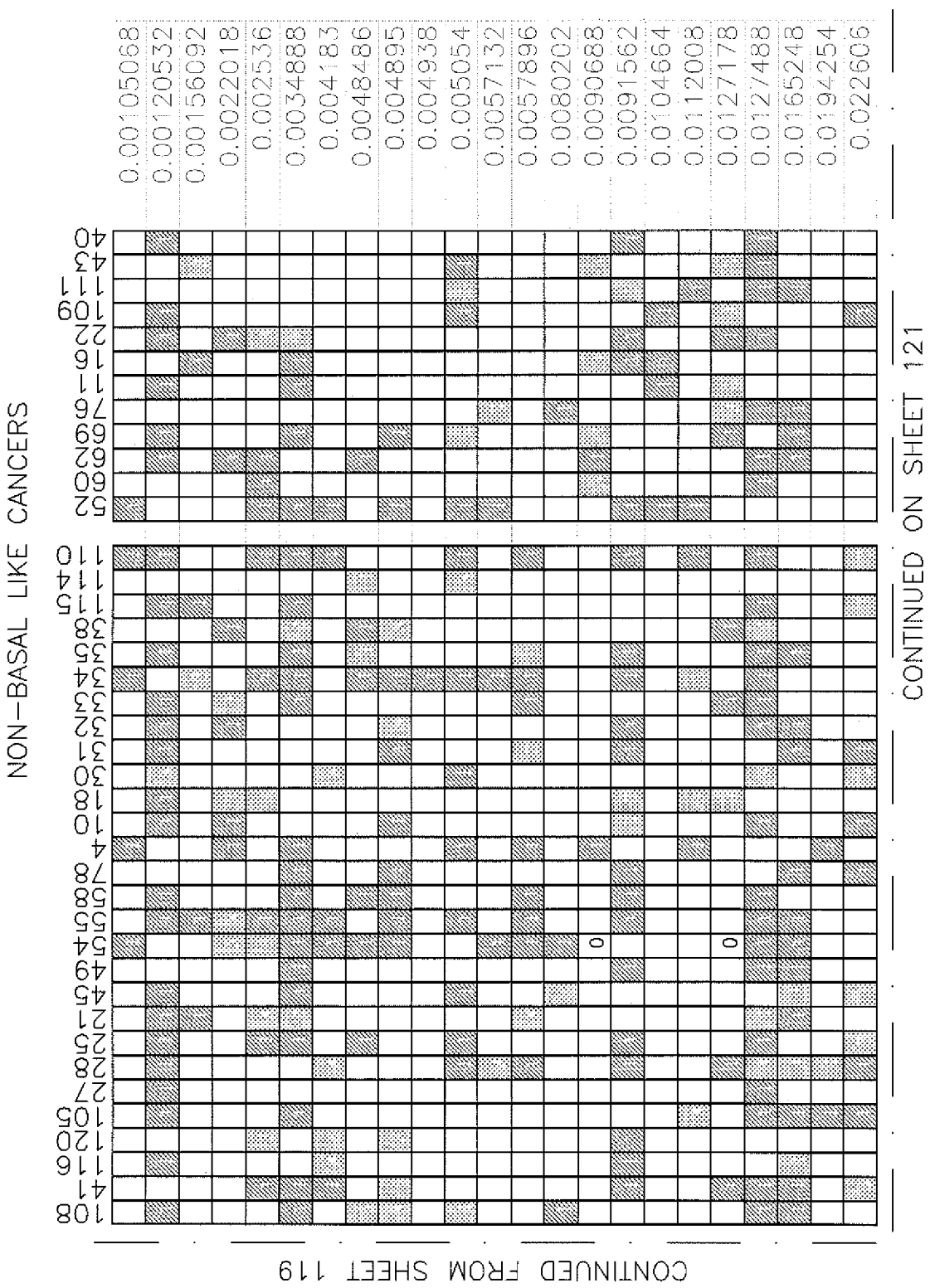

CONTINUED ON SHEET 120
NON-BASAL LIKE CANCERS
IGFBP7
FLJ10493
CH1
FGF10
DIO2
HAS1
GNG11
PRSC
AK001865
BTEB1
THBS2
AF009314
NOX4
IGF1R
KIAA1523
LOC56932
SC65
KIAA1288
DKFZP434G232
SLU7
HML2
LIPA
KRT19

FIG. 24


NON-BASAL LIKE CANCERS
CONTINUED FROM SHEET 119
CONTINUED ON SHEET 121
0.001105068
0.001120532
0.001156092
0.0022018
0.002536
0.0034888
0.004183
0.0048486
0.004895
0.004938
0.005054
0.0057132
0.0057896
0.0080202
0.0090688
0.0091562
0.0104664
0.0112008
0.0127178
0.012748
0.0165248
0.0194254
0.022606

120

FIG. 24

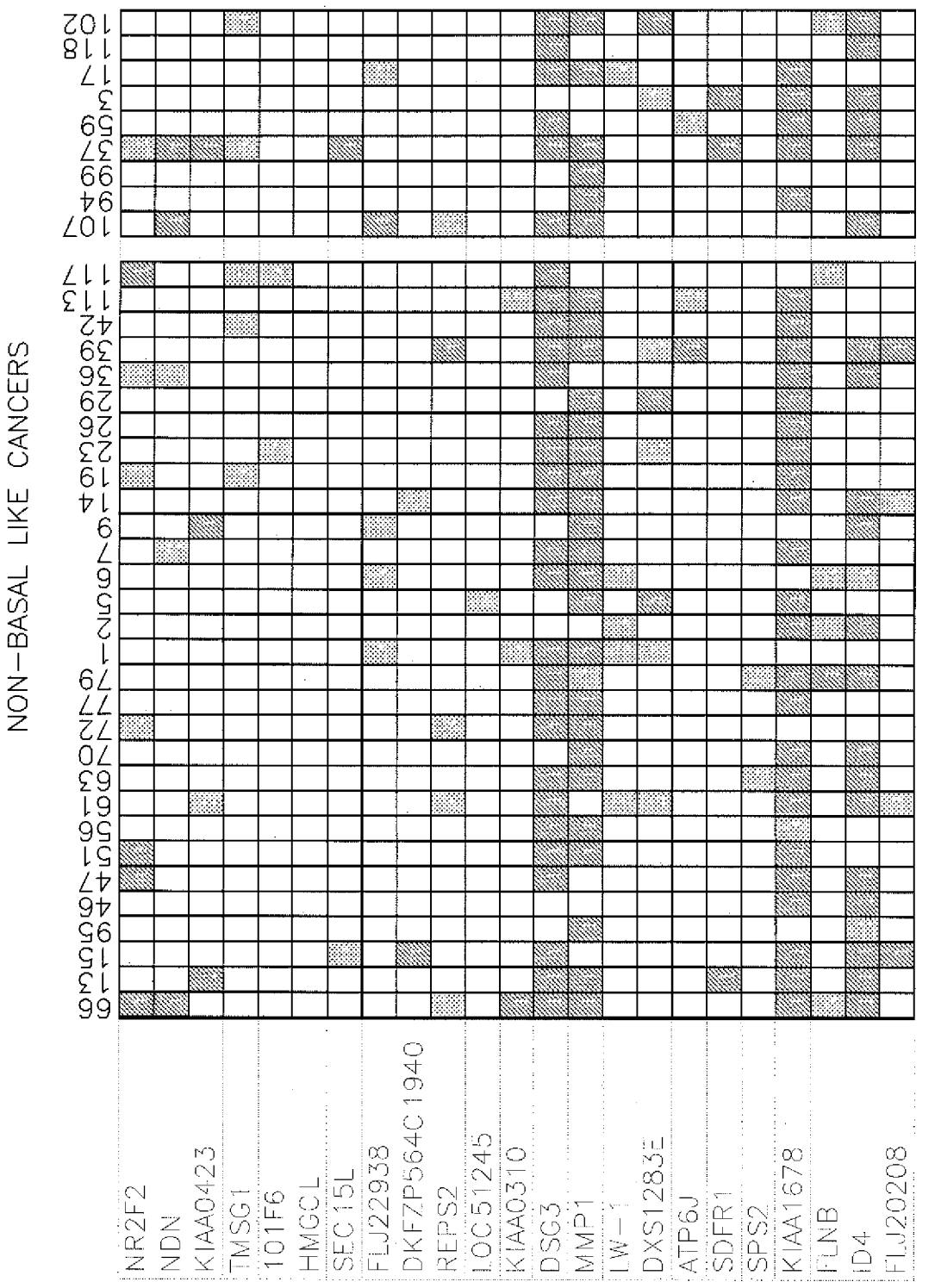
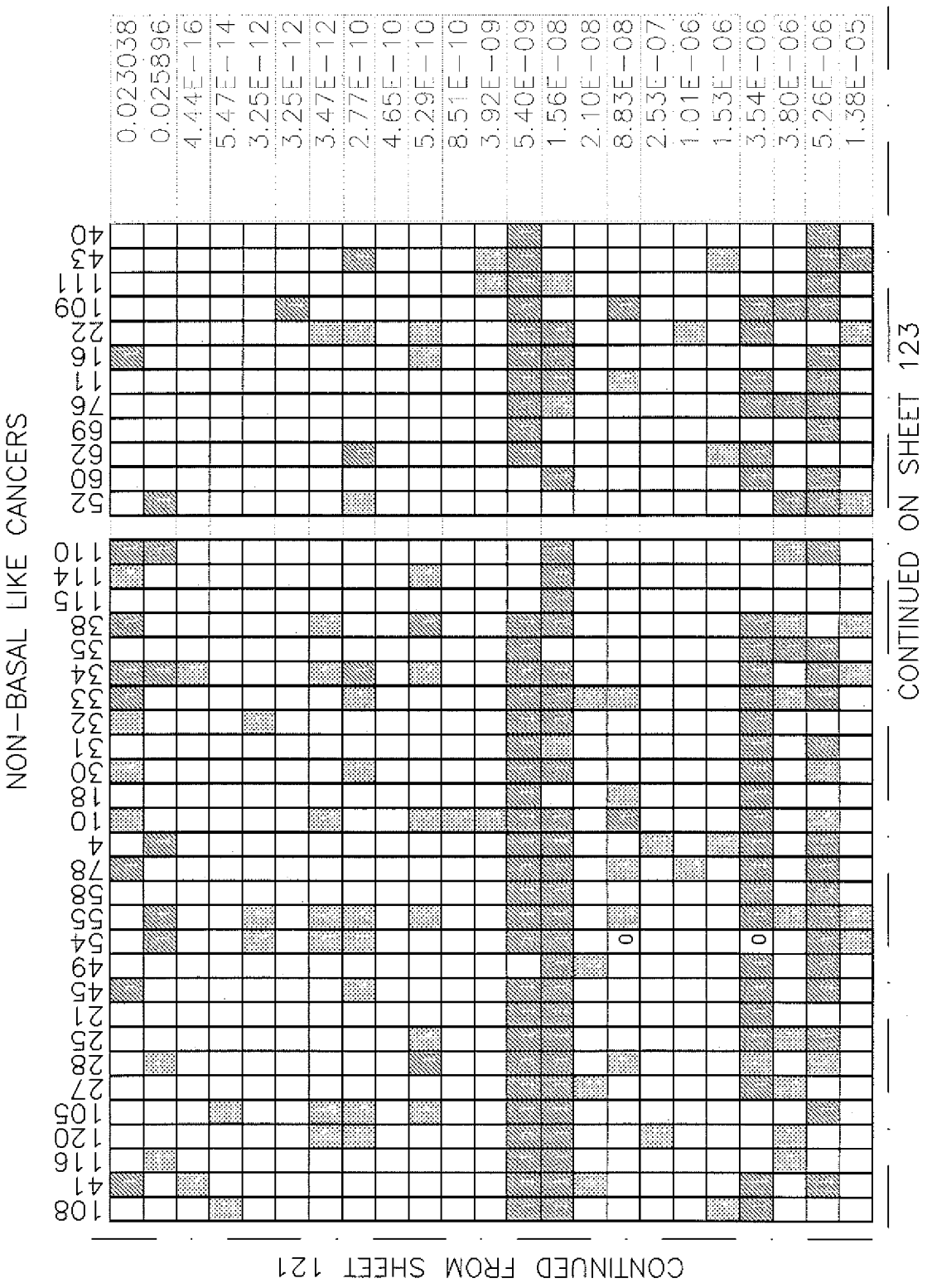

NON-BASAL LIKE CANCERS
CONTINUED ON SHEET 122
NR2F2
NDN
KIAA0423
TMSG1
101F6
HMGCL
SEC15L
FLJ22938
DKFZP564C1940
REPS2
LOC51245
KIAA0310
DSG3
MMP1
LW-1
DXS1283E
ATP6J
SDFR1
SPS2
KIAA1678
FLNB
ID4
FLJ20208

FIG. 24


NON-BASAL LIKE CANCERS
CONTINUED FROM SHEET 121
CONTINUED ON SHEET 123
0.0230338
0.0258896
4.44E-16
5.47E-14
3.25E-12
3.25E-12
3.47E-12
2.77E-10
4.65E-10
5.29E-10
8.51E-10
3.92E-09
5.40E-09
1.56E-08
2.10E-08
8.83E-08
2.53E-07
1.01E-06
1.53E-06
3.54E-06
3.80E-06
5.26E-06
1.38E-05

122

FIG. 24

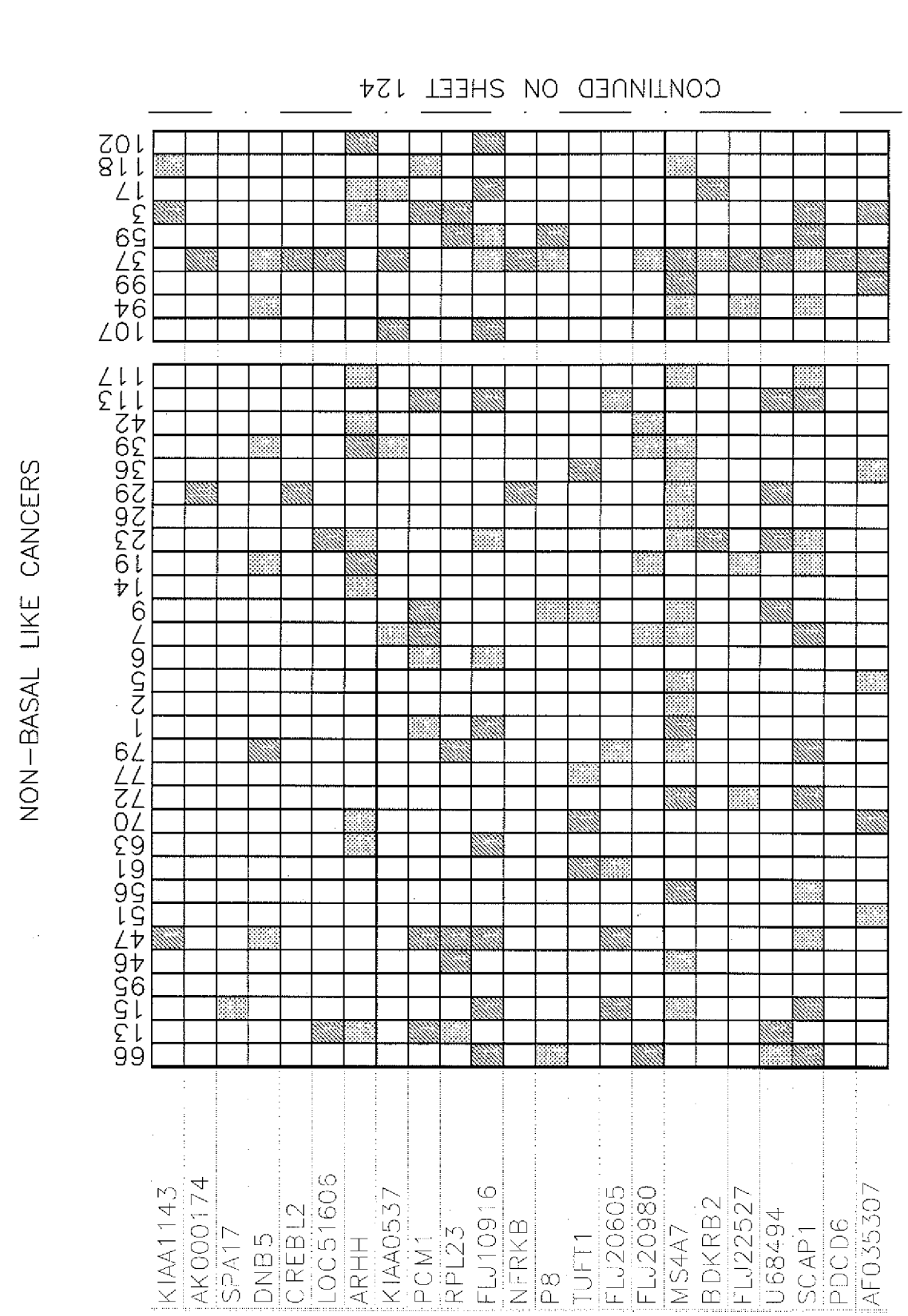

NON-BASAL LIKE CANCERS
CONTINUED ON SHEET 124
KIAA1143
AK000174
SPA17
DNB5
CREBL2
LOC51606
ARHH
KIAA0537
PCM1
RPL23
FLJ10916
NFRKB
P8
TJFT1
FLJ20605
FLJ20980
MS4A7
BDKRB2
FLJ22527
U68494
SCAP1
PDCD6
AF035307

FIG. 24

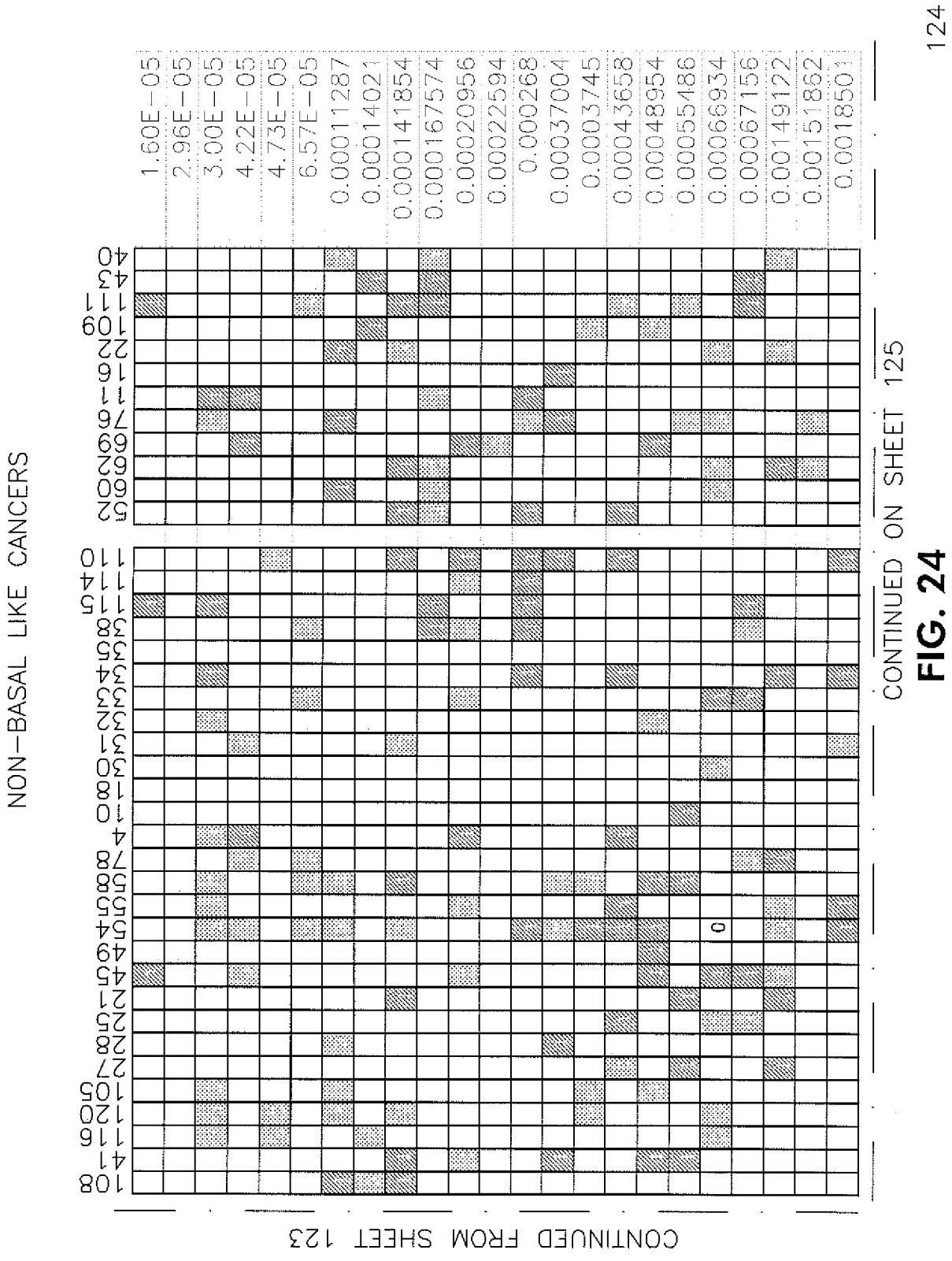

NON-BASAL LIKE CANCERS
CONTINUED FROM SHEET 123
CONTINUED ON SHEET 125
124
1.60E-05
2.96E-05
3.00E-05
4.22E-05
4.73E-05
6.57E-05
0.00011287
0.00014021
0.00014185 4
0.00016757 4
0.00020956
0.00022594
0.000268
0.00037004
0.0003745
0.00043658
0.00048954
0.00055486
0.00066934
0.00067156
0.00149122
0.00151862
0.0018501

FIG. 24

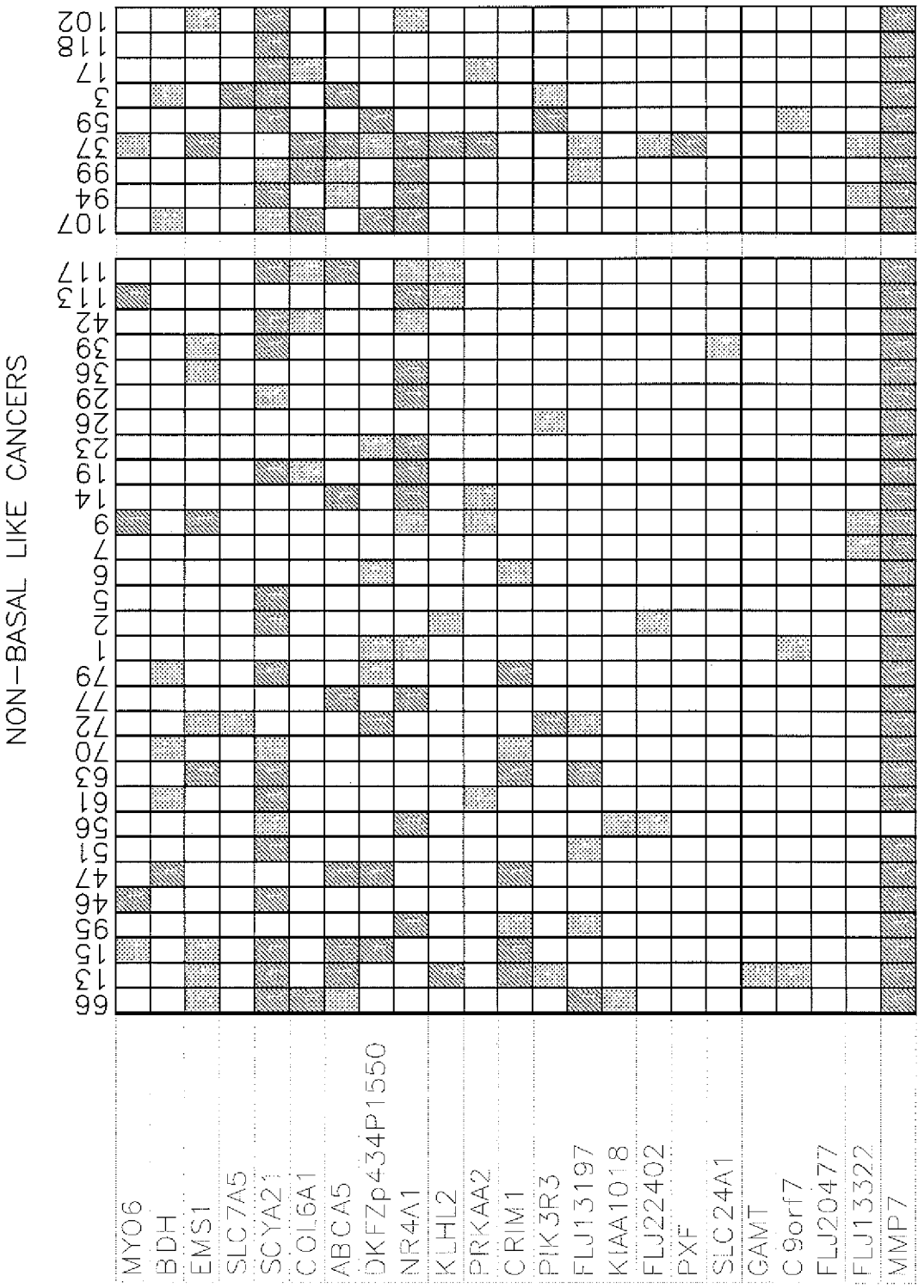
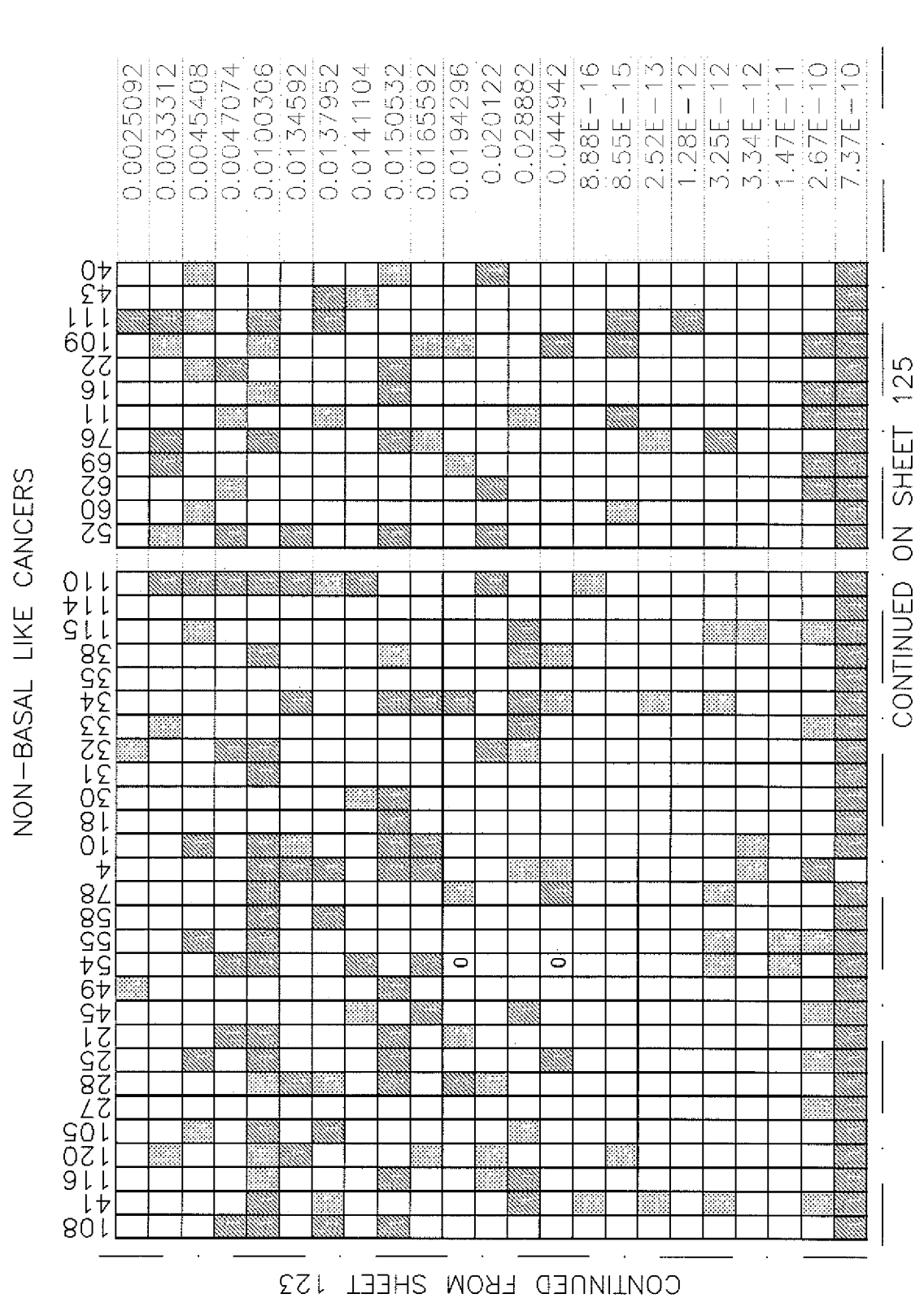

NON-BASAL LIKE CANCERS
CONTINUED ON SHEET 124
MYO6
BDH
EMS1
SLC7A5
SCYA21
COL6A1
ABCA5
DKFZp434P1550
NR4A1
KLHL2
PRKAA2
CRIM1
PIK3R3
FLJ13197
KIAA1018
FLJ22402
PXF
SLC24A1
GAMT
C9orf7
FLJ20477
FLJ13322
MMP7

FIG. 24


CONTINUED FROM SHEET 123
NON-BASAL LIKE CANCERS
108 41 116 120 105 27 28 25 21 45 49 54 55 58 78 4 10 30 31 32 33 34 35 38 115 14 10
52 60 62 69 76 11 16 22 109 1 43 40
0.0025092
0.0033312
0.0045408
0.0047074
0.0100306
0.0134592
0.0137952
0.0141104
0.0150532
0.0165592
0.0194296
0.020122
0.028882
0.044942
8.88E-16
8.55E-15
2.52E-13
1.28E-12
3.25E-12
3.34E-12
1.47E-11
2.67E-10
7.37E-10
CONTINUED ON SHEET 125

126

FIG. 24

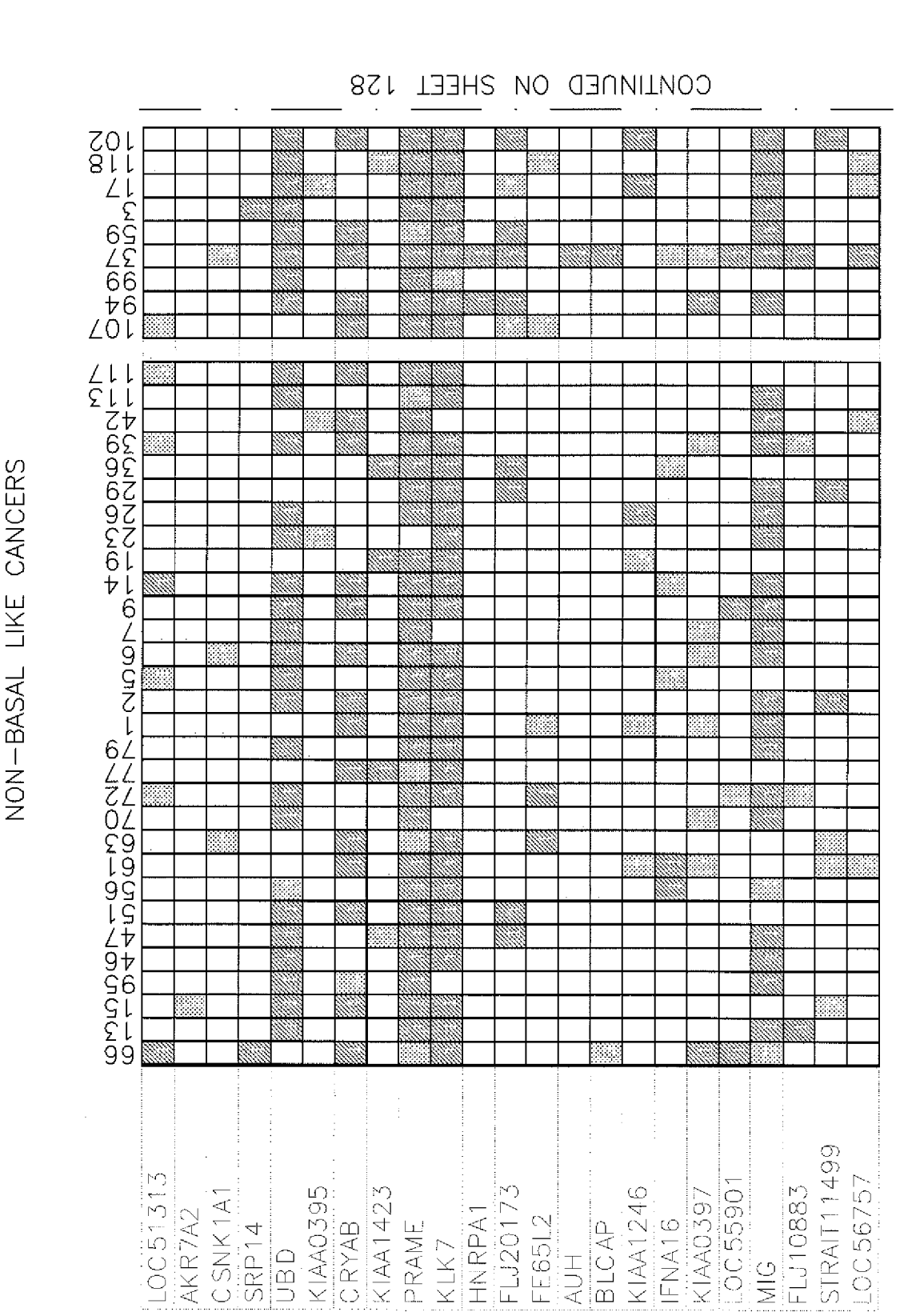

NON-BASAL LIKE CANCERS
CONTINUED ON SHEET 128
LOC51313
AKR7A2
CSNK1A1
SRP14
UBD
KIAA0395
CRYAB
KIAA1423
PRAME
KLK7
HNRPA1
FLJ20173
FE65L2
AUH
BLCAP
KIAA1246
IFNA16
KIAA0397
LOC55901
MIG
FLJ10883
STRAIT11499
LOC56757

FIG. 24

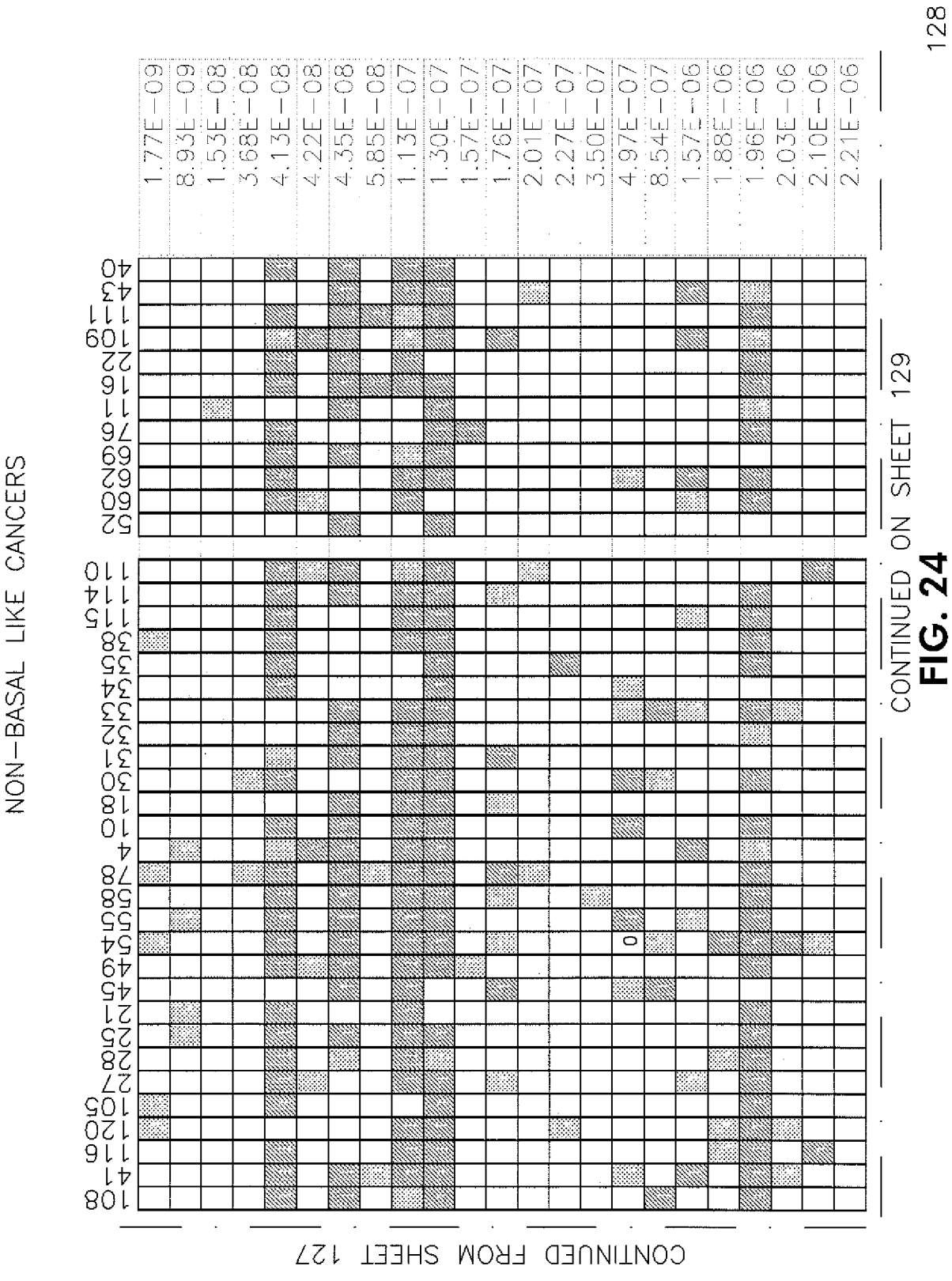

NON-BASAL LIKE CANCERS
CONTINUED FROM SHEET 127
CONTINUED ON SHEET 129
1.77E-09
8.93E-09
1.53E-08
3.68E-08
4.13E-08
4.22E-08
4.35E-08
5.85E-08
1.13E-07
1.30E-07
1.57E-07
1.76E-07
2.01E-07
2.27E-07
3.50E-07
4.97E-07
8.54E-07
1.57E-06
1.88E-06
1.96E-06
2.03E-06
2.10E-06
2.21E-06

FIG. 24

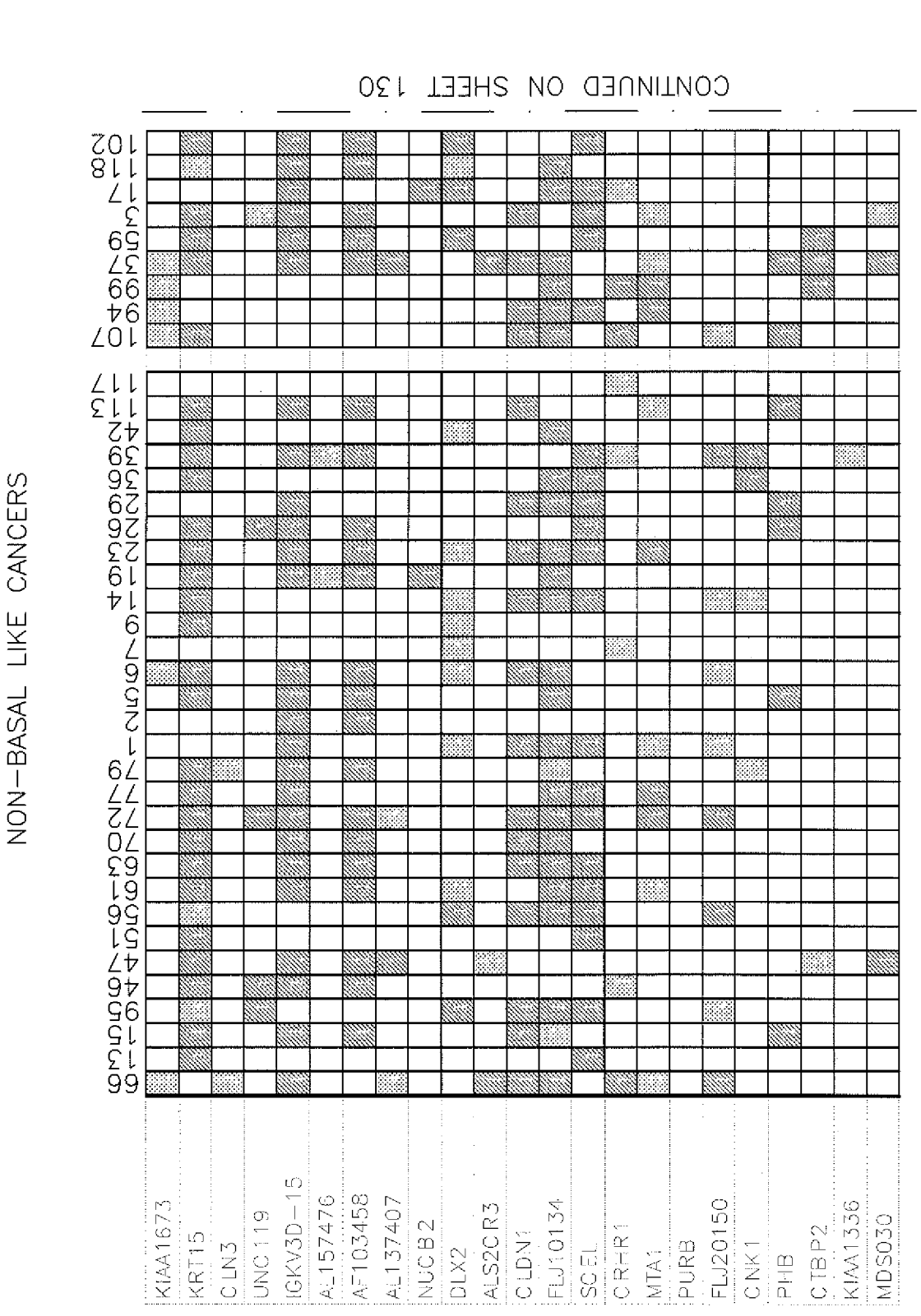
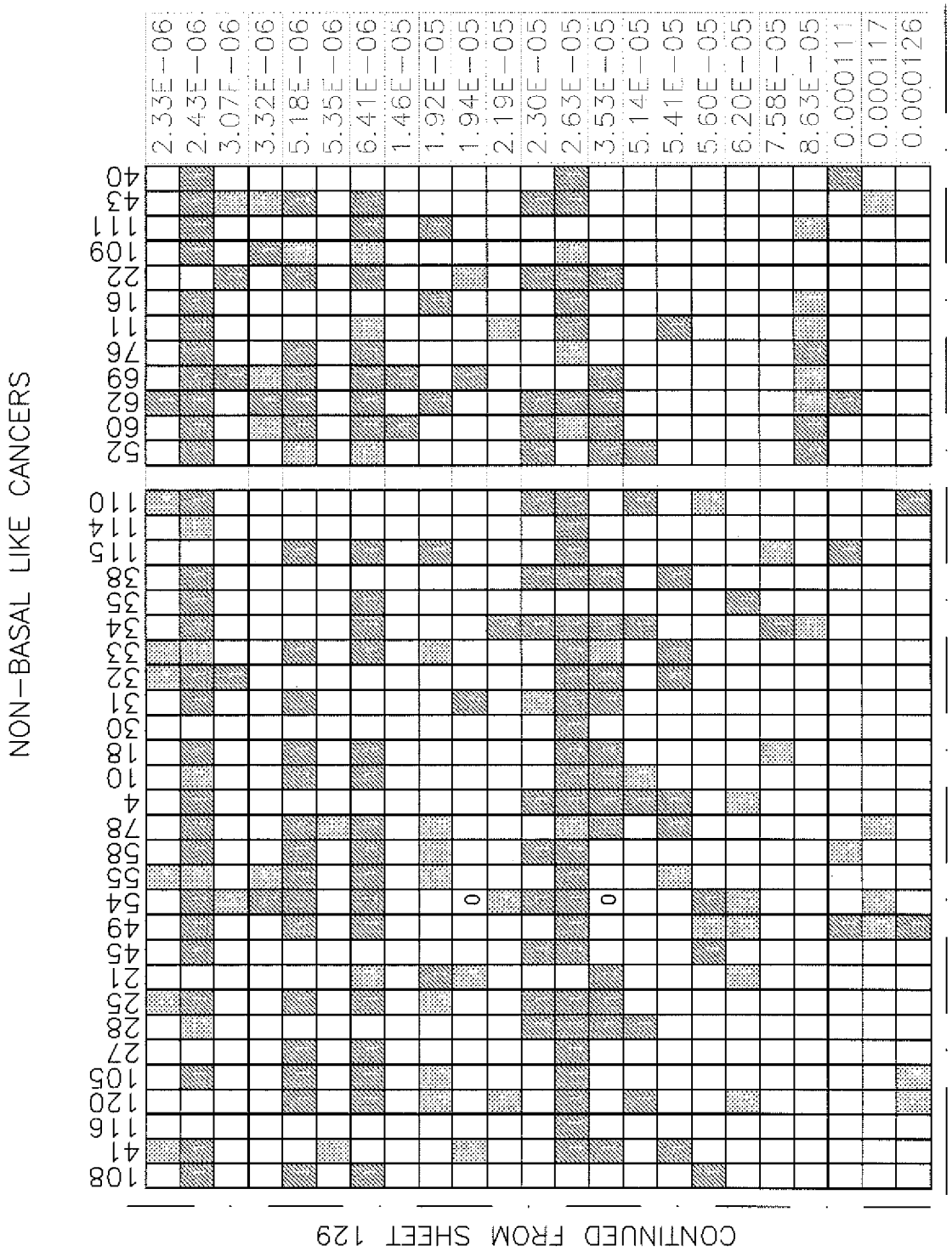
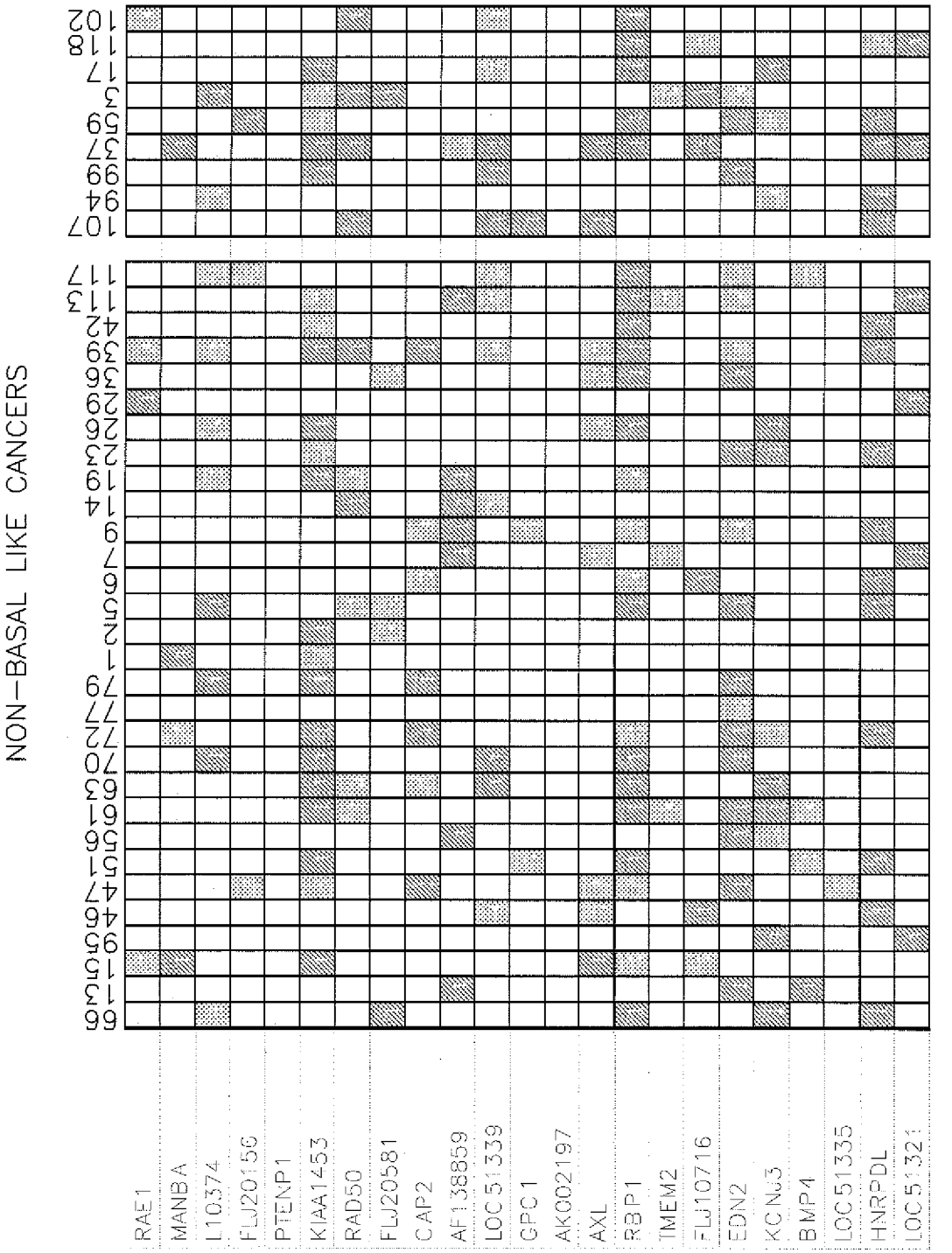

NON-BASAL LIKE CANCERS
CONTINUED ON SHEET 130
KIAA1673
KRT15
CLN3
UNC119
IGKV3D-15
AL157476
AF103458
AL137407
NUCB2
DLX2
ALS2CR3
CLDN1
FLJ10134
SCEL
CR1-R1
MTA1
PURB
FLJ20150
CNK1
PHB
CTBP2
KIAA1336
MDS030

FIG. 24


NON-BASAL LIKE CANCERS
CONTINUED FROM SHEET 129
CONTINUED ON SHEET 131
2.33E-06
2.43E-06
3.07E-06
3.32E-06
5.18E-06
5.35E-06
6.41E-06
1.46E-05
1.92E-05
1.94E-05
2.19E-05
2.30E-05
2.63E-05
3.53E-05
5.14E-05
5.41E-05
5.60E-05
6.20E-05
7.58E-05
8.63E-05
0.000111
0.000117
0.000126

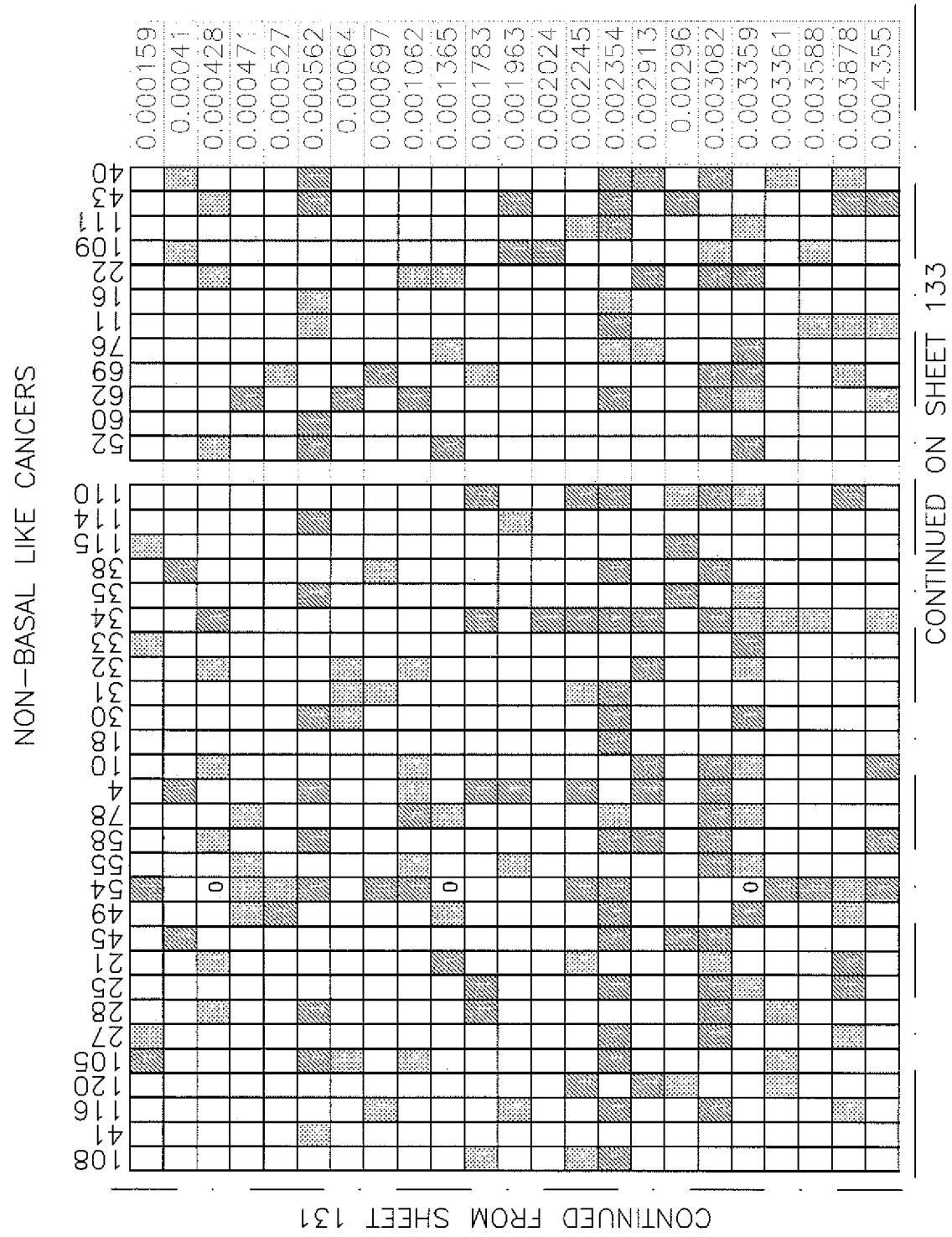
130

FIG. 24


CONTINUED ON SHEET 132
NON-BASAL LIKE CANCERS
RAE1
MANBA
L10374
FLJ20156
PTENP1
KIAA1453
RAD50
FLJ20581
CAP2
AF138859
LOC51339
GPC1
AK002197
AXL
RBP1
TMEM2
FLJ10716
EDN2
KCNJ3
BMP4
LOC51335
HNRPDL
LOC51321

131

FIG. 24


NON-BASAL LIKE CANCERS
CONTINUED FROM SHEET 131
CONTINUED ON SHEET 133
0.000159
0.00041
0.000428
0.00047
0.000527
0.000562
0.00064
0.000697
0.001062
0.001365
0.001783
0.001963
0.002024
0.002245
0.002354
0.002913
0.00296
0.003082
0.003359
0.003361
0.003588
0.003878
0.004355

132

FIG. 24

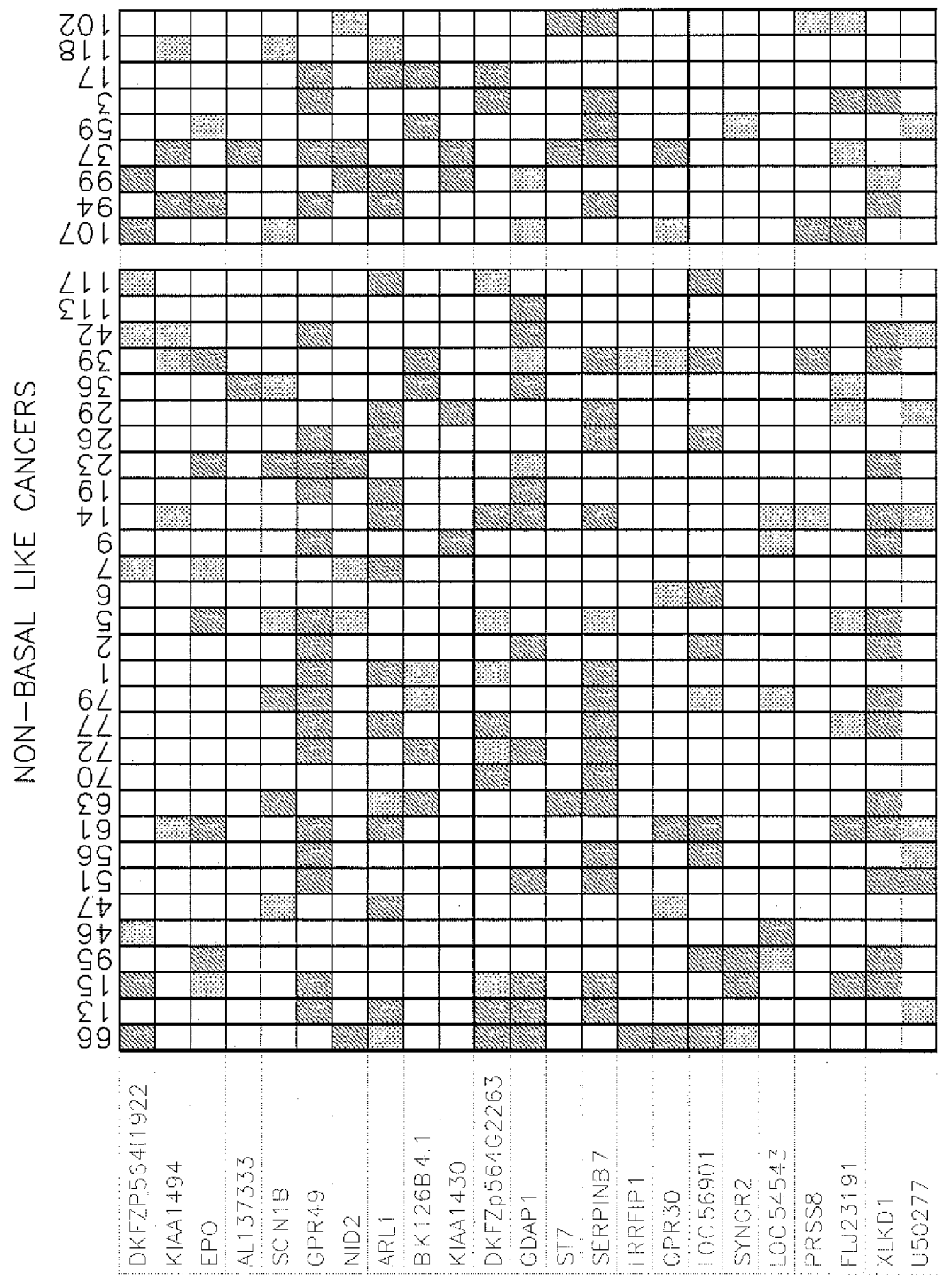

NON-BASAL LIKE CANCERS
DKFZP564I1922
KIAA1494
EPO
AL137333
SCN1B
GPR49
NID2
ARL1
BK126B4.1
KIAA1430
DKFZp564G2263
CDAP1
ST7
SERPINB7
LRRFIP1
CPR3D
LOC56901
SYNGR2
LOC54543
PRSS8
FLJ23191
XLKD1
U50277
CONTINUED ON SHEET 134

FIG. 24

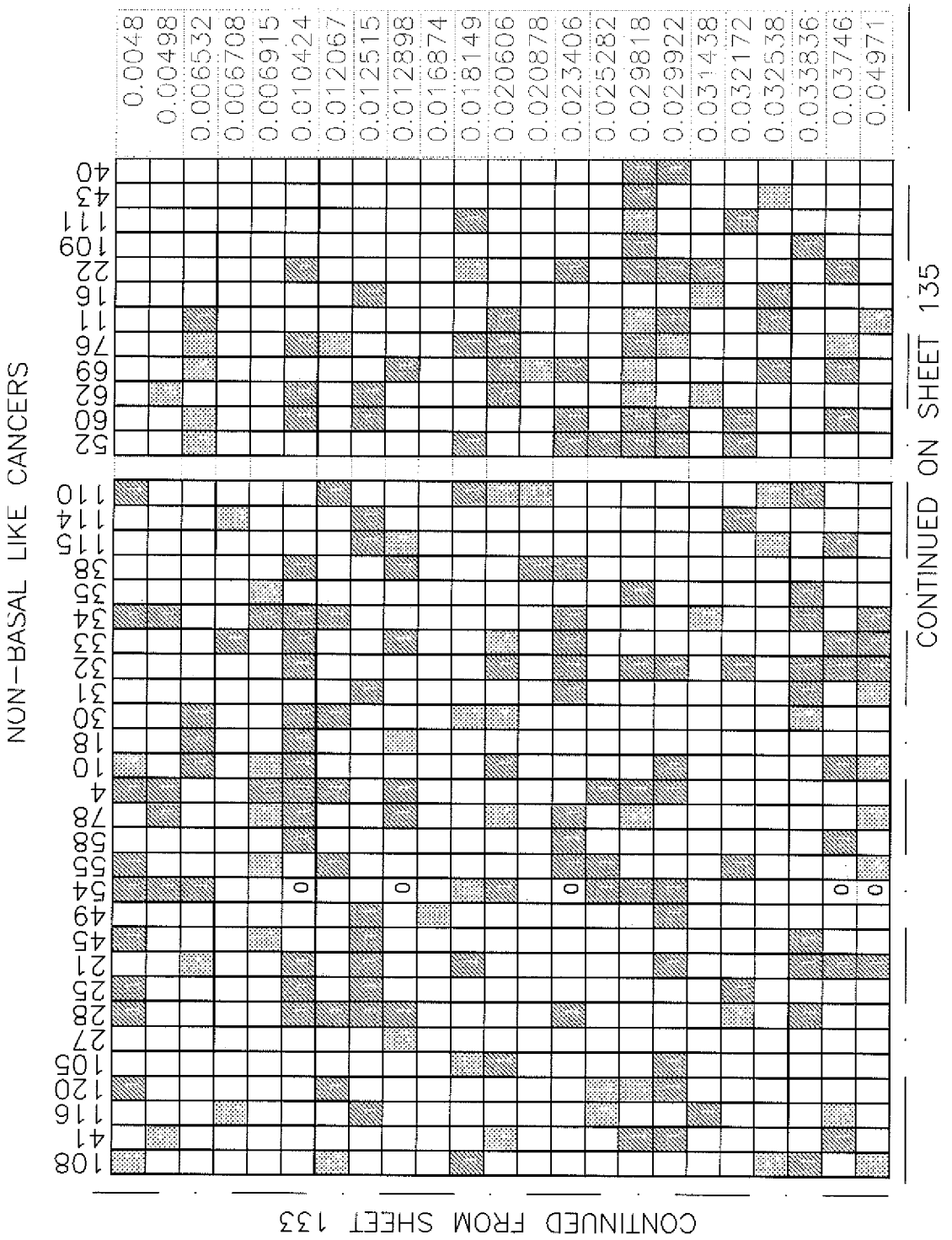

NON-BASAL LIKE CANCERS
CONTINUED FROM SHEET 133
CONTINUED ON SHEET 135
0.00048
0.00498
0.006532
0.006708
0.006915
0.010424
0.012067
0.012515
0.012898
0.016874
0.018149
0.020606
0.020878
0.023406
0.025282
0.029818
0.029922
0.031438
0.032172
0.032538
0.033836
0.03746
0.04971

FIG. 24

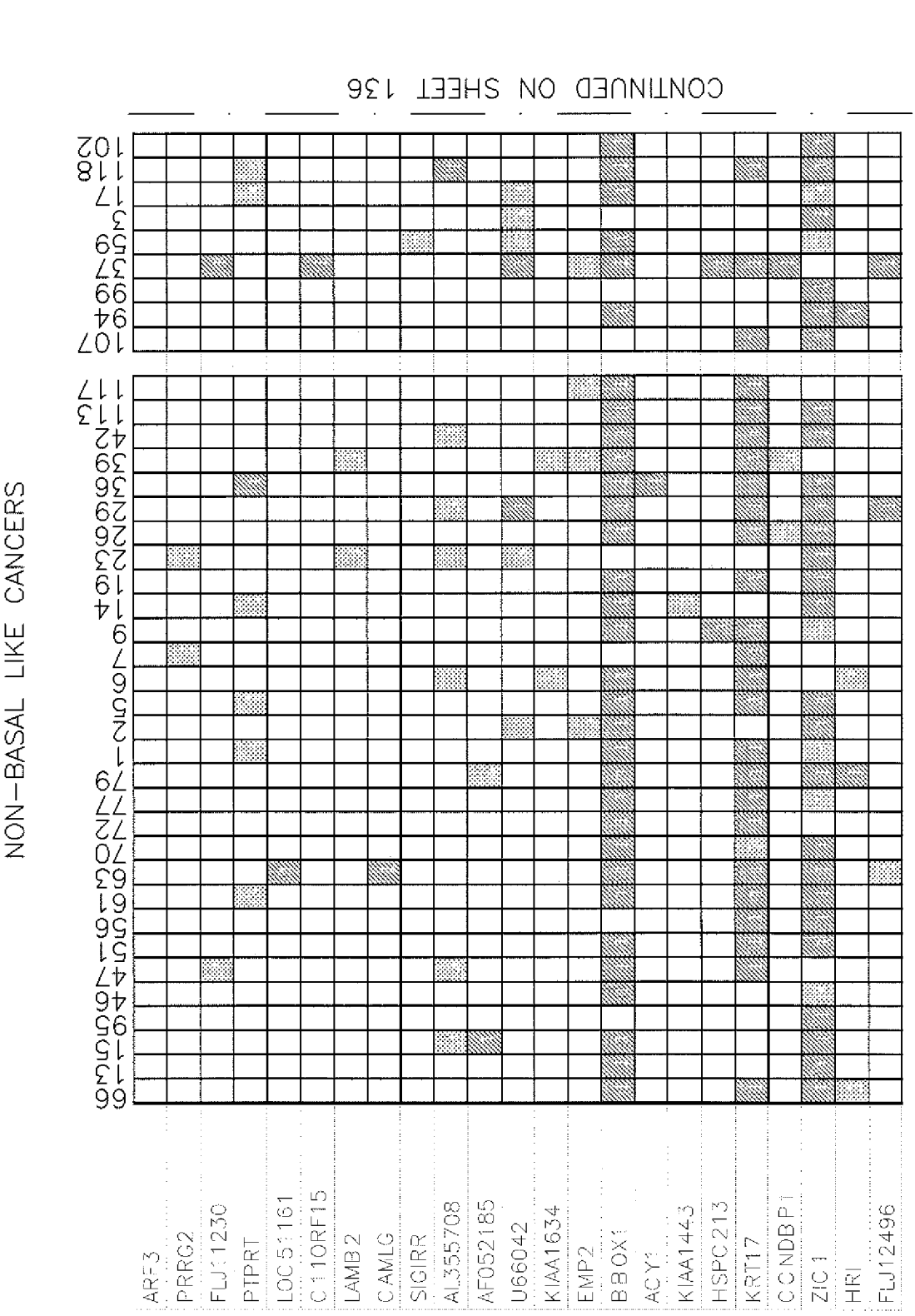
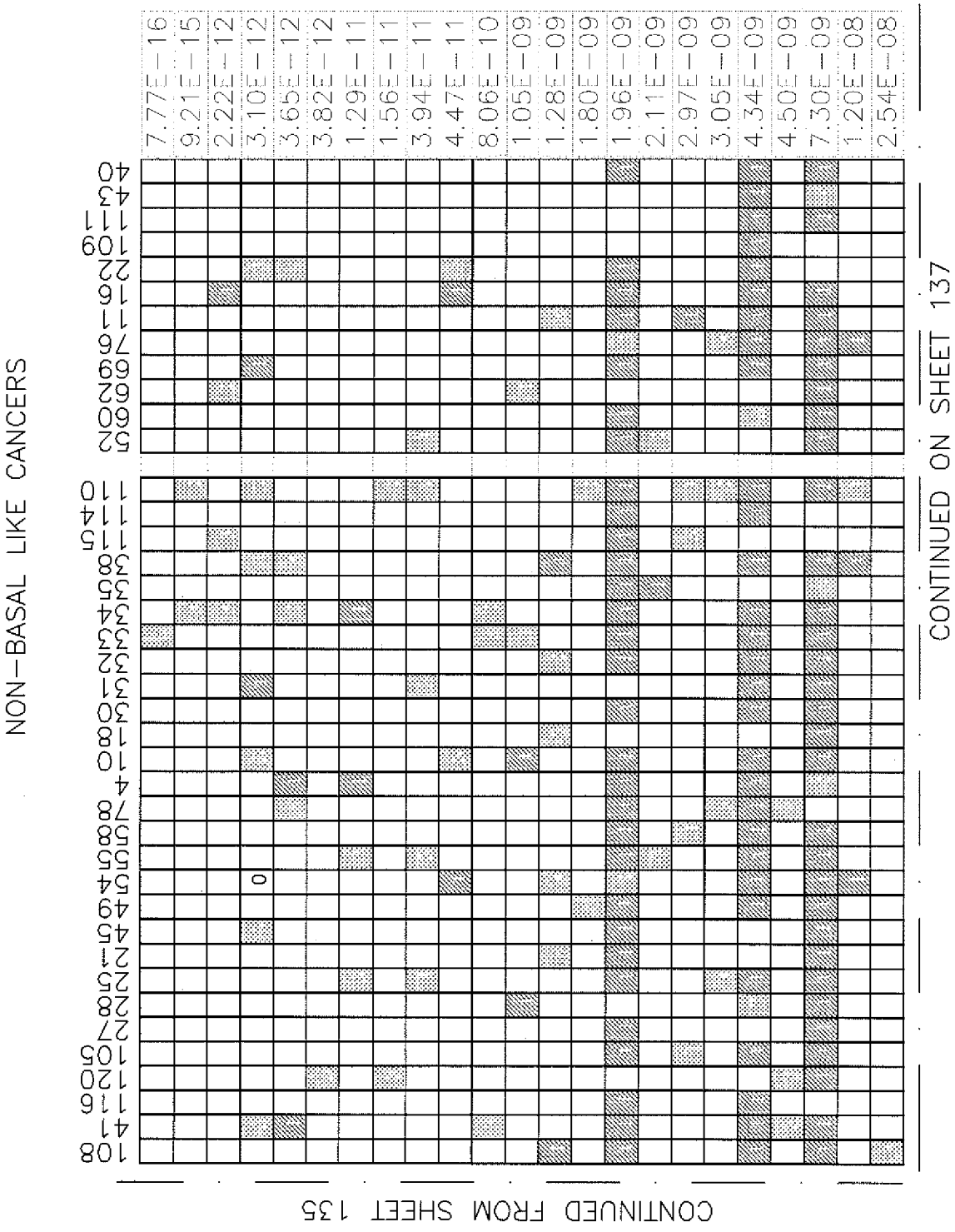

NON-BASAL LIKE CANCERS
CONTINUED ON SHEET 136
ARF3
PRRG2
FLJ11230
PTPRT
LOC51161
C110RF15
LAMB2
CAMLG
SIGIRR
AI355708
AF052185
U66042
KIAA1634
EMP2
BBOX1
ACY1
KIAA1443
HSPC213
KRT17
CCNDBP1
ZIC1
HRI
FLJ12496

FIG. 24


NON-BASAL LIKE CANCERS
CONTINUED FROM SHEET 135
CONTINUED ON SHEET 137
7.77E-16
9.21E-15
2.22E-12
3.10E-12
3.65E-12
3.82E-12
1.29E-11
1.56E-11
3.94E-11
4.47E-11
8.06E-10
1.05E-09
1.28E-09
1.80E-09
1.96E-09
2.11E-09
2.97E-09
3.05E-09
4.34E-09
4.50E-09
7.30E-09
1.20E-08
2.54E-08

136

FIG. 24

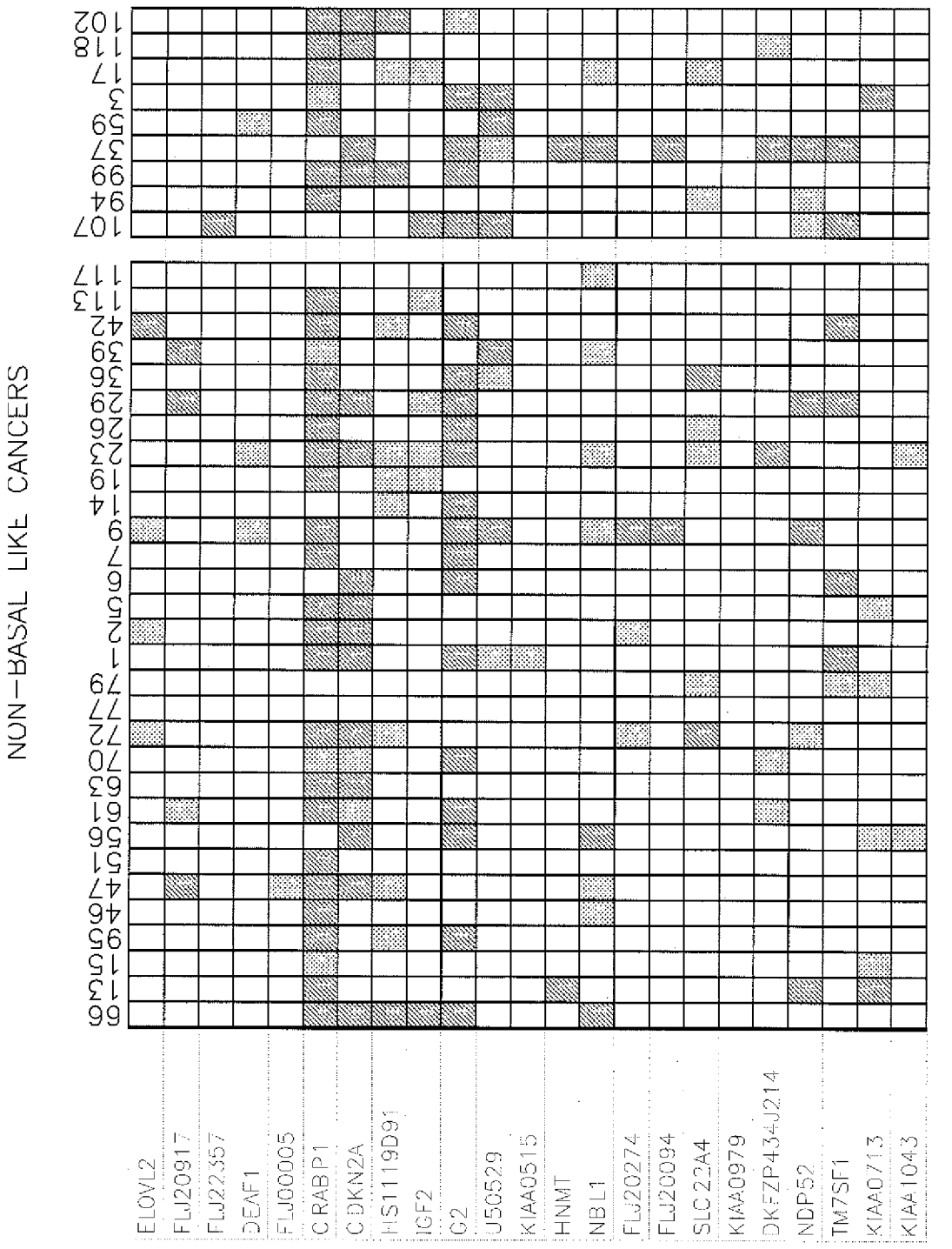
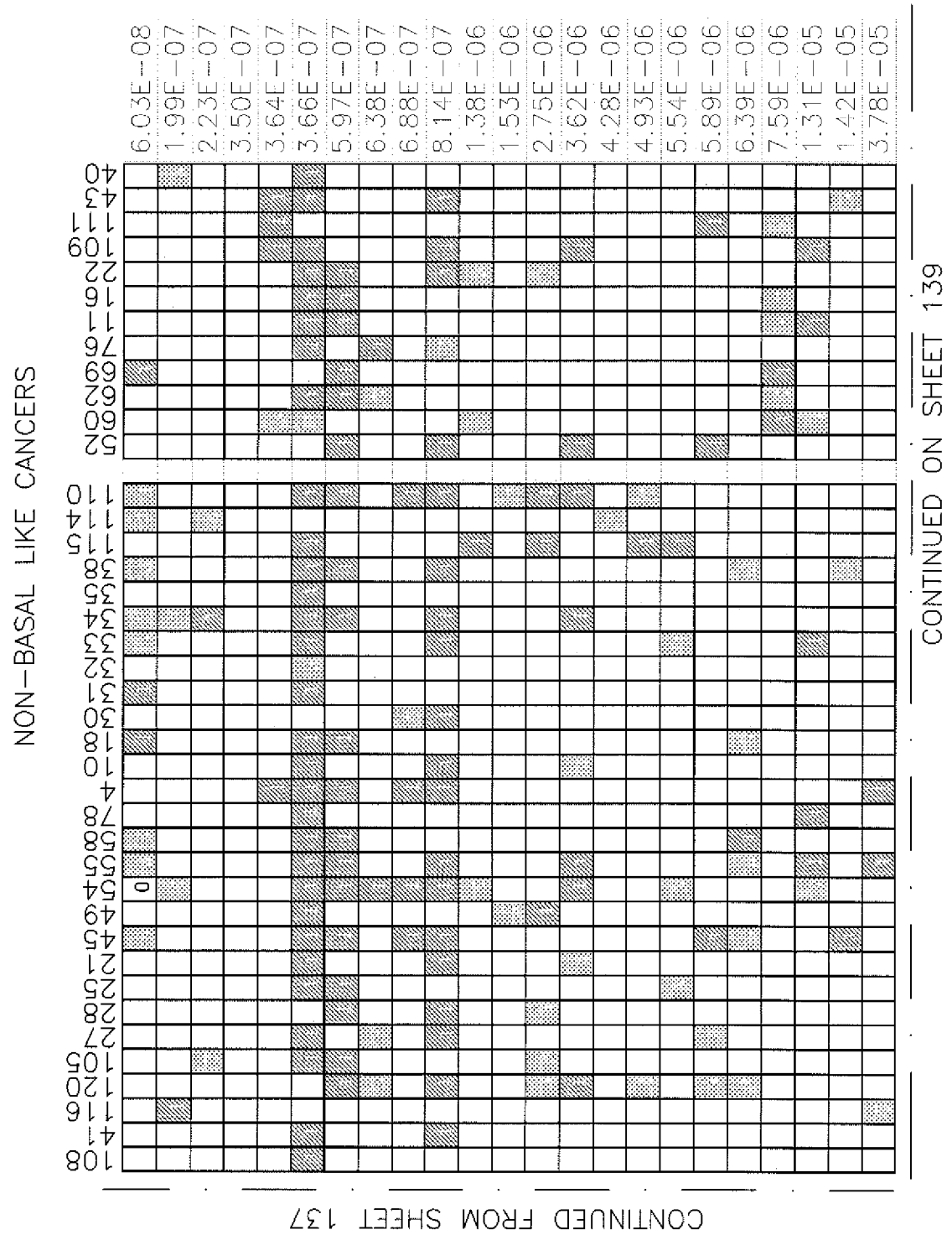

NON-BASAL LIKE CANCERS
CONTINUED ON SHEET 138
ELOVL2
FLJ20917
FLJ22357
DEAF1
FLJ00005
CRABP1
CDKN2A
HS1119D91
IGF2
G2
J50529
KIAA0515
HNMT
NBL1
FLJ20274
FLJ20094
SLC22A4
KIAA0979
DKFZP434J214
NDP52
TM7SF1
KIAA0713
KIAA1043

FIG. 24


CONTINUED FROM SHEET 137
NON-BASAL LIKE CANCERS
6.03E-08
1.99E-07
2.23E-07
3.50E-07
3.64E-07
3.66E-07
5.97E-07
6.38E-07
6.88E-07
8.14E-07
1.38E-06
1.53E-06
2.75E-06
3.62E-06
4.28E-06
4.93E-06
5.54E-06
5.89E-06
6.39E-06
7.59E-06
1.31E-05
1.42E-05
3.78E-05
CONTINUED ON SHEET 139

138

FIG. 24

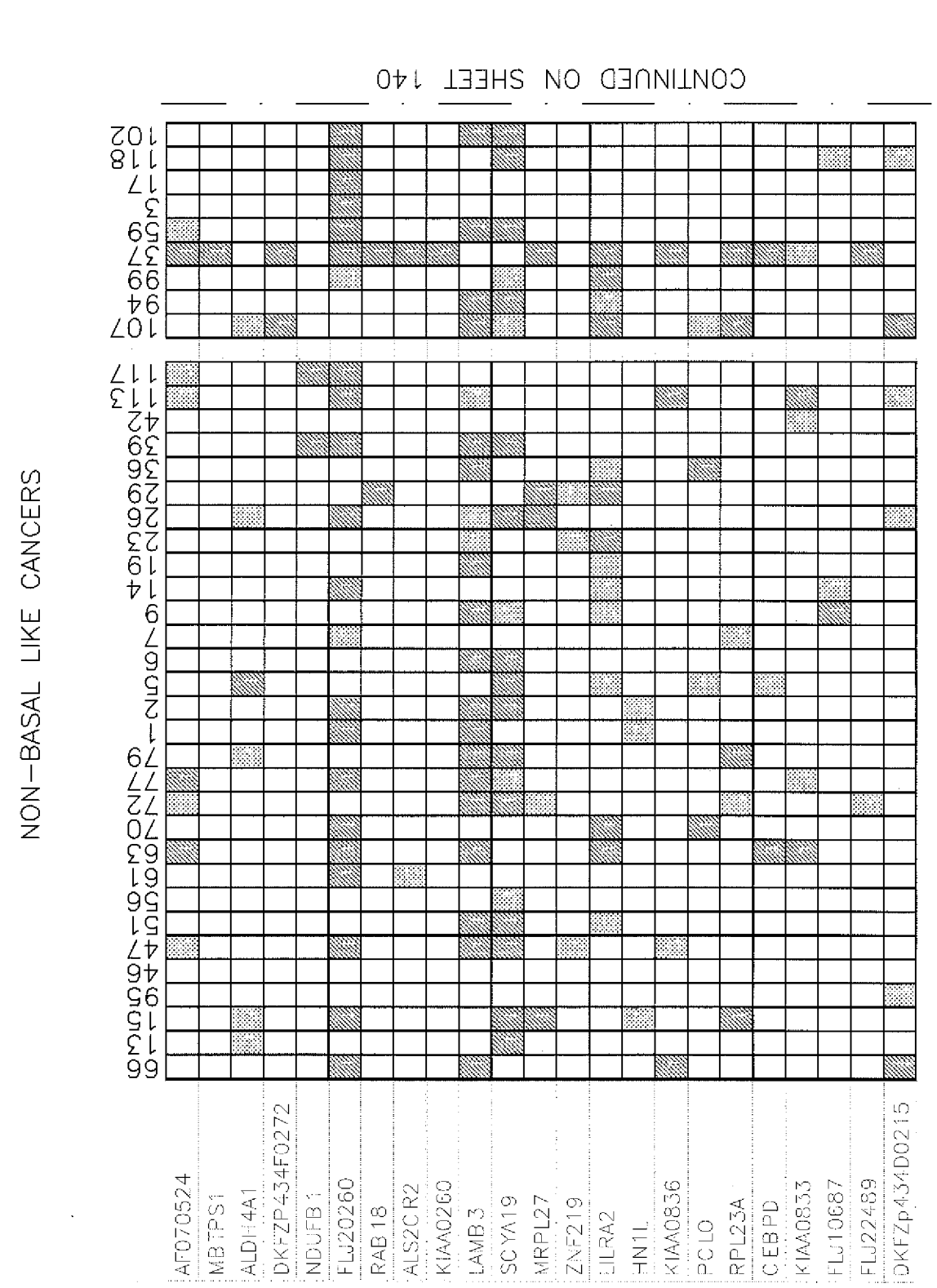

NON-BASAL LIKE CANCERS
CONTINUED ON SHEET 140
AF070524
MBTPS1
ALDH4A1
DKFZP434F0272
NDUFB1
FLJ20260
RAB18
ALS2CR2
KIAA0260
LAMB3
SCYA19
MRPL27
ZNF219
LILRA2
HN1L
KIAA0836
PCLO
RPL23A
CEBPD
KIAA0833
FLJ10687
FLJ22489
DKFZp434D0215

FIG. 24

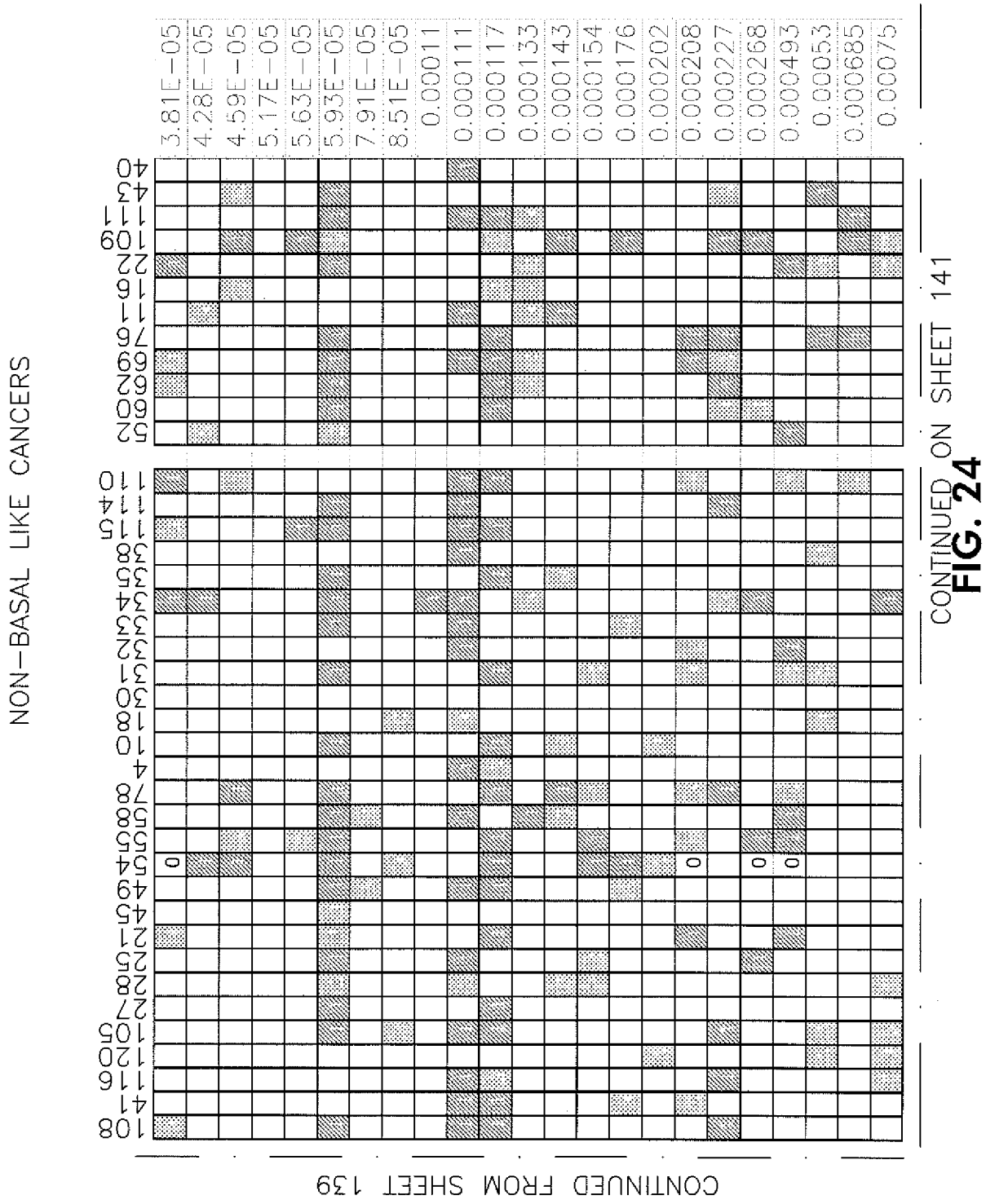

NON-BASAL LIKE CANCERS
CONTINUED FROM SHEET 139
CONTINUED ON SHEET 141
140
3.81E-05
4.28E-05
4.59E-05
5.17E-05
5.63E-05
5.93E-05
7.91E-05
8.51E-05
0.00011
0.000111
0.000117
0.000133
0.000143
0.000154
0.000176
0.000202
0.000208
0.000227
0.000268
0.000493
0.00053
0.000685
0.00075

FIG. 24

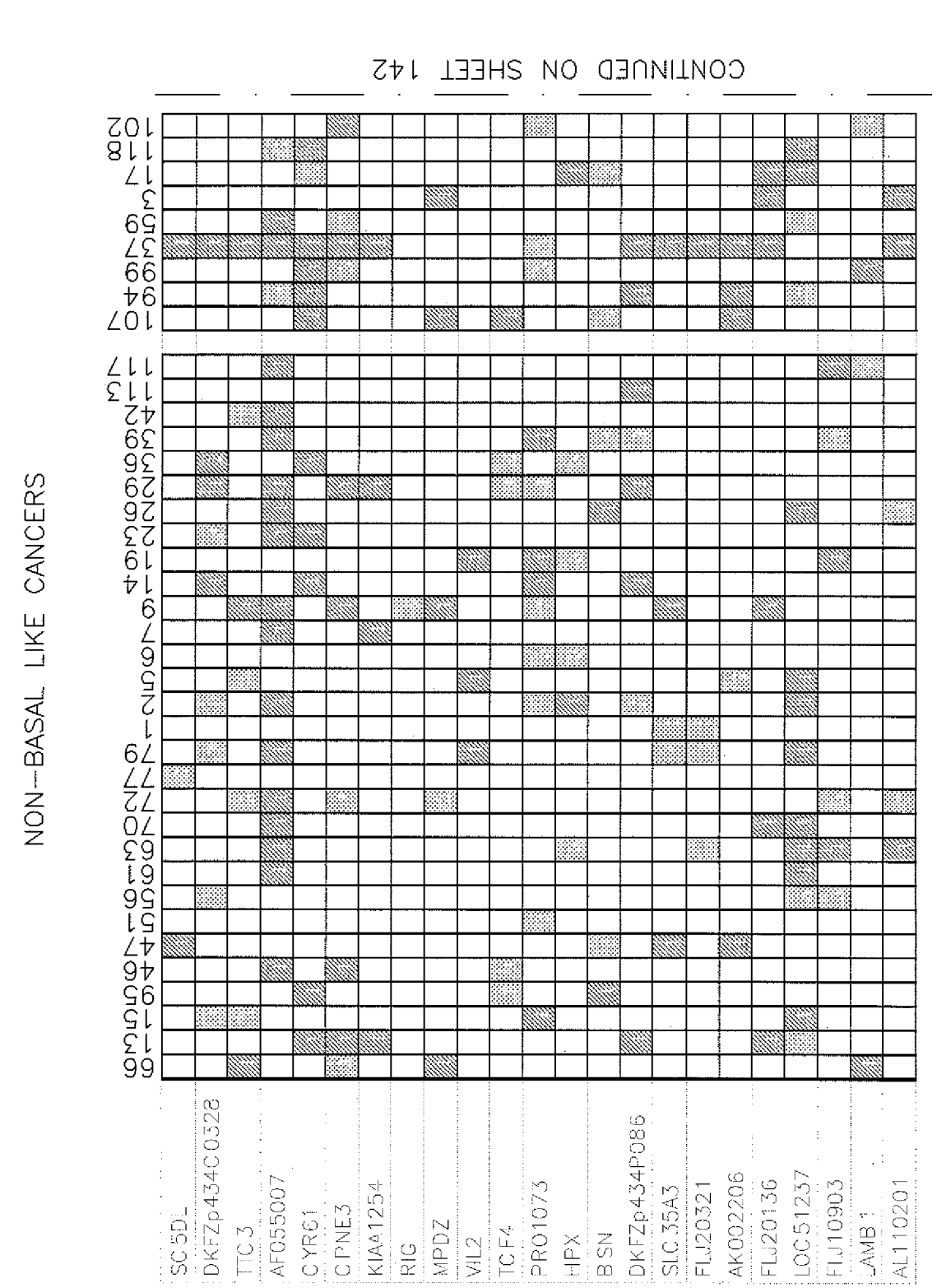
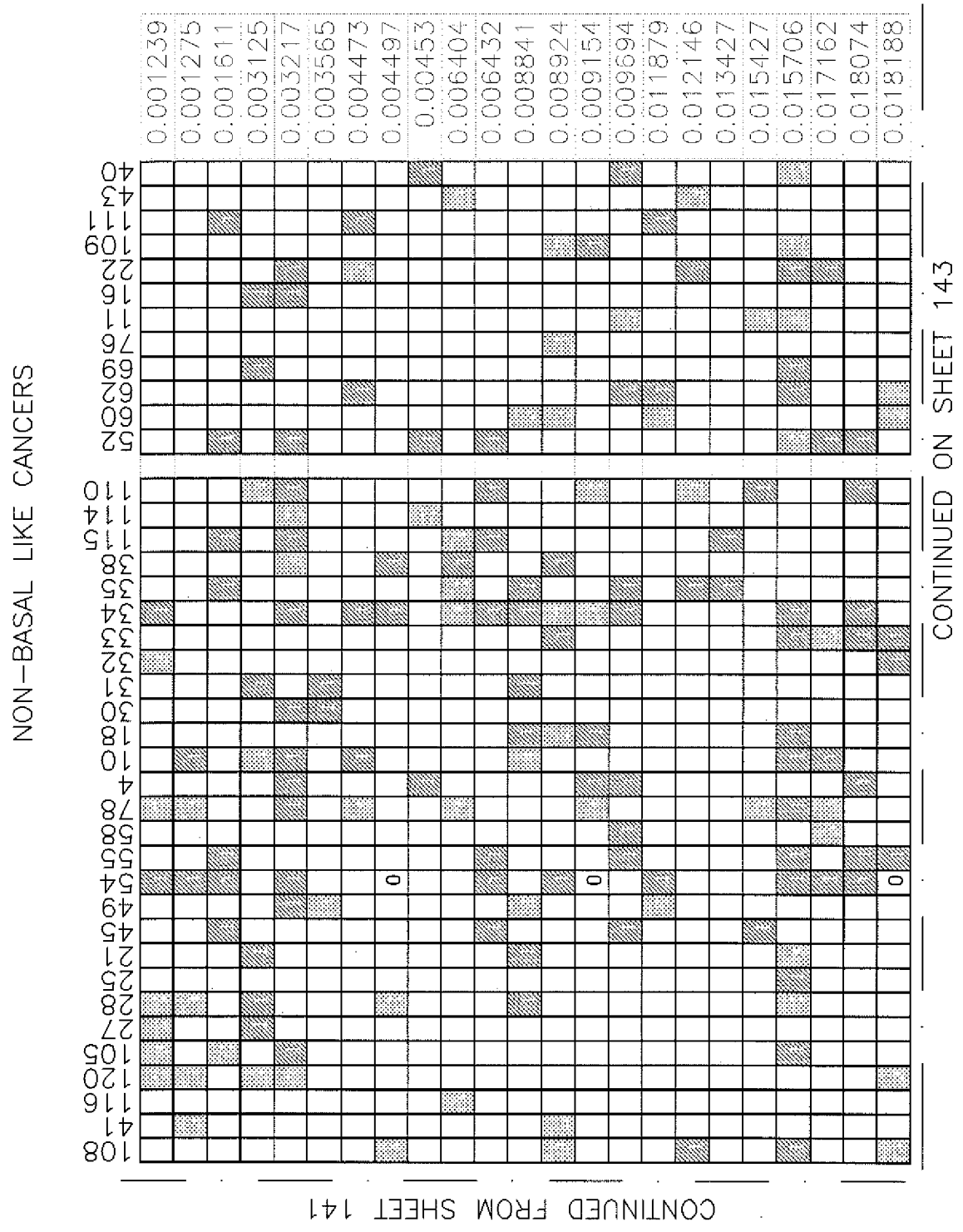

NON-BASAL LIKE CANCERS
SC5D
DKFZp434C0328
TTC3
AF055007
CYR61
CPNE3
KIAA1254
RIG
MPDZ
VIL2
TCF4
PRO1073
HPX
BSN
DKFZp434P086
SLC35A3
FLJ20321
AK002206
FLJ20136
LOC51237
FLJ10903
LAMB1
AL110201
CONTINUED ON SHEET 142

FIG. 24


CONTINUED FROM SHEET 141
NON-BASAL LIKE CANCERS
0.001239
0.001275
0.001611
0.003125
0.003217
0.003565
0.004473
0.004497
0.00453
0.006404
0.006432
0.008841
0.008924
0.009154
0.009694
0.011879
0.012146
0.013427
0.015427
0.015706
0.017162
0.018074
0.018188
CONTINUED ON SHEET 143

142

FIG. 24

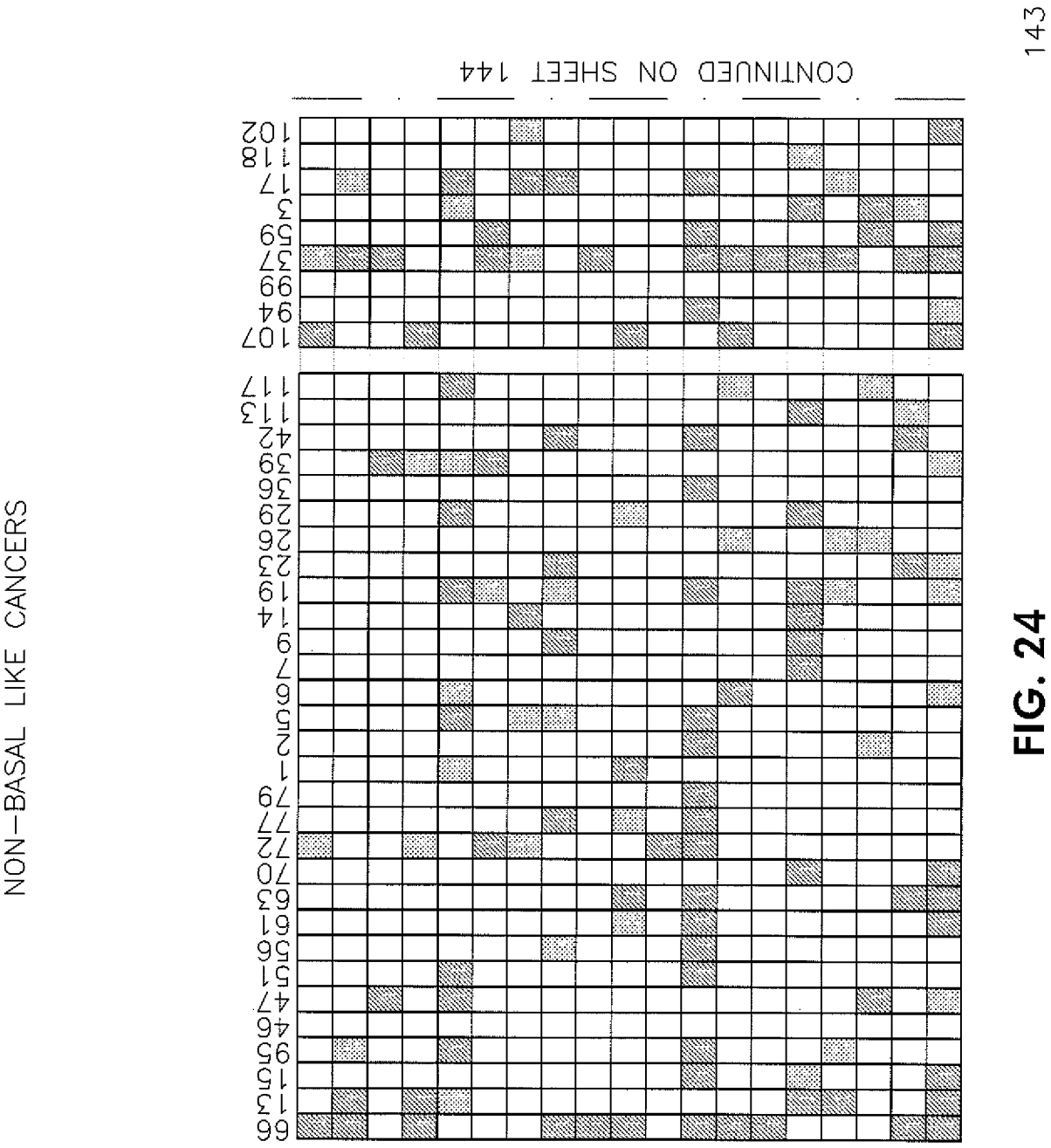


FIG. 24

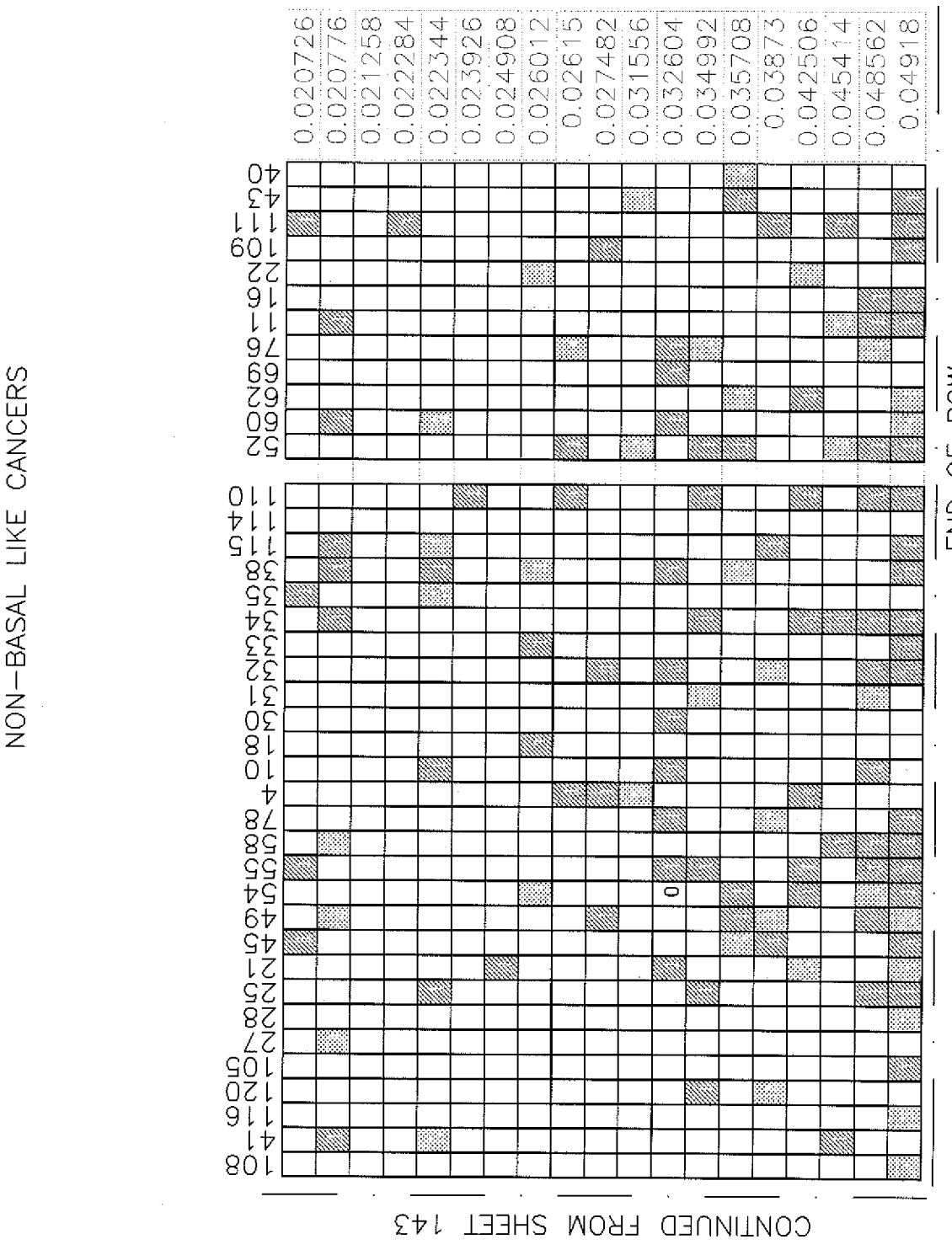

NON-BASAL LIKE CANCERS
CONTINUED FROM SHEET 143
END OF ROW
0.020726
0.020776
0.021258
0.022284
0.022344
0.023926
0.024908
0.026012
0.02615
0.027482
0.031556
0.032604
0.034992
0.035708
0.03873
0.042506
0.045414
0.048562
0.04918

FIG. 24

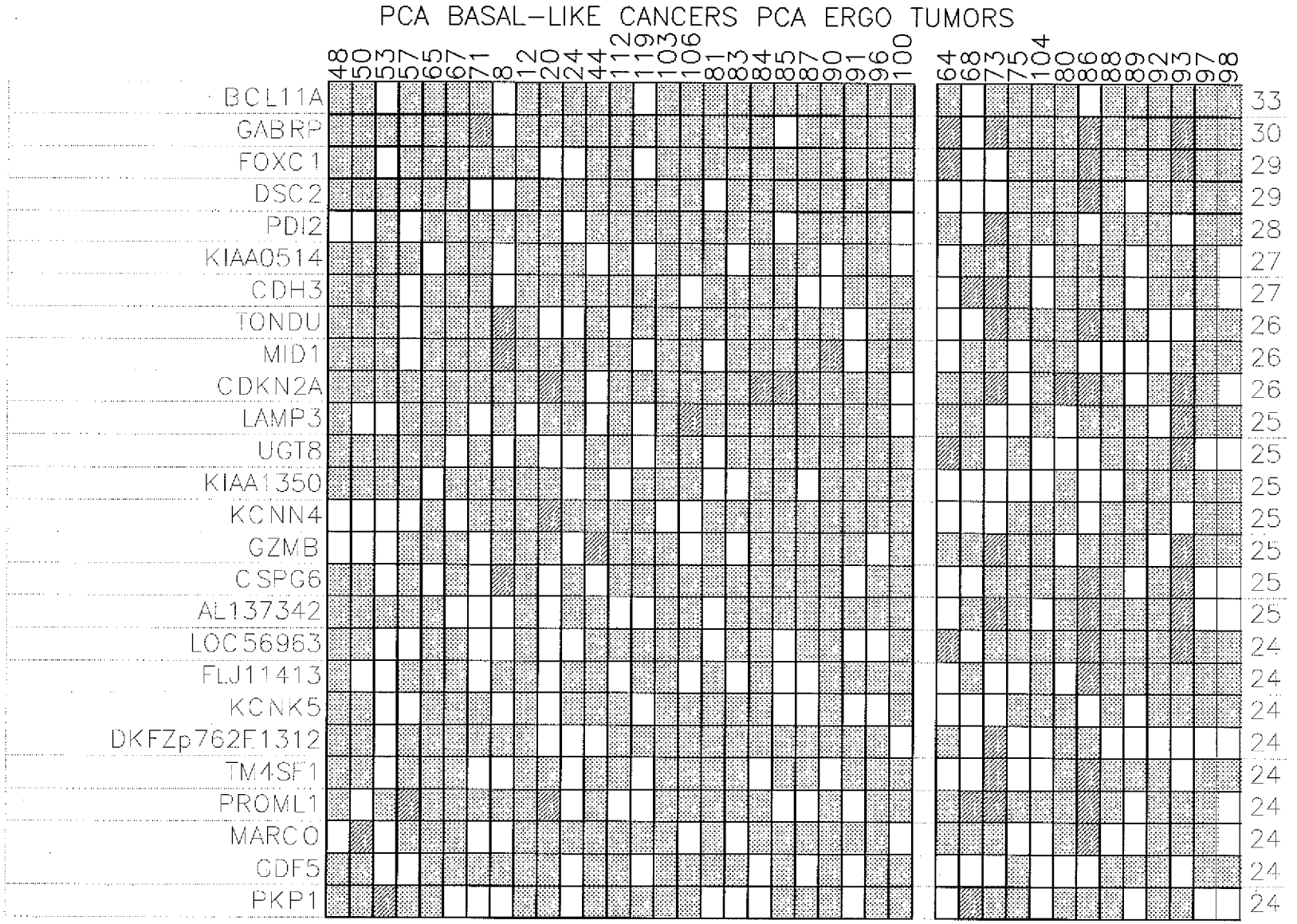

PCA BASAL–LIKE CANCERS PCA ERGO TUMORS
48 50 53 57 65 67 71 8 12 20 24 44 112 119 103 106 81 83 84 85 87 90 91 96 100 64 68 73 75 104 80 86 88 89 92 93 97 98
BCL11A 33
GABRP 30
FOXC1 29
DSC2 29
PDI2 28
KIAA0514 27
CDH3 27
TONDU 26
MID1 26
CDKN2A 26
LAMP3 25
UGT8 25
KIAA1350 25
KCNN4 25
GZMB 25
CSPG6 25
AL137342 25
LOC56963 24
FLJ11413 24
KCNK5 24
DKFZp762E1312 24
TM4SF1 24
PROML1 24
MARCO 24
CDF5 24
PKP1 24
CONTINUED ON SHEET 2

FIG. 25

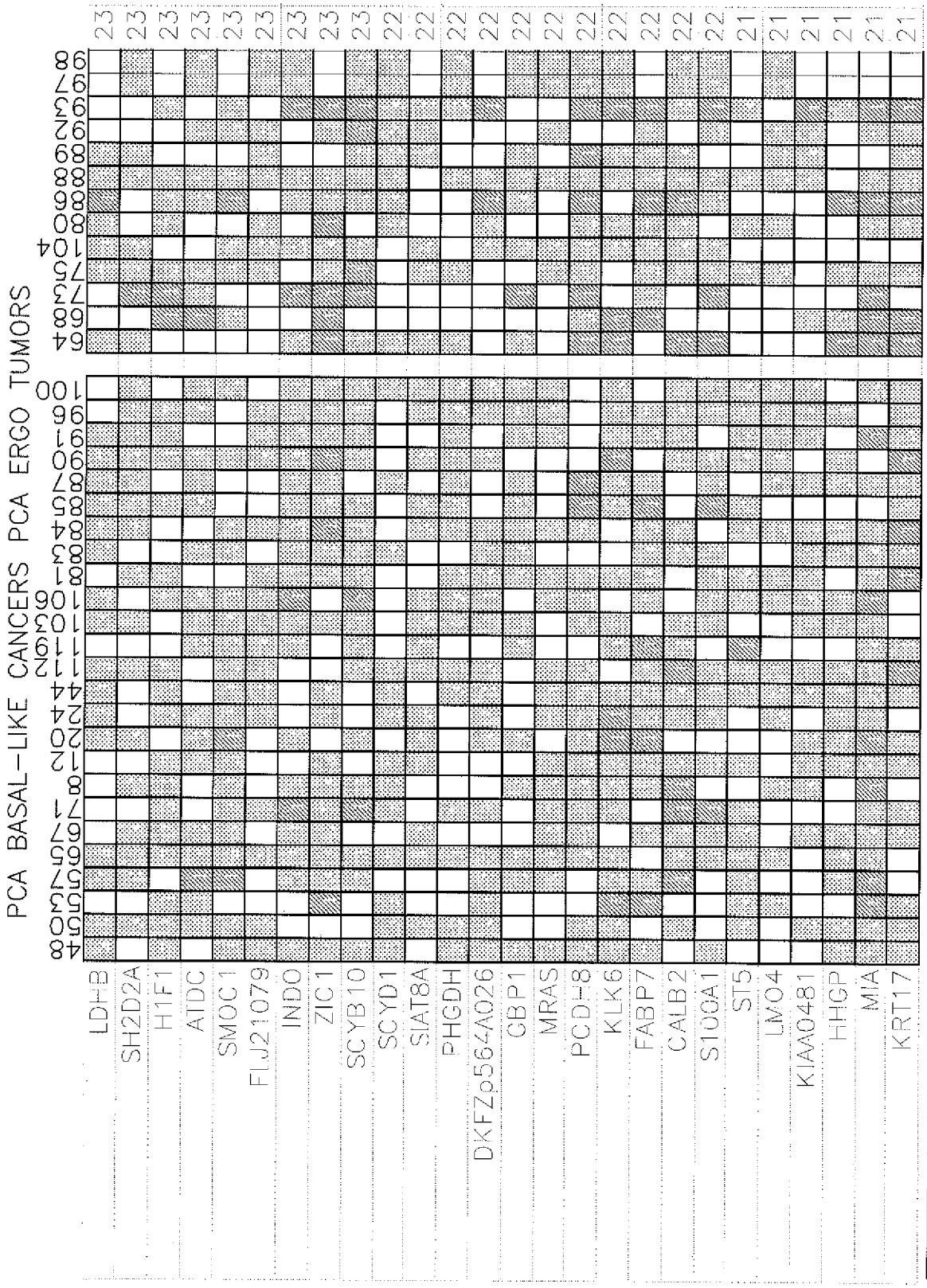
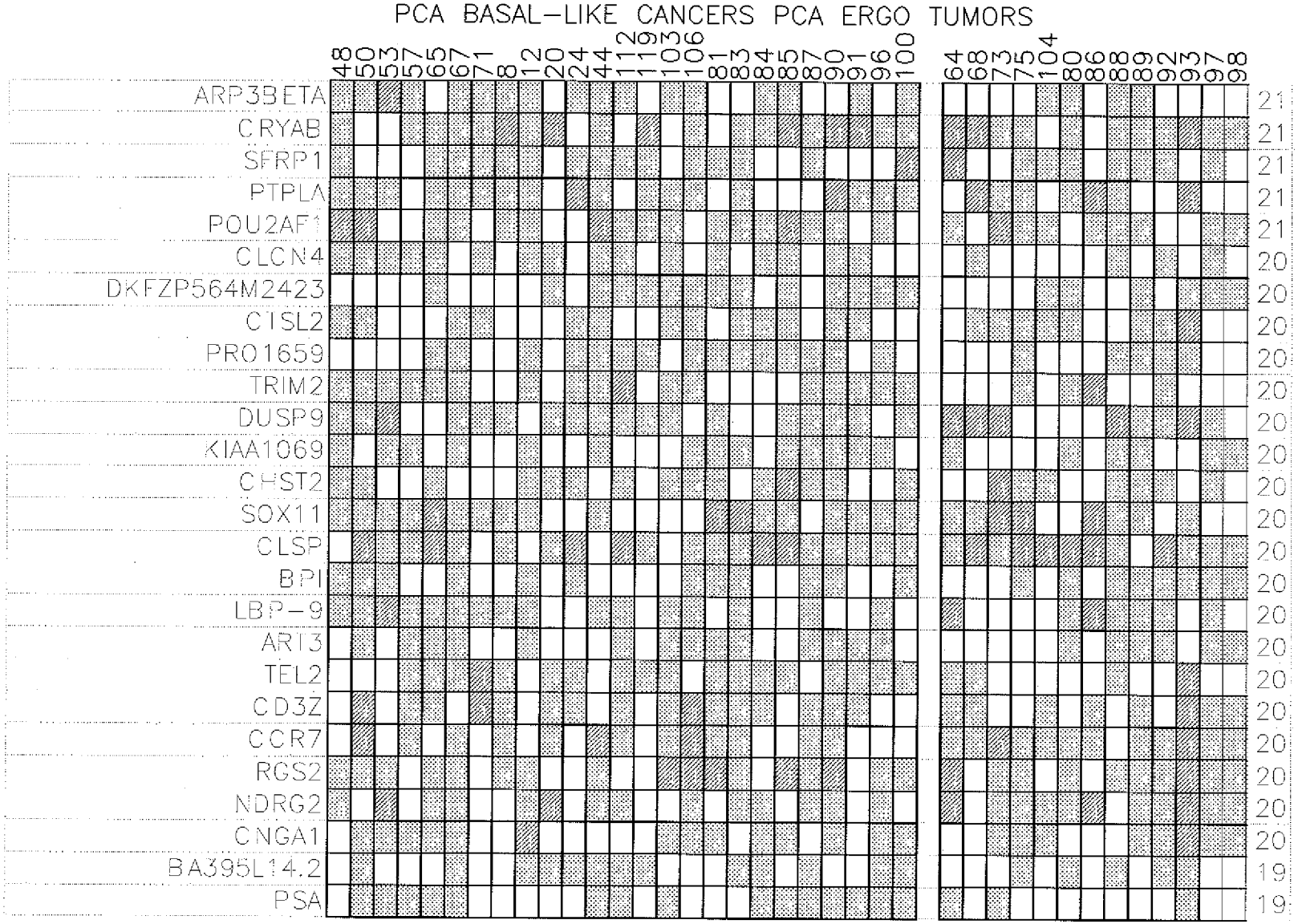

PCA BASAL-LIKE CANCERS PCA ERGO TUMORS
LDHB
SH2D2A
H1F1
AIDC
SMOC1
FLJ21079
INDO
ZIC1
SCYB10
SCYD1
SIAT8A
PHGDH
DKFZp564A026
GBP1
MRAS
PCDH8
KLK6
FABP7
CALB2
S100A1
ST5
LMO4
KIAA0481
HHGP
MIA
KRT17
CONTINUED ON SHEET 3

FIG. 25 2



CONTINUED ON SHEET 4

FIG. 25

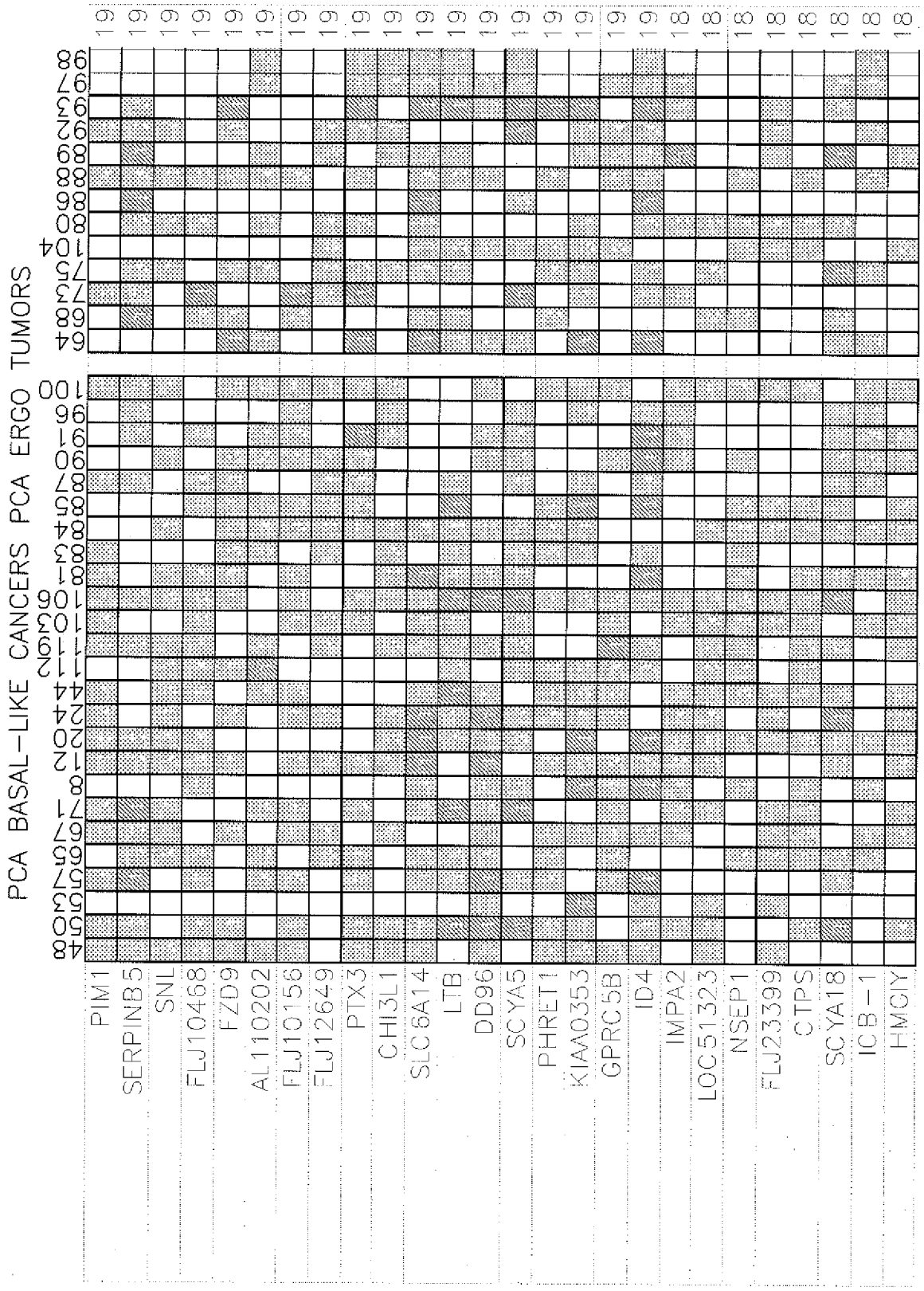

PCA BASAL-LIKE CANCERS PCA ERGO TUMORS
PIM1
SERPINB5
SNL
FLJ10468
FZD9
AL110202
FLJ10156
FLJ12649
PTX3
CHI3L1
SLC6A14
LTB
DD96
SCYA5
PHRET1
KIAA0353
GPRC5B
ID4
IMPA2
LOC51323
NSEP1
FLJ23399
CTPS
SCYA18
ICB-1
HMGIY
CONTINUED ON SHEET 5

FIG. 25

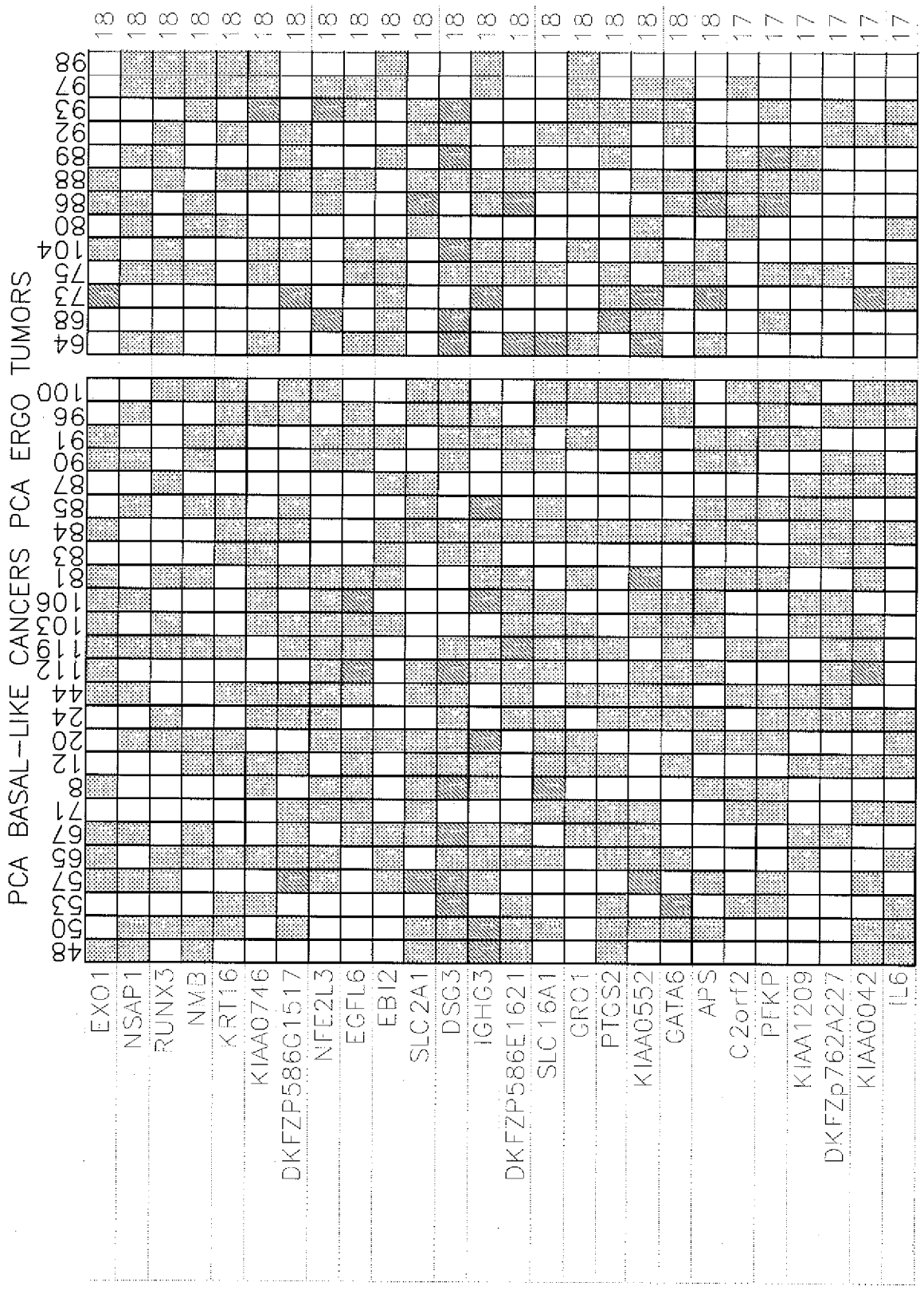

PCA BASAL-LIKE CANCERS PCA ERGO TUMORS
EXO1
NSAP1
RUNX3
NMB
KRT16
KIAA0746
DKFZP586G1517
NFE2L3
EGFL6
EB12
SLC2A1
DSG3
IGHG3
DKFZP586E1621
SLC16A1
GRO1
PTGS2
KIAA0552
CATA6
APS
C2orf2
PFKP
KIAA1209
DKFZp762A227
KIAA0042
IL6
CONTINUED ON SHEET 6

FIG. 25

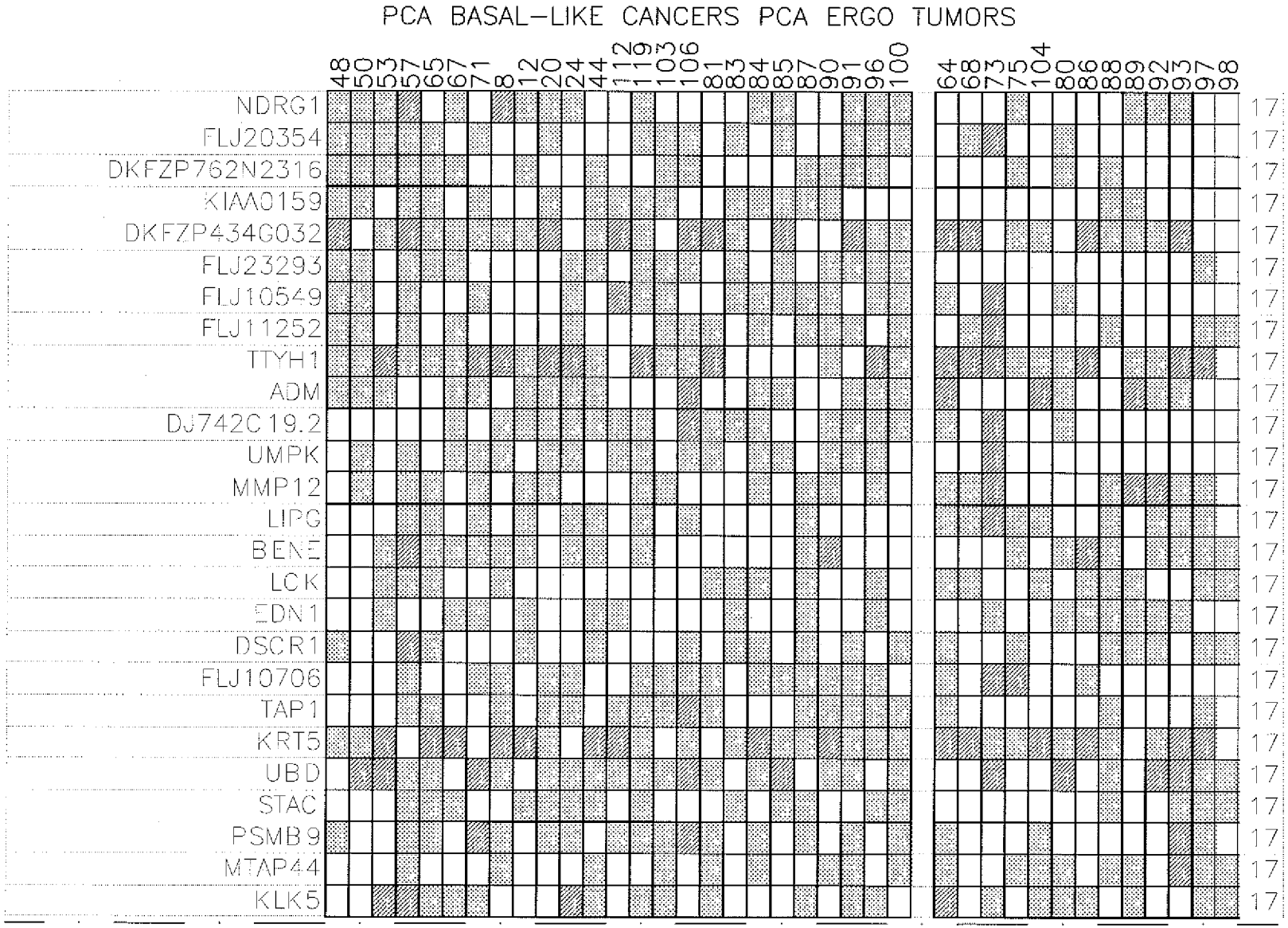

PCA BASAL–LIKE CANCERS PCA ERGO TUMORS
48 50 53 57 65 67 71 8 12 20 24 44 112 119 103 106 81 83 84 85 87 90 91 96 100
64 68 73 75 104 80 86 88 89 92 93 97 98
NDRG1
FLJ20354
DKFZP762N2316
KIAA0159
DKFZP434G032
FLJ23293
FLJ10549
FLJ11252
TTYH1
ADM
DJ742C19.2
UMPK
MMP12
LIPG
BENE
LCK
EDN1
DSCR1
FLJ10706
TAP1
KRT5
UBD
STAC
PSMB9
MTAP44
KLK5
17
CONTINUED ON SHEET 7

FIG. 25

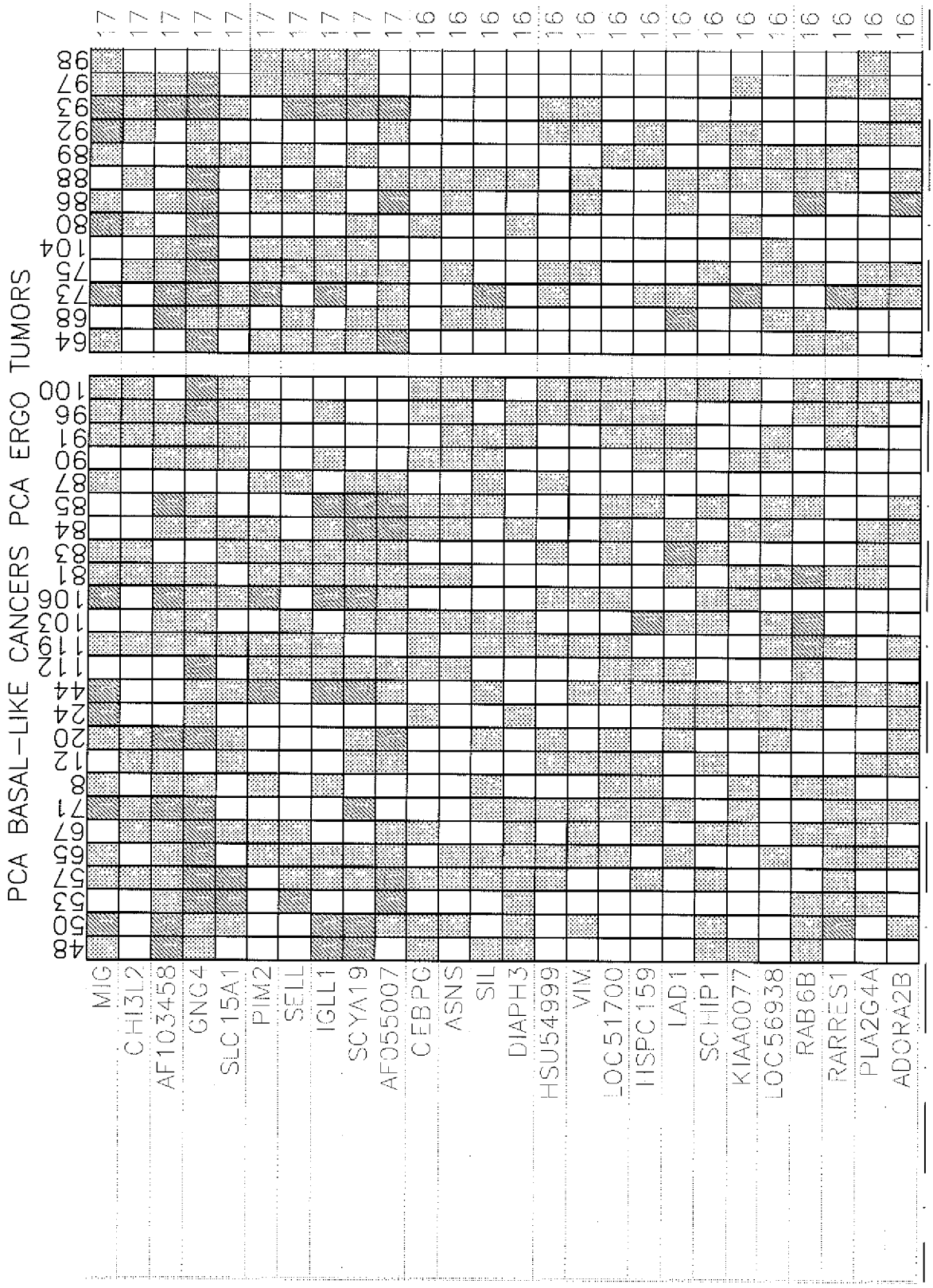

PCA BASAL-LIKE CANCERS PCA ERGO TUMORS
MIG
CHI3L2
AF103458
GNG4
SLC15A1
PIM2
SELL
IGLL1
SCYA19
AF055007
CEBPG
ASNS
SIL
DIAPH3
HSU54999
VIM
LOC51700
IISPC159
IAD1
SCHIP1
KIAA0077
LOC56938
RAB6B
RARRES1
PLA2G4A
ADORA2B
CONTINUED ON SHEET 8

FIG. 25

7

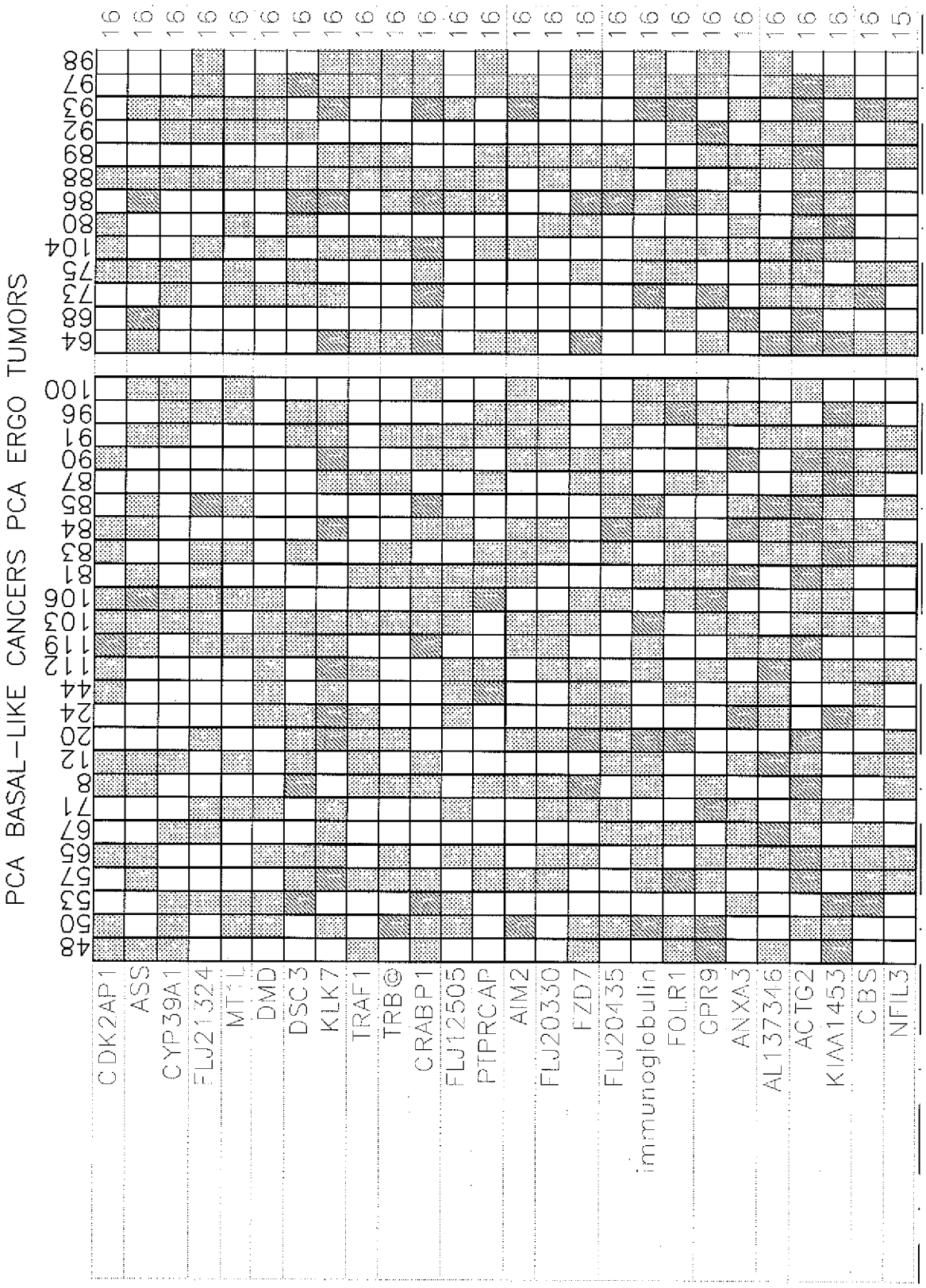

PCA BASAL-LIKE CANCERS PCA ERGO TUMORS
CDK2AP1
ASS
CYP39A1
FLJ21324
MT1L
DMD
DSC3
KLK7
TRAF1
TRB@
CRABP1
FLJ12505
PTPRCAP
AIM2
FLJ20330
FZD7
FLJ20435
immunoglobulin
FOLR1
GPR9
ANXA3
AL137346
ACTG2
KIAA1453
CBS
NFIL3
CONTINUED ON SHEET 9

FIG. 25

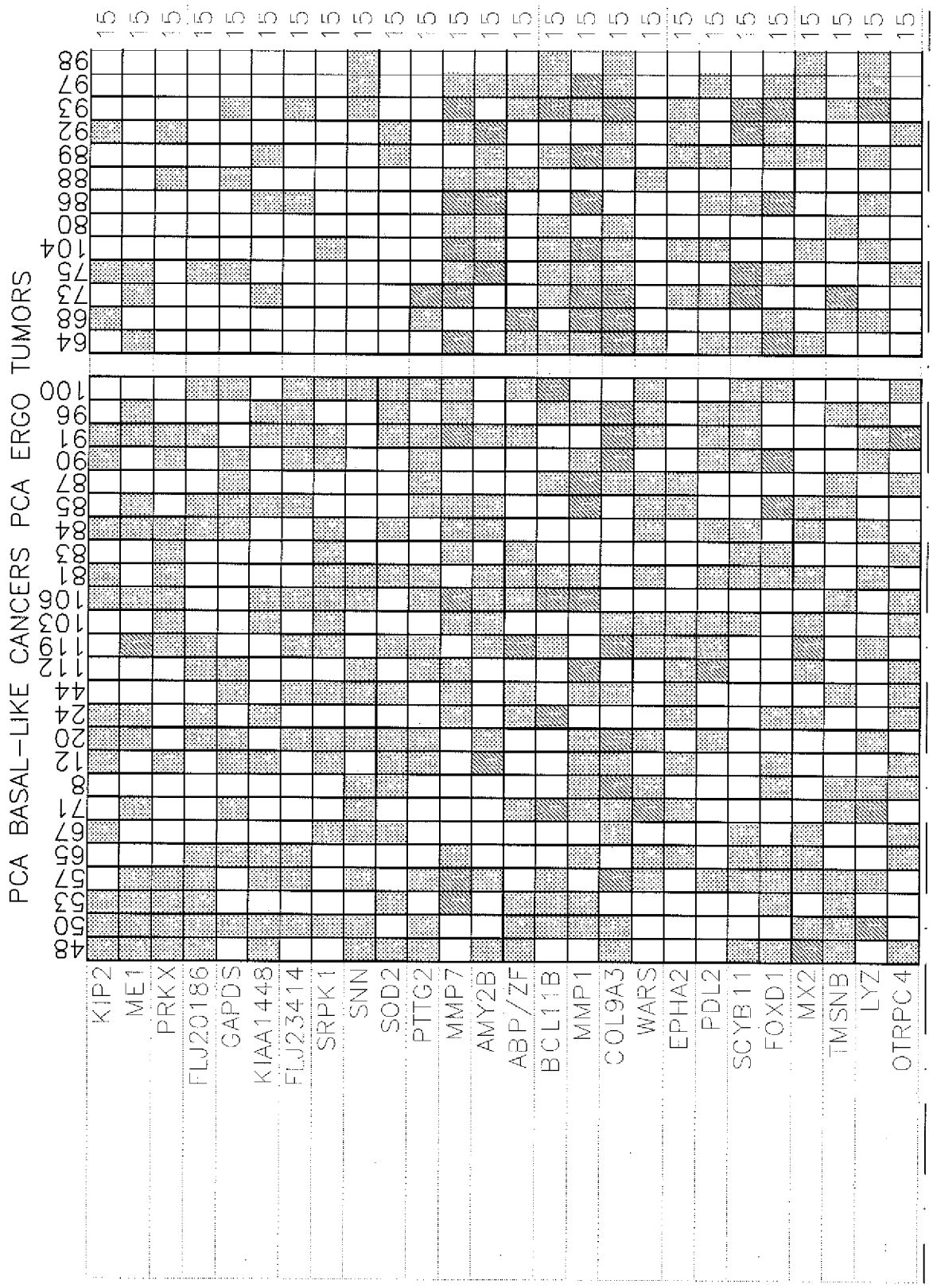

PCA BASAL-LIKE CANCERS PCA ERGO TUMORS
KIP2
ME1
PRKX
FLJ20186
GAPDS
KIAA1448
FLJ23414
SRPK1
SNN
SOD2
PTTG2
MMP7
AMY2B
ABP/ZF
BCL11B
MMP1
COL9A3
WARS
EPHA2
PDL2
SCYB11
FOXD1
MX2
TMSNB
LYZ
OTRPC4
15
CONTINUED ON SHEET 10

FIG. 25

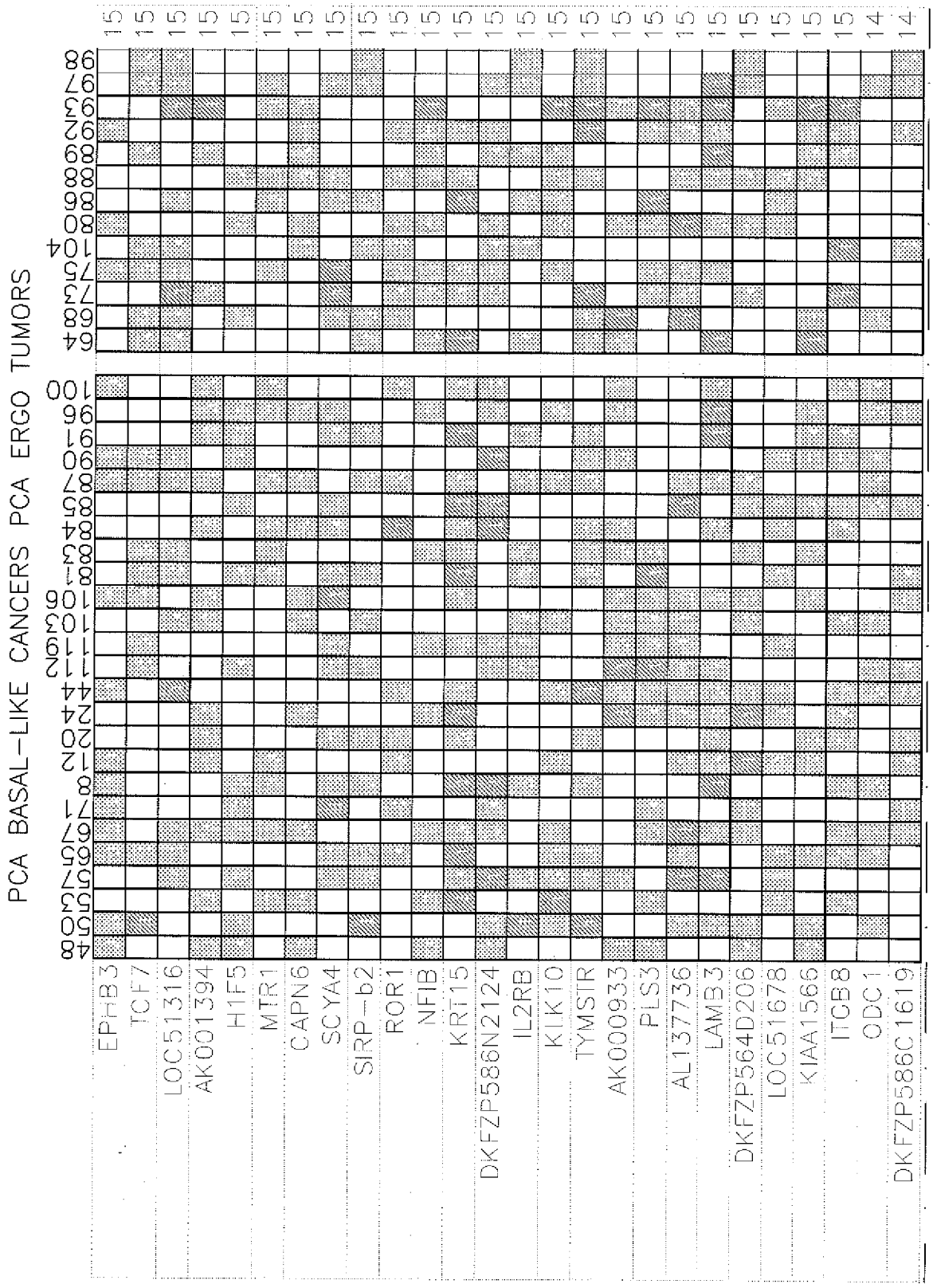

PCA BASAL-LIKE CANCERS PCA ERGO TUMORS
EPHB3
TCF7
LOC51316
AK001394
H1F5
MTR1
CAPN6
SCYA4
SIRP-b2
ROR1
NFIB
KRT15
DKFZP586N2124
IL2RB
KIK10
TYMSTR
AK000933
PLS3
AL137736
LAMB3
DKFZP564D206
LOC51678
KIAA1566
ITCB8
ODC1
DKFZP586C1619
CONTINUED ON SHEET 11

FIG. 25 10

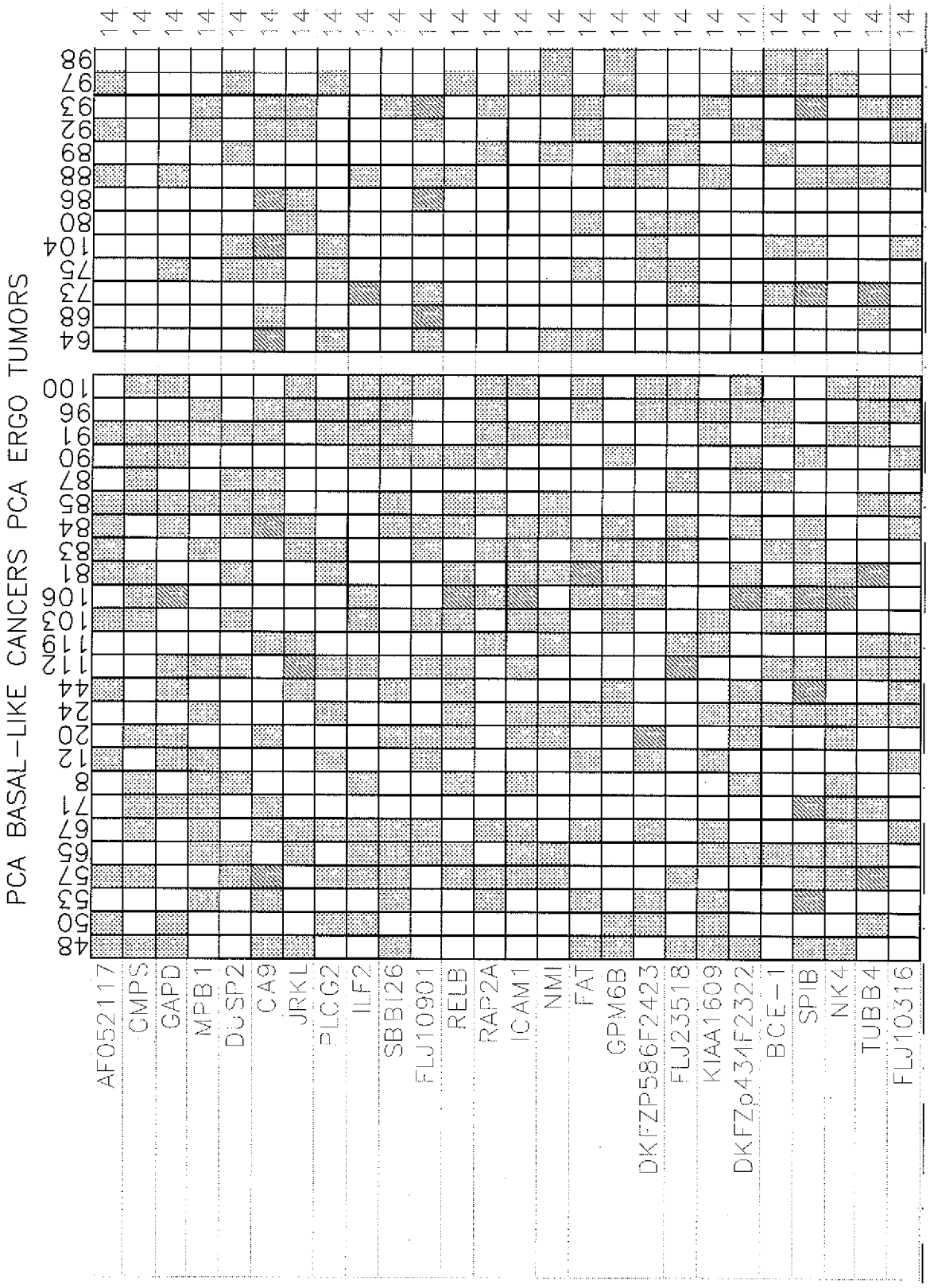


FIG. 25

CONTINUED ON SHEET 12

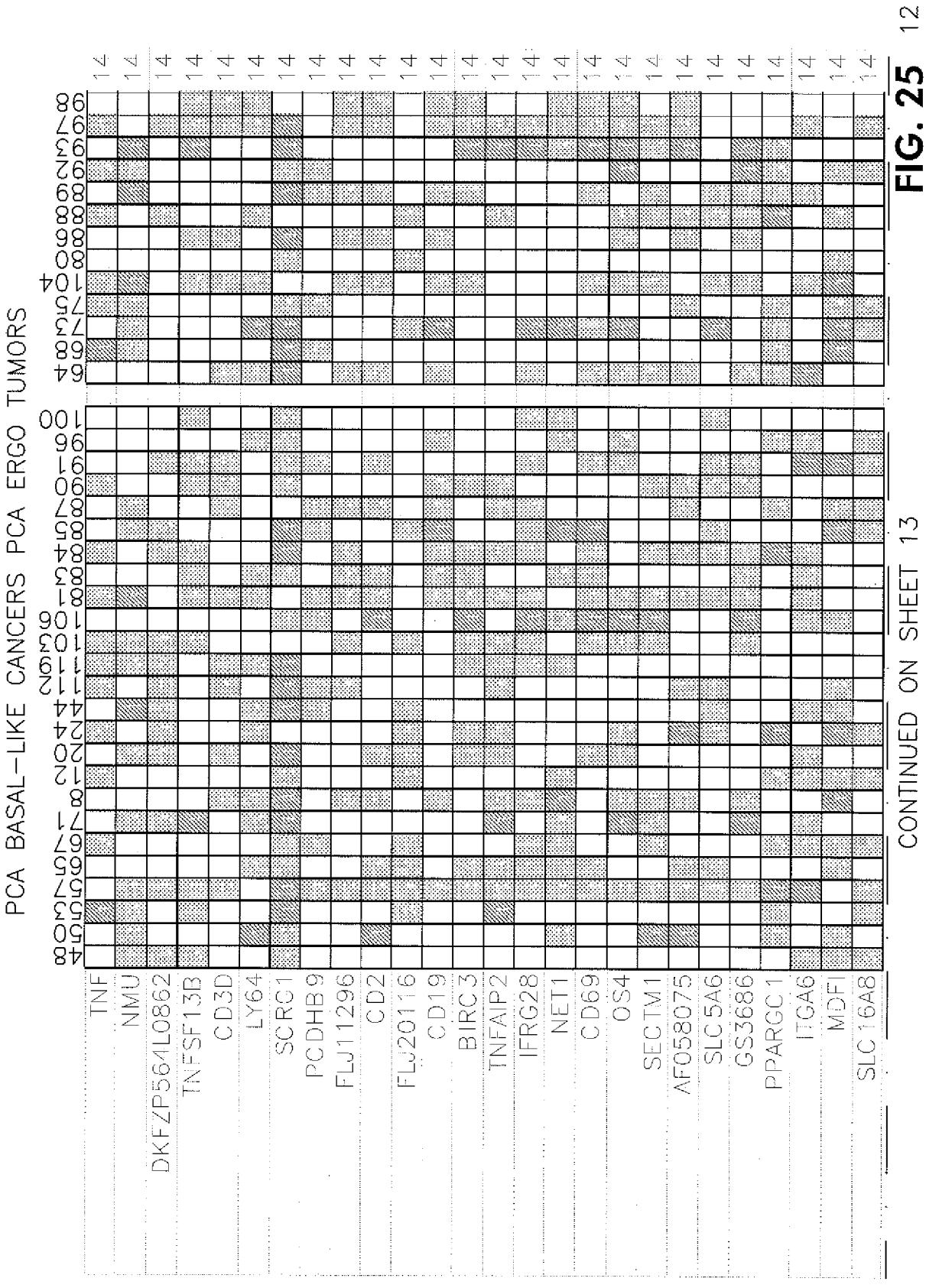
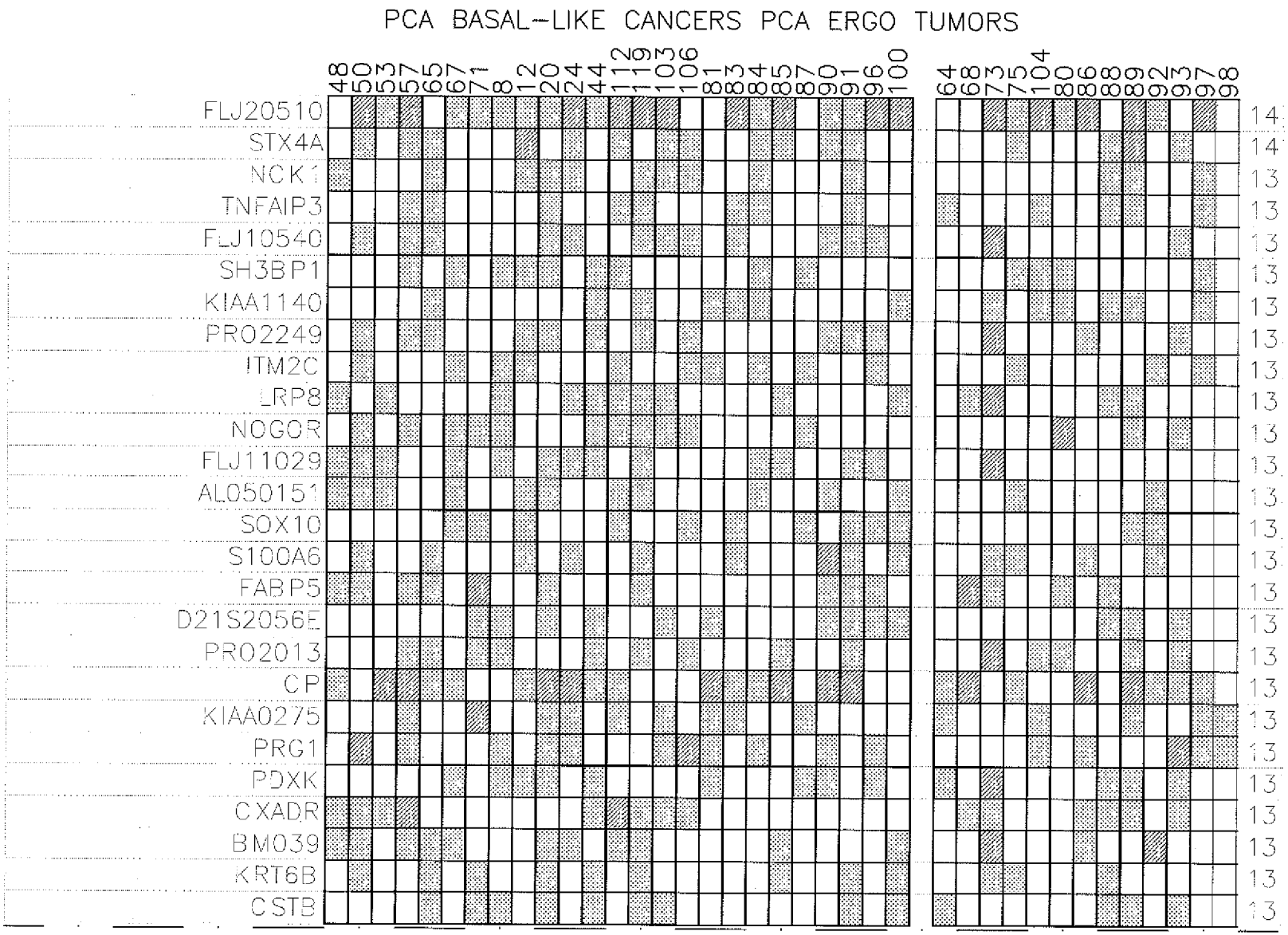

PCA BASAL-LIKE CANCERS PCA ERGO TUMORS
TNF
NMU
DKFZP564L0862
TNFSF13B
CD3D
LY64
SCRC1
PCDHB9
FLJ11296
CD2
FLJ20116
CD19
BIRC3
TNFAIP2
IFRG28
NET1
CD69
OS4
SECTM1
AF058075
SLC5A6
GS3686
PPARGC1
ITGA6
MDFI
SLC16A8
CONTINUED ON SHEET 13

FIG. 25 12



CONTINUED ON SHEET 14

FIG. 25

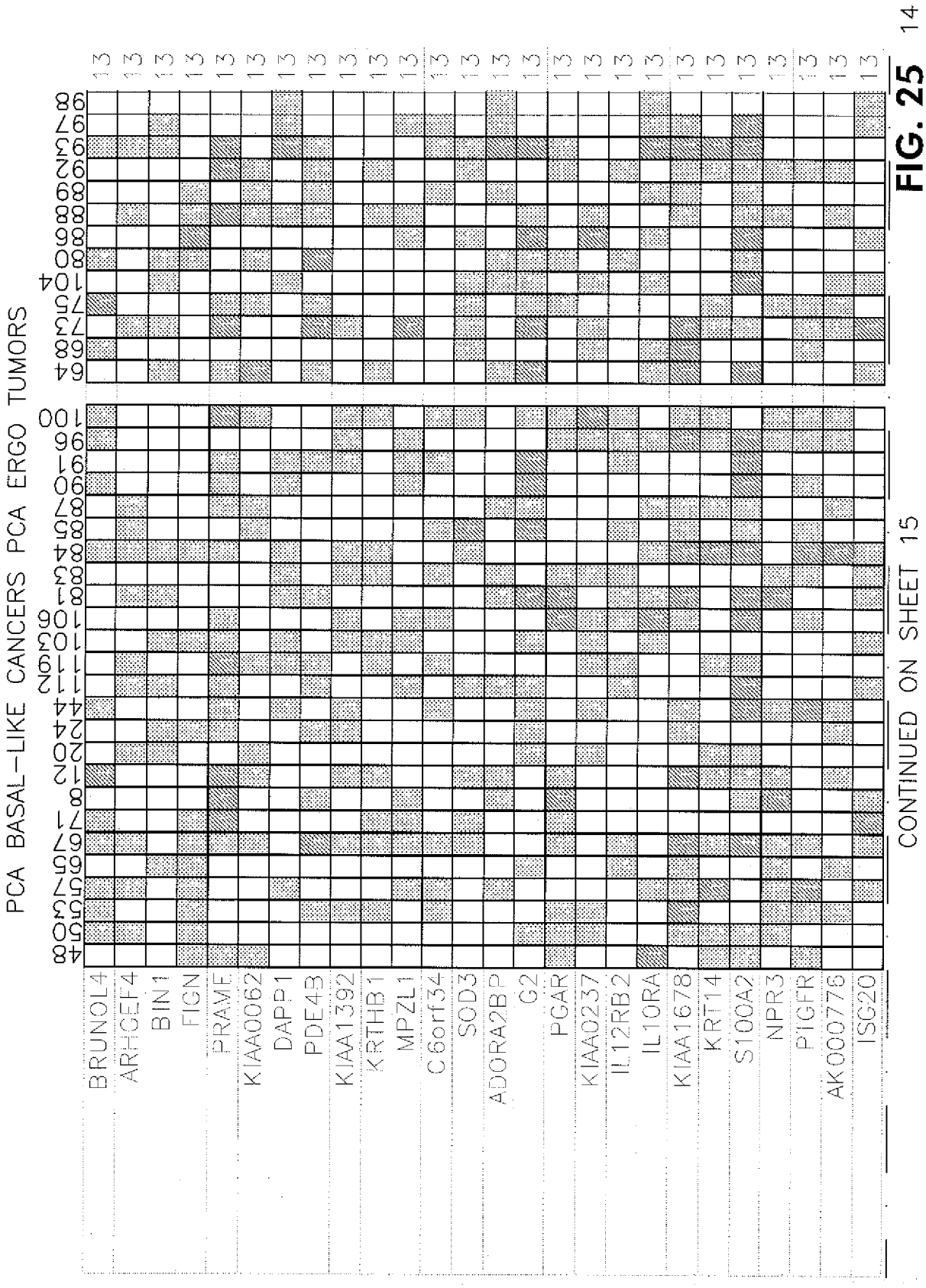

PCA BASAL-LIKE CANCERS PCA ERGO TUMORS
BRUNOL4
ARHGEF4
BIN1
FIGN
PRAME
KIAA0062
DAPP1
PDE4B
KIAA1392
KRTHB1
MPZL1
C6orf34
SOD3
ADORA2BP
G2
PGAR
KIAA0237
IL12RB2
IL10RA
KIAA1678
KRT14
S100A2
NPR3
PIGFR
AK000776
ISG20
CONTINUED ON SHEET 15

FIG. 25 14

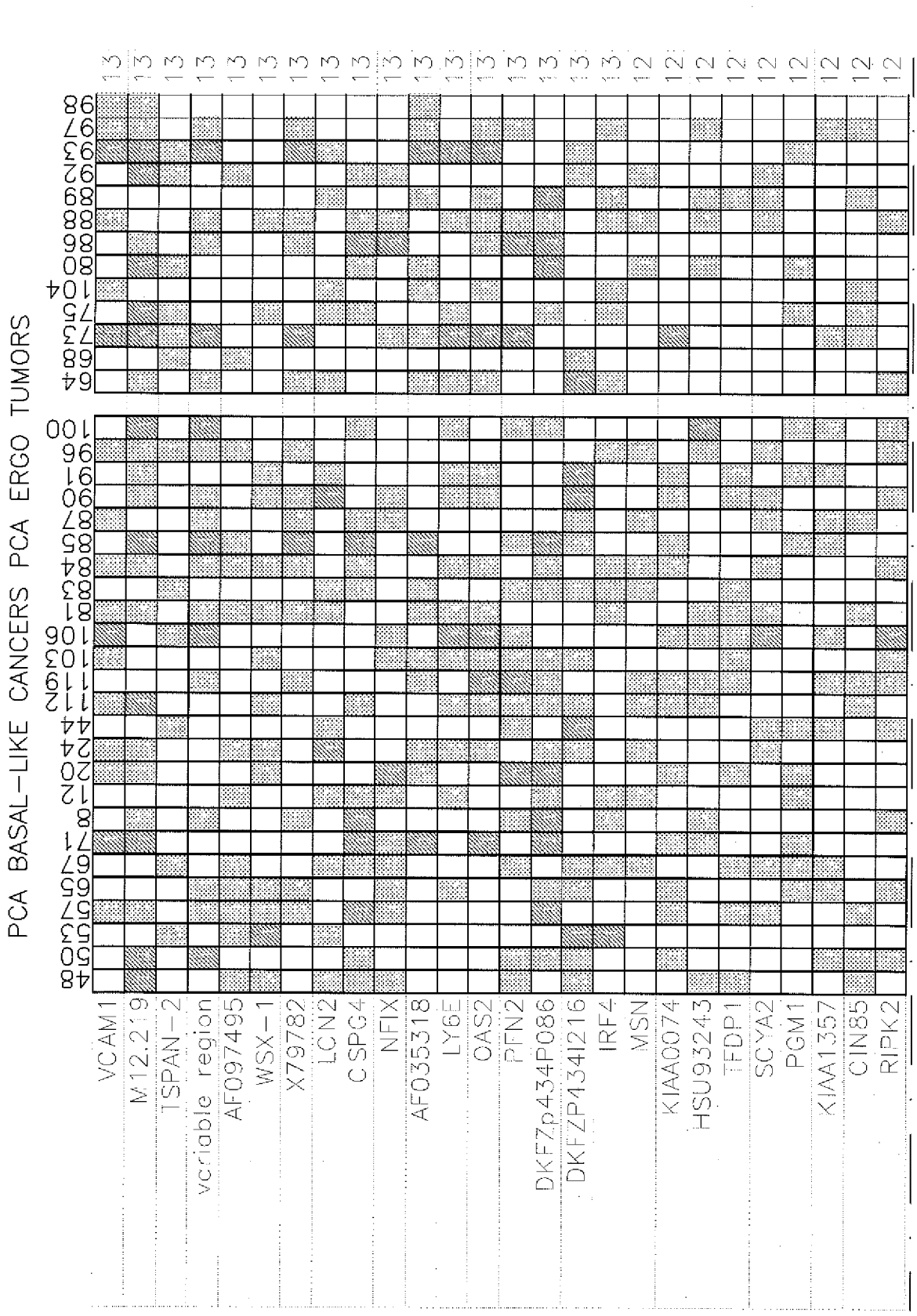

PCA BASAL-LIKE CANCERS PCA ERGO TUMORS
VCAM1
M12.219
TSPAN-2
variable region
AF097495
WSX-1
X79782
LCN2
CSPG4
NFIX
AF035318
LY6E
OAS2
PFN2
DKFZp434P086
DKFZP1341216
IRF4
MSN
KIAA0074
HSU93243
TFDP1
SCYA2
PGM1
KIAA1357
CIN85
RIPK2
CONTINUED ON SHEET 16

FIG. 25 15

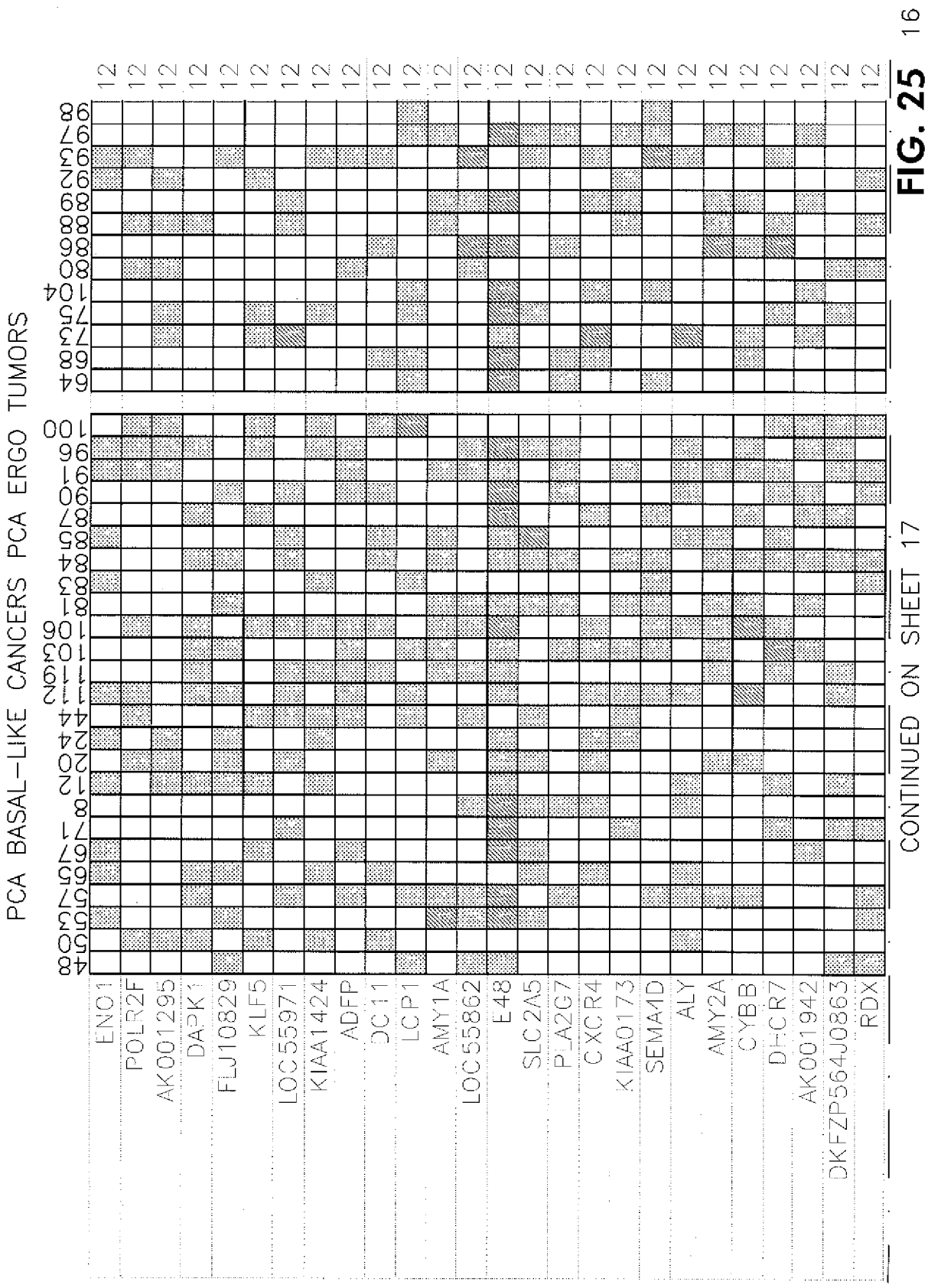

PCA BASAL-LIKE CANCERS PCA ERGO TUMORS
ENO1
POLR2F
AK001295
DAPK1
FLJ10829
KLF5
LOC55971
KIAA1424
ADFP
DC11
LCP1
AMY1A
LOC55862
E48
SLC2A5
P_A2G7
CXCR4
KIAA0173
SEMA4D
ALY
AMY2A
CYBB
DHCR7
AK001942
DKFZP564J0863
RDX
CONTINUED ON SHEET 17

FIG. 25

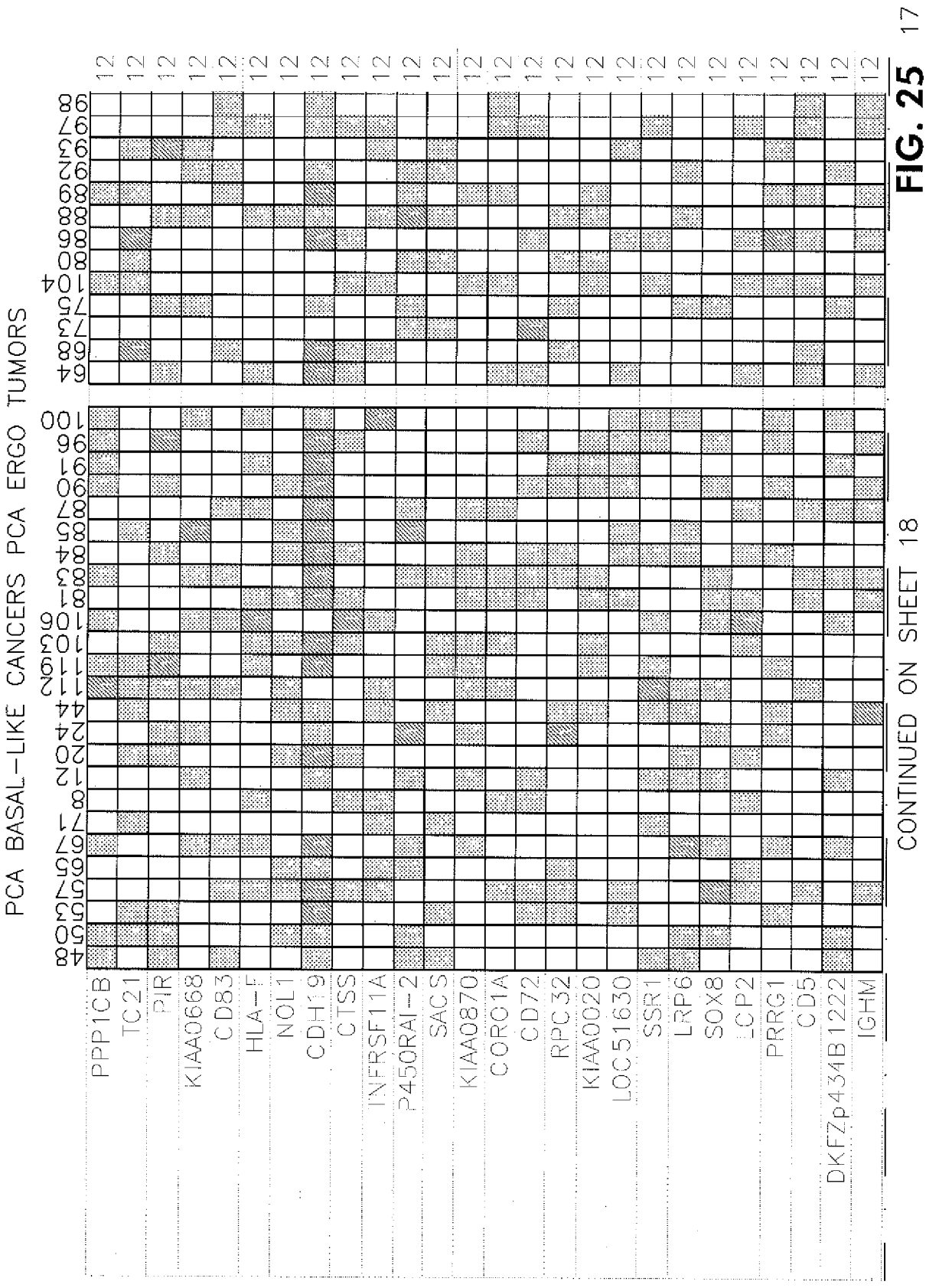

PCA BASAL-LIKE CANCERS PCA ERGO TUMORS
PPP1CB
TC21
PIR
KIAA0668
CD83
HLA-F
NOL1
CDH19
CTSS
TNFRSF11A
P450RAI-2
SACS
KIAA0870
CORO1A
CD72
RPC32
KIAA0020
LOC51630
SSR1
LRP6
SOX8
LCP2
PRRG1
CD5
DKFZp434B1222
IGHM
CONTINUED ON SHEET 18

FIG. 25 17

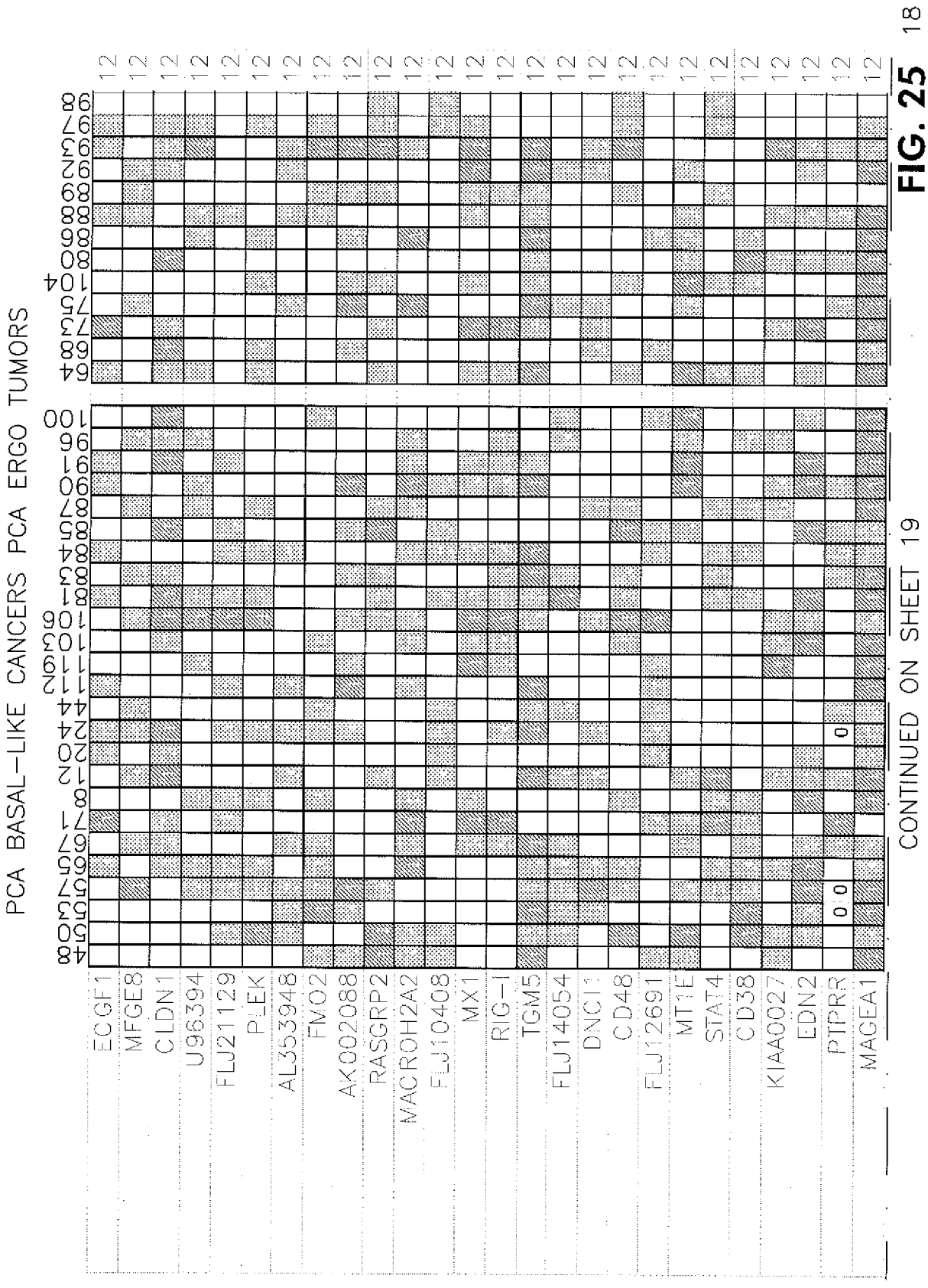

PCA BASAL-LIKE CANCERS PCA ERGO TUMORS
ECGF1
MFGE8
CLDN1
U96394
FLJ21129
PLEK
AL353948
FMO2
AK002088
RASGRP2
MACROH2A2
FLJ10408
MX1
RIG-I
TGM5
FLJ14054
DNC1
CD48
FLJ12691
MT1E
STAT4
CD38
KIAA0027
EDN2
PTPRR
MAGEA1
CONTINUED ON SHEET 19

FIG. 25 18

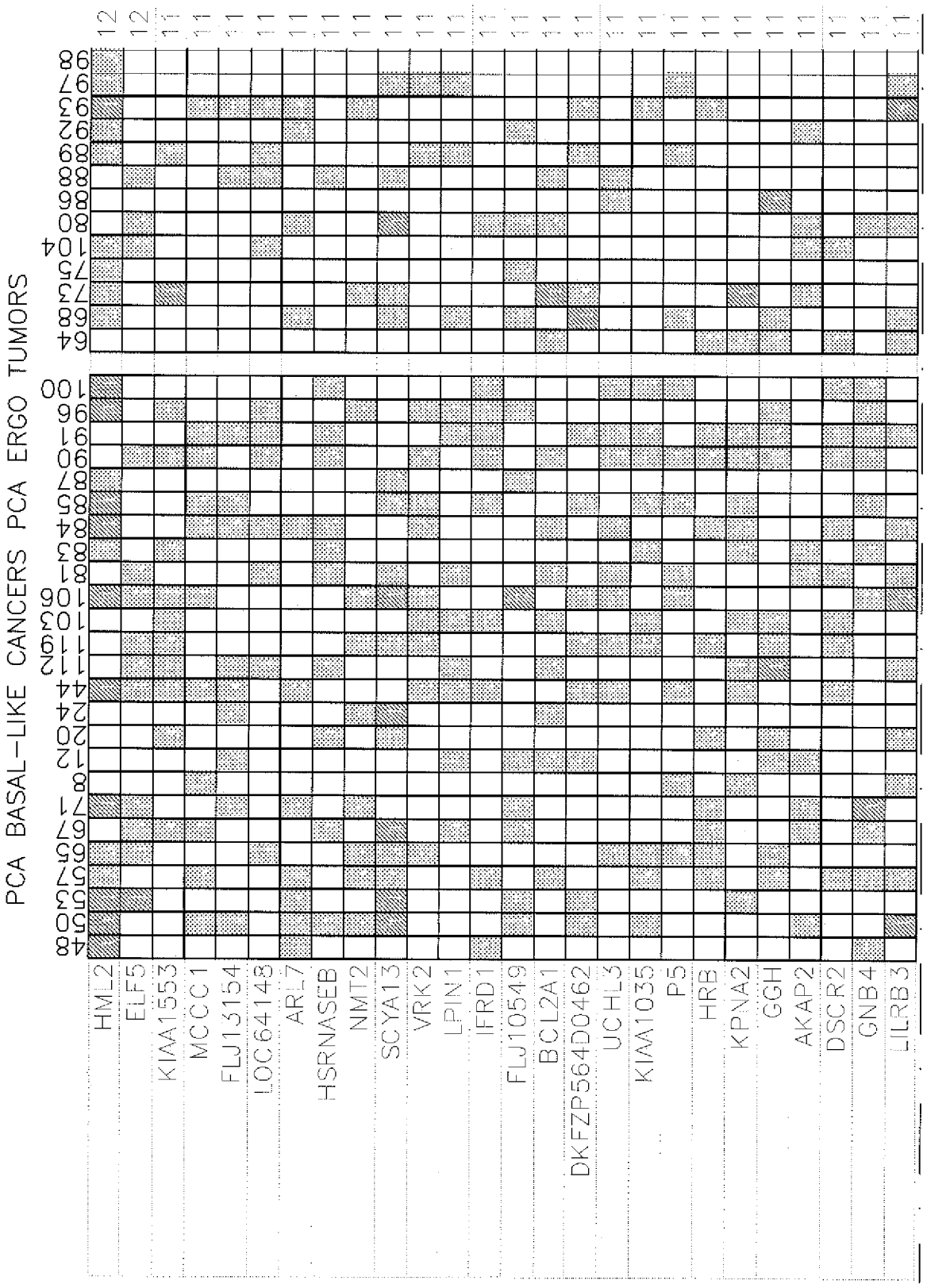

PCA BASAL-LIKE CANCERS PCA ERGO TUMORS
HML2
ELF5
KIAA1553
MCCC1
FLJ13154
LOC64143
ARL7
HSRNASEB
NMT2
SCYA13
VRK2
LPIN1
IFRD1
FLJ10549
BCL2A1
DKFZP564D0462
UCHL3
KIAA1035
P5
HRB
KPNA2
GGH
AKAP2
DSCR2
GNB4
LILRB3
CONTINUED ON SHEET 20

FIG. 25

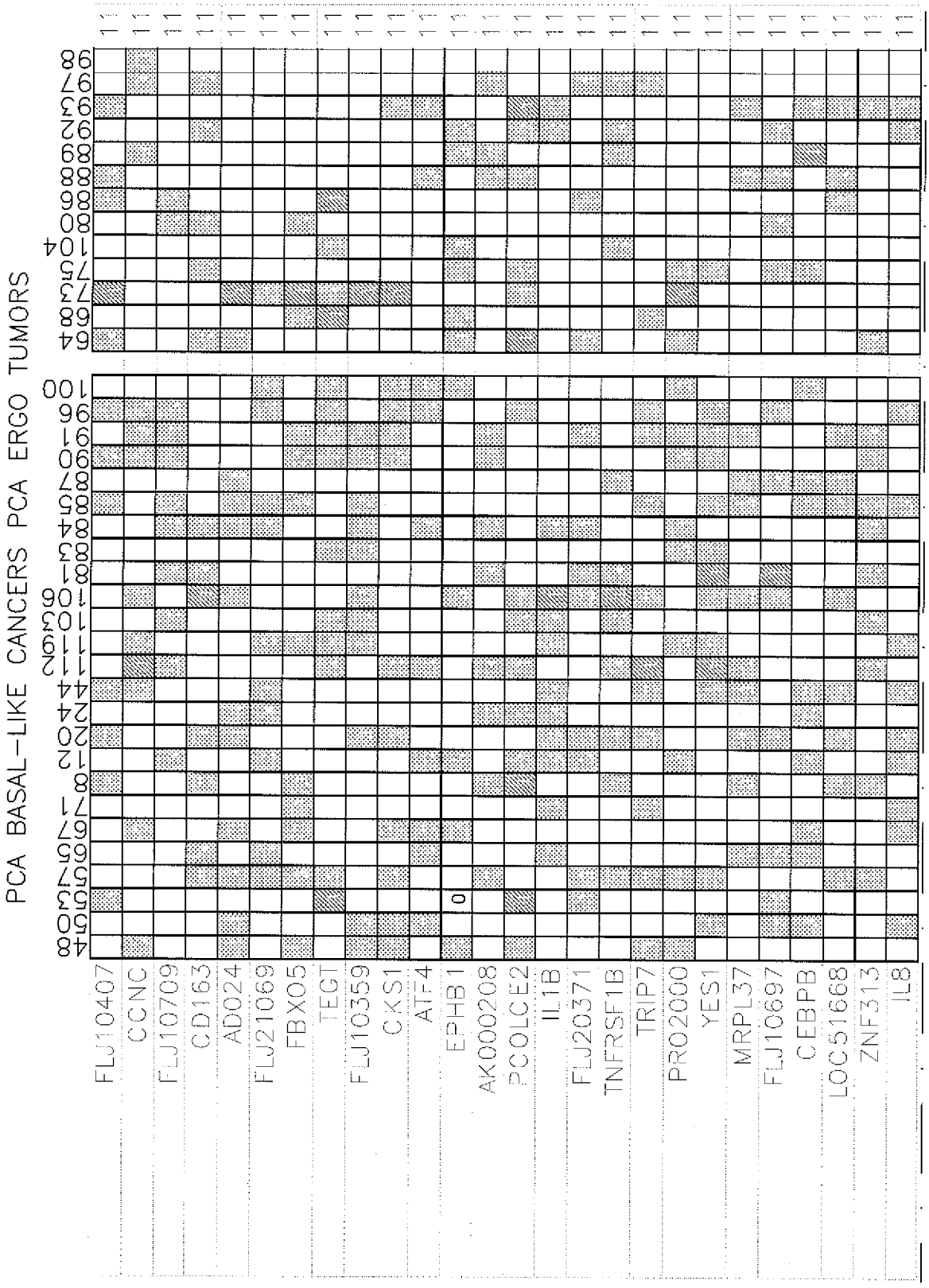

PCA BASAL-LIKE CANCERS PCA ERGO TUMORS
FLJ10407
CCNC
FLJ10709
CD163
AD024
FLJ21069
FBXO5
TEGT
FLJ10359
CKS1
ATF4
EPHB1
AK000208
PCOLCE2
IL1B
FLJ20371
TNFRSF1B
TRIP7
PRO2000
YES1
MRPL37
FLJ10697
CEBPB
LOC51668
ZNF313
IL8
CONTINUED ON SHEET 21

FIG. 25

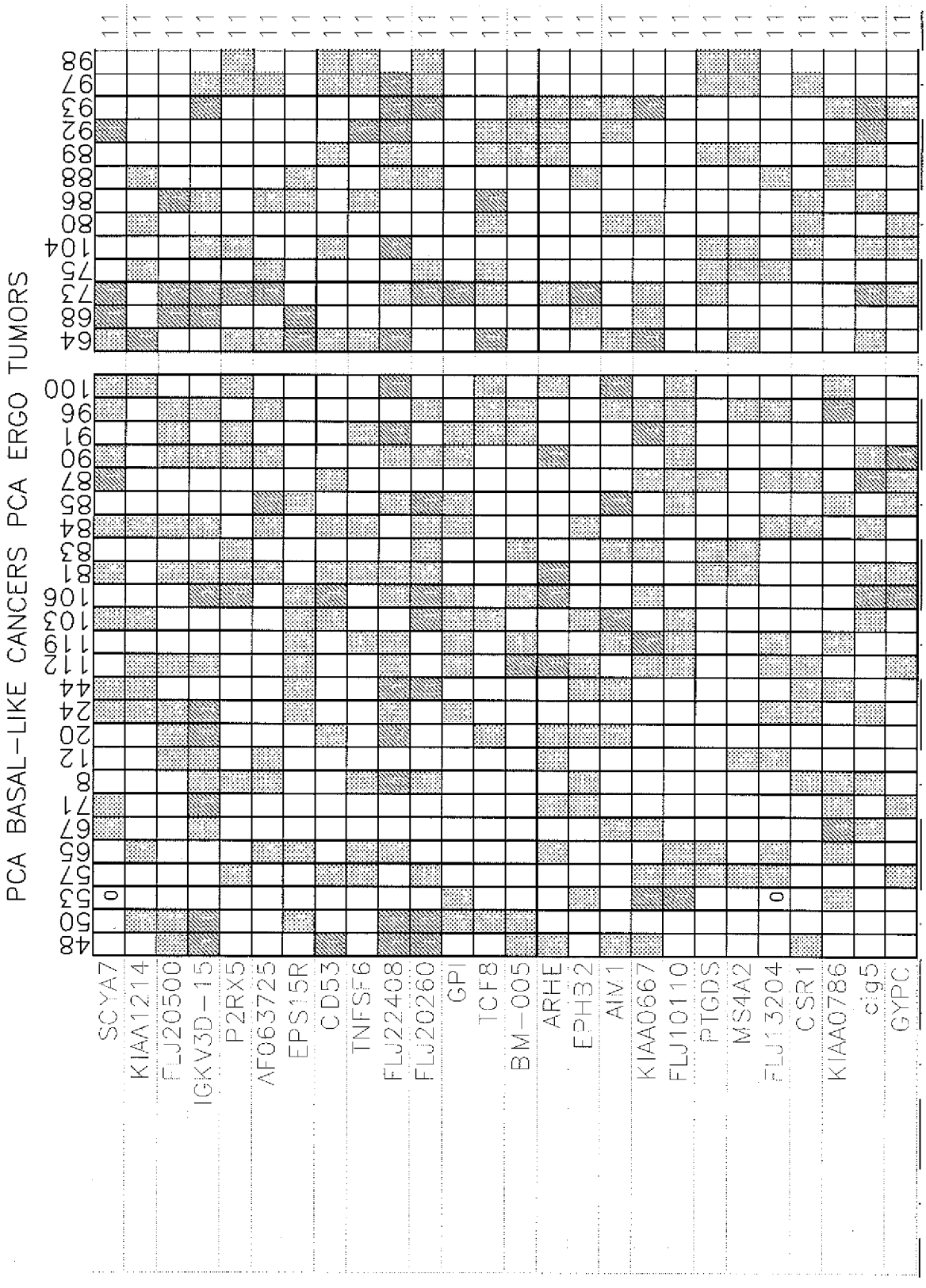

PCA BASAL-LIKE CANCERS PCA ERGO TUMORS
SCYA7
KIAA1214
FLJ20500
IGKV3D-15
P2RX5
AF063725
EPS15R
CD53
TNFSF6
FLJ22408
FLJ20260
GPI
TCF8
BM-005
ARHE
EPH32
AIM1
KIAA0667
FLJ10110
PTGDS
MS4A2
FLJ13204
CSR1
KIAA0786
cig5
GYPC
CONTINUED ON SHEET 22

FIG. 25 21

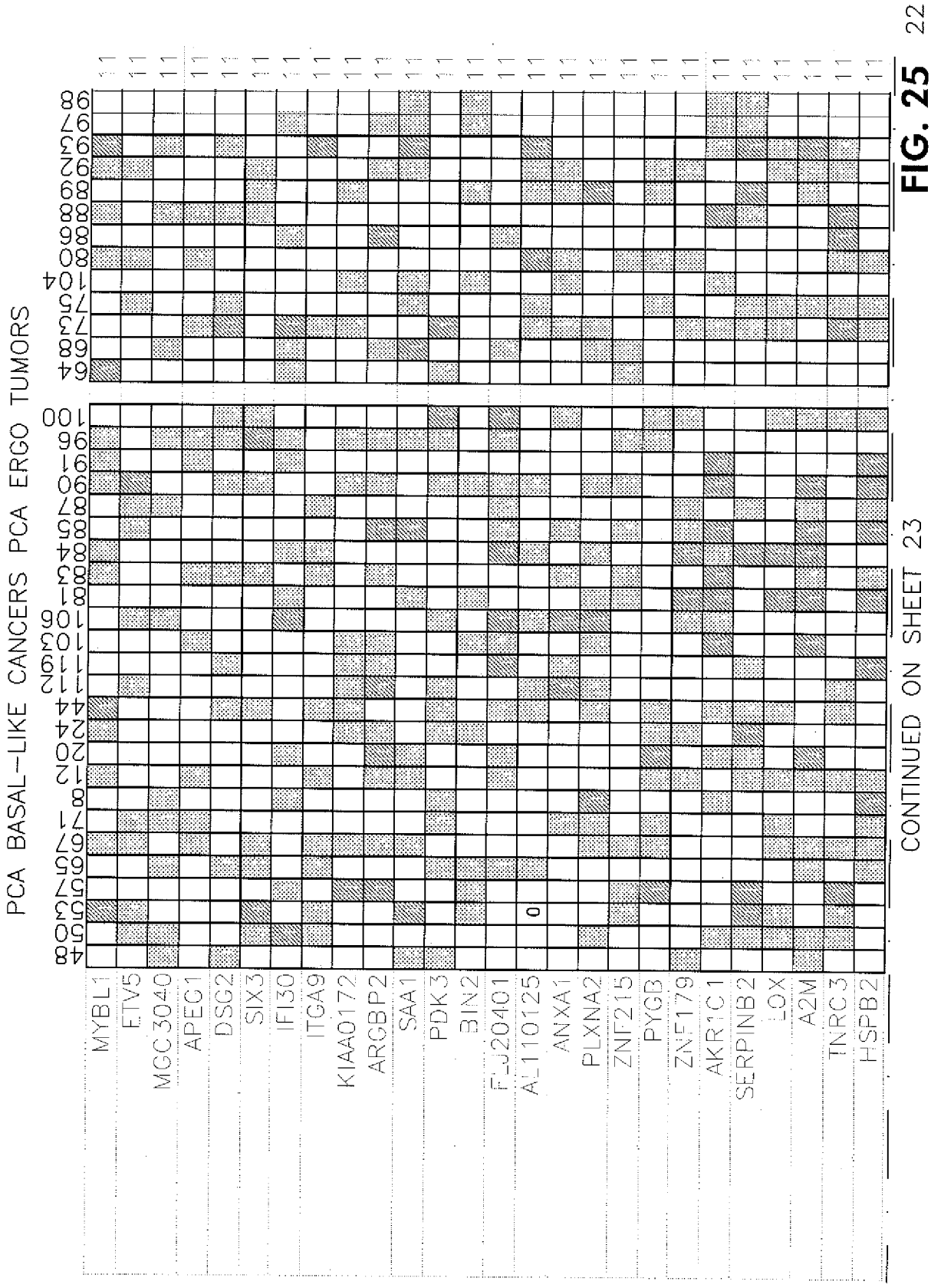

PCA BASAL-LIKE CANCERS PCA ERGO TUMORS
MYBL1
ETV5
MGC3040
APEG1
DSG2
SIX3
IFI30
ITGA9
KIAA0172
ARGBP2
SAA1
PDK3
BIN2
FLJ20401
AL110125
ANXA1
PLXNA2
ZNF215
PYGB
ZNF179
AKR1C1
SERPINB2
LOX
A2M
TNRC3
HSPB2
CONTINUED ON SHEET 23

FIG. 25 22

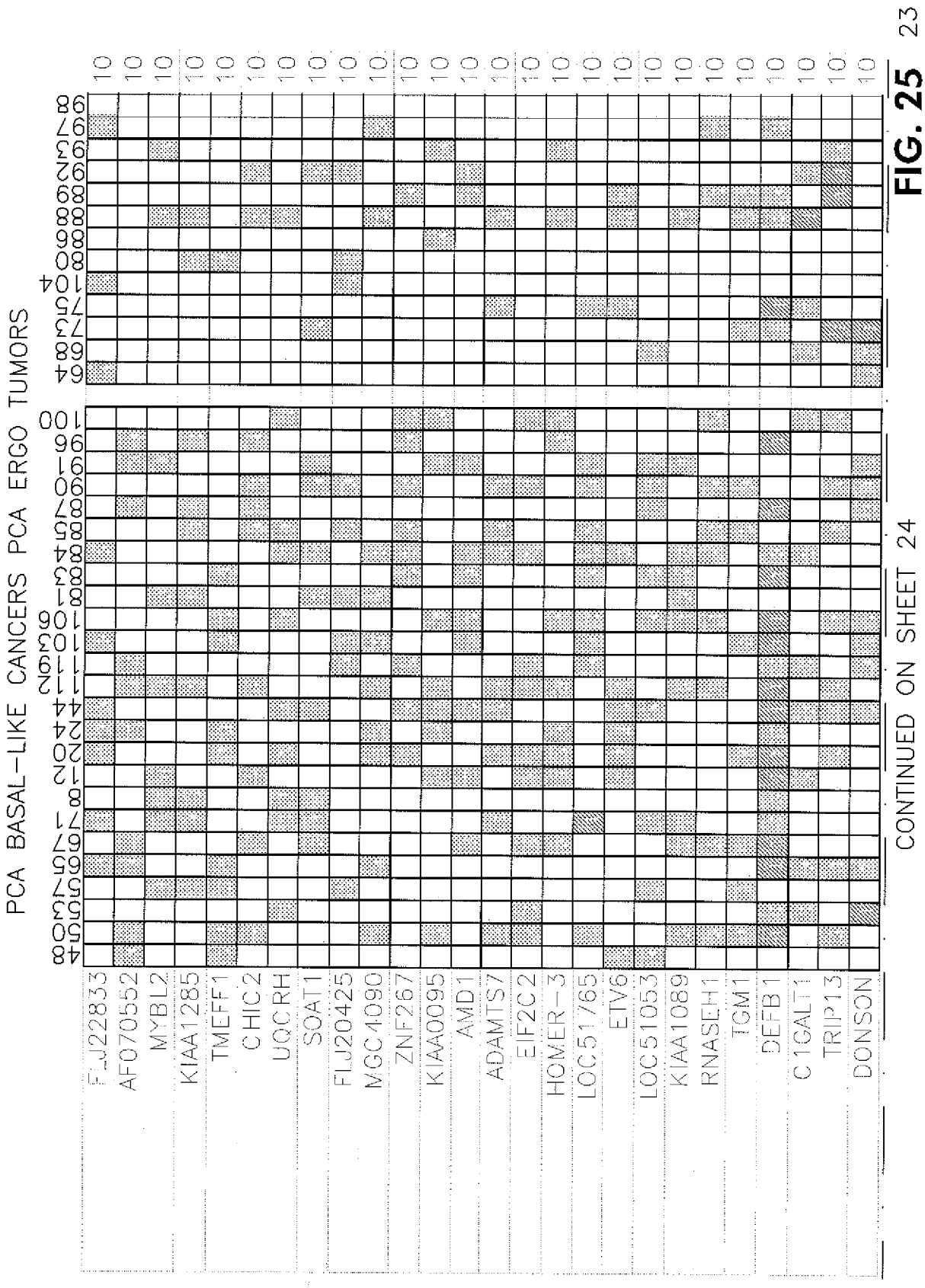

PCA BASAL-LIKE CANCERS PCA ERGO TUMORS
FLJ22833
AF070552
MYBL2
KIAA1285
TMEFF1
CHIC2
UQCRH
SOAT1
FLJ20425
MGC4090
ZNF267
KIAA0095
AMD1
ADAMTS7
EIF2C2
HOMER-3
LOC51765
ETV6
LOC51053
KIAA1089
RNASEH1
TGM1
DEFB1
C1GALT1
TRIP13
DONSON
CONTINUED ON SHEET 24

FIG. 25 23

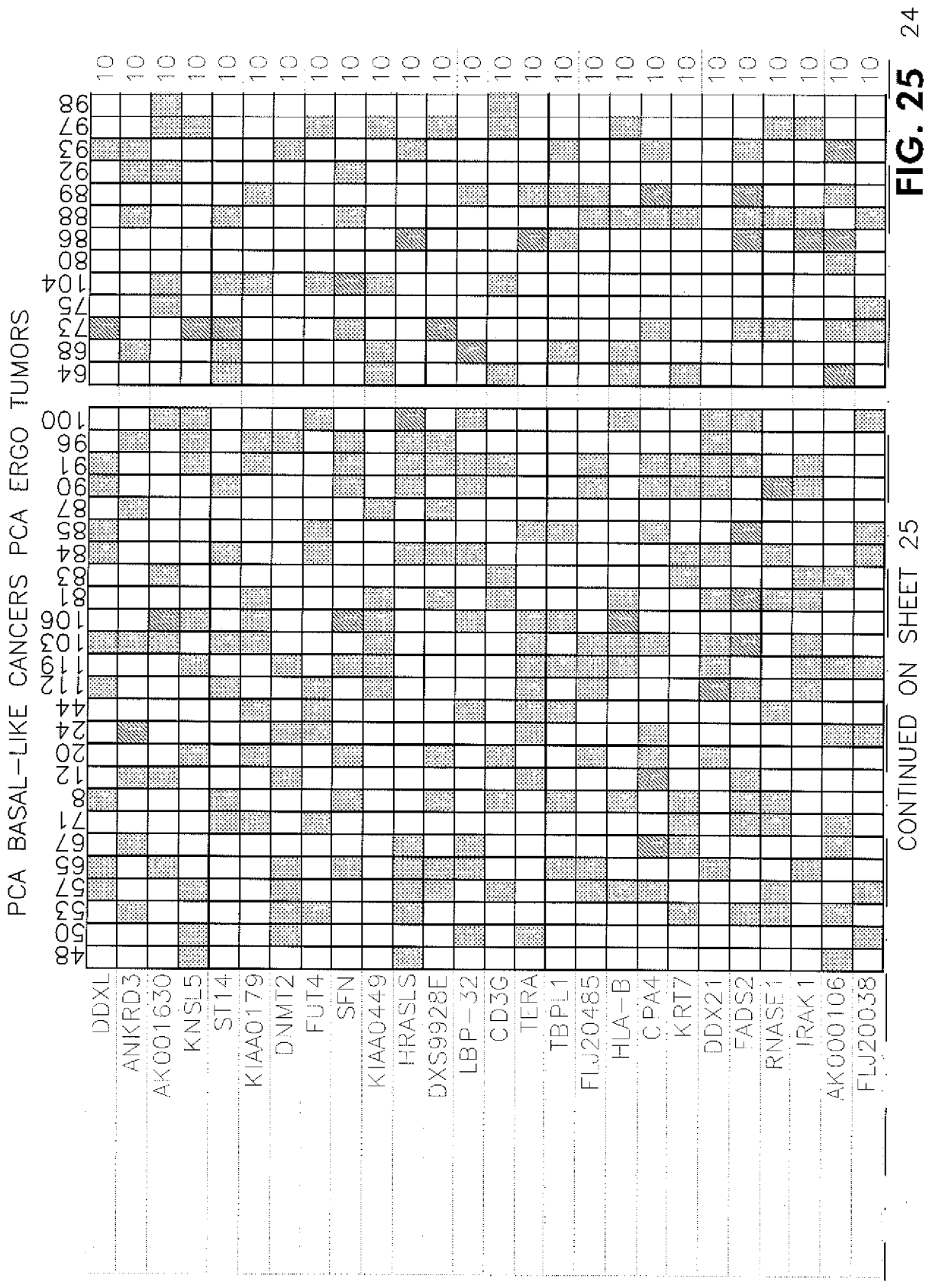

PCA BASAL-LIKE CANCERS PCA ERGO TUMORS
DDXL
ANKRD3
AK001630
KNSL5
ST14
KIAA0179
DNMT2
FUT4
SFN
KIAA0449
HRASLS
DXS9928E
LBP-32
CD3G
TERA
TBPL1
FLJ20485
HLA-B
CPA4
KRT7
DDX21
EADS2
RNASE1
IRAK1
AK000106
FLJ20038
CONTINUED ON SHEET 25

FIG. 25 24

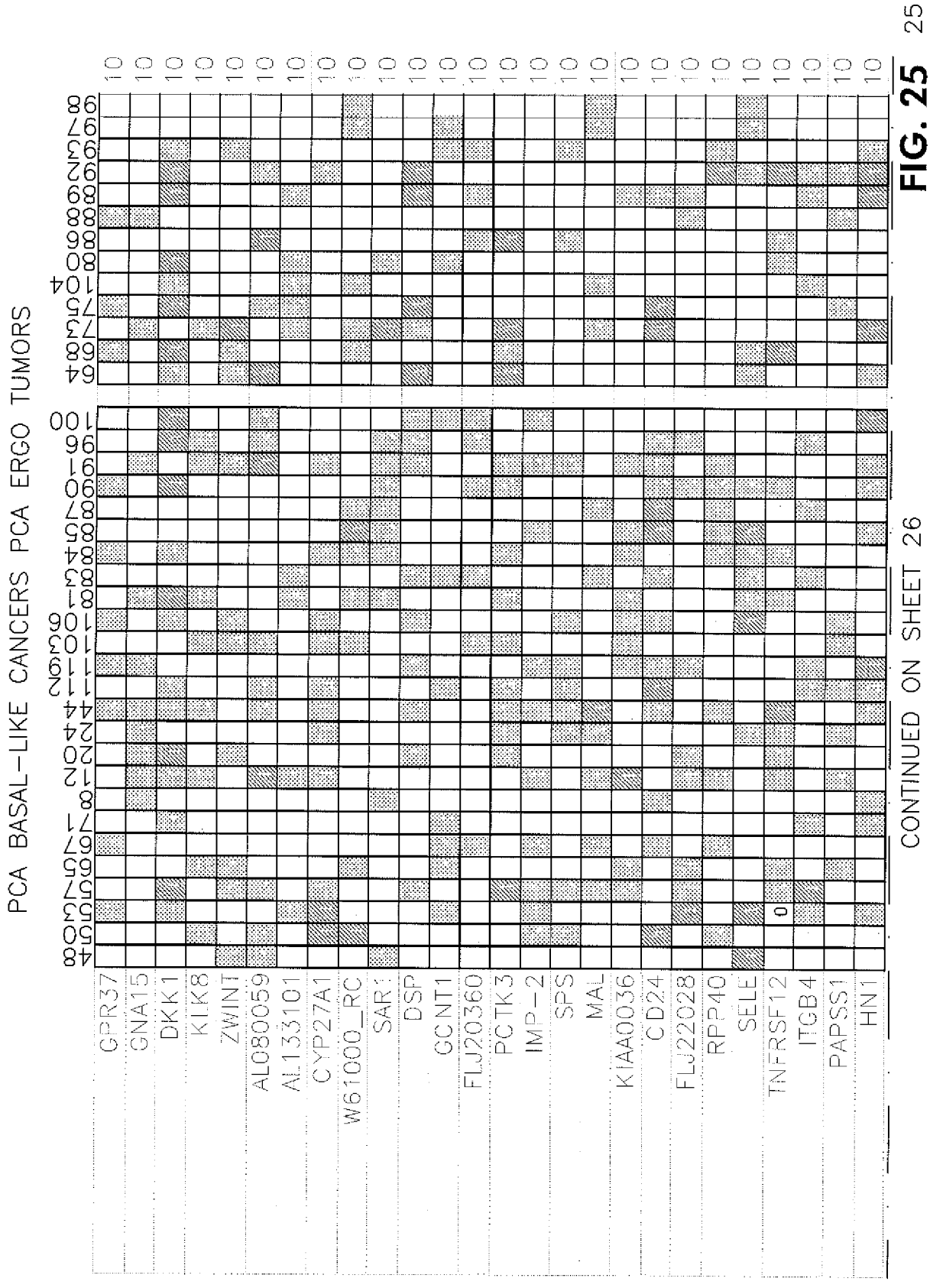

PCA BASAL-LIKE CANCERS PCA ERGO TUMORS
GPR37
GNA15
DKK1
KIK8
ZWINT
AL080059
AL133101
CYP27A1
W61000_RC
SAR1
DSP
GCNT1
FLJ20360
PCTK3
IMP-2
SPS
MAL
KIAA0036
CD24
FLJ22028
RPP40
SELE
TNFRSF12
ITGB4
PAPSS1
HN1
10
0
CONTINUED ON SHEET 26

FIG. 25

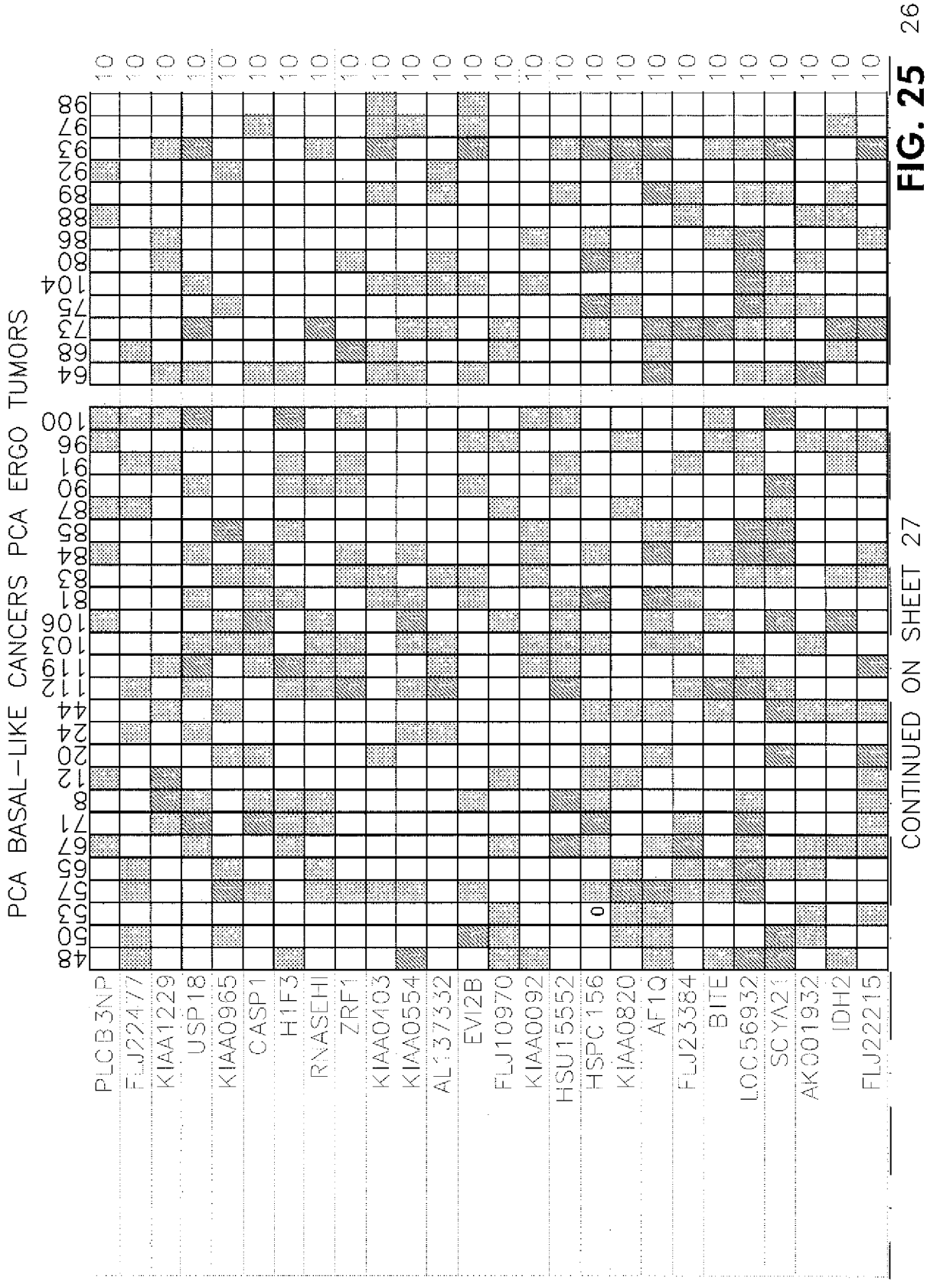

PCA BASAL-LIKE CANCERS PCA ERGO TUMORS
PLCB3NP
FLJ22477
KIAA1229
USP18
KIAA0965
CASP1
H1F3
RVASEHI
ZRF1
KIAA0403
KIAA0554
AL137332
EVI2B
FLJ10970
KIAA0092
HSU15552
HSPC156
KIAA0820
AF1Q
FLJ23384
BITE
LOC56932
SCYA2
AK001932
IDH2
FLJ22215
CONTINUED ON SHEET 27

FIG. 25

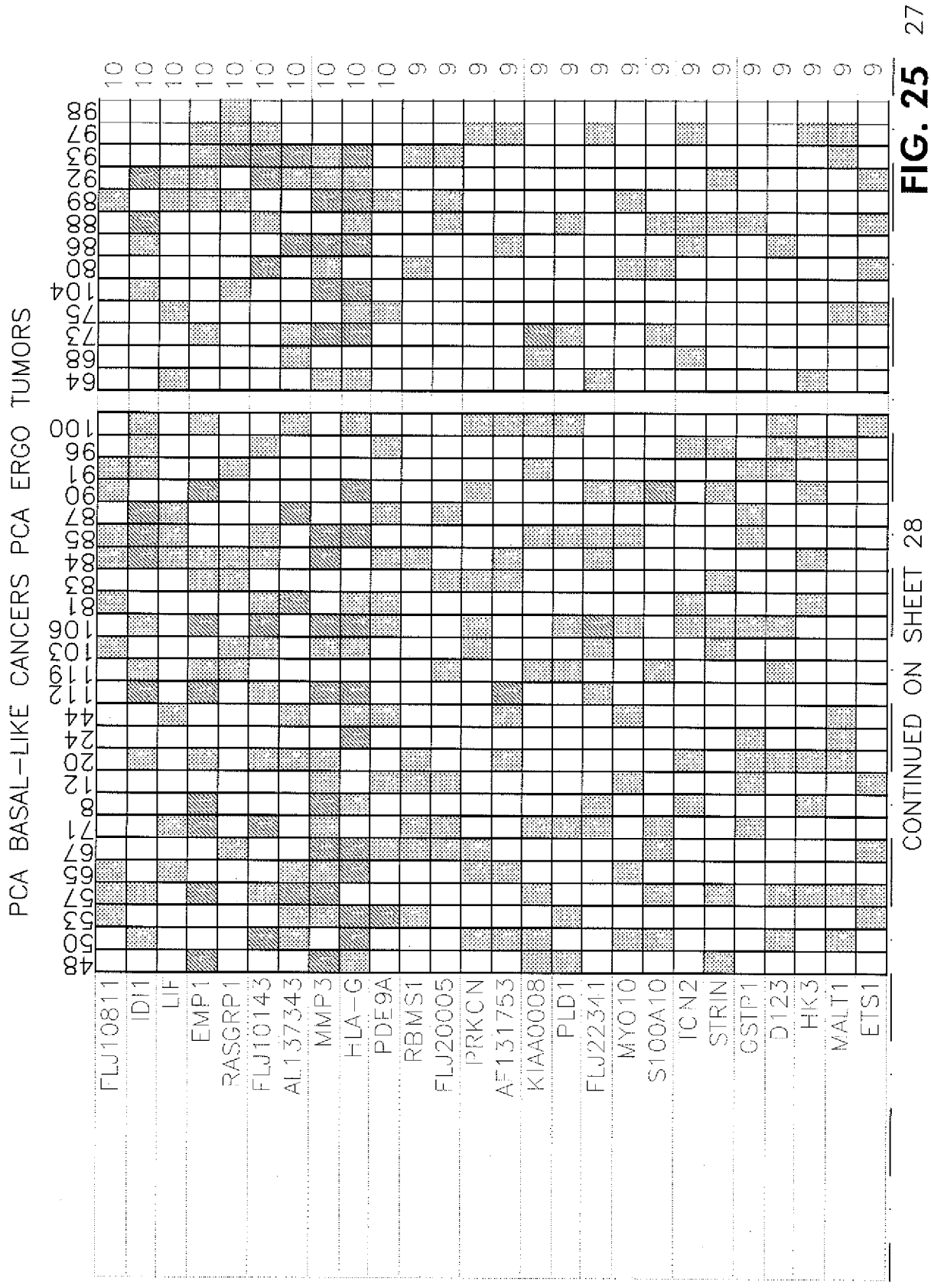

PCA BASAL-LIKE CANCERS PCA ERGO TUMORS
FLJ10811
IDI1
LIF
EMP1
RASGRP1
FLJ10143
AL137343
MMP3
HLA-G
PDE9A
RBMS1
FLJ20005
PRKCN
AF131753
KIAA0008
PLD1
FLJ22341
MYO10
S100A10
ICN2
STRIN
GSTP1
D123
HK3
MALT1
ETS1
CONTINUED ON SHEET 28

FIG. 25 27

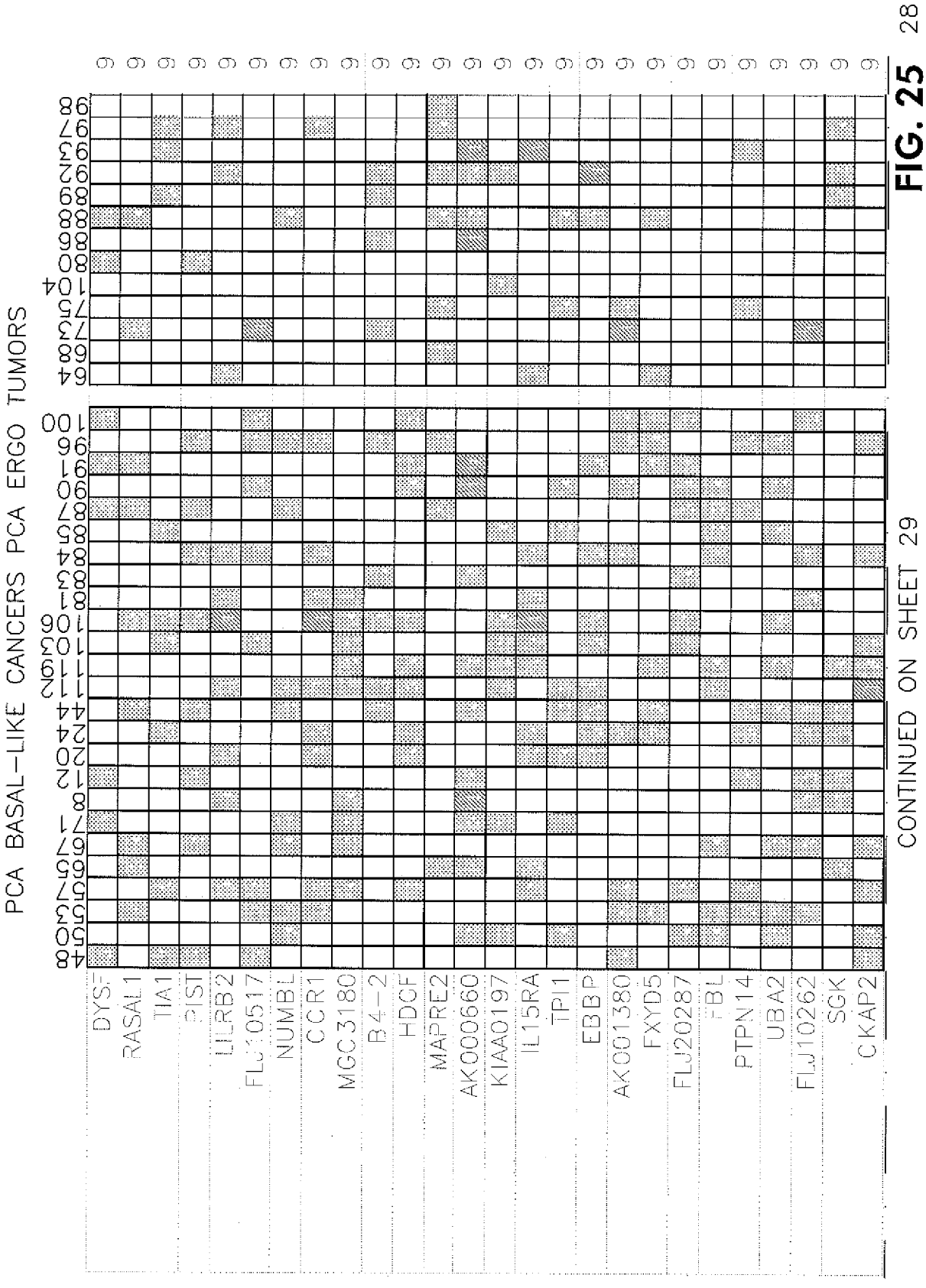

PCA BASAL-LIKE CANCERS PCA ERGO TUMORS
DYS-
RASAL1
TIA1
SIST
LILRB2
FLJ10517
NUMBL
CCR1
MGC3180
B4-2
HDCF
MAPRE2
AK000660
KIAA0197
IL15RA
TPI1
EBP
AK001380
FXYD5
FLJ20287
FBL
PTPN14
UBA2
FLJ10262
SGK
CKAP2
CONTINUED ON SHEET 29

FIG. 25

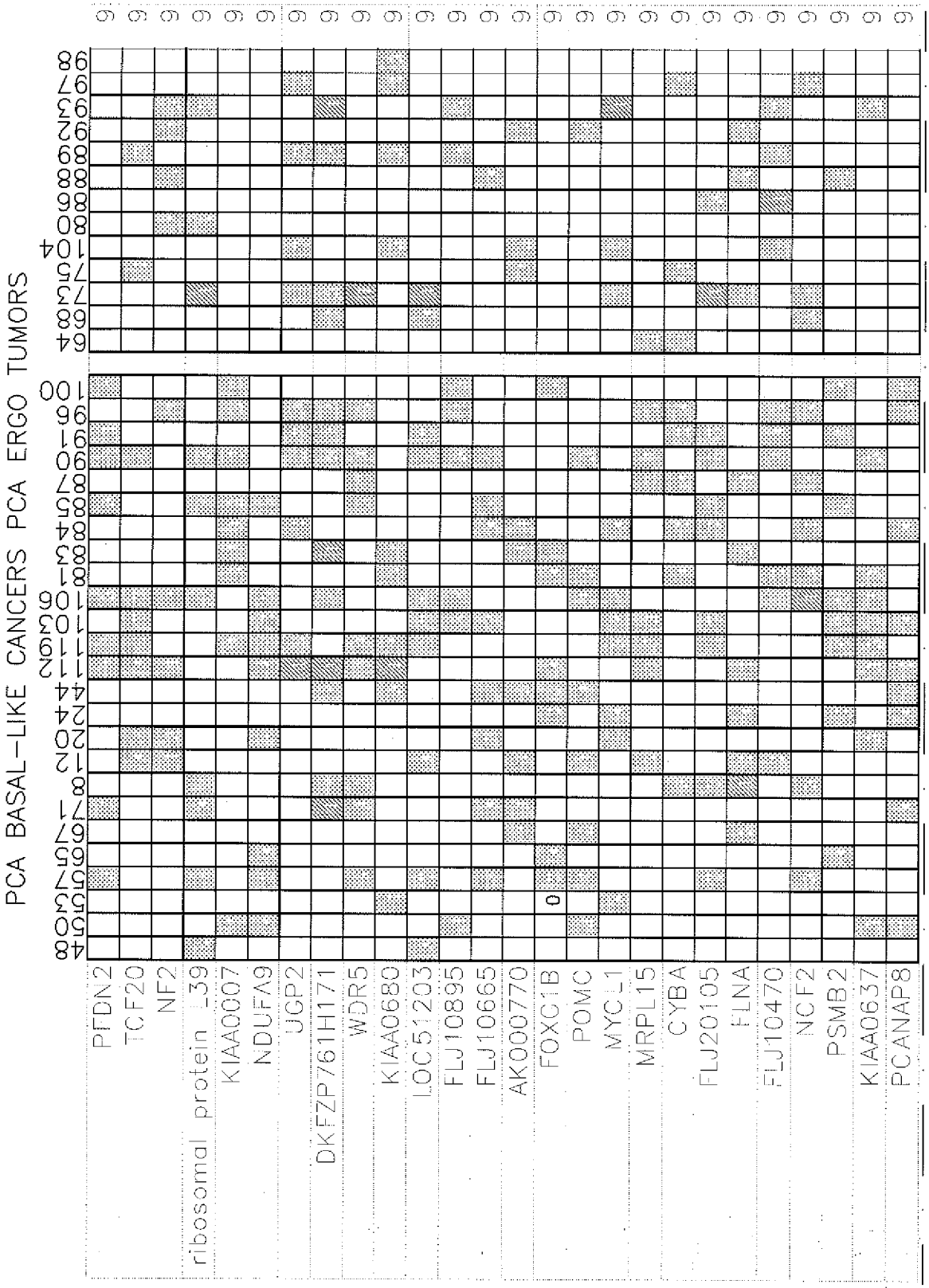

PCA BASAL-LIKE CANCERS PCA ERGO TUMORS
PFDN2
TCF20
NF2
ribosomal protein _39
KIAA0007
NDUFA9
UGP2
DKFZP761H171
WDR5
KIAA0680
LOC51203
FLJ10895
FLJ10665
AK000770
FOXC1B
POMC
MYC_1
MRPL15
CYBA
FLJ20105
FLNA
FLJ10470
NCF2
PSMB2
KIAA0637
PCANAP8
CONTINUED ON SHEET 30

FIG. 25

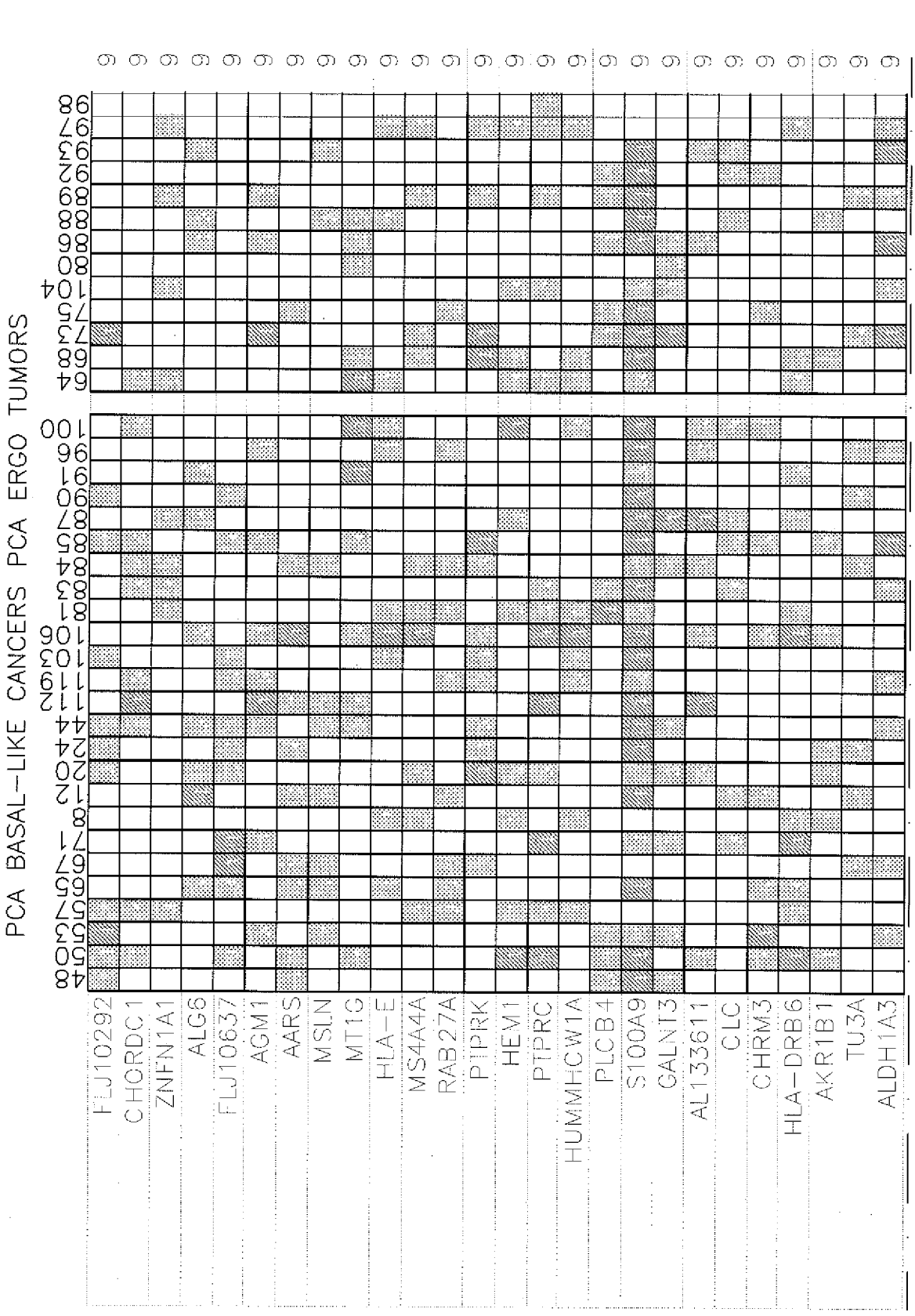

PCA BASAL-LIKE CANCERS PCA ERGO TUMORS
FLJ10292
CHORDC1
ZNFN1A1
ALG6
FLJ10637
AGM1
AARS
MSLN
MT1G
HLA-E
MS4A4A
RAB27A
PIPRK
HEM1
PTPRC
HUMMHCW1A
PLCB4
S100A9
GALNT3
AL133611
CLC
CHRM3
HLA-DRB6
AKR1B1
TU3A
ALDH1A3
CONTINUED ON SHEET 31

FIG. 25

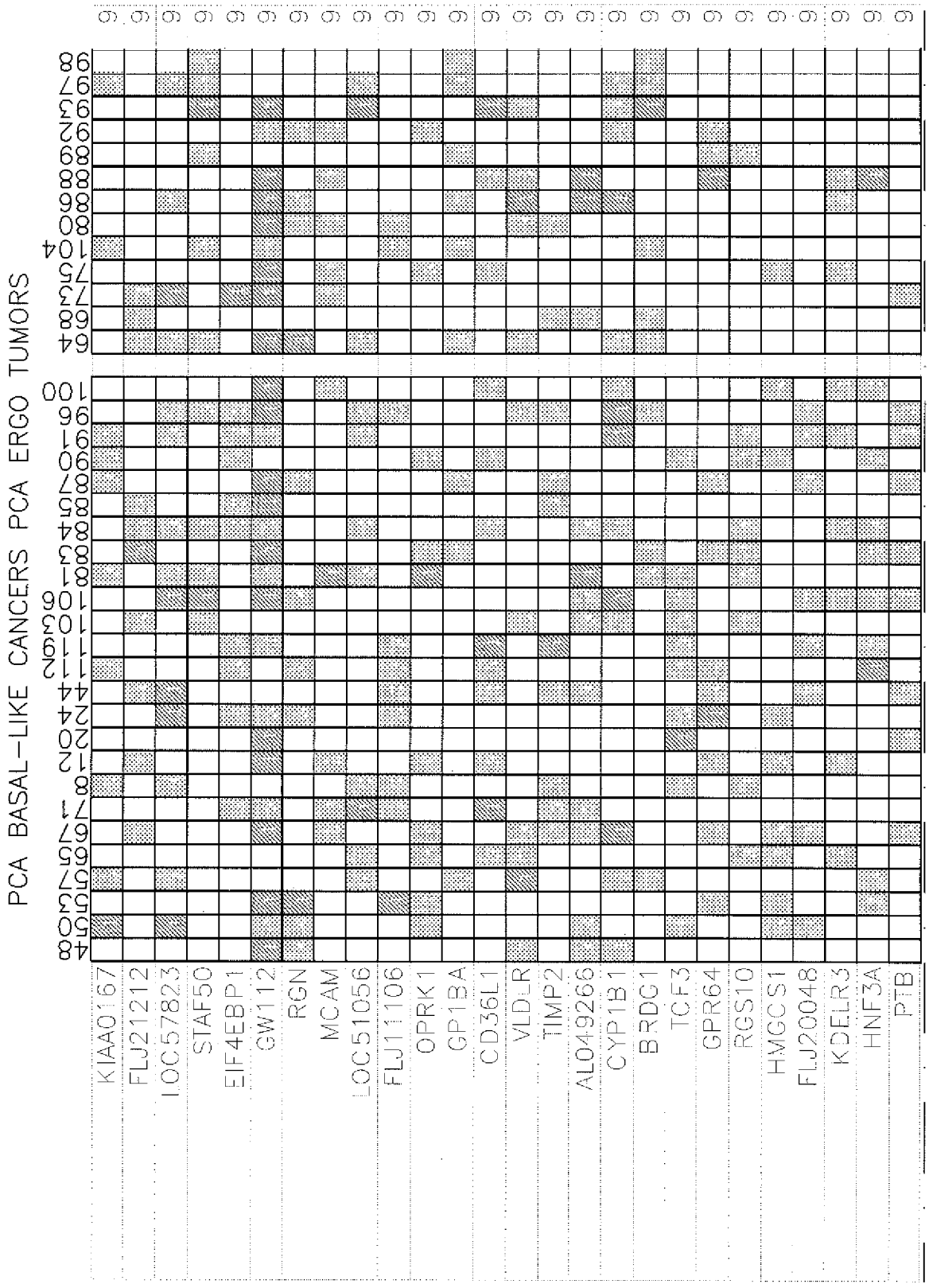

PCA BASAL-LIKE CANCERS PCA ERGO TUMORS
KIAA0167
FLJ21212
LOC57823
STAF50
EIF4EBP1
GW112
RGN
MCAM
LOC51056
FLJ11106
OPRK1
GP1BA
CD36L1
VLDLR
TIMP2
AL049266
CYP1B1
BRDC1
TCF3
GPR64
RGS10
HMGCS1
FLJ20048
KDELR3
HNF3A
PTB
CONTINUED ON SHEET 32

FIG. 25 31

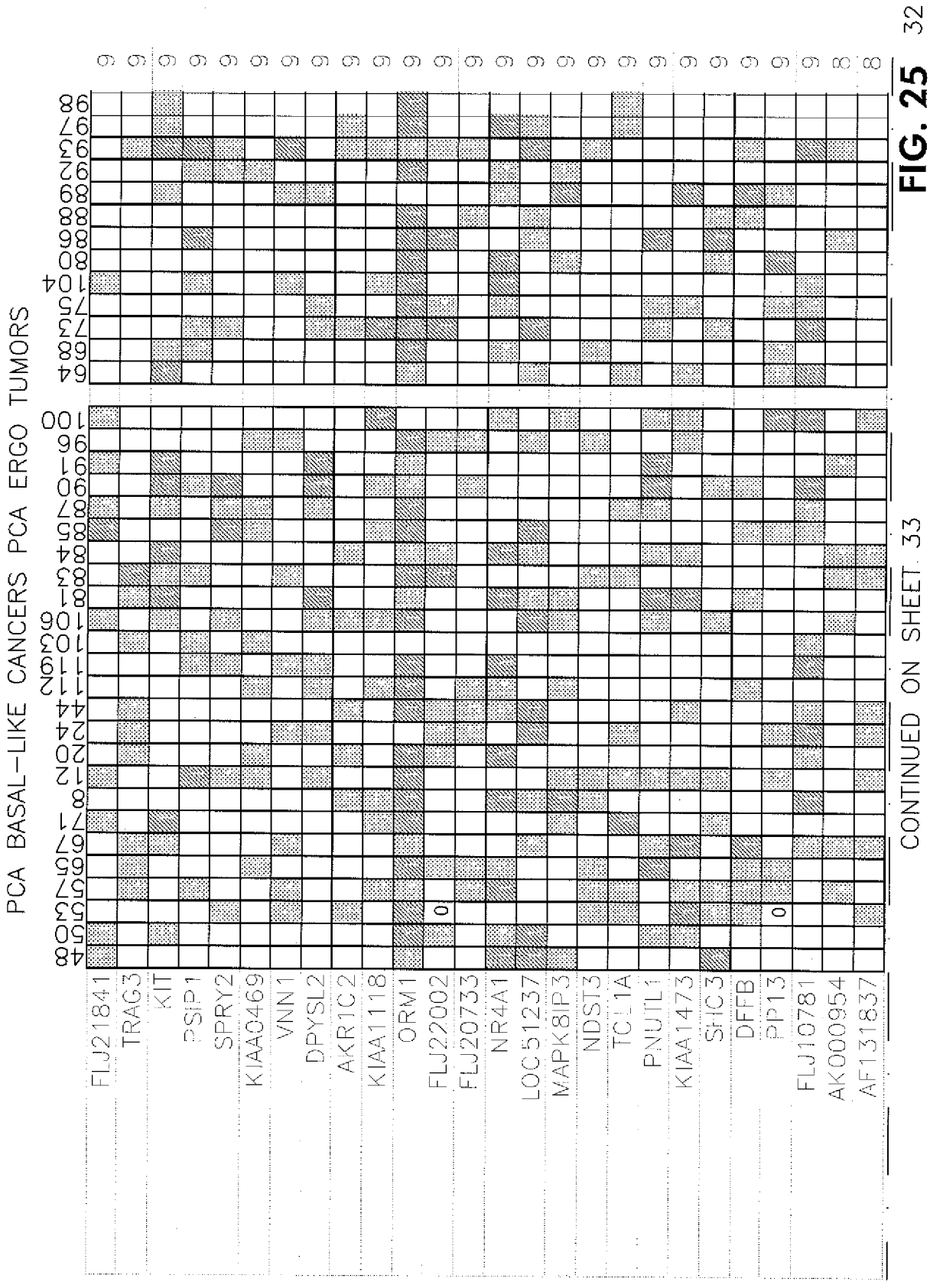

PCA BASAL-LIKE CANCERS PCA ERGO TUMORS
FLJ21841
TRAG3
KIT
PSP1
SPRY2
KIAA0469
VNN1
DPYSL2
AKR1C2
KIAA1118
ORM1
FLJ22002
FLJ20733
NR4A1
LOC51237
MAPK8IP3
NDST3
TCL1A
PNUTL1
KIAA1473
SIC3
DFFB
PP13
FLJ10781
AK000954
AF131837
CONTINUED ON SHEET 33

FIG. 25

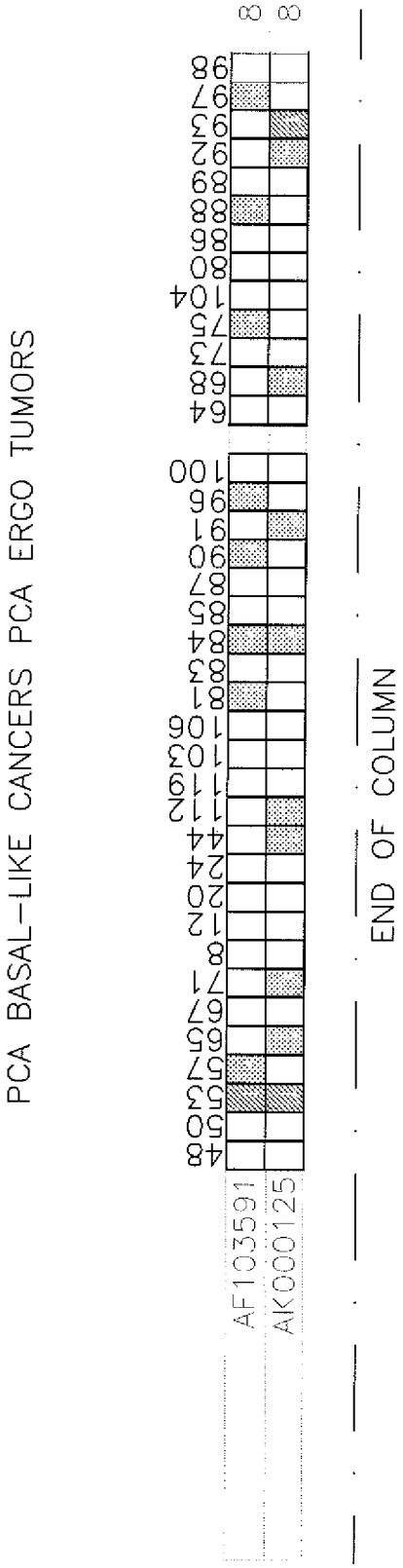

PCA BASAL–LIKE CANCERS PCA ERGO TUMORS
END OF COLUMN
AF103591
AK000125

FIG. 25

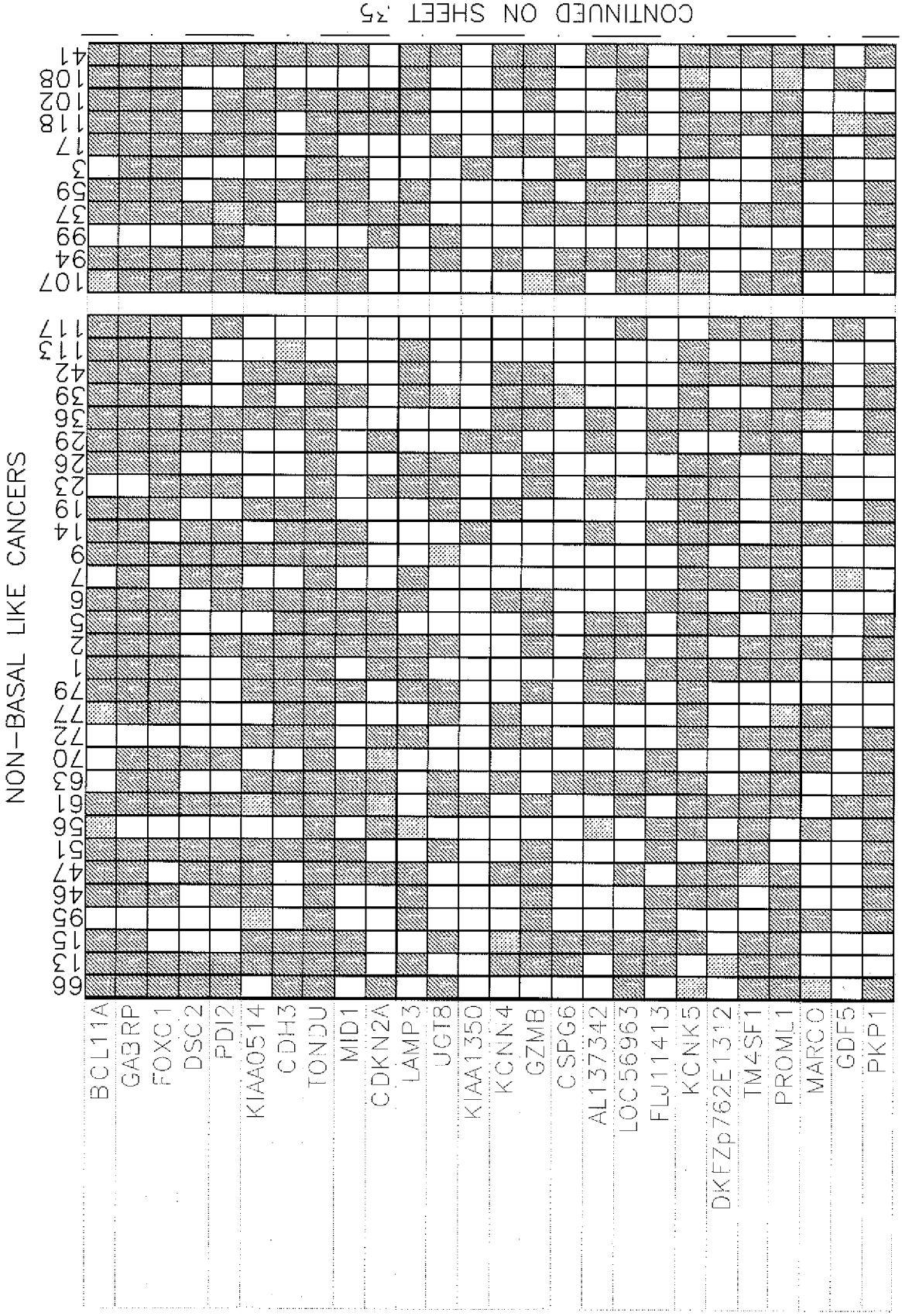

CONTINUED ON SHEET 35
NON-BASAL LIKE CANCERS
BCL11A
GABRP
FOXC1
DSC2
PDI2
KIAA0514
CDH3
TONDU
MID1
CDKN2A
LAMP3
UGT8
KIAA1350
KCNN4
GZMB
CSPG6
AL137342
LOC56963
FLJ11413
KCNK5
DKFZp762E1312
TM4SF1
PROML1
MARCO
GDF5
PKP1

FIG. 25 34

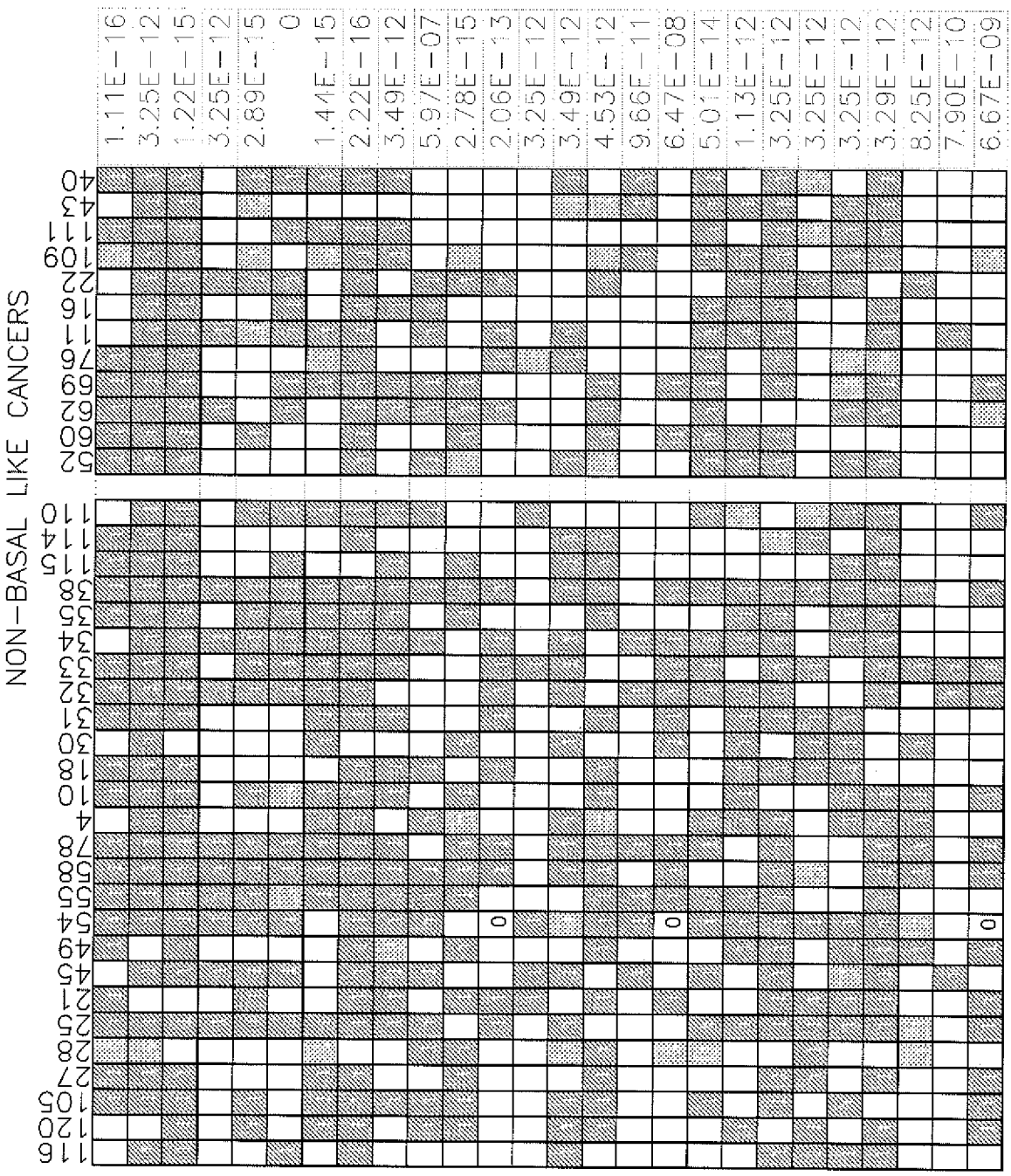

NON-BASAL LIKE CANCERS
1.11E-16
3.25E-12
1.22E-15
3.25E-12
2.89E-15
0
1.44E-15
2.22E-16
3.49E-12
5.97E-07
2.78E-15
2.06E-13
3.25E-12
3.49E-12
4.53E-12
9.66E-11
6.47E-08
5.01E-14
1.13E-12
3.25E-12
3.25E-12
3.25E-12
3.29E-12
8.25E-12
7.90E-10
6.67E-09

FIG. 25

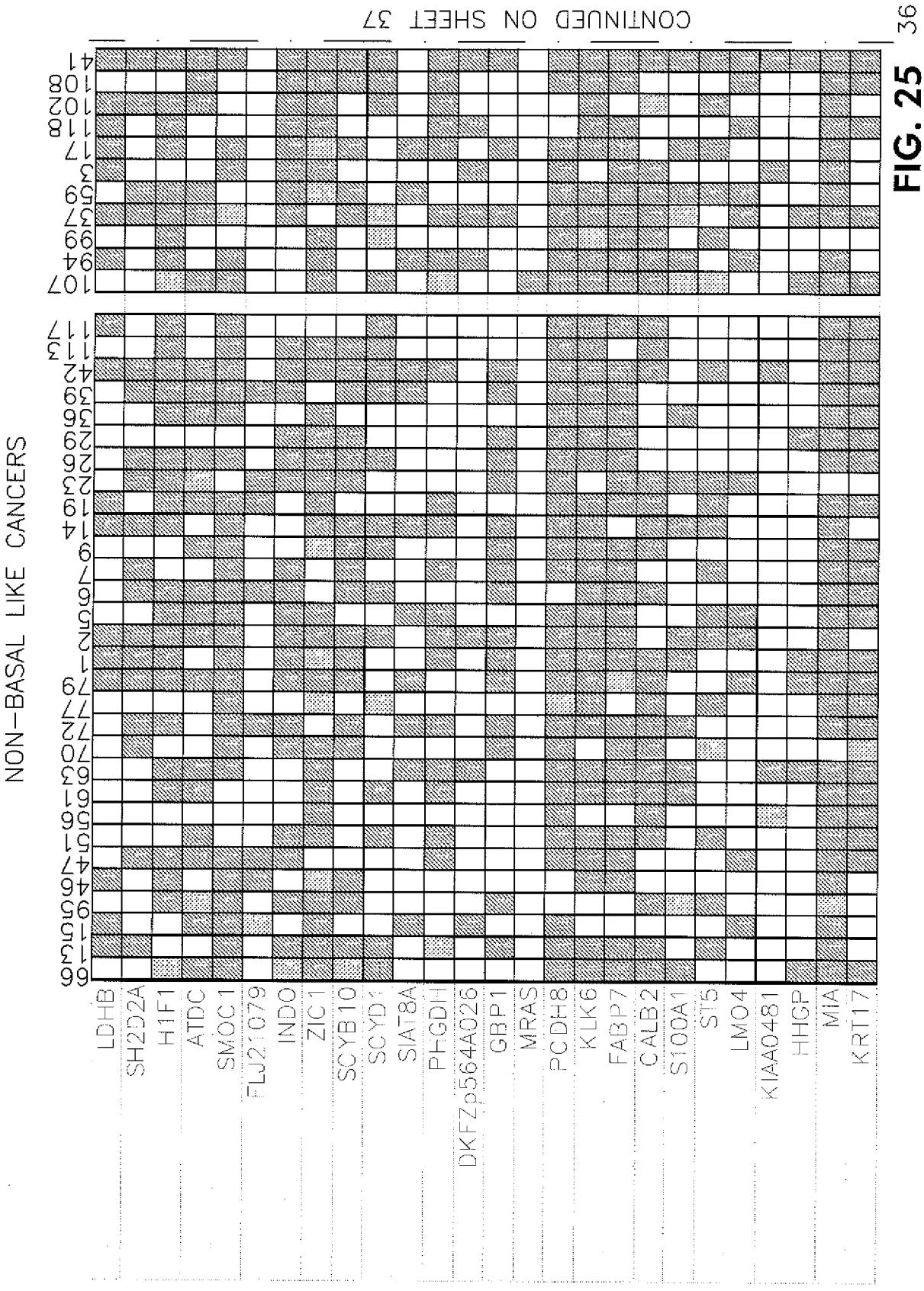

CONTINUED ON SHEET 37
NON-BASAL LIKE CANCERS
LDHB
SH2D2A
H1F1
ATDC
SMOC1
FLJ21079
INDO
ZIC1
SCYB10
SCYD1
SIAT8A
PHGDH
DKFZp564A026
GBP1
MRAS
PCDH8
KLK6
FABP7
CALB2
S100A1
ST5
LMO4
KIAA0481
HHGP
MIA
KRT17

FIG. 25

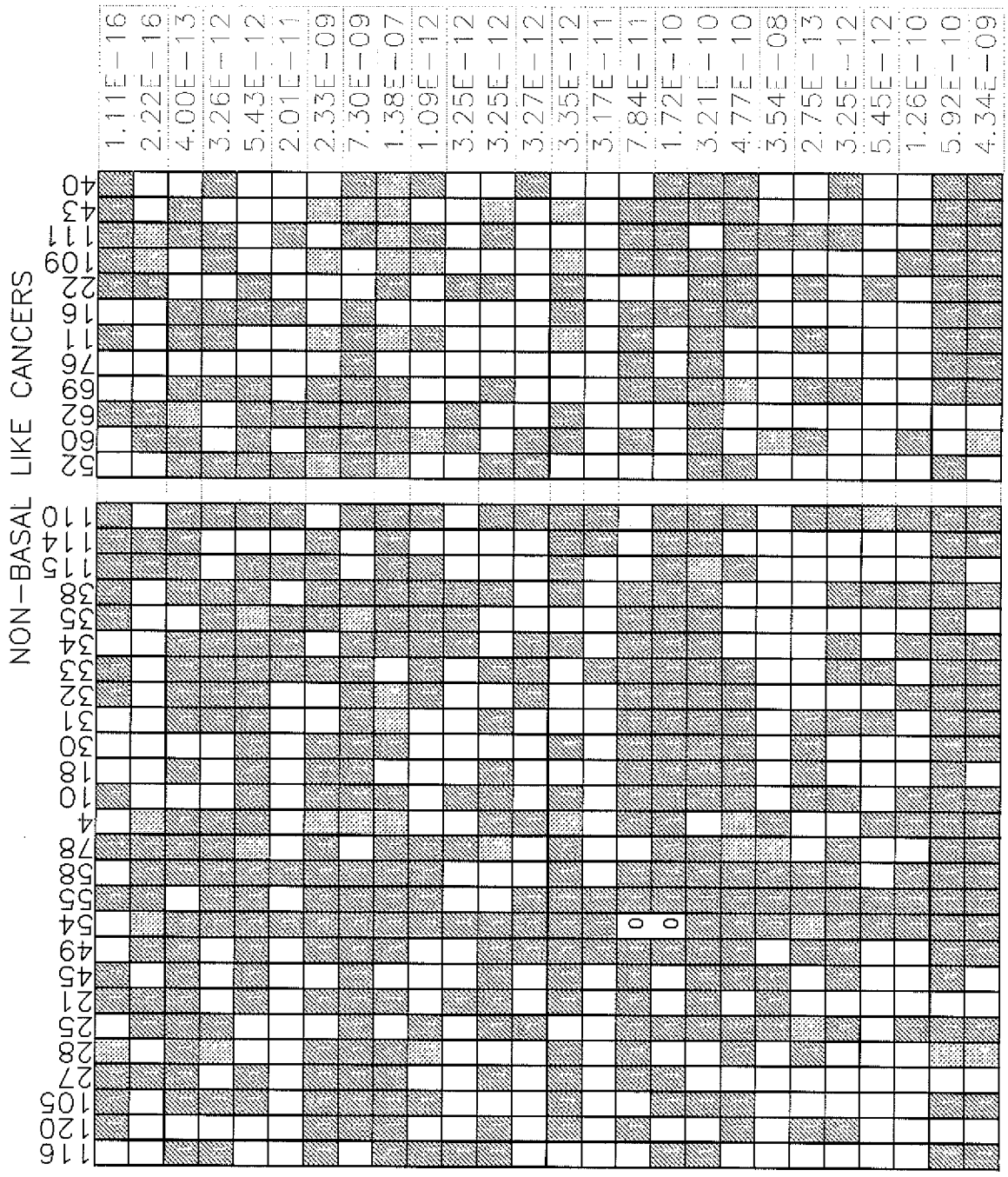

NON-BASAL LIKE CANCERS
1.11E-16
2.22E-16
4.00E-13
3.26E-12
5.43E-12
2.01E-11
2.33E-09
7.30E-09
1.38E-07
1.09E-12
3.25E-12
3.25E-12
3.27E-12
3.35E-12
3.17E-11
7.84E-11
1.72E-10
3.21E-10
4.77E-10
3.54E-08
2.75E-13
3.25E-12
5.45E-12
1.26E-10
5.92E-10
4.34E-09

FIG. 25

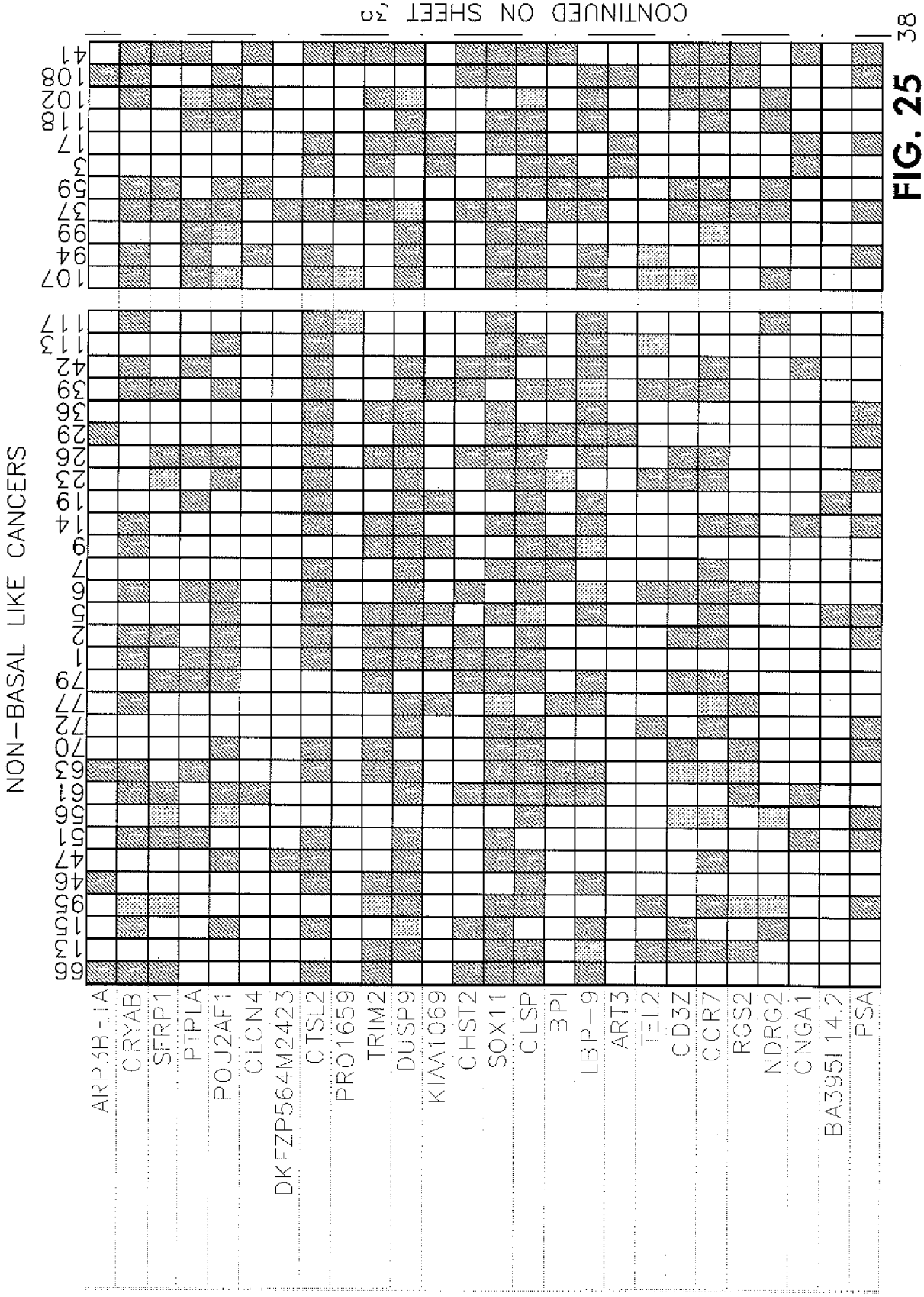

CONTINUED ON SHEET 39
38
NON-BASAL LIKE CANCERS
ARP3BETA
CRYAB
SFRP1
PTPLA
POU2AF1
CLCN4
DKFZP564M2423
CTSL2
PRO1659
TRIM2
DUSP9
KIAA1069
CHST2
SOX11
CLSP
BPI
LBP-9
ART3
TEL2
CD3Z
CCR7
RGS2
NDRG2
CNGA1
BA395I14.2
PSA

FIG. 25

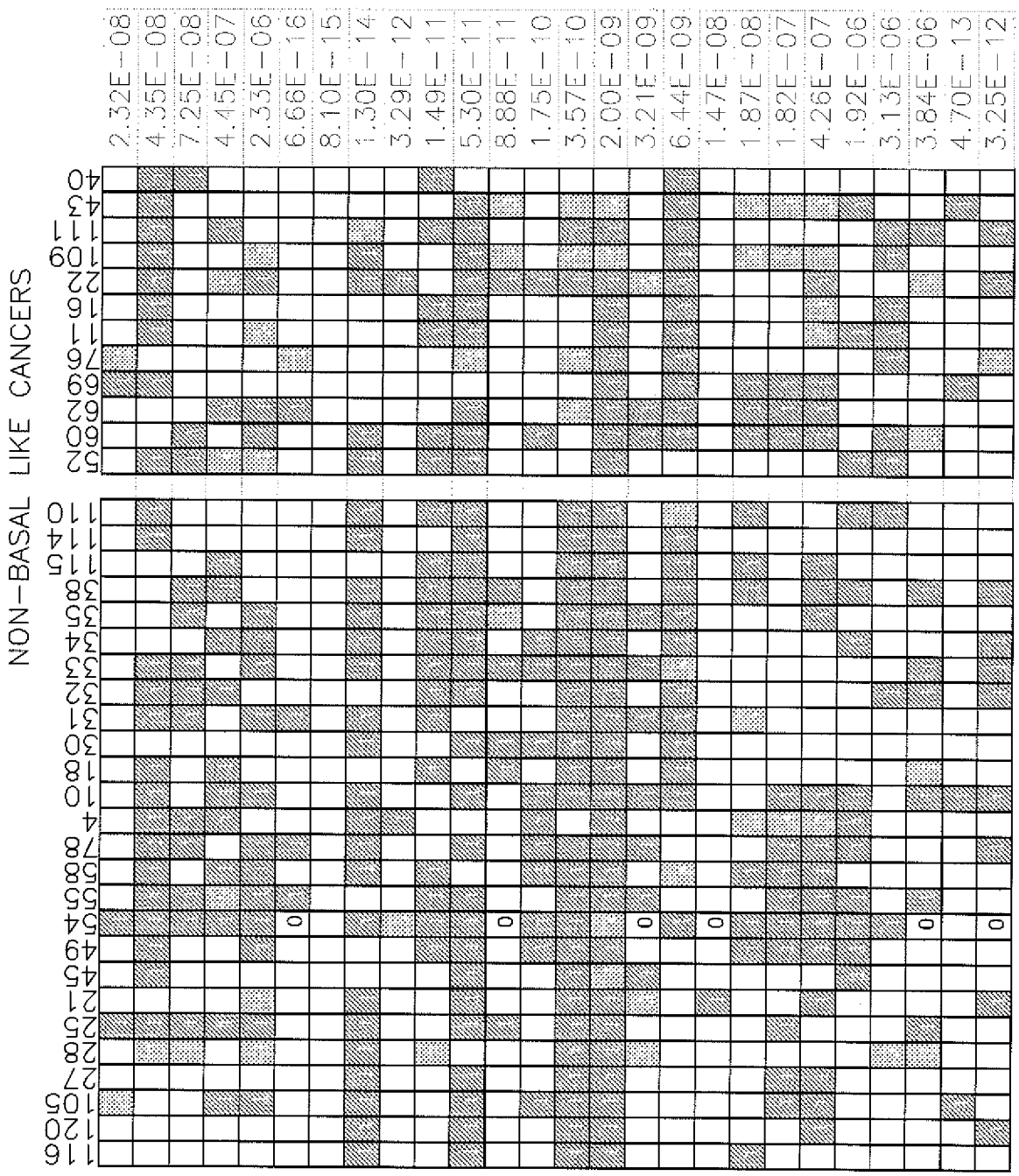

NON-BASAL LIKE CANCERS
2.32E-08
4.35E-08
7.25E-08
4.45E-07
2.33E-06
6.66E-16
8.10E-15
1.30E-14
3.29E-12
1.49E-11
5.30E-11
8.88E-11
1.75E-10
3.57E-10
2.00E-09
3.21E-09
6.44E-09
1.47E-08
1.87E-08
1.82E-07
4.26E-07
1.92E-06
3.13E-06
3.84E-06
4.70E-13
3.25E-12

FIG. 25

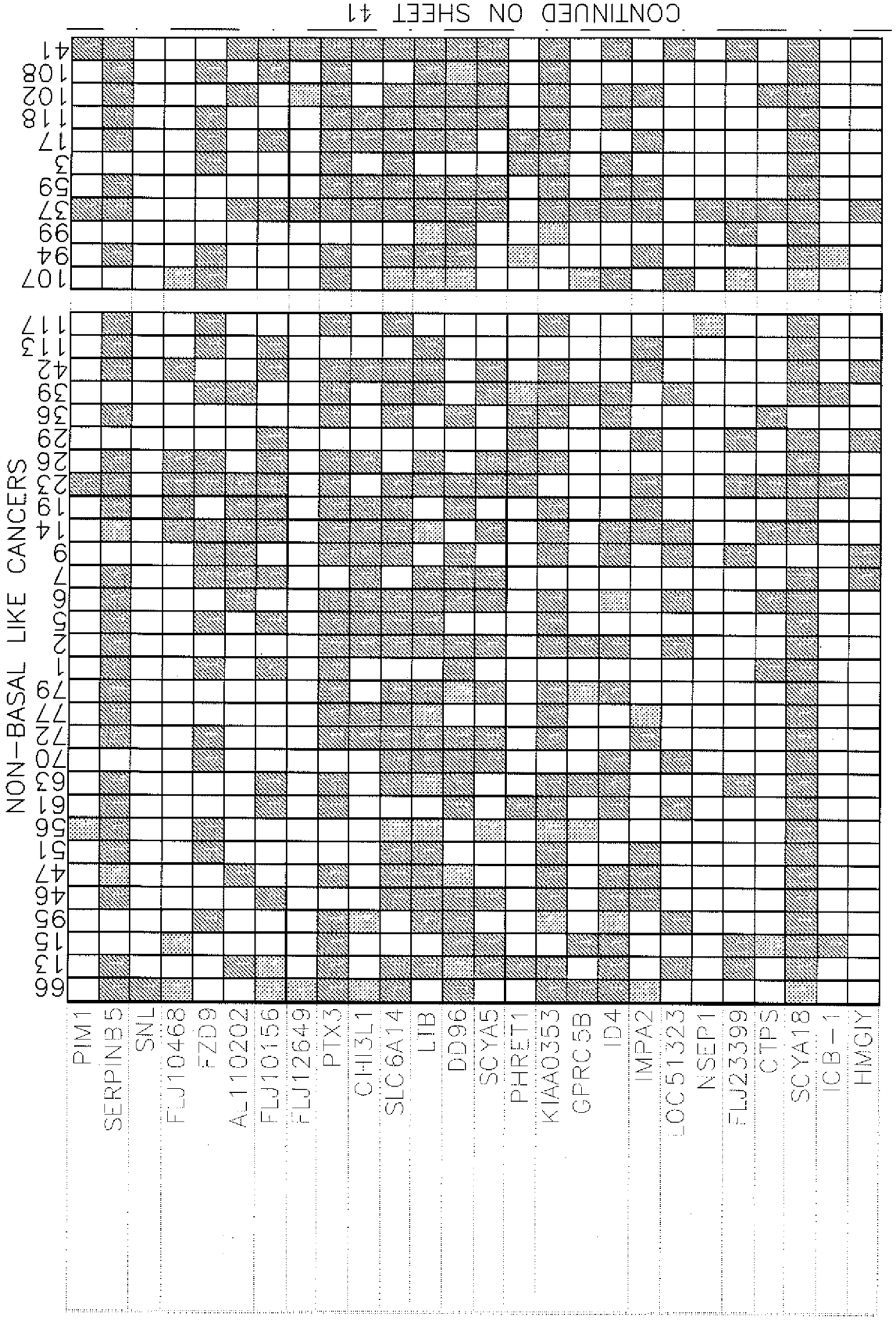

CONTINUED ON SHEET 41
NON-BASAL LIKE CANCERS
PIM1
SERPINB5
SNL
FLJ10468
FZD9
AL110202
FLJ10156
FLJ12649
PTX3
CHI3L1
SLC6A14
LIB
DD96
SCYA5
PHRET1
KIAA0353
GPRC5B
ID4
IMPA2
LOC51323
NSEP1
FLJ23399
CTPS
SCYA18
ICB-1
HMGIY

FIG. 25 40

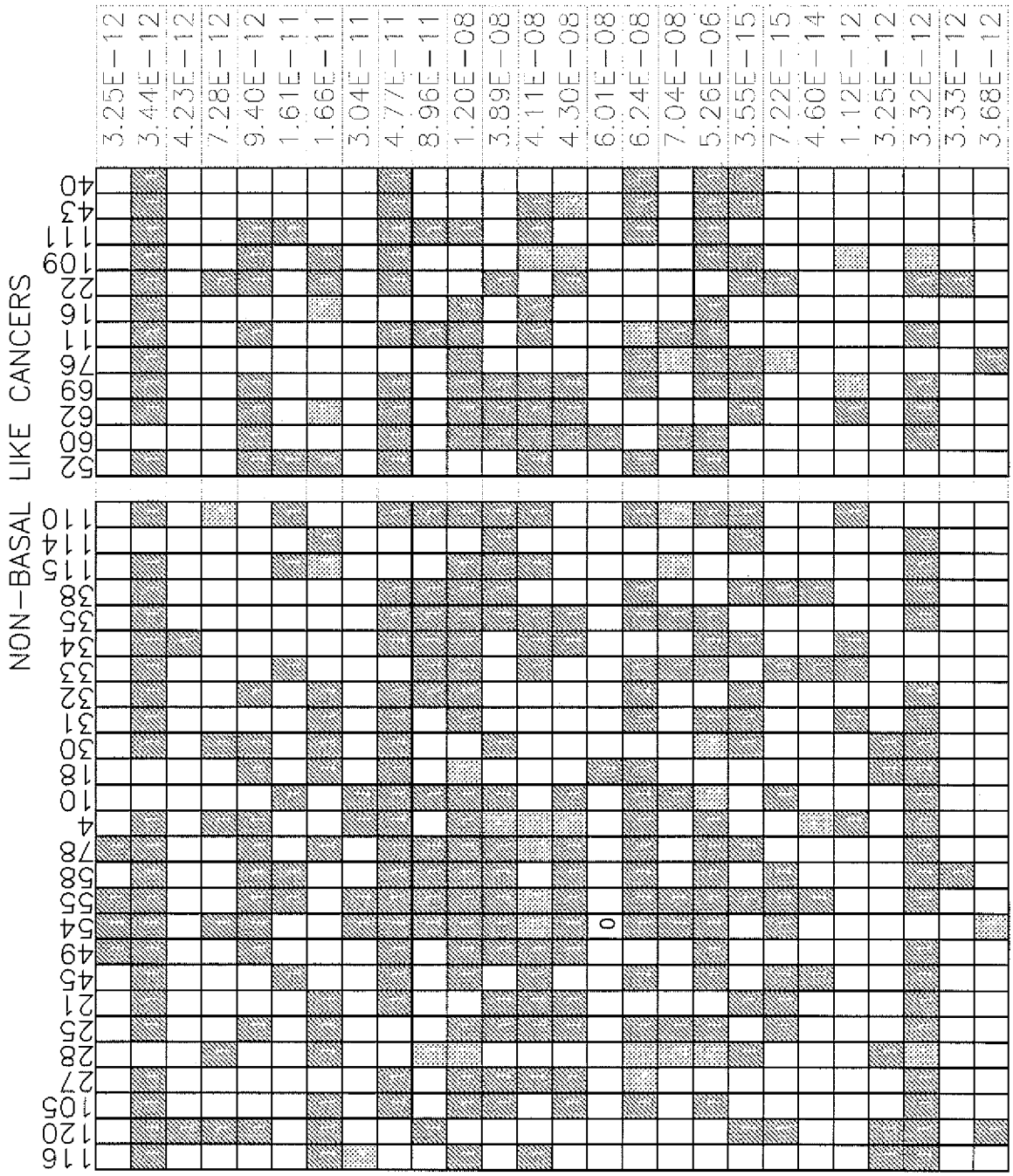

NON−BASAL LIKE CANCERS
52 60 62 69 76 11 16 22 09 11 43 40
116 120 105 27 28 25 21 45 49 54 55 58 78 4 10 18 30 31 32 34 35 38 115 114 110
3.25E−12
3.44E−12
4.23E−12
7.28E−12
9.40E−12
1.61E−11
1.66E−11
3.04E−11
4.77E−11
8.96E−11
1.20E−08
3.89E−08
4.11E−08
4.30E−08
6.01E−08
6.24E−08
7.04E−08
5.26E−06
3.55E−15
7.22E−15
4.60E−14
1.12E−12
3.25E−12
3.32E−12
3.33E−12
3.68E−12

FIG. 25 41

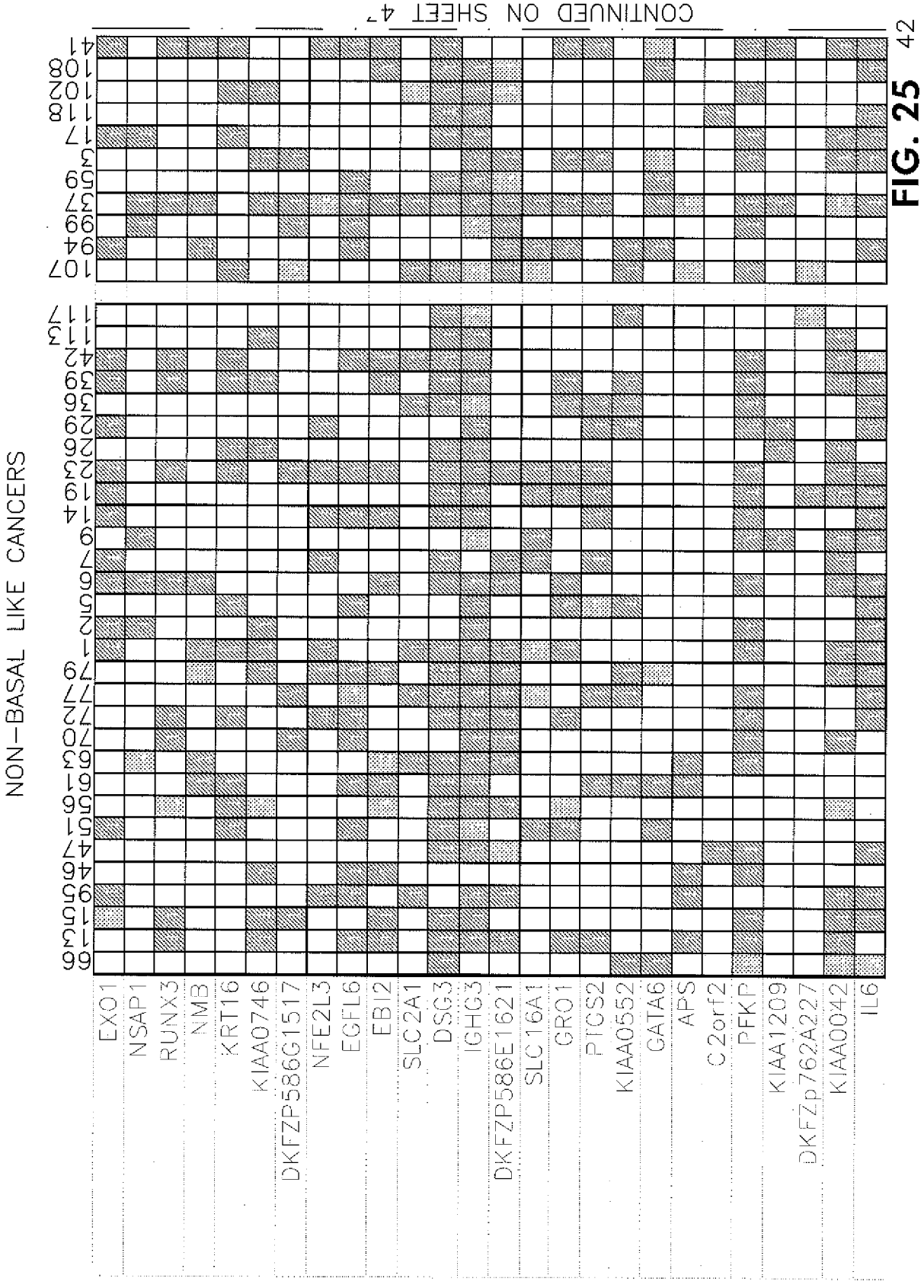

CONTINUED ON SHEET 47
NON-BASAL LIKE CANCERS
EXO1
NSAP1
RUNX3
NMB
KRT16
KIAA0746
DKFZP586G1517
NFE2L3
EGFL6
EBI2
SLC2A1
DSG3
IGHG3
DKFZP586E1621
SLC16A1
GRO1
PTCS2
KIAA0552
GATA6
APS
C2orf2
PFKP
KIAA1209
DKFZp762A227
KIAA0042
IL6

FIG. 25 42

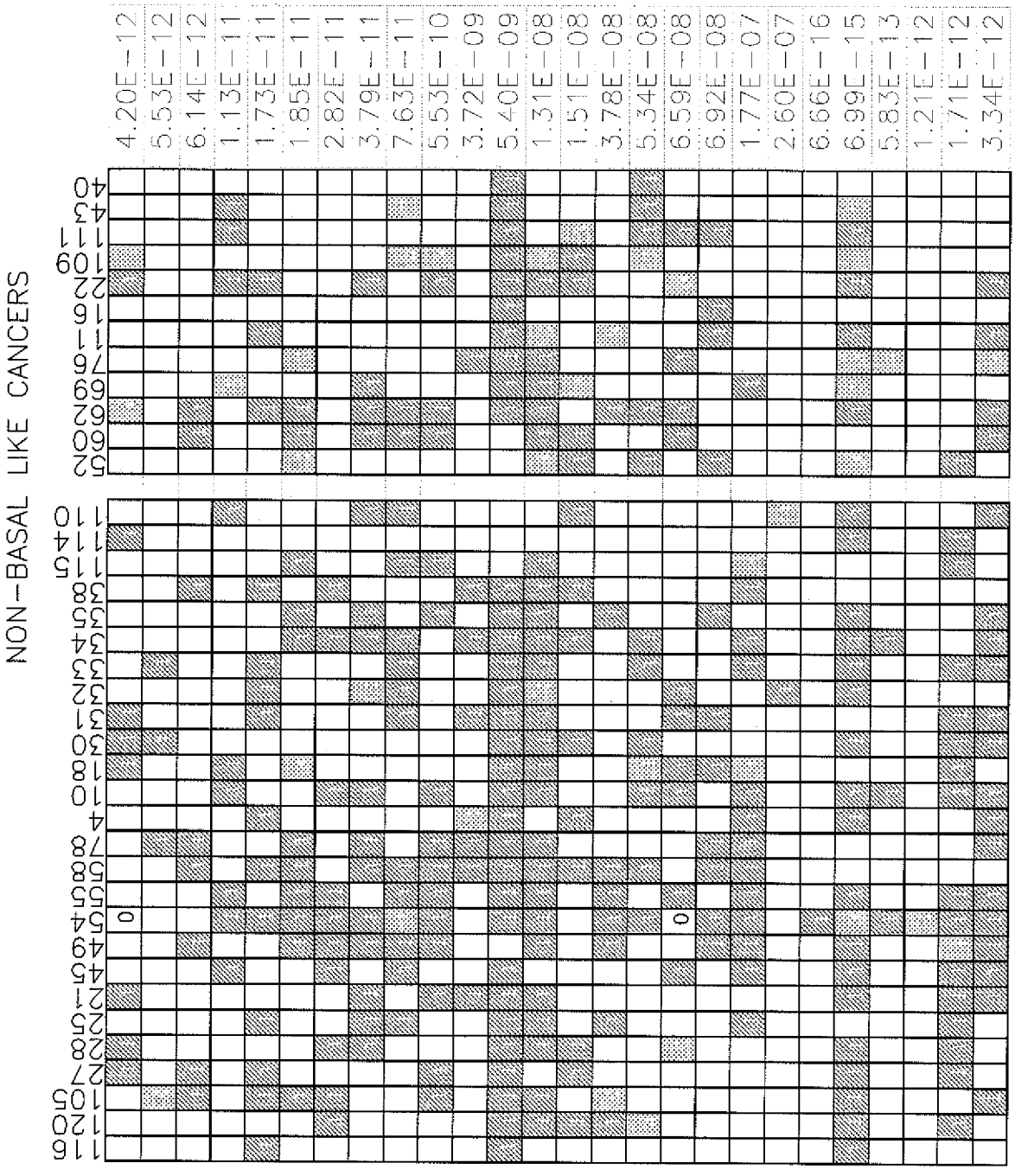

NON−BASAL LIKE CANCERS
52 60 62 69 76 11 16 22 109 1 43 40
116 120 105 27 28 25 21 45 49 54 55 58 78 4 10 18 30 31 32 34 35 38 15 14 10
4.20E−12
5.53E−12
6.14E−12
1.13E−11
1.73E−11
1.85E−11
2.82E−11
3.79E−11
7.63E−11
5.53E−10
3.72E−09
5.40E−09
1.31E−08
1.51E−08
3.78E−08
5.34E−08
6.59E−08
6.92E−08
1.77E−07
2.60E−07
6.66E−16
6.99E−15
5.83E−13
1.21E−12
1.71E−12
3.34E−12

FIG. 25

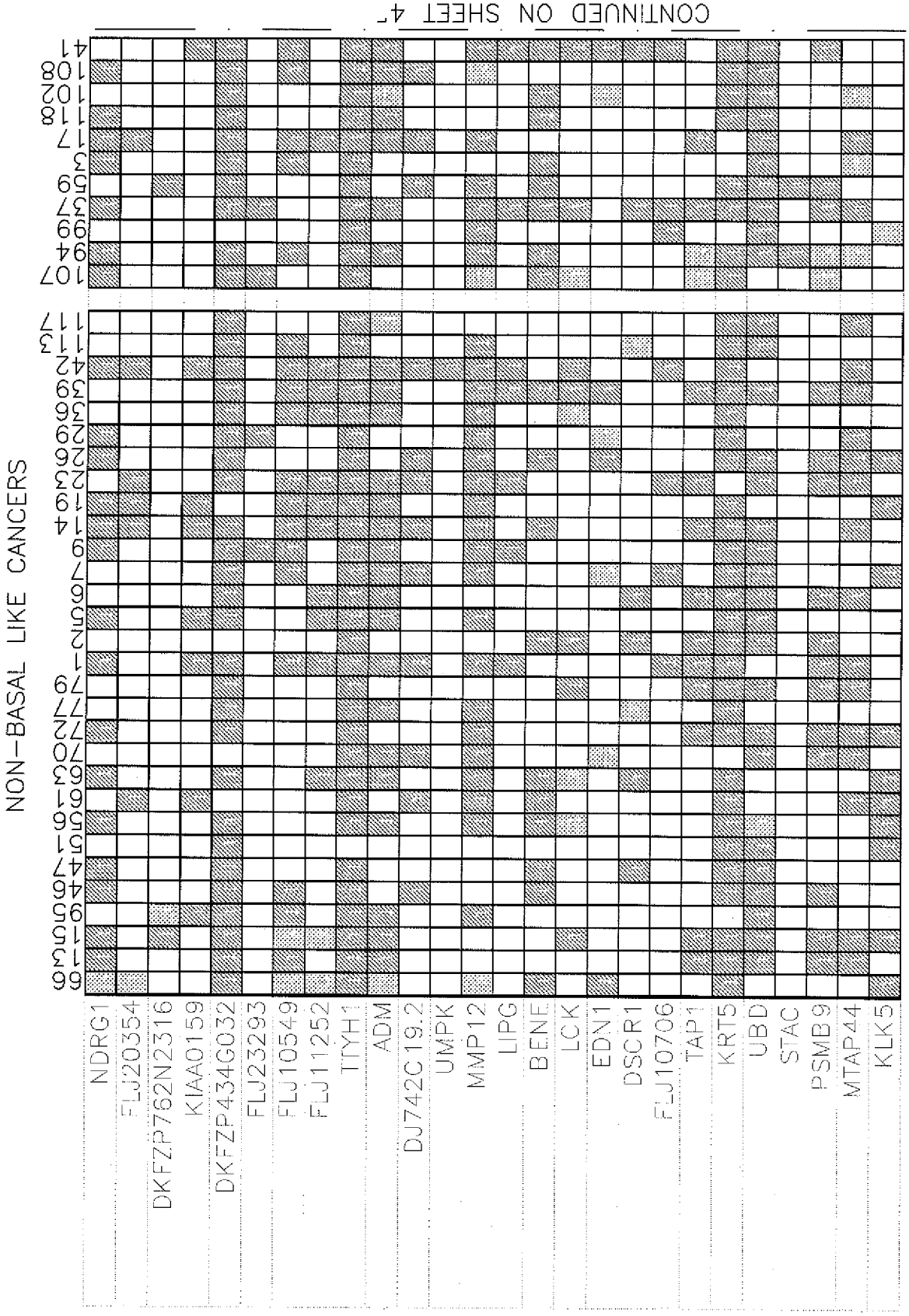

CONTINUED ON SHEET 47
NON-BASAL LIKE CANCERS
NDRG1
FLJ20354
DKFZP762N2316
KIAA0159
DKFZP434G032
FLJ23293
FLJ10549
FLJ11252
TTYH1
ADM
DJ742C19.2
UMPK
MMP12
LIPG
BENE
LCK
EDN1
DSCR1
FLJ10706
TAP1
KRT5
UBD
STAC
PSMB9
MTAP44
KLK5

FIG. 25 44

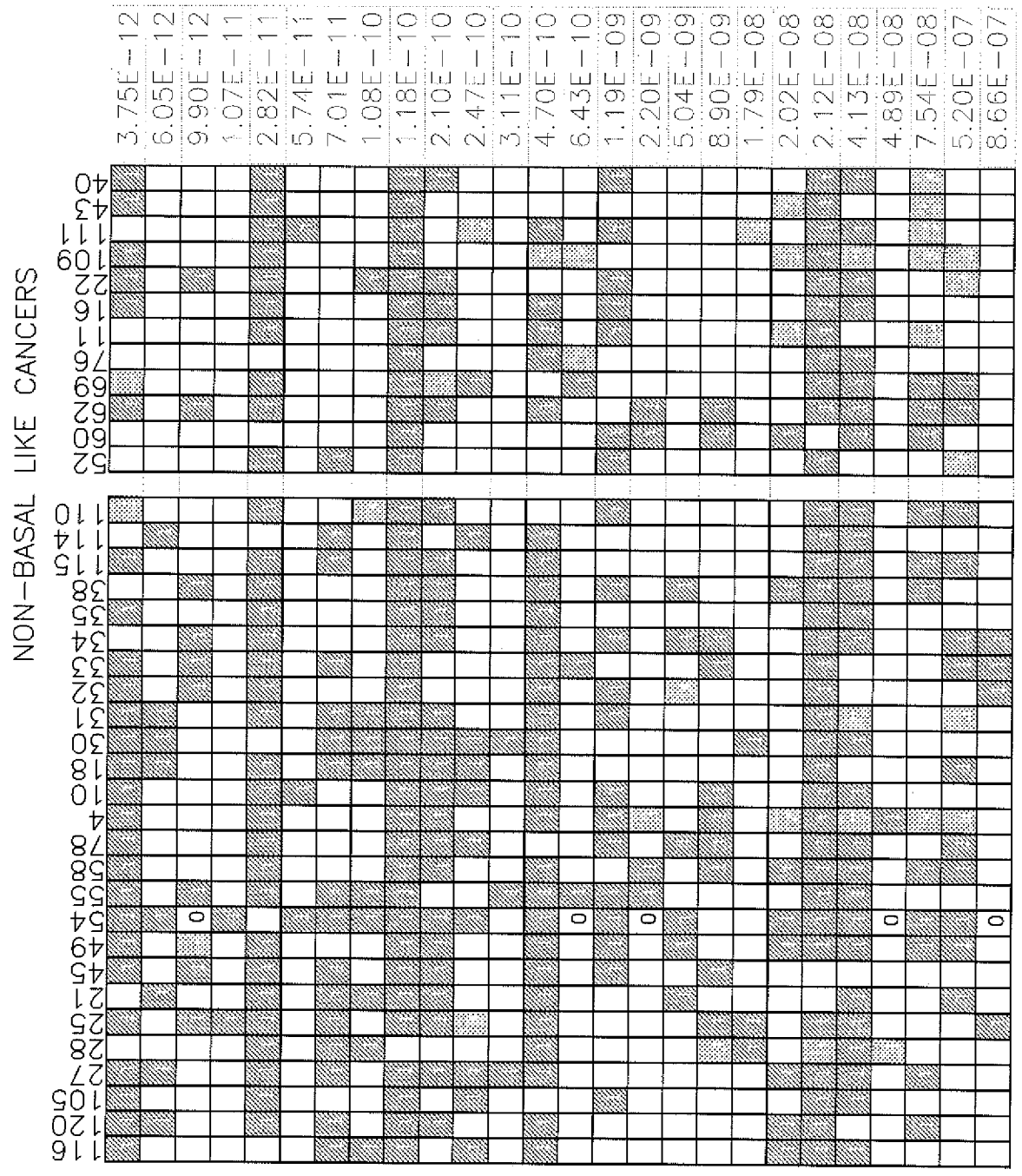

NON-BASAL LIKE CANCERS
3.75E-12
6.05E-12
9.90E-12
1.07E-11
2.82E-11
5.74E-11
7.01E-11
1.08E-10
1.18E-10
2.10E-10
2.47E-10
3.11E-10
4.70E-10
6.43E-10
1.19E-09
2.20E-09
5.04E-09
8.90E-09
1.79E-08
2.02E-08
2.12E-08
4.13E-08
4.89E-08
7.54E-08
5.20E-07
8.66E-07

FIG. 25

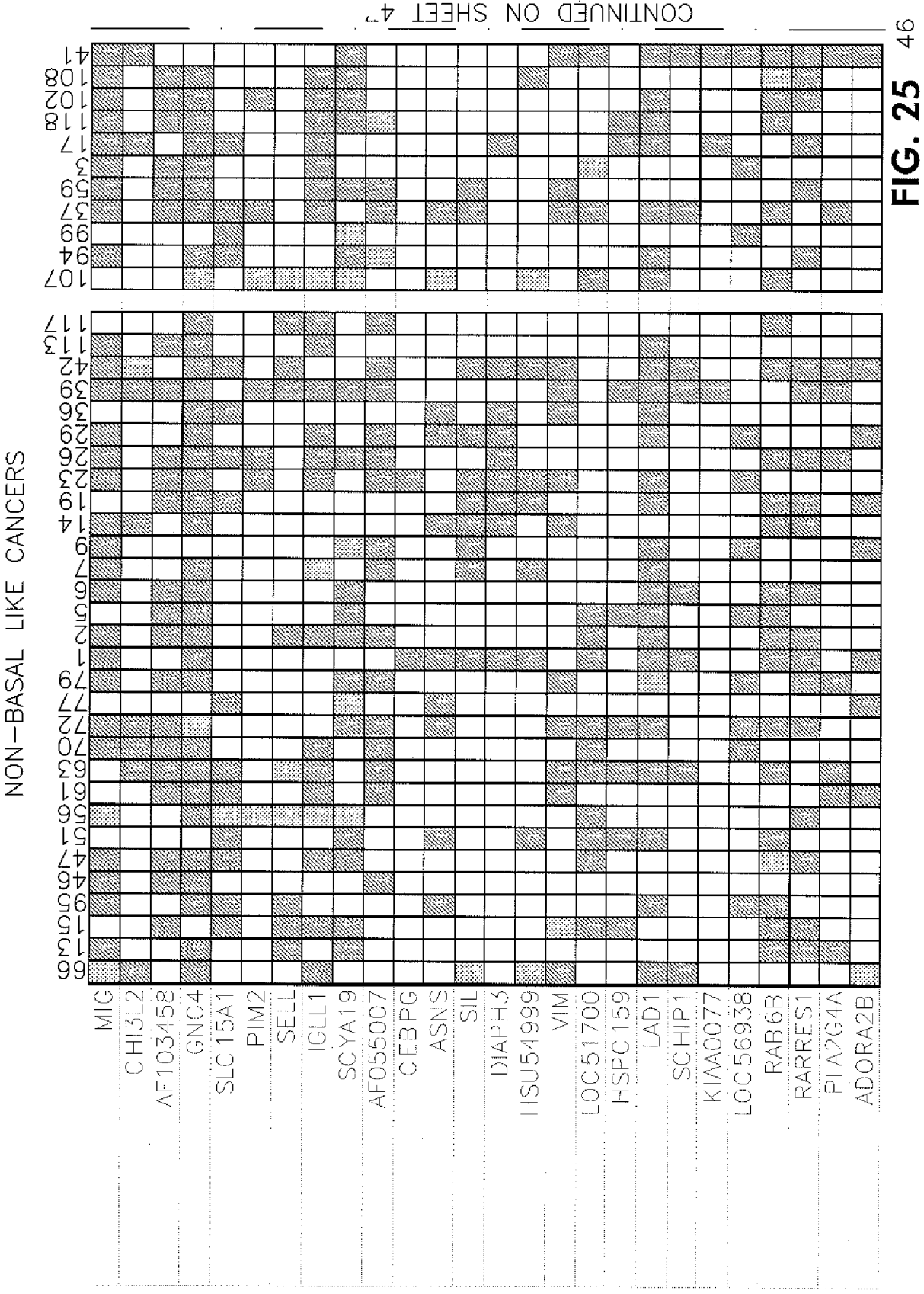

CONTINUED ON SHEET 47
NON-BASAL LIKE CANCERS
MIG
CHI3L2
AF103458
GNG4
SLC15A1
PIM2
SELL
IGLL1
SCYA19
AF055007
CEBPG
ASNS
SIL
DIAPH3
HSU54999
VIM
LOC51700
HSPC159
LAD1
SCHIP1
KIAA0077
LOC56938
RAB6B
RARRES1
PLA2G4A
ADORA2B

FIG. 25 46

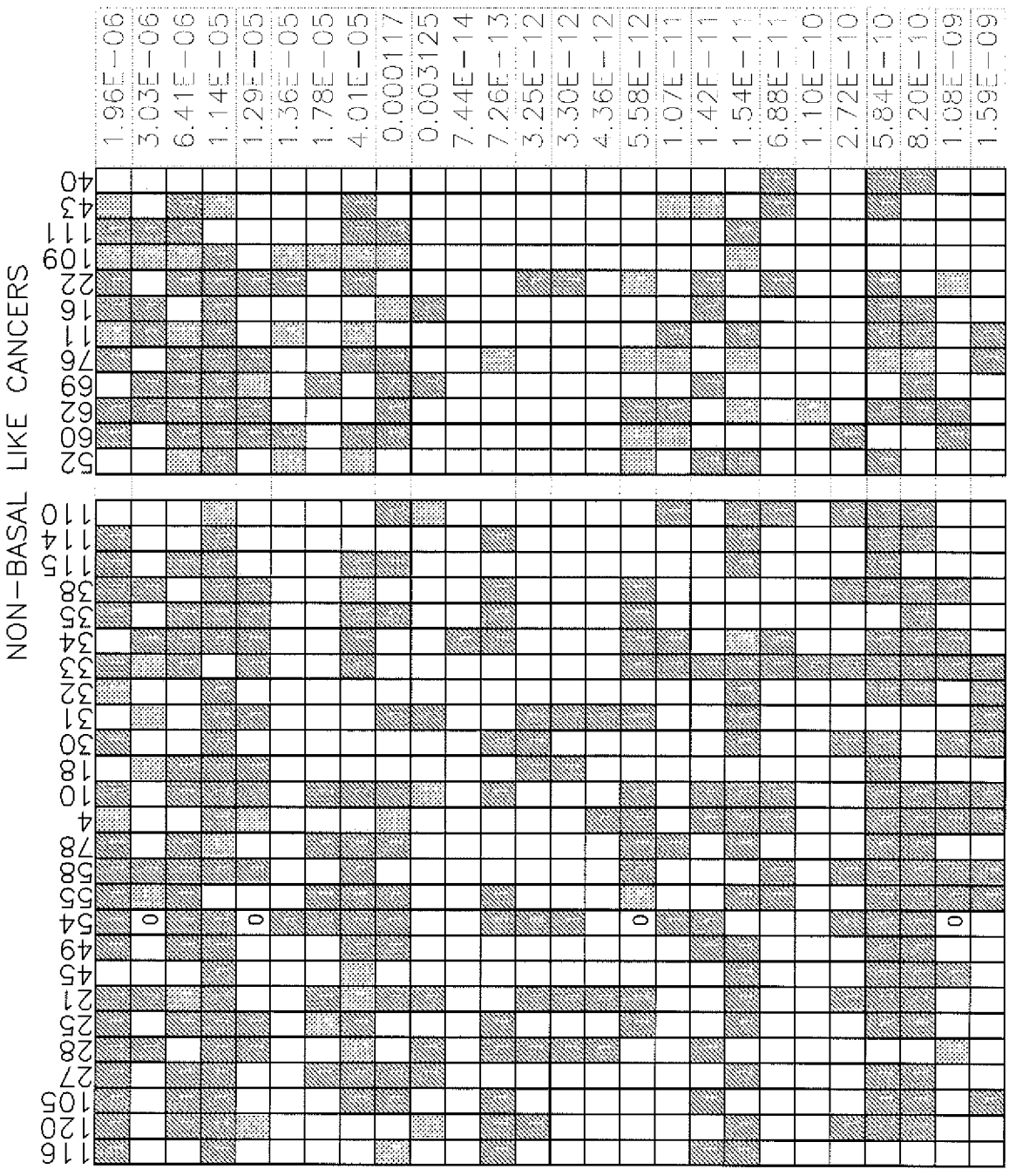

NON-BASAL LIKE CANCERS
52 60 62 69 76 11 16 22 109 11 43 40
116 120 105 27 228 225 21 45 49 54 55 78 4 10 18 30 31 22 23 24 25 28 115 104 11
1.96E-06
3.03E-06
6.41E-06
1.14E-05
1.29E-05
1.36E-05
1.78E-05
4.01E-05
0.000117
0.003125
7.44E-14
7.26E-13
3.25E-12
3.30E-12
4.36E-12
5.58E-12
1.07E-11
1.42E-11
1.54E-11
6.88E-11
1.10E-10
2.72E-10
5.84E-10
8.20E-10
1.08E-09
1.59E-09

FIG. 25

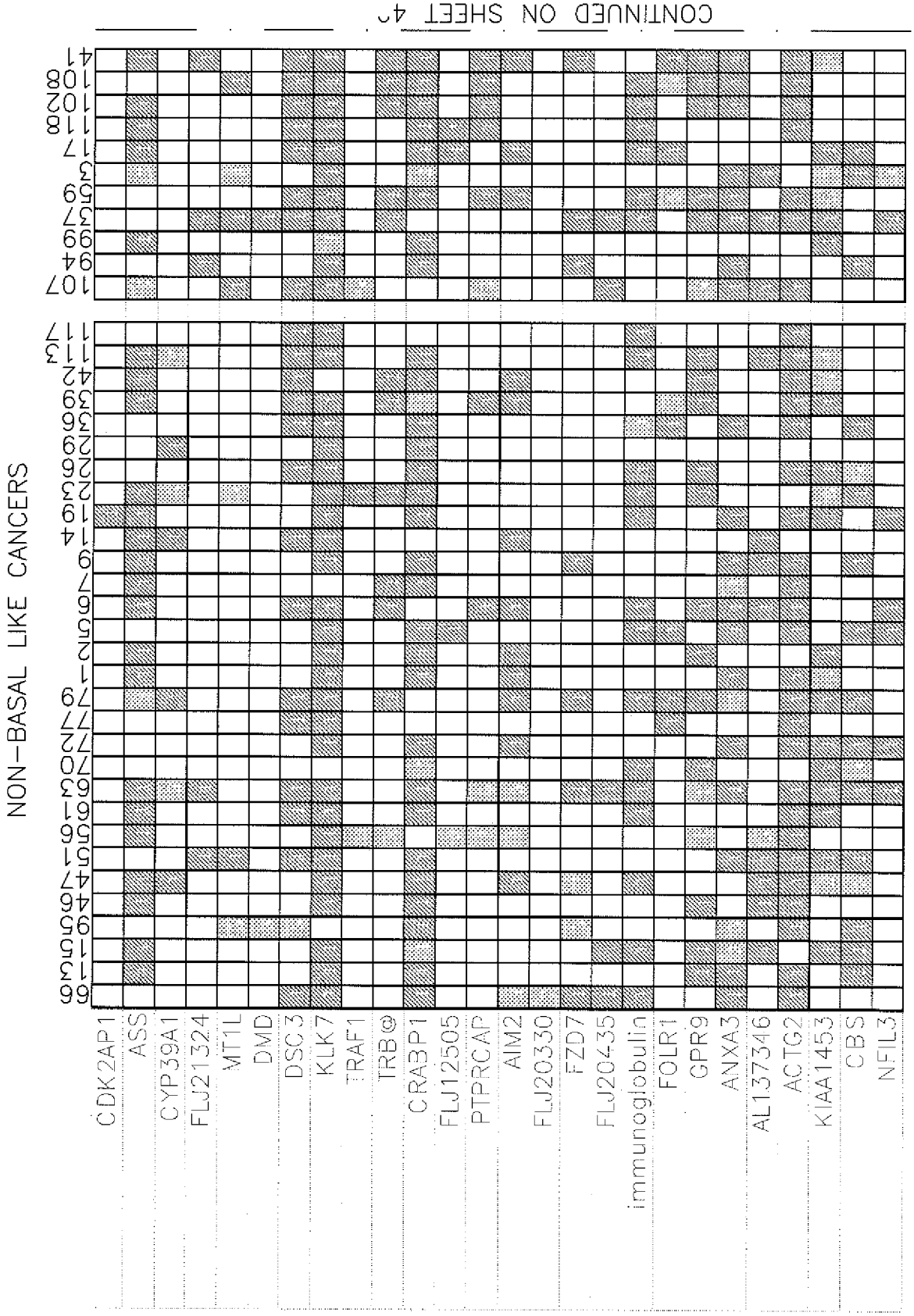

CONTINUED ON SHEET 4C
NON-BASAL LIKE CANCERS
CDK2AP1
ASS
CYP39A1
FLJ21324
MT1L
DMD
DSC3
KLK7
TRAF1
TRB@
CRA3P1
FLJ12505
PTPRCAP
AIM2
FLJ20330
FZD7
FLJ20435
immunoglobulin
FOLR1
GPR9
ANXA3
AL137346
ACTG2
KIAA1453
CBS
NFIL3

FIG. 25

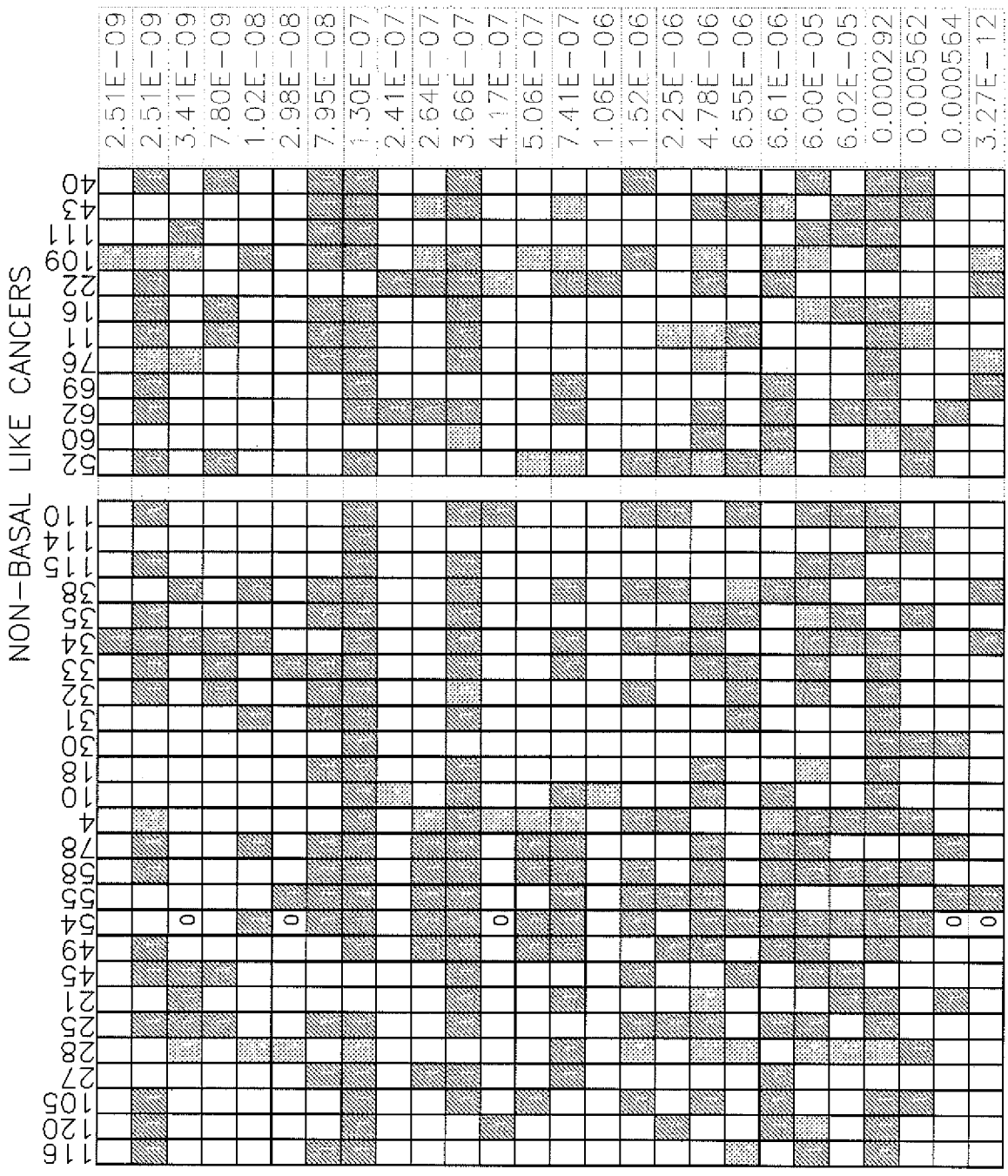

NON−BASAL LIKE CANCERS
2.51E−09
2.51E−09
3.41E−09
7.80E−09
1.02E−08
2.98E−08
7.95E−08
1.30E−07
2.41E−07
2.64E−07
3.66E−07
4.17E−07
5.06E−07
7.41E−07
1.06E−06
1.52E−06
2.25E−06
4.78E−06
6.55E−06
6.61E−06
6.00E−05
6.02E−05
0.000292
0.000562
0.000564
3.27E−12

FIG. 25

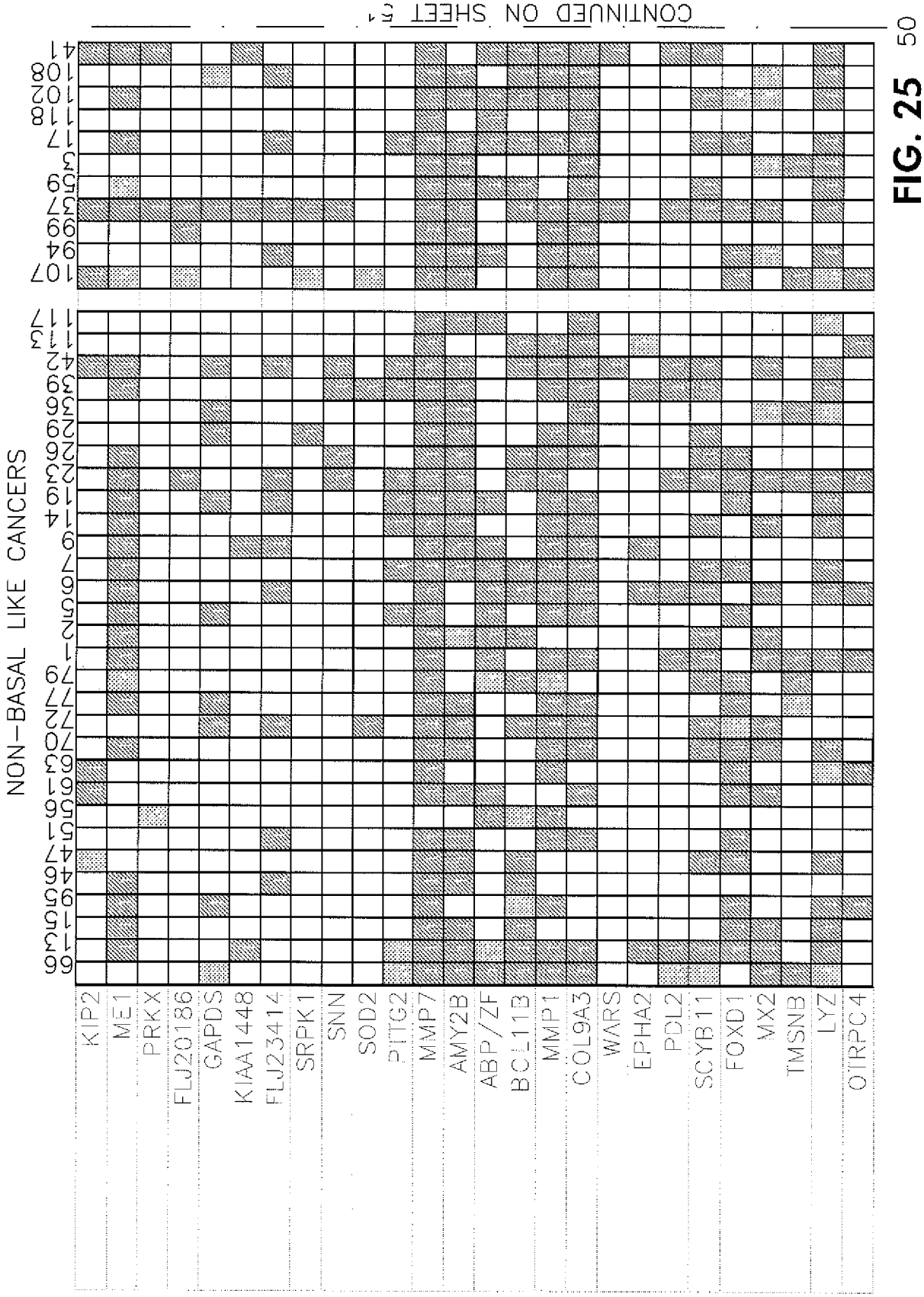

CONTINUED ON SHEET 51
NON-BASAL LIKE CANCERS
KIP2
ME1
PRKX
FLJ20186
GAPDS
KIAA1448
FLJ23414
SRPK1
SNN
SOD2
PTTG2
MMP7
AMY2B
ABP/ZF
BCL11B
MMP1
COL9A3
WARS
EPHA2
PDL2
SCYB11
FOXD1
MX2
TMSNB
LYZ
OTRPC4

FIG. 25

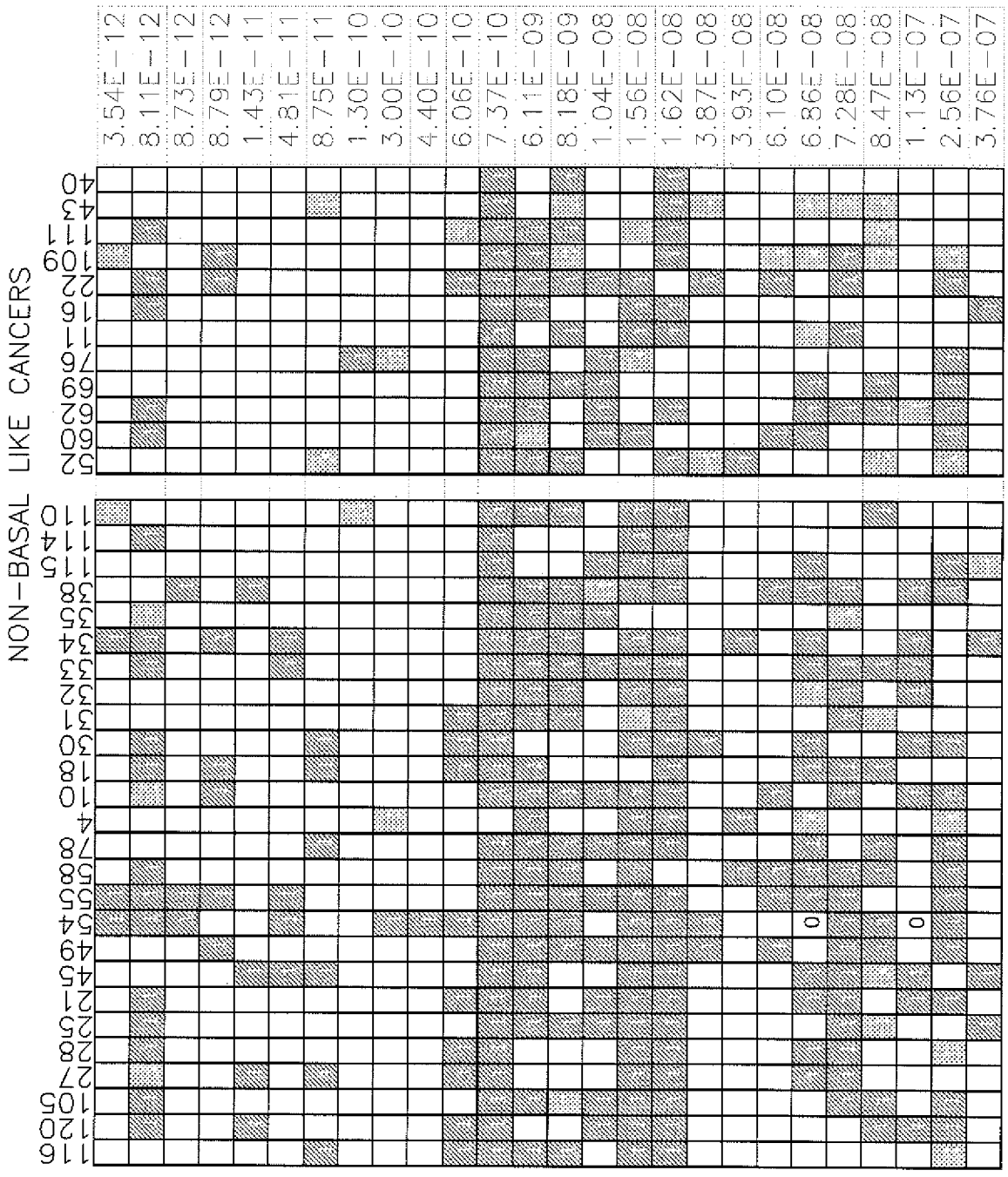

NON-BASAL LIKE CANCERS
3.54E-12
8.11E-12
8.73E-12
8.79E-12
1.43E-11
4.81E-11
8.75E-11
1.30E-10
3.00E-10
4.40E-10
6.06E-10
7.37E-10
6.11E-09
8.18E-09
1.04E-08
1.56E-08
1.62E-08
3.87E-08
3.93E-08
6.10E-08
6.86E-08
7.28E-08
8.47E-08
1.13E-07
2.56E-07
3.76E-07

FIG. 25 51

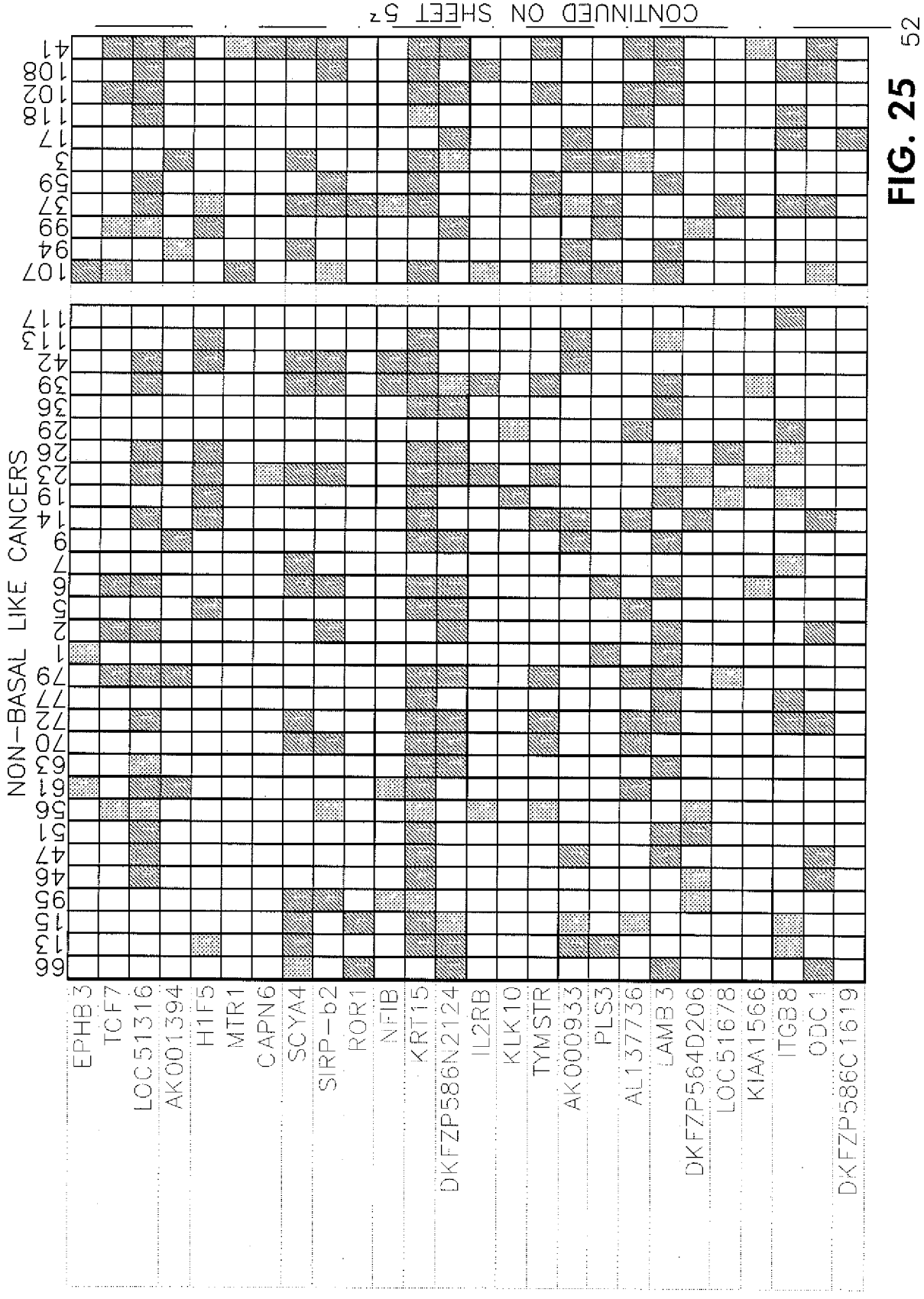

CONTINUED ON SHEET 52
NON-BASAL LIKE CANCERS
EPHB3
TCF7
LOC51316
AK001394
H1F5
MTR1
CAPN6
SCYA4
SIRP-b2
ROR1
NFIB
KRT15
DKFZP586N2124
IL2RB
KLK10
TYMSTR
AK000933
PLS3
AL137736
LAMB3
DKFZP564D206
LOC51678
KIAA1566
ITGB8
ODC1
DKFZP586C1619

FIG. 25

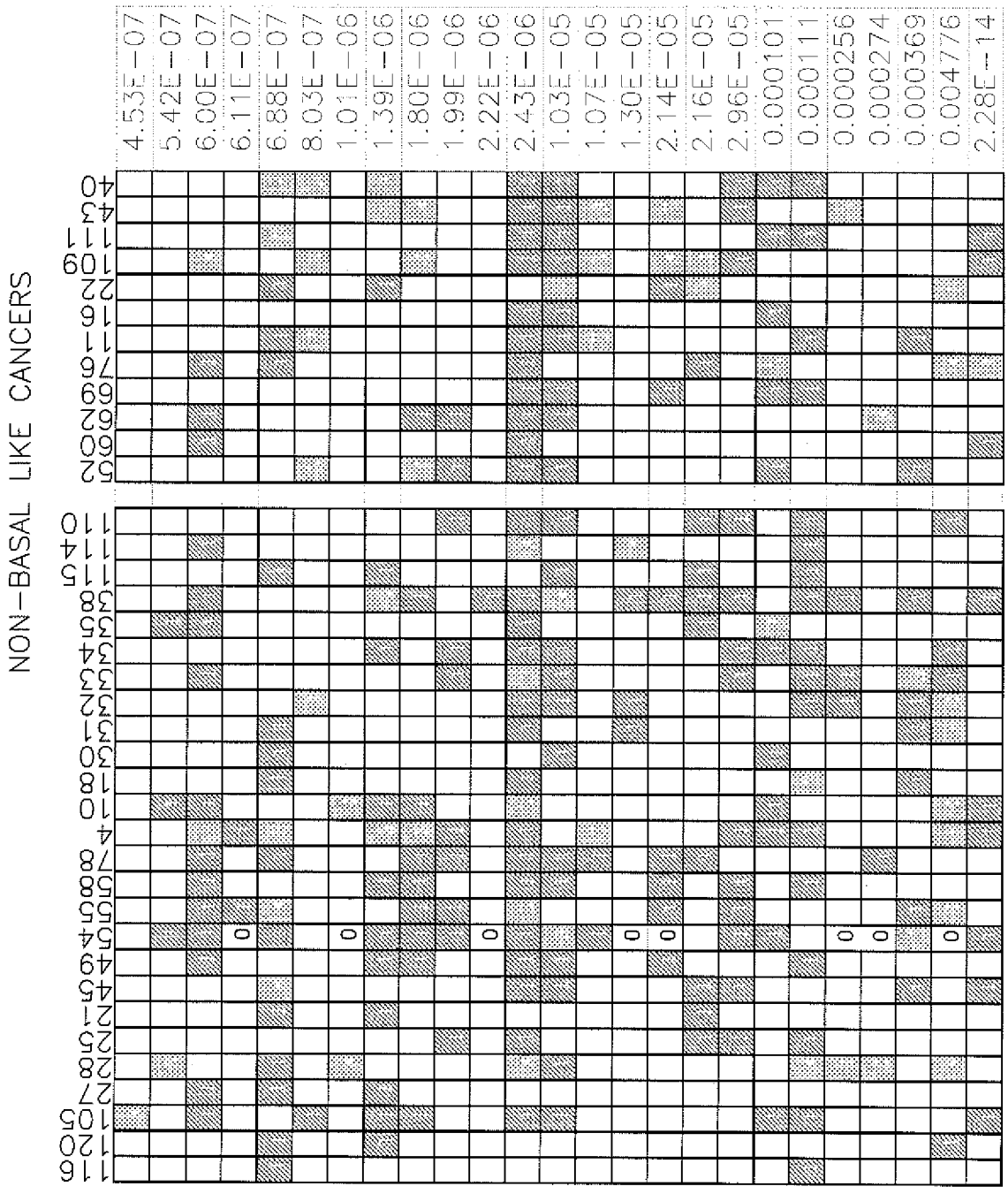

NON-BASAL LIKE CANCERS
4.53E-07
5.42E-07
6.00E-07
6.11E-07
6.88E-07
8.03E-07
1.01E-06
1.39E-06
1.80E-06
1.99E-06
2.22E-06
2.43E-06
1.03E-05
1.07E-05
1.30E-05
2.14E-05
2.16E-05
2.96E-05
0.000101
0.000111
0.000256
0.000274
0.000369
0.004776
2.28E-14

FIG. 25 53

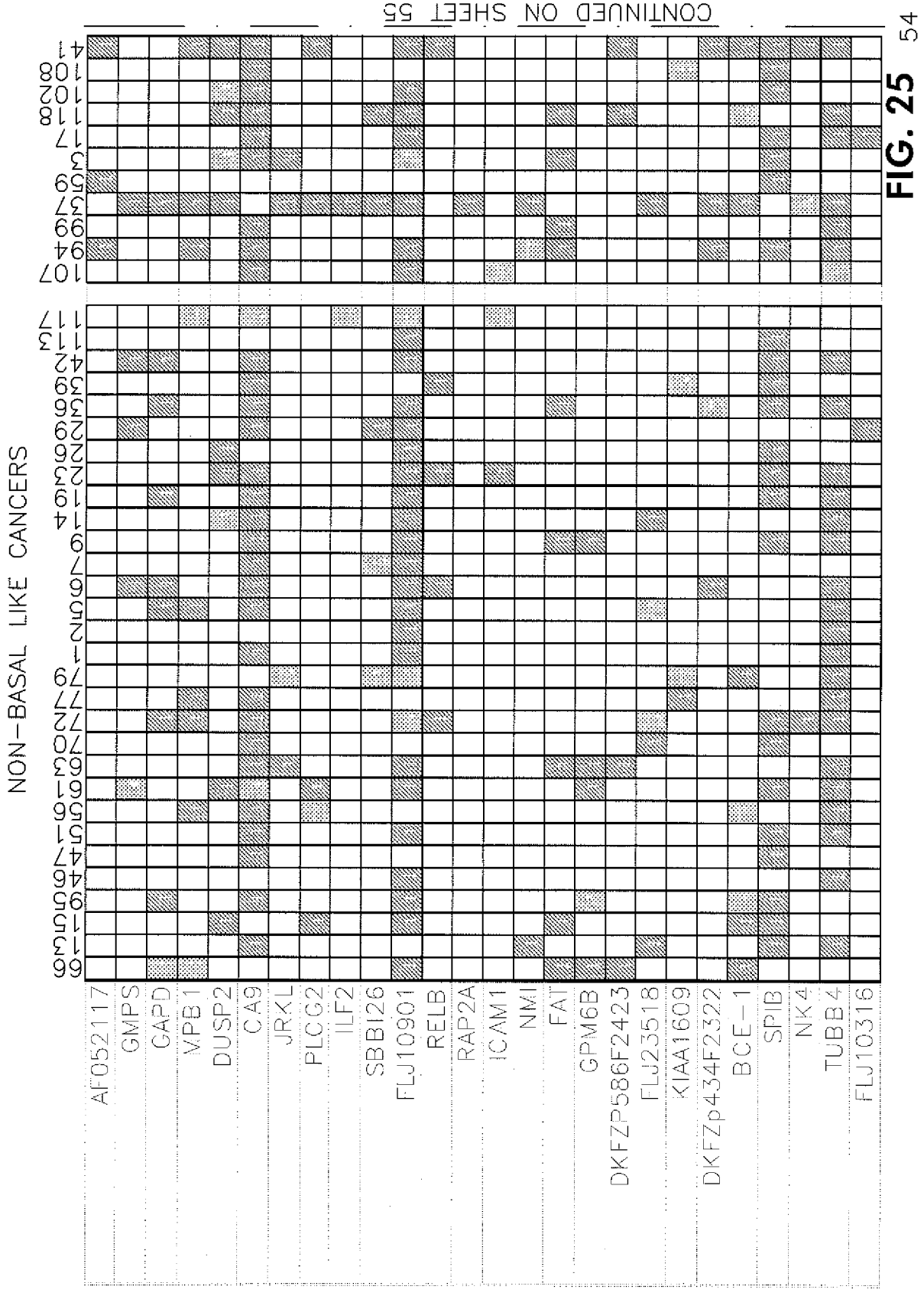

CONTINUED ON SHEET 55
NON-BASAL LIKE CANCERS
AF052117
GMPS
GAPD
VPB1
DUSP2
CA9
JRKL
PLCG2
ILF2
SBBI26
FLJ10901
RELB
RAP2A
ICAM1
NMI
FAT
GPM6B
DKFZP586F2423
FLJ23518
KIAA1609
DKFZp434F2322
BCE-1
SPIB
NK4
TUBB4
FLJ10316

FIG. 25

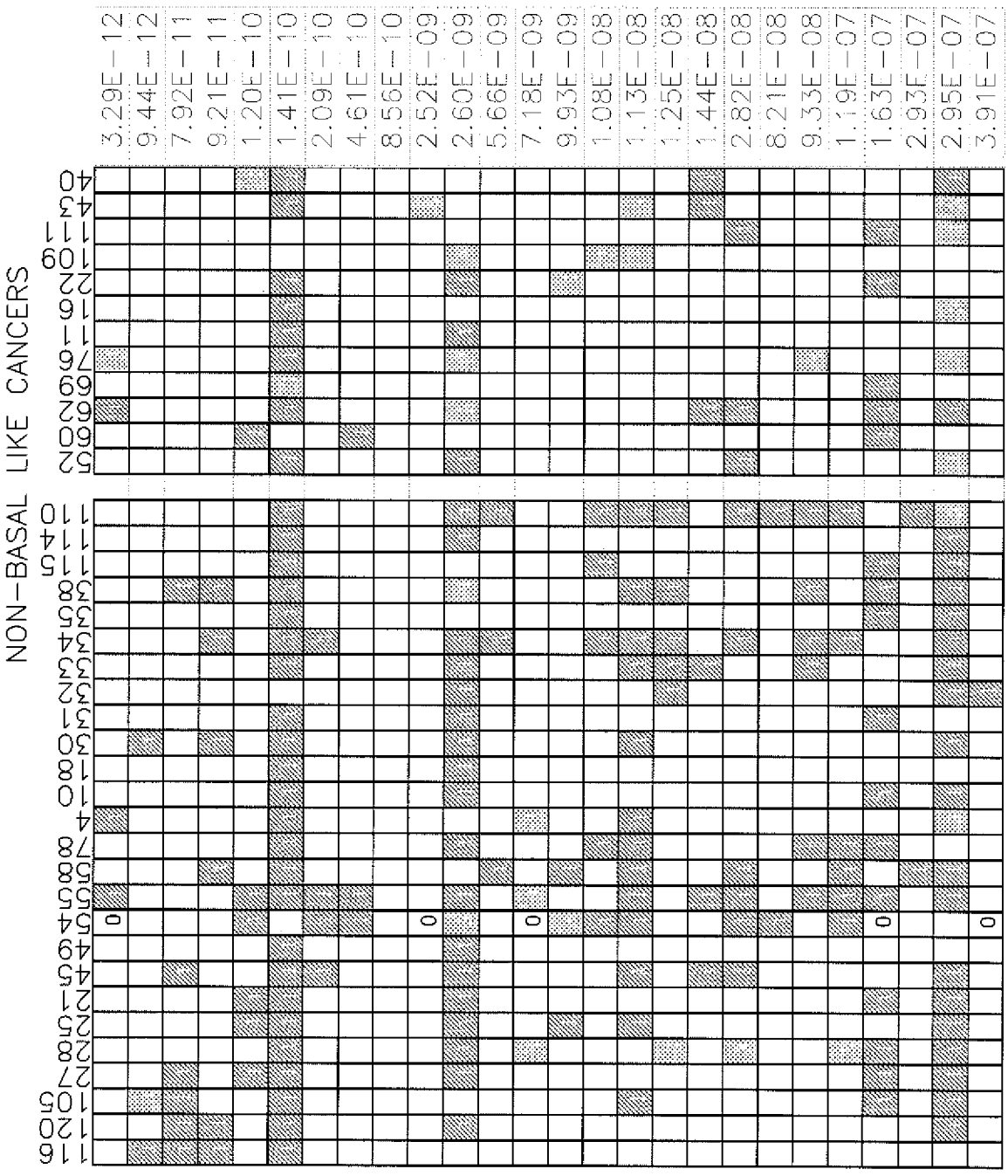

NON-BASAL LIKE CANCERS
3.29E-12
9.44E-12
7.92E-11
9.21E-11
1.20E-10
1.41E-10
2.09E-10
4.61E-10
8.56E-10
2.52E-09
2.60E-09
5.66E-09
7.18E-09
9.93E-09
1.08E-08
1.13E-08
1.25E-08
1.44E-08
2.82E-08
8.21E-08
9.33E-08
1.19E-07
1.63E-07
2.93E-07
2.95E-07
3.91E-07

FIG. 25

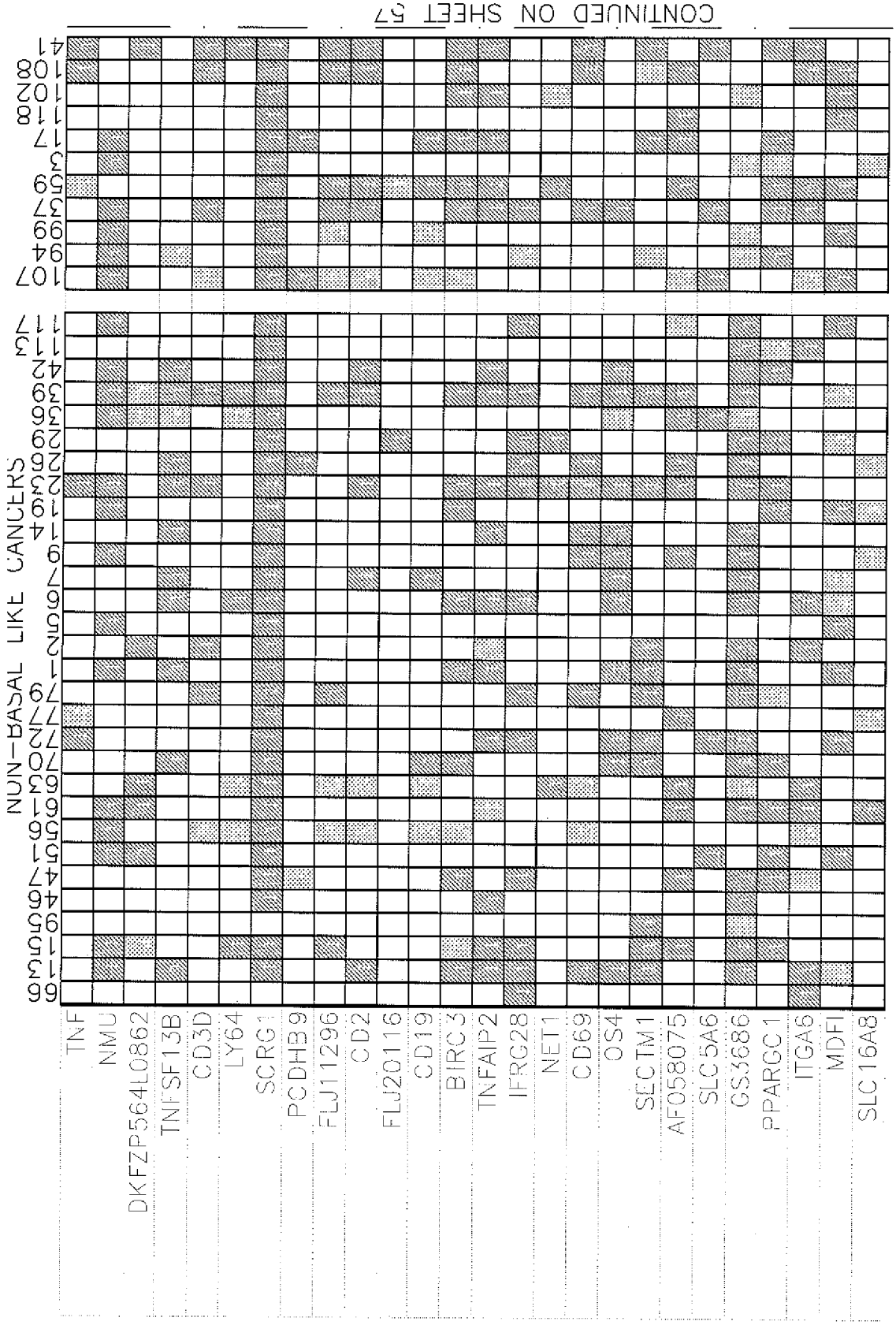

CONTINUED ON SHEET 57
NON-BASAL LIKE CANCERS
TNF
NMU
DKFZP564L0862
TNFSF13B
CD3D
LY64
SCRG1
PCDHB9
FLJ11296
CD2
FLJ20116
CD19
BIRC3
TNFAIP2
IFRG28
NET1
CD69
OS4
SLCTM1
AF058075
SLC5A6
GS3686
PPARGC1
ITGA6
MDFI
SLC16A8

FIG. 25 56

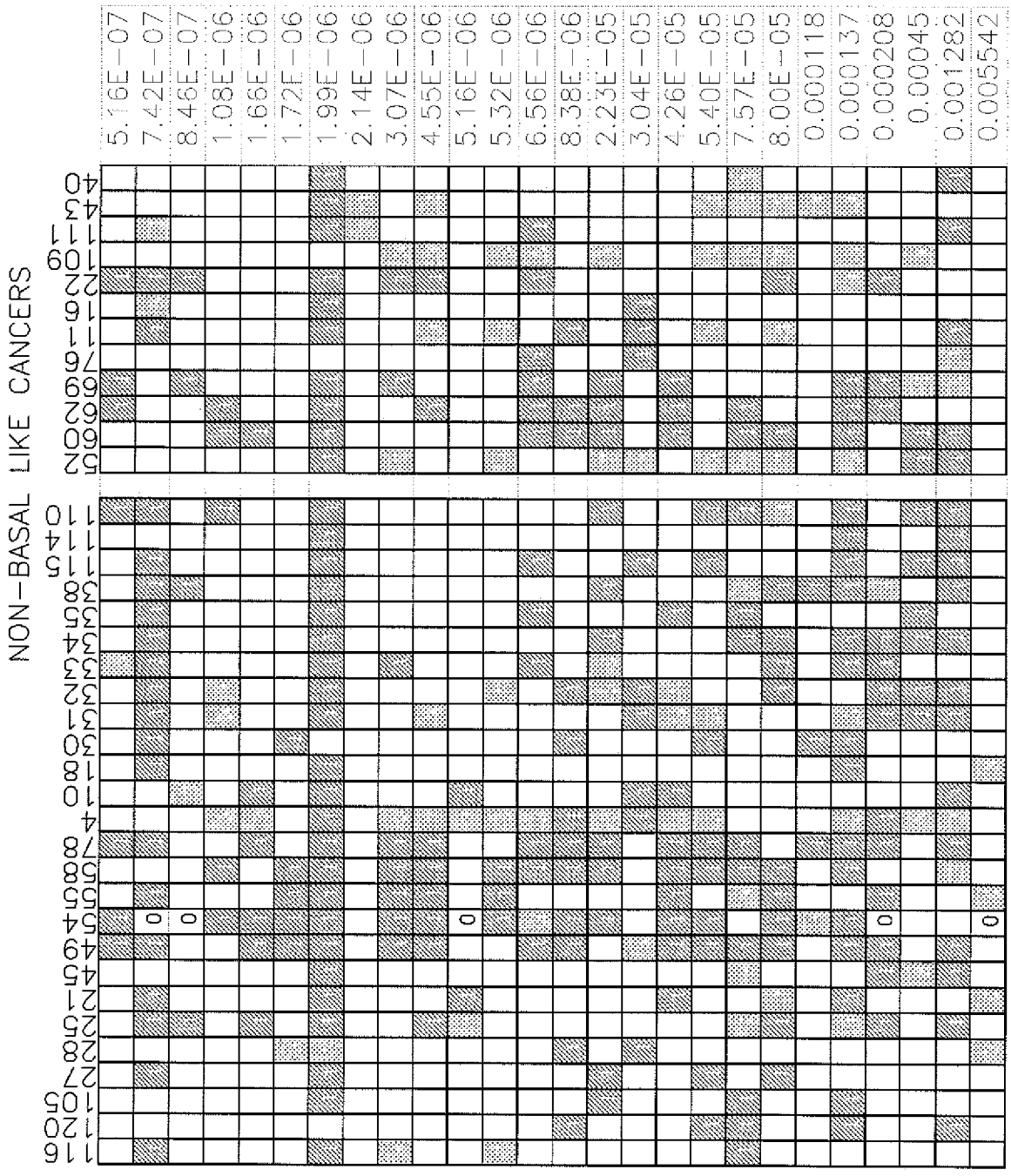

NON-BASAL LIKE CANCERS
5.16E-07
7.42E-07
8.46E-07
1.08E-06
1.66E-06
1.72E-06
1.99E-06
2.14E-06
3.07E-06
4.55E-06
5.16E-06
5.32E-06
6.56E-06
8.38E-06
2.23E-05
3.04E-05
4.26E-05
5.40E-05
7.57E-05
8.00E-05
0.000118
0.000137
0.000208
0.00045
0.001282
0.005542

FIG. 25

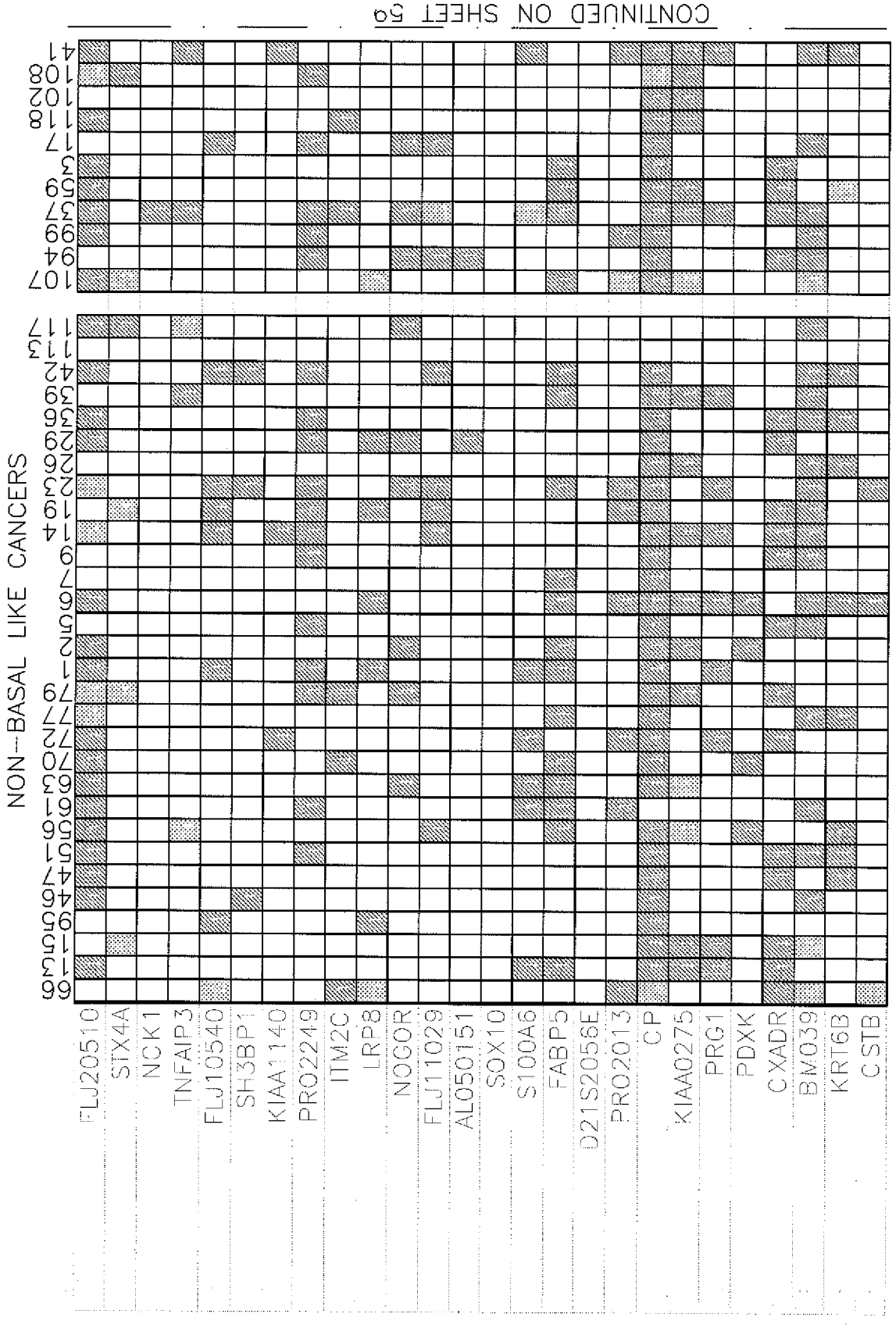

CONTINUED ON SHEET 59
NON-BASAL LIKE CANCERS
FLJ20510
STX4A
NCK1
TNFAIP3
FLJ10540
SH3BP1
KIAA1140
PRO2249
ITM2C
LRP8
NOGOR
FLJ11029
AL050151
SOX10
S100A6
FABP5
D21S2056E
PRO2013
CP
KIAA0275
PRG1
PDXK
CXADR
BM039
KRT6B
CSTB

FIG. 25 58

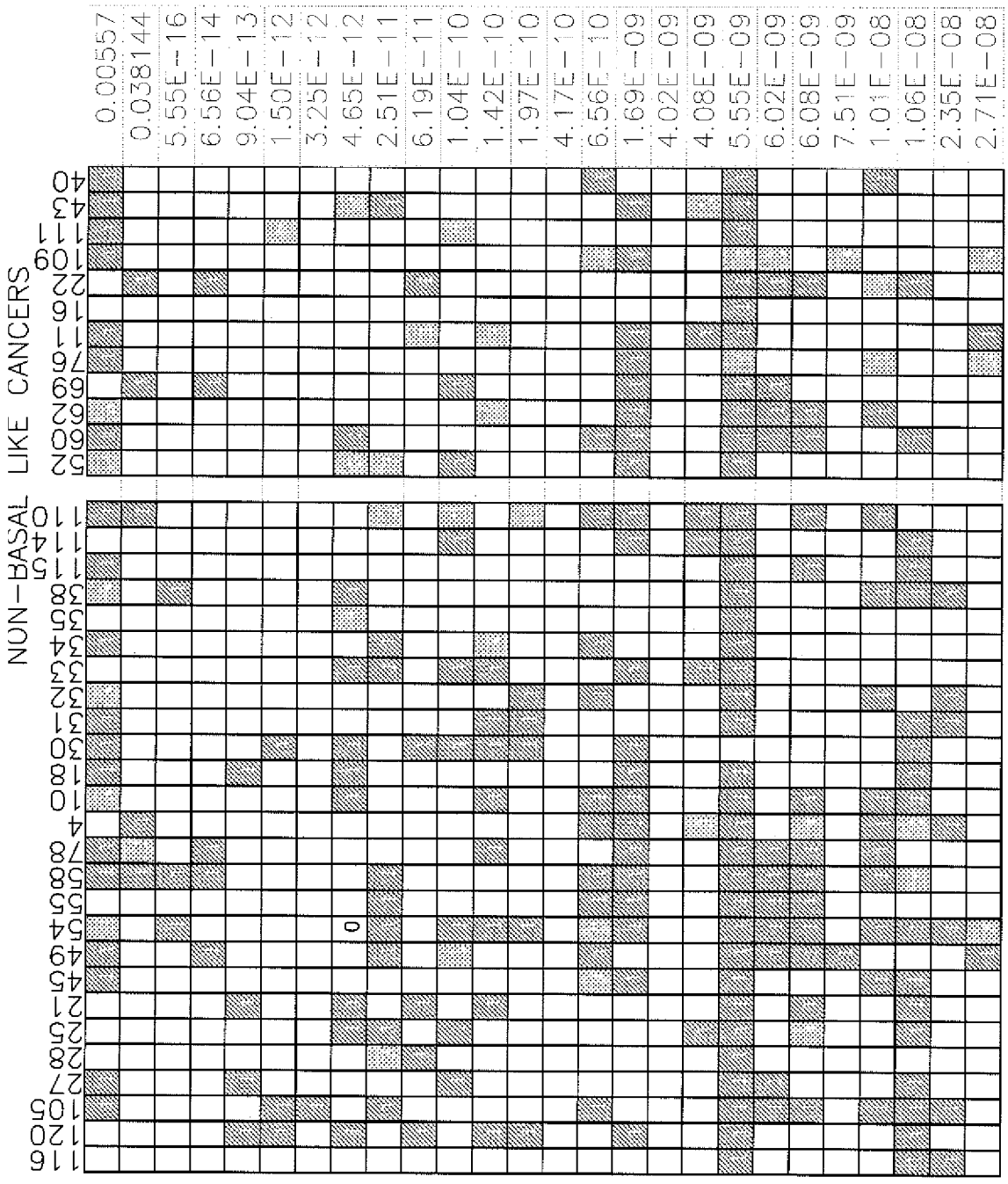

NON-BASAL LIKE CANCERS
52 60 62 69 76 11 16 22 109 111 43 40
116 120 105 27 28 25 21 45 49 54 55 58 78 4 10 30 31 32 33 34 35 38 115 114 110
0.00557
0.038144
5.55E-16
6.56E-14
9.04E-13
1.50E-12
3.25E-12
4.65E-12
2.51E-11
6.19E-11
1.04E-10
1.42E-10
1.97E-10
4.17E-10
6.56E-10
1.69E-09
4.02E-09
4.08E-09
5.55E-09
6.02E-09
6.08E-09
7.51E-09
1.01E-08
1.06E-08
2.35E-08
2.71E-08

FIG. 25

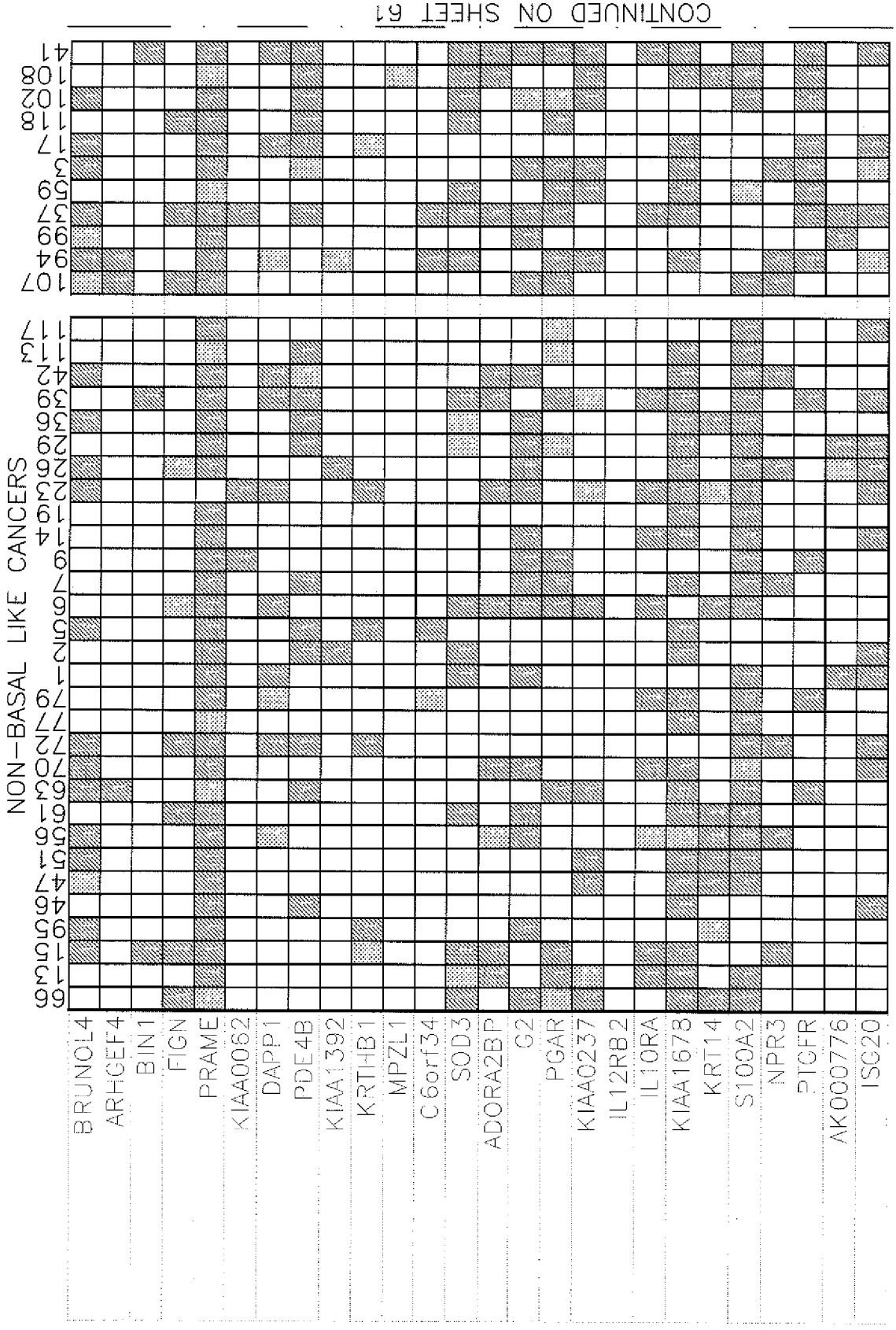

CONTINUED ON SHEET 61
NON-BASAL LIKE CANCERS
BRUNOL4
ARHGEF4
BIN1
FIGN
PRAME
KIAA0062
DAPP1
PDE4B
KIAA1392
KRTHB1
MPZL1
C6orf34
SOD3
ADORA2BP
G2
PGAR
KIAA0237
IL12RB2
IL10RA
KIAA1678
KRT14
S100A2
NPR3
PTGFR
AK000776
ISG20

FIG. 25 60

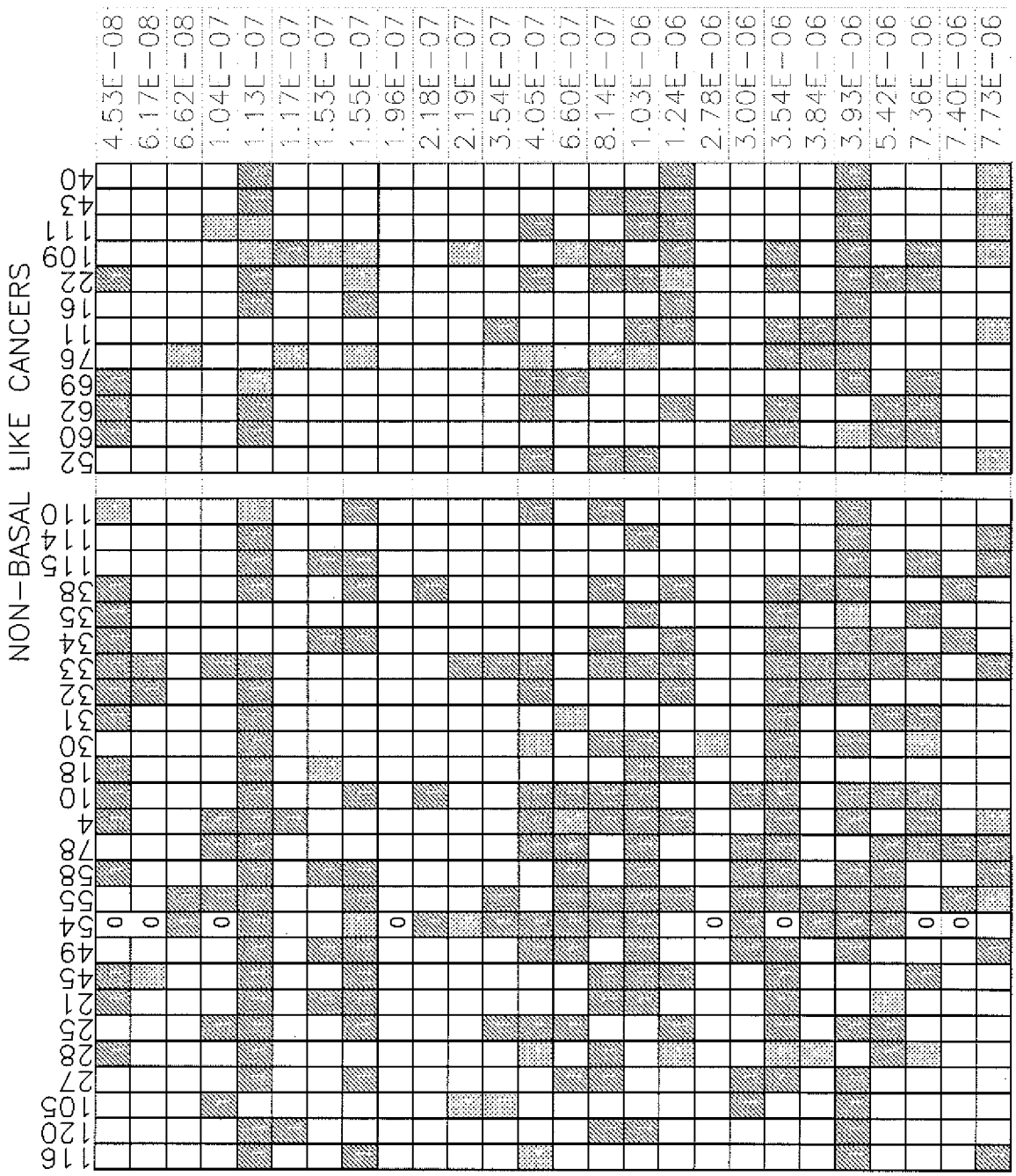

NON-BASAL LIKE CANCERS
4.53E-08
6.17E-08
6.62E-08
1.04E-07
1.13E-07
1.17E-07
1.53E-07
1.55E-07
1.96E-07
2.18E-07
2.19E-07
3.54E-07
4.05E-07
6.60E-07
8.14E-07
1.03E-06
1.24E-06
2.78E-06
3.00E-06
3.54E-06
3.84E-06
3.93E-06
5.42E-06
7.36E-06
7.40E-06
7.73E-06

FIG. 25

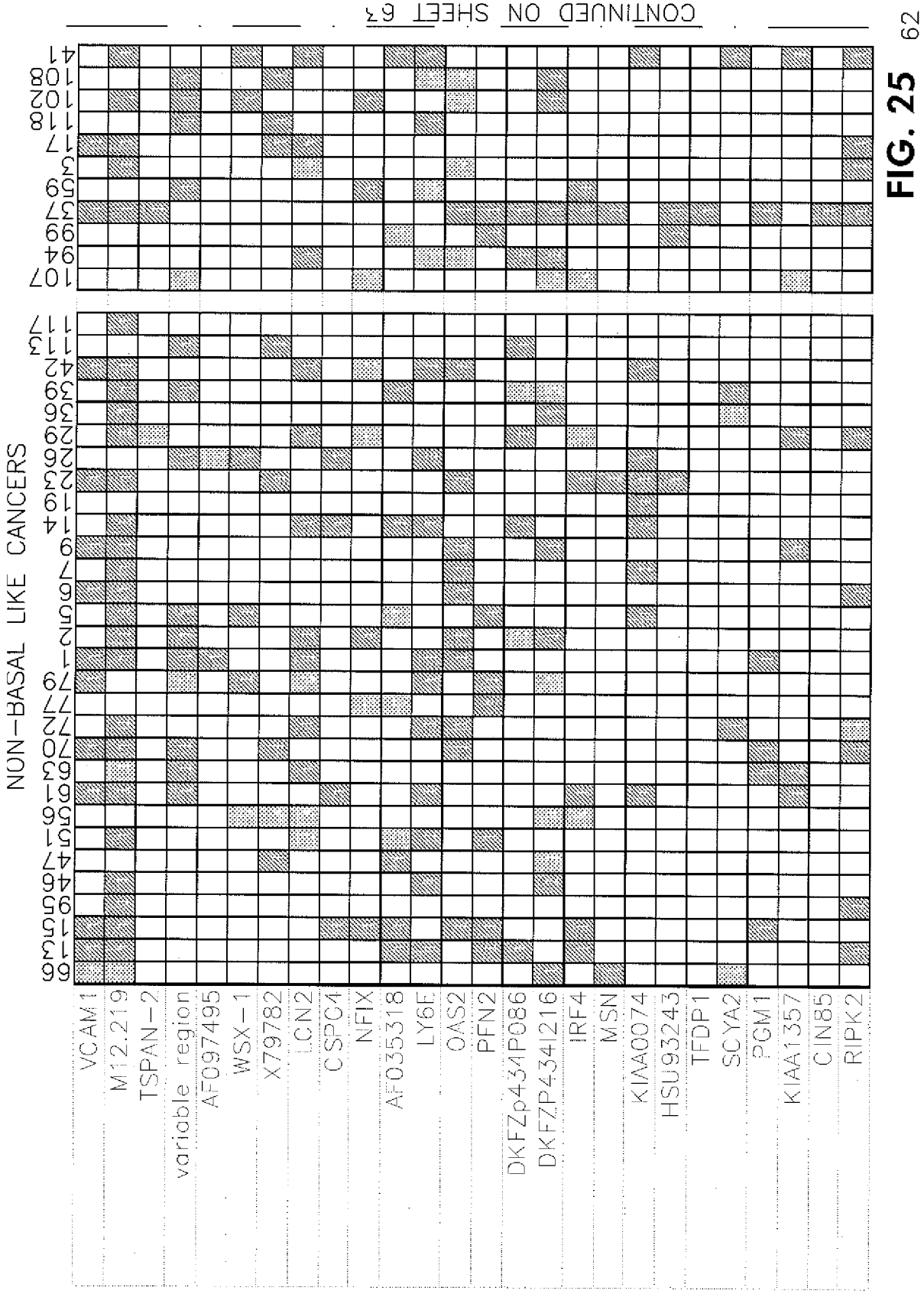

NON-BASAL LIKE CANCERS
VCAM1
M12.219
TSPAN-2
variable region
AF097495
WSX-1
X79782
LCN2
CSPC4
NFIX
AF035318
LY6E
OAS2
PFN2
DKFZp434P086
DKFZP434I216
IRF4
MSN
KIAA0074
HSU93243
TFDP1
SCYA2
PGM1
KIAA1357
CIN85
RIPK2
CONTINUED ON SHEET 63

FIG. 25 62

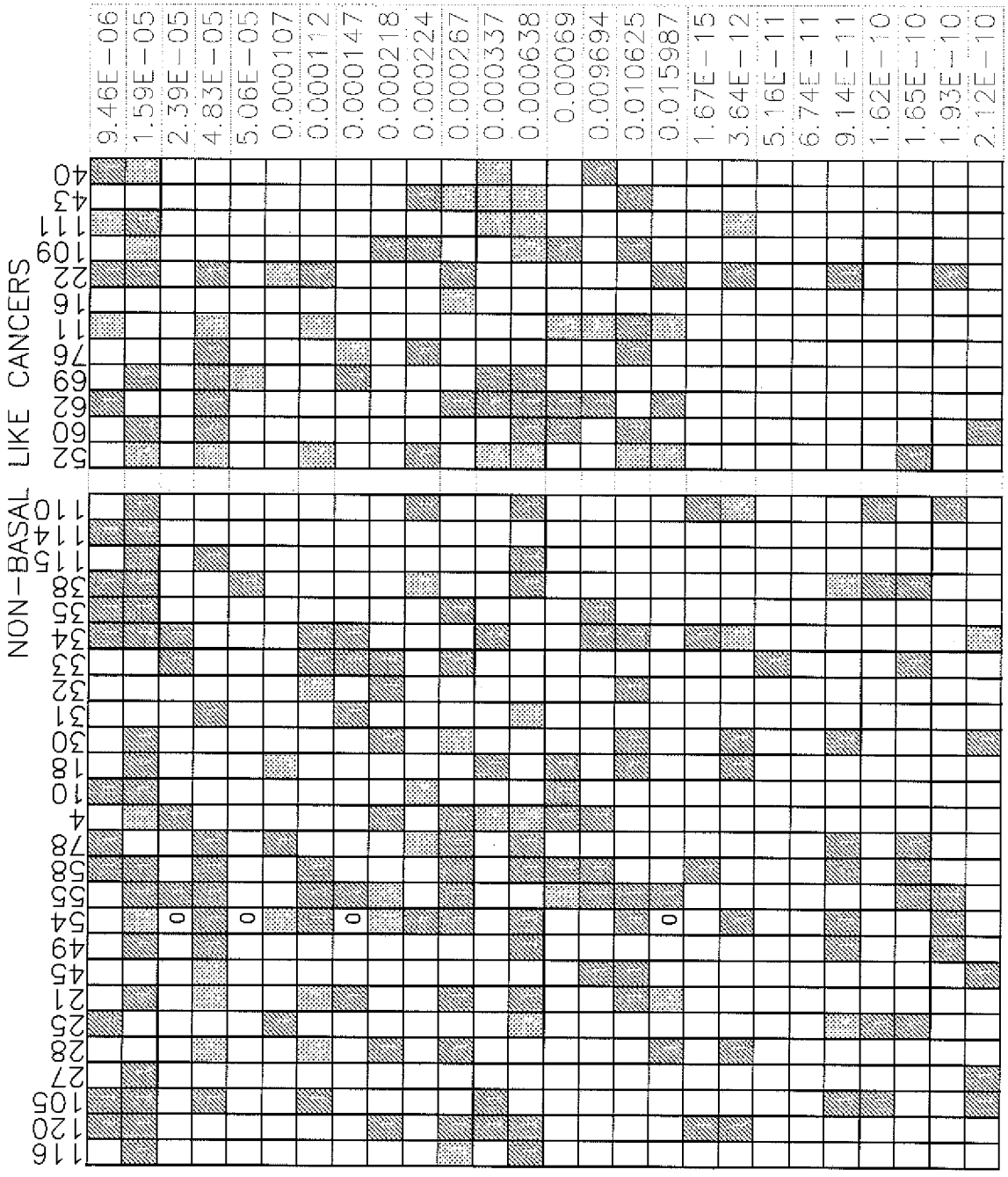

NON-BASAL LIKE CANCERS
52 60 62 69 76 11 16 22 109 11 43 40
116 120 105 27 228 225 211 45 49 54 55 58 78 4 10 18 30 31 22 24 25 38 45 14 10 116
9.46E-06
1.59E-05
2.39E-05
4.83E-05
5.06E-05
0.000107
0.000112
0.000147
0.000218
0.000224
0.000267
0.000337
0.000638
0.00069
0.009694
0.010625
0.015987
1.67E-15
3.64E-12
5.16E-11
6.74E-11
9.14E-11
1.62E-10
1.65E-10
1.93E-10
2.12E-10

FIG. 25 63

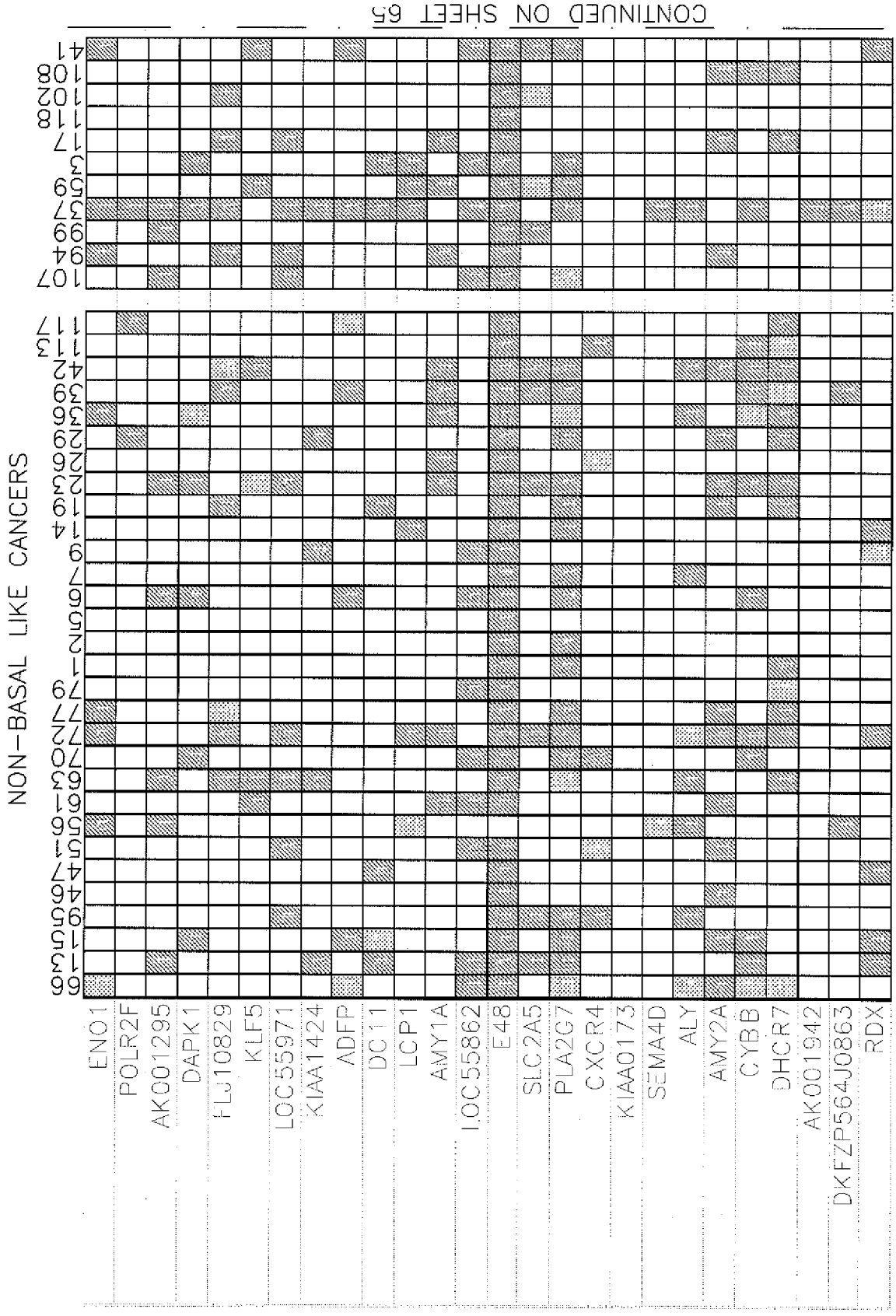

CONTINUED ON SHEET 65
NON-BASAL LIKE CANCERS
ENO1
POLR2F
AK001295
DAPK1
FLJ10829
KLF5
LOC55971
KIAA1424
ADFP
DC11
LCP1
AMY1A
LOC55862
E48
SLC2A5
PLA2G7
CXCR4
KIAA0173
SEMA4D
ALY
AMY2A
CYBB
DHCR7
AK001942
DKFZP564J0863
RDX

FIG. 25 64

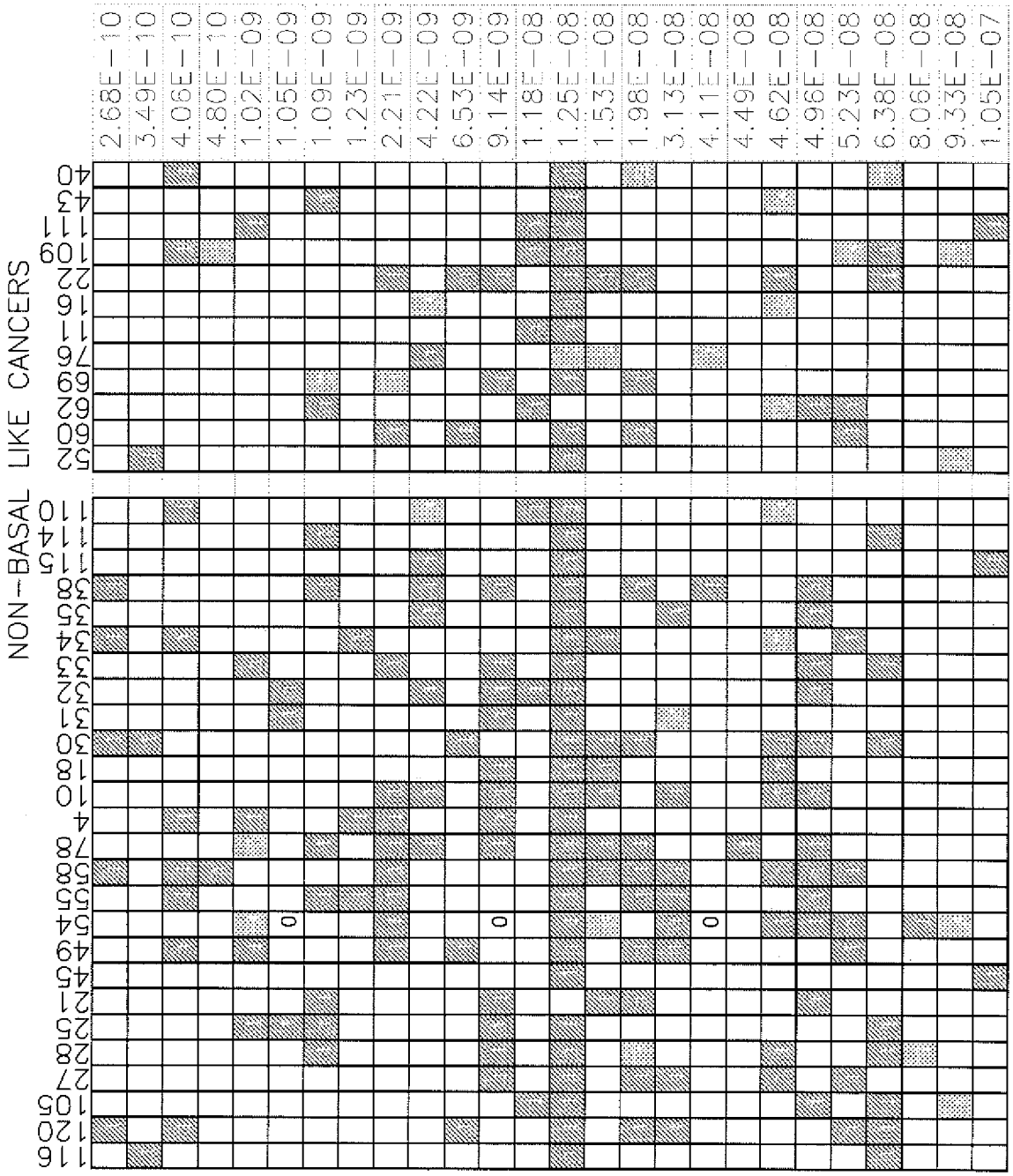

NON-BASAL LIKE CANCERS
116 120 105 127 128 125 121 145 149 154 155 158 178 4 110 130 131 132 133 134 135 138 115 114 110
52 60 62 69 76 111 116 122 109 111 43 40
2.68E-10
3.49E-10
4.06E-10
4.80E-10
1.02E-09
1.05E-09
1.09E-09
1.23E-09
2.21E-09
4.22E-09
6.53E-09
9.14E-09
1.18E-08
1.25E-08
1.53E-08
1.98E-08
3.13E-08
4.11E-08
4.49E-08
4.62E-08
4.96E-08
5.23E-08
6.38E-08
8.06E-08
9.33E-08
1.05E-07

FIG. 25 65

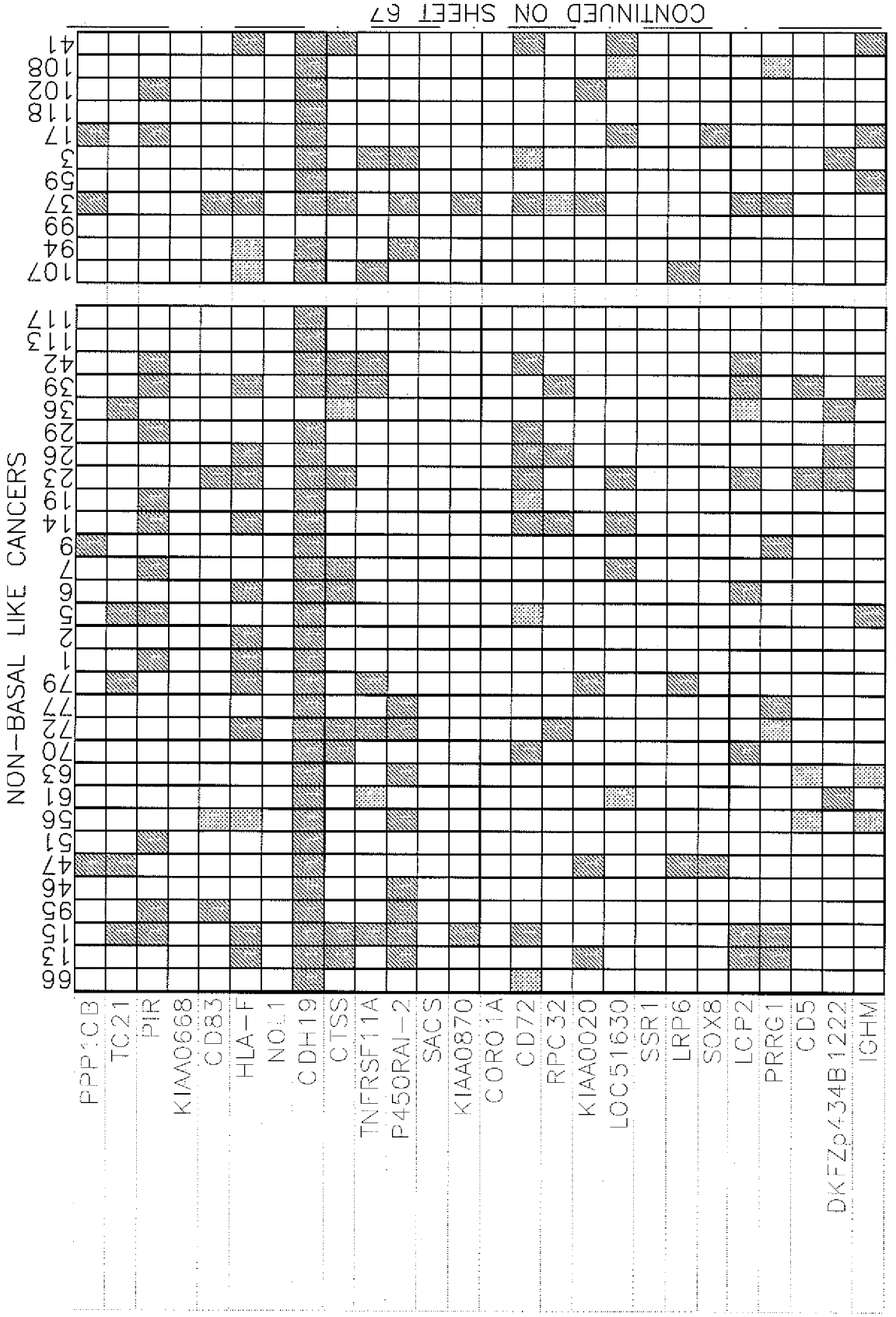

NON-BASAL LIKE CANCERS
PPP1CB
TC21
PIR
KIAA0668
CD83
HLA-F
NOL1
CDH19
CTSS
TNFRSF11A
P450RAI-2
SACS
KIAA0870
CORO1A
CD72
RPC32
KIAA0020
LOC51630
SSR1
LRP6
SOX8
LCP2
PRRG1
CD5
DKFZp434B1222
IGHM
CONTINUED ON SHEET 67

FIG. 25 66

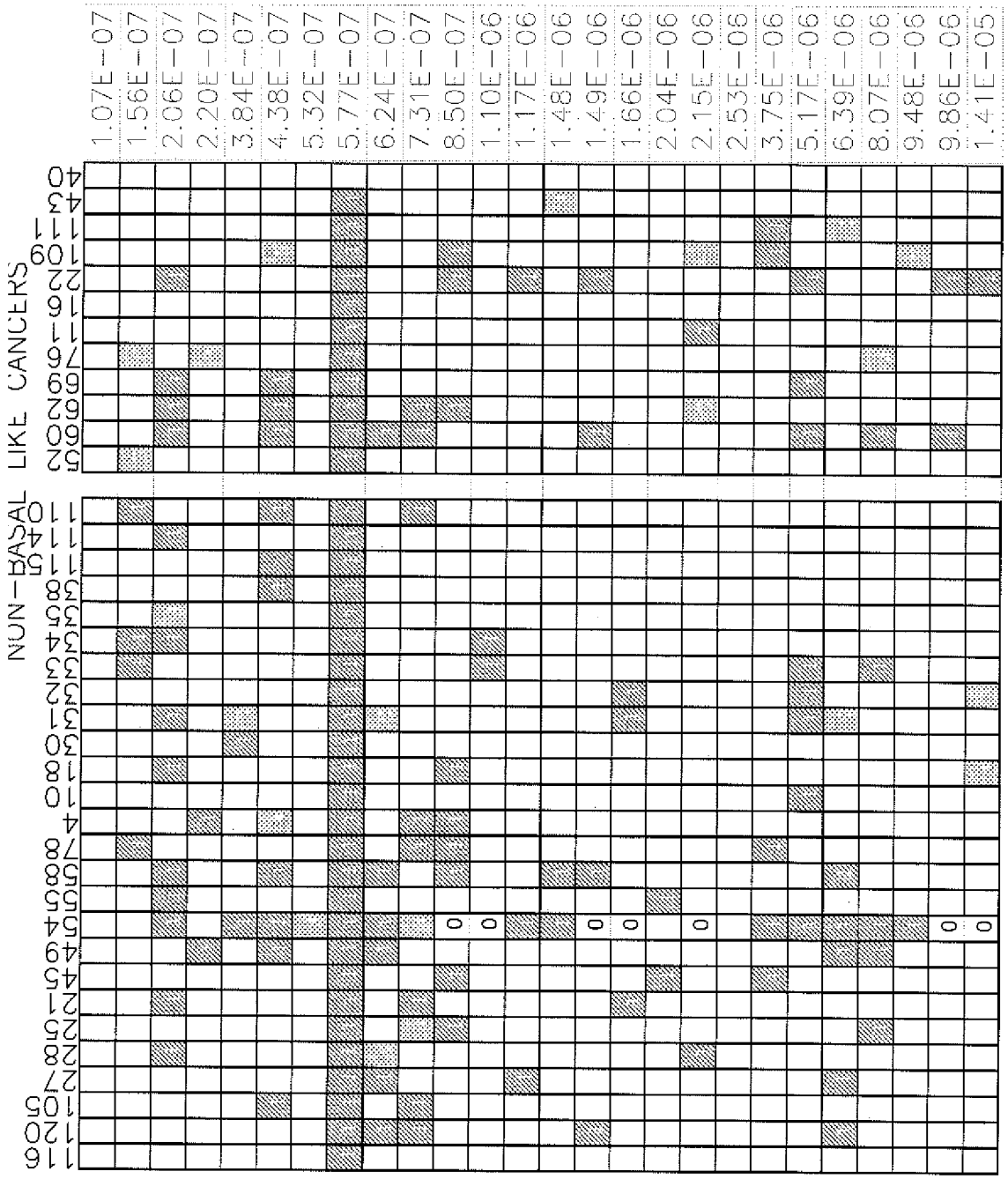

NON-BASAL LIKE CANCERS
1.07E-07
1.56E-07
2.06E-07
2.20E-07
3.84E-07
4.38E-07
5.32E-07
5.77E-07
6.24E-07
7.31E-07
8.50E-07
1.10E-06
1.17E-06
1.48E-06
1.49E-06
1.66E-06
2.04E-06
2.15E-06
2.53E-06
3.75E-06
5.17E-06
6.39E-06
8.07E-06
9.48E-06
9.86E-06
1.41E-05

FIG. 25 67

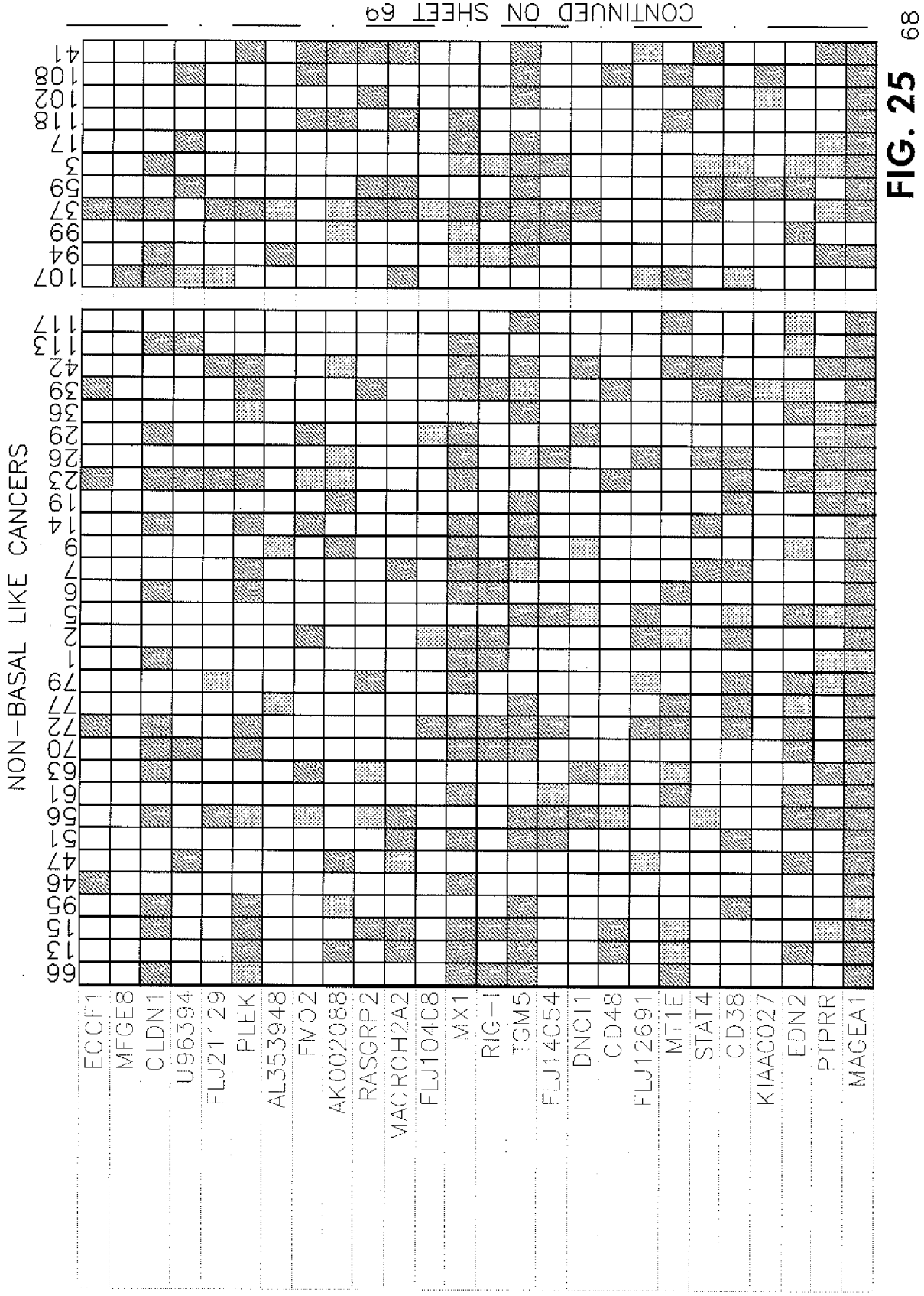

NON-BASAL LIKE CANCERS
CONTINUED ON SHEET 69
ECGF1
MFGE8
CLDN1
U96394
FLJ21129
PLEK
AL353948
FMO2
AK002088
RASGRP2
MACROH2A2
FLJ10408
MX1
RIG-I
TCM5
FLJ14054
DNC11
CD48
FLJ12691
MT1E
STAT4
CD38
KIAA0027
EDN2
PTPRR
MAGEA1

FIG. 25

68

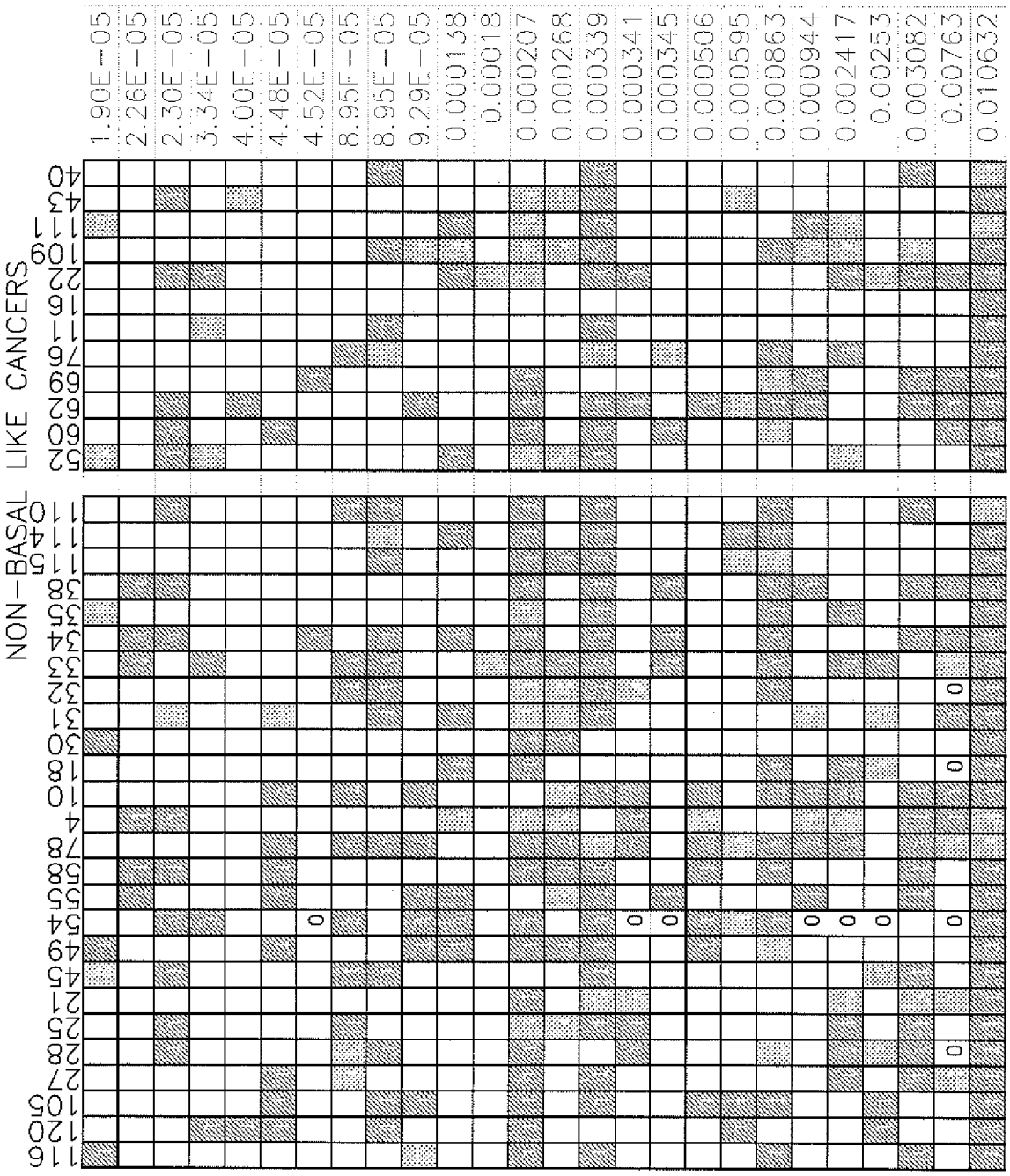

NON-BASAL LIKE CANCERS
1.90E-05
2.26E-05
2.30E-05
3.34E-05
4.00E-05
4.48E-05
4.52E-05
8.95E-05
8.95E-05
9.29E-05
0.000138
0.00018
0.000207
0.000268
0.000339
0.000341
0.000345
0.000506
0.000595
0.000863
0.000944
0.002417
0.00253
0.003082
0.00763
0.010632

FIG. 25

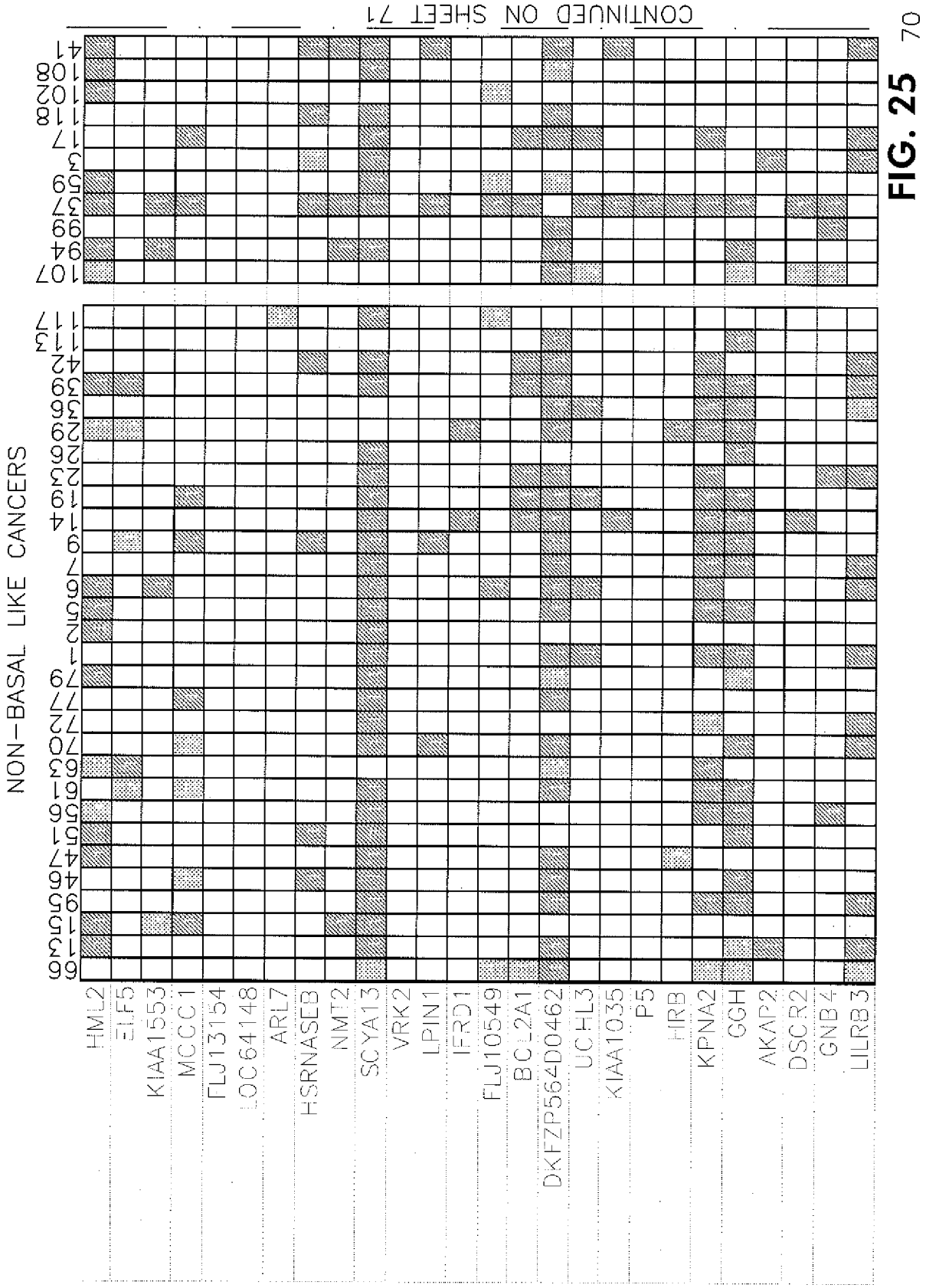

CONTINUED ON SHEET 71
NON-BASAL LIKE CANCERS
HML2
ELF5
KIAA1553
MCCC1
FLJ13154
LOC64148
ARL7
HSRNASEB
NMT2
SCYA13
VRK2
LPIN1
IFRD1
FLJ10549
BCL2A1
DKFZP564D0462
UCHL3
KIAA1035
P5
HRB
KPNA2
GGH
AKAP2
DSCR2
GNB4
LILRB3

FIG. 25 70

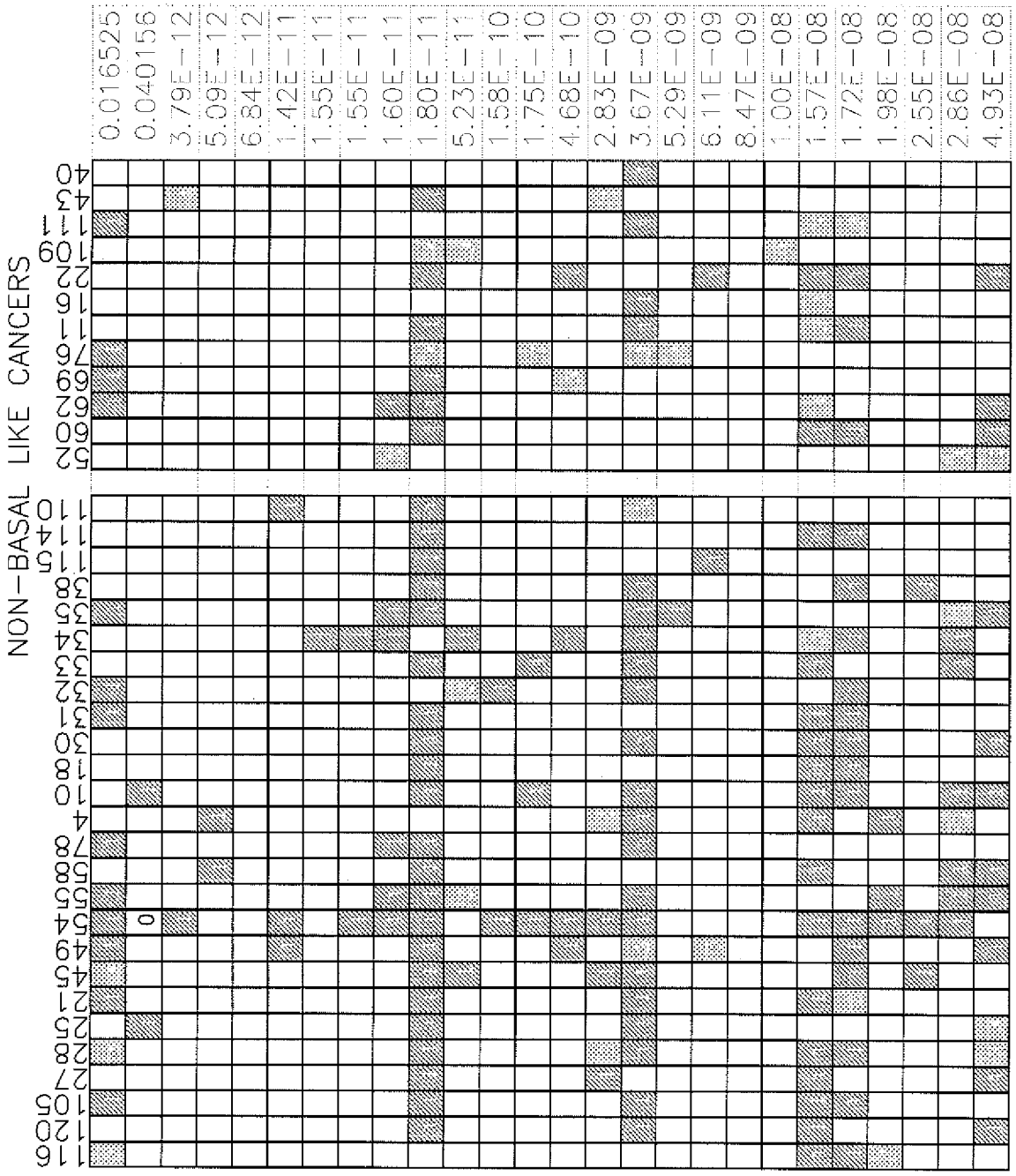

NON-BASAL LIKE CANCERS
0.016525
0.040156
3.79E-12
5.09E-12
6.84E-12
1.42E-11
1.55E-11
1.55E-11
1.60E-11
1.80E-11
5.23E-11
1.58E-10
1.75E-10
4.68E-10
2.83E-09
3.67E-09
5.29E-09
6.11E-09
8.47E-09
1.00E-08
1.57E-08
1.72E-08
1.98E-08
2.55E-08
2.86E-08
4.93E-08

FIG. 25 71

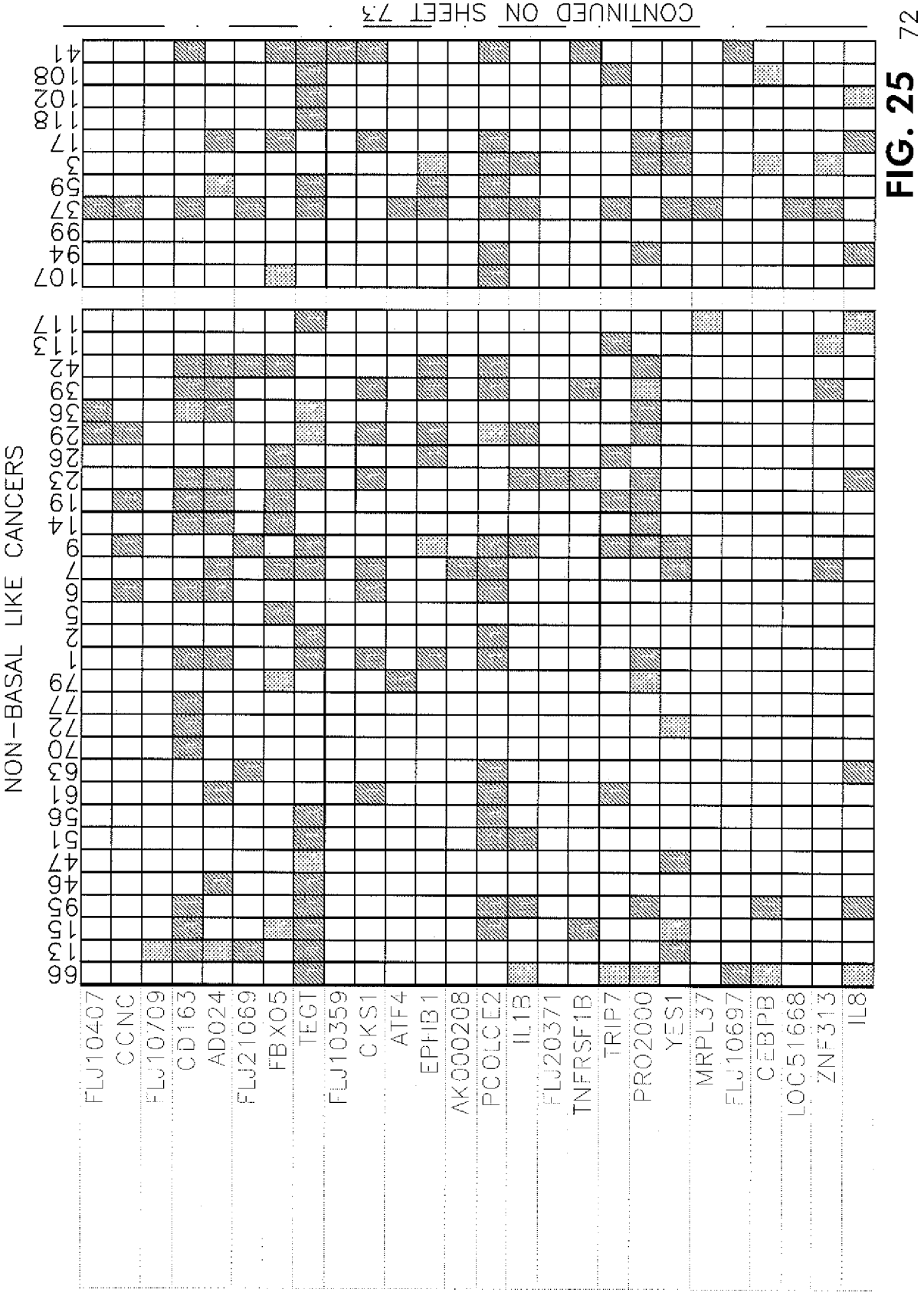

CONTINUED ON SHEET 73
NON-BASAL LIKE CANCERS
FLJ10407
CCNC
FLJ10709
CD163
AD024
FLJ21069
FBXO5
TEGT
FLJ10359
CKS1
ATF4
EPHB1
AK000208
PCOLCE2
IL1B
FLJ20371
TNFRSF1B
TRIP7
PRO2000
YES1
MRPL37
FLJ10697
CEBPB
LOC51668
ZNF313
IL8

FIG. 25 72

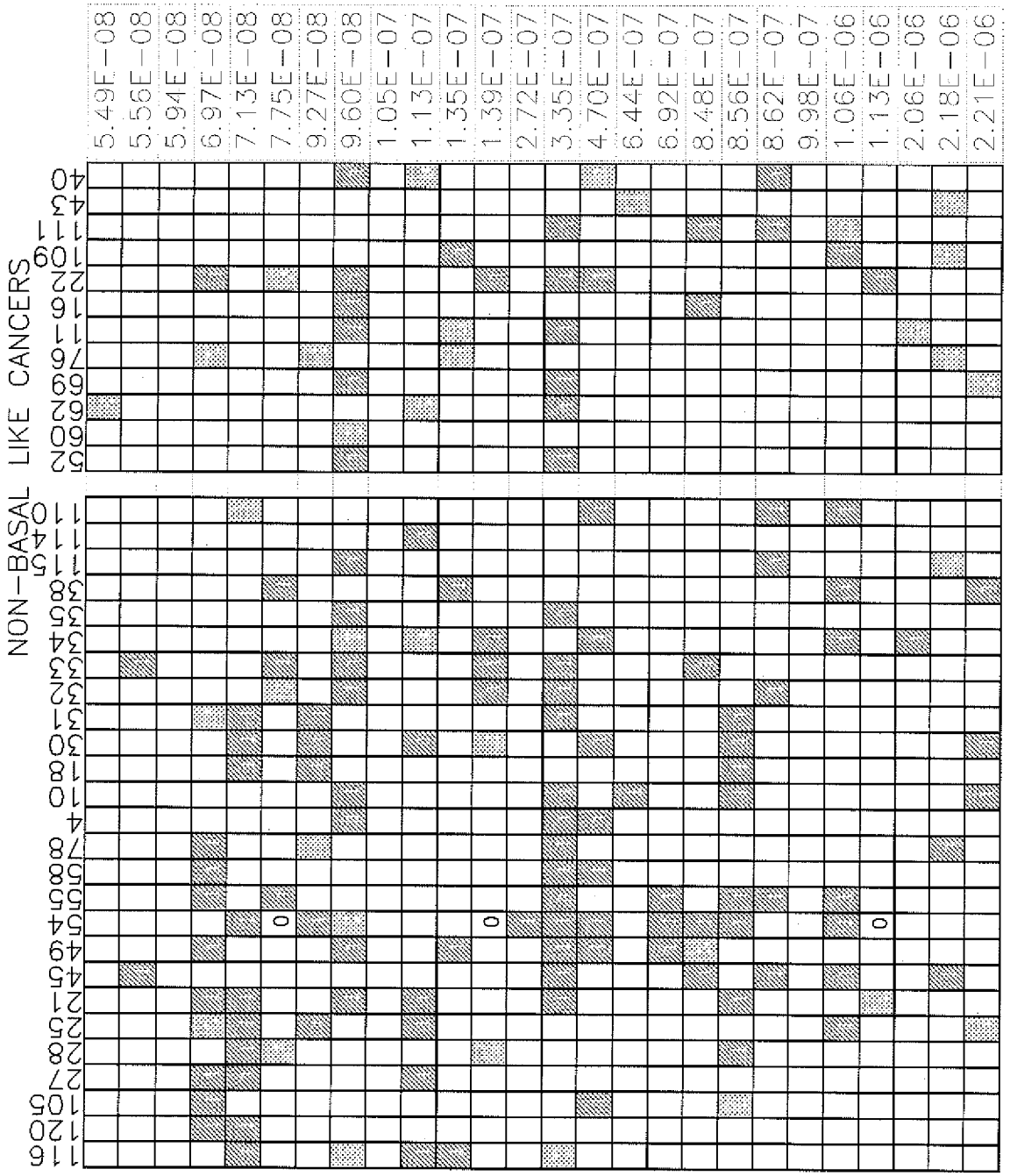

NON-BASAL LIKE CANCERS
5.49E-08
5.56E-08
5.94E-08
6.97E-08
7.13E-08
7.75E-08
9.27E-08
9.60E-08
1.05E-07
1.13E-07
1.35E-07
1.39E-07
2.72E-07
3.35E-07
4.70E-07
6.44E-07
6.92E-07
8.48E-07
8.56E-07
8.62E-07
9.98E-07
1.06E-06
1.13E-06
2.06E-06
2.18E-06
2.21E-06

FIG. 25 73

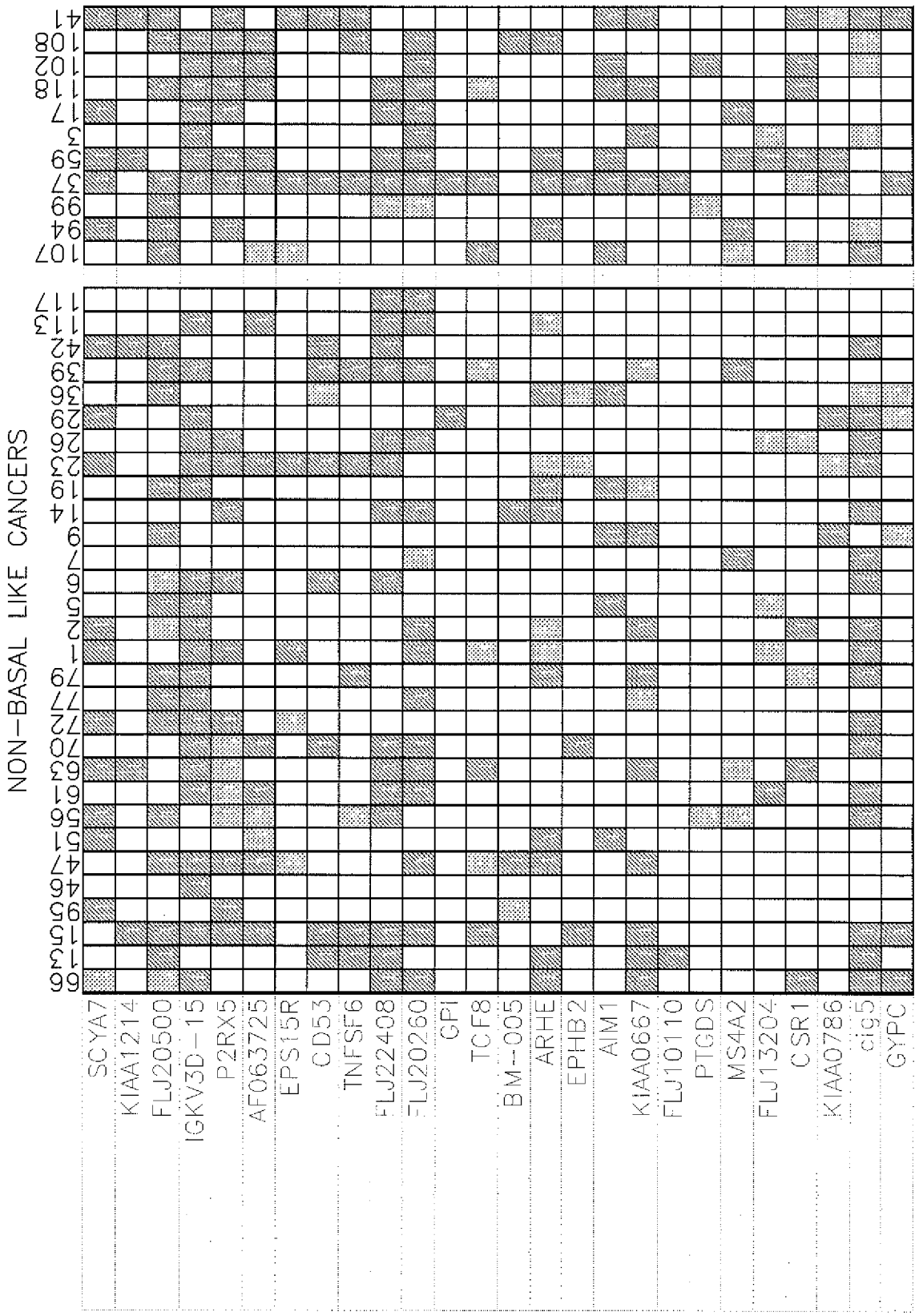

CONTINUED ON SHEET 75
NON-BASAL LIKE CANCERS
SCYA7
KIAA1214
FLJ20500
IGKV3D-15
P2RX5
AF063725
EPS15R
CD53
TNFSF6
FLJ22408
FLJ20260
GPI
TCF8
BM-005
ARHE
EPHB2
AIM1
KIAA0667
FLJ10110
PTGDS
MS4A2
FLJ13204
CSR1
KIAA0786
cig5
GYPC

FIG. 25 74

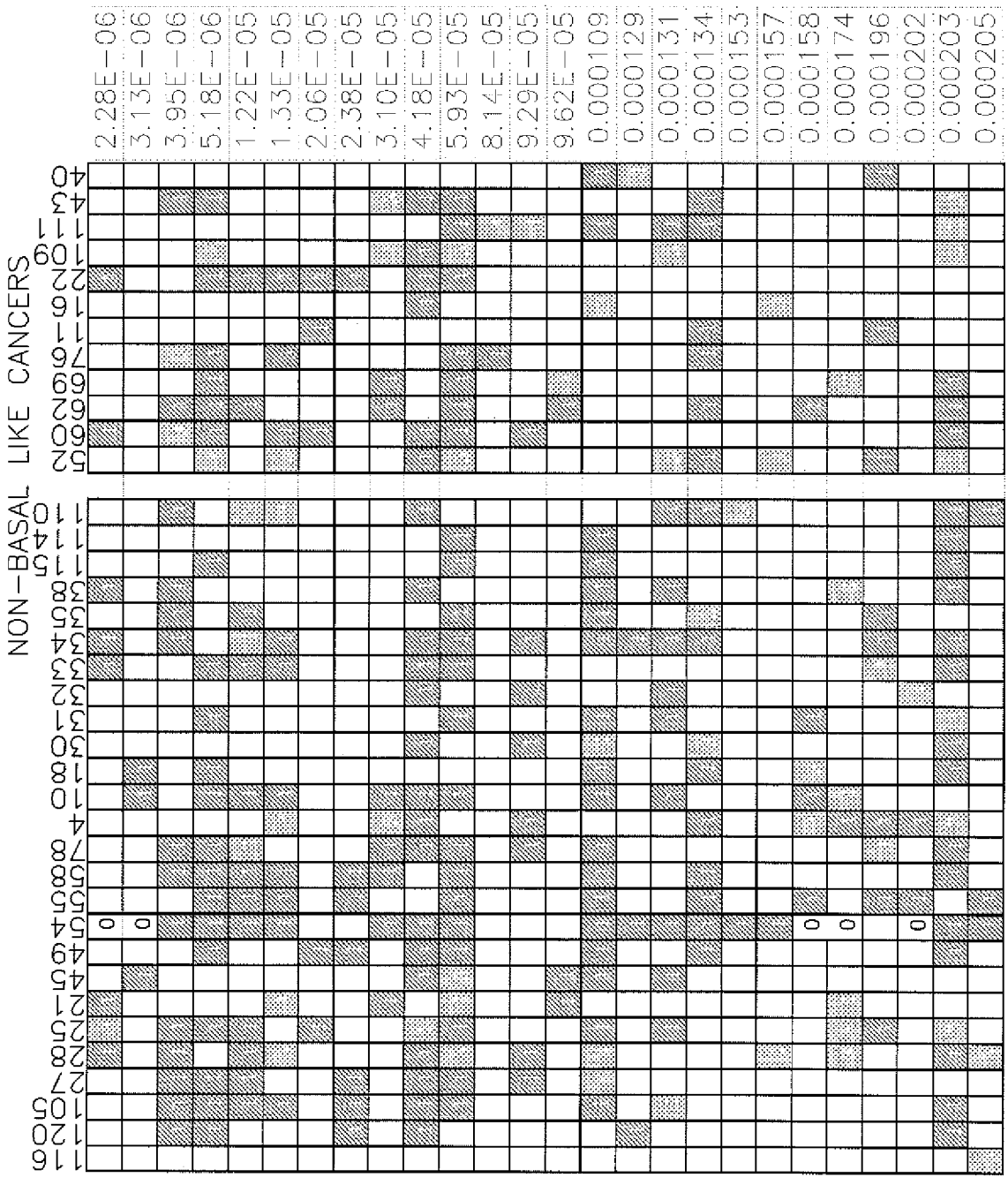

NON−BASAL LIKE CANCERS
LIKE CANCERS
2.28E−06
3.13E−06
3.95E−06
5.18E−06
1.22E−05
1.33E−05
2.06E−05
2.38E−05
3.10E−05
4.18E−05
5.93E−05
8.14E−05
9.29E−05
9.62E−05
0.000109
0.000129
0.000131
0.000134
0.000153
0.000157
0.000158
0.000174
0.000196
0.000202
0.000203
0.000205

FIG. 25

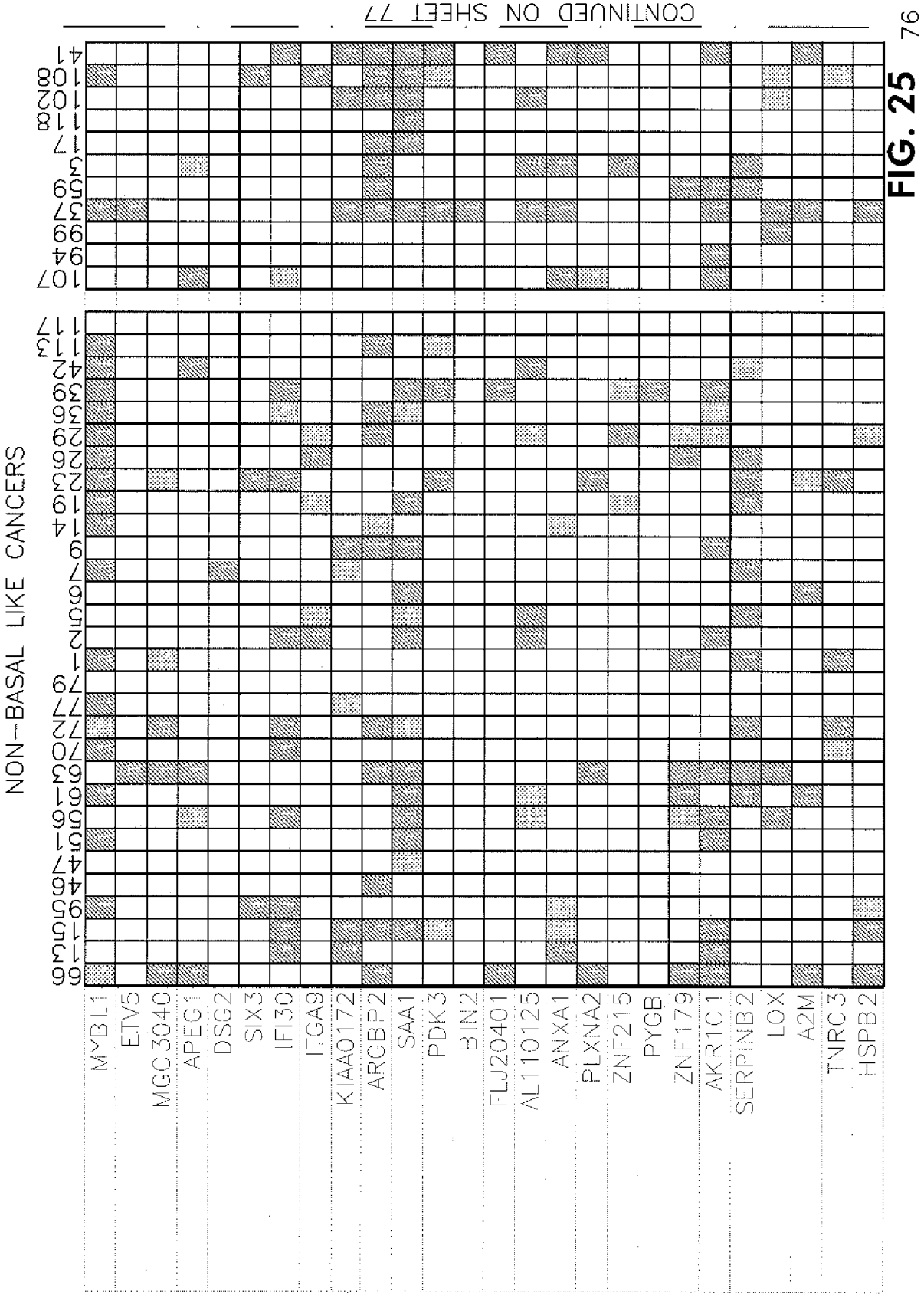

CONTINUED ON SHEET 77
NON-BASAL LIKE CANCERS
MYBL1
ETV5
MGC3040
APEG1
DSG2
SIX3
IFI30
ITGA9
KIAA0172
ARGBP2
SAA1
PDK3
BIN2
FLJ20401
AL110125
ANXA1
PLXNA2
ZNF215
PYGB
ZNF179
AKR1C1
SERPINB2
LOX
A2M
TNRC3
HSPB2

FIG. 25

76

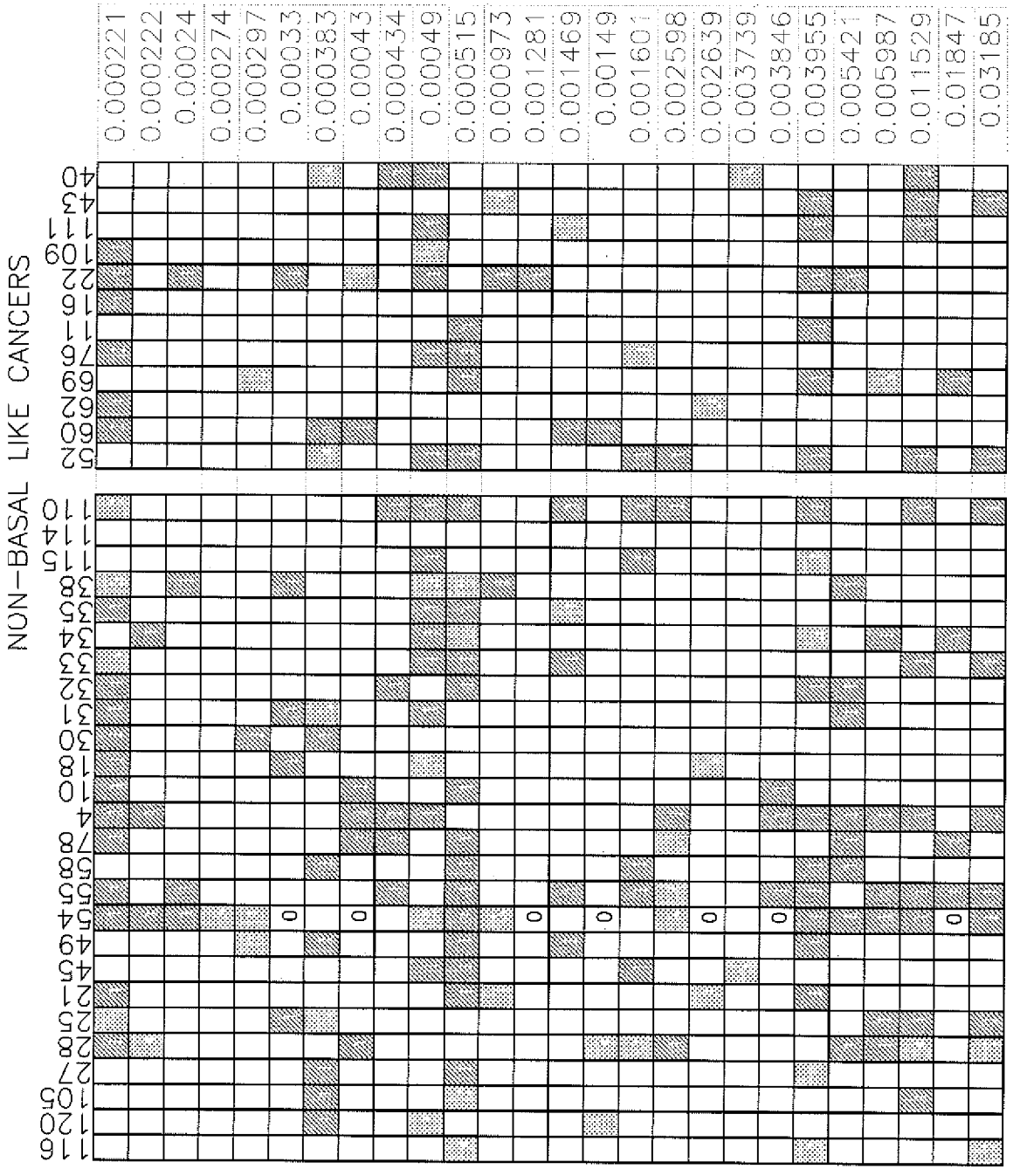

NON-BASAL LIKE CANCERS
0.000221
0.000222
0.00024
0.000274
0.000297
0.00033
0.000383
0.00043
0.000434
0.00049
0.000515
0.000973
0.001281
0.001469
0.00149
0.001601
0.002598
0.002639
0.003739
0.003846
0.003955
0.005421
0.005987
0.011529
0.01847
0.03185

FIG. 25 77

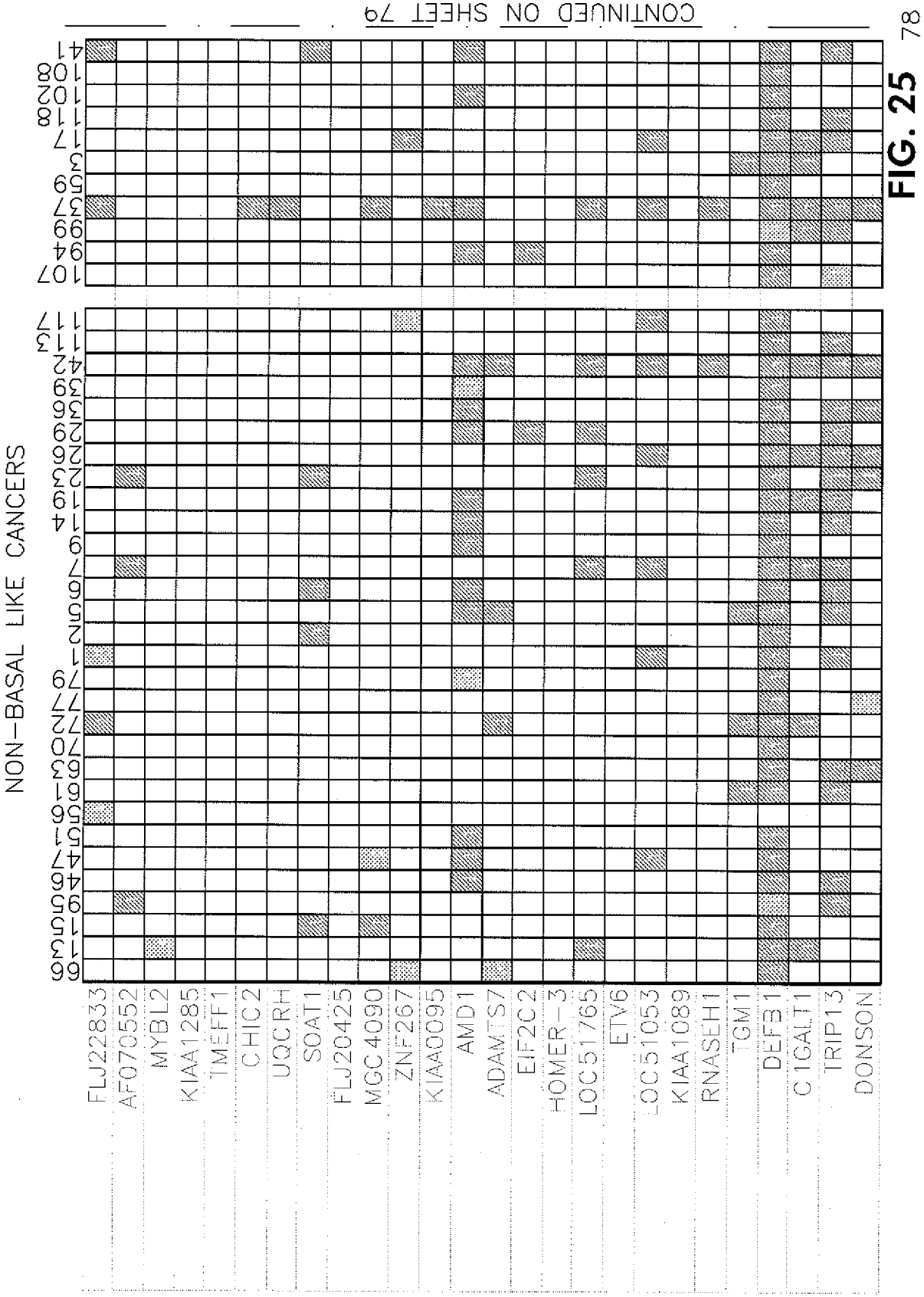

CONTINUED ON SHEET 79
NON-BASAL LIKE CANCERS
FLJ22833
AF070552
MYBL2
KIAA1285
TMEFF1
CHIC2
UQCRH
SOAT1
FLJ20425
MGC4090
ZNF267
KIAA0095
AMD1
ADAMTS7
EIF2C2
HOMER-3
LOC51765
ETV6
LOC51053
KIAA1089
RNASEH1
TGM1
DEFB1
C1GALT1
TRIP13
DONSON

FIG. 25

78

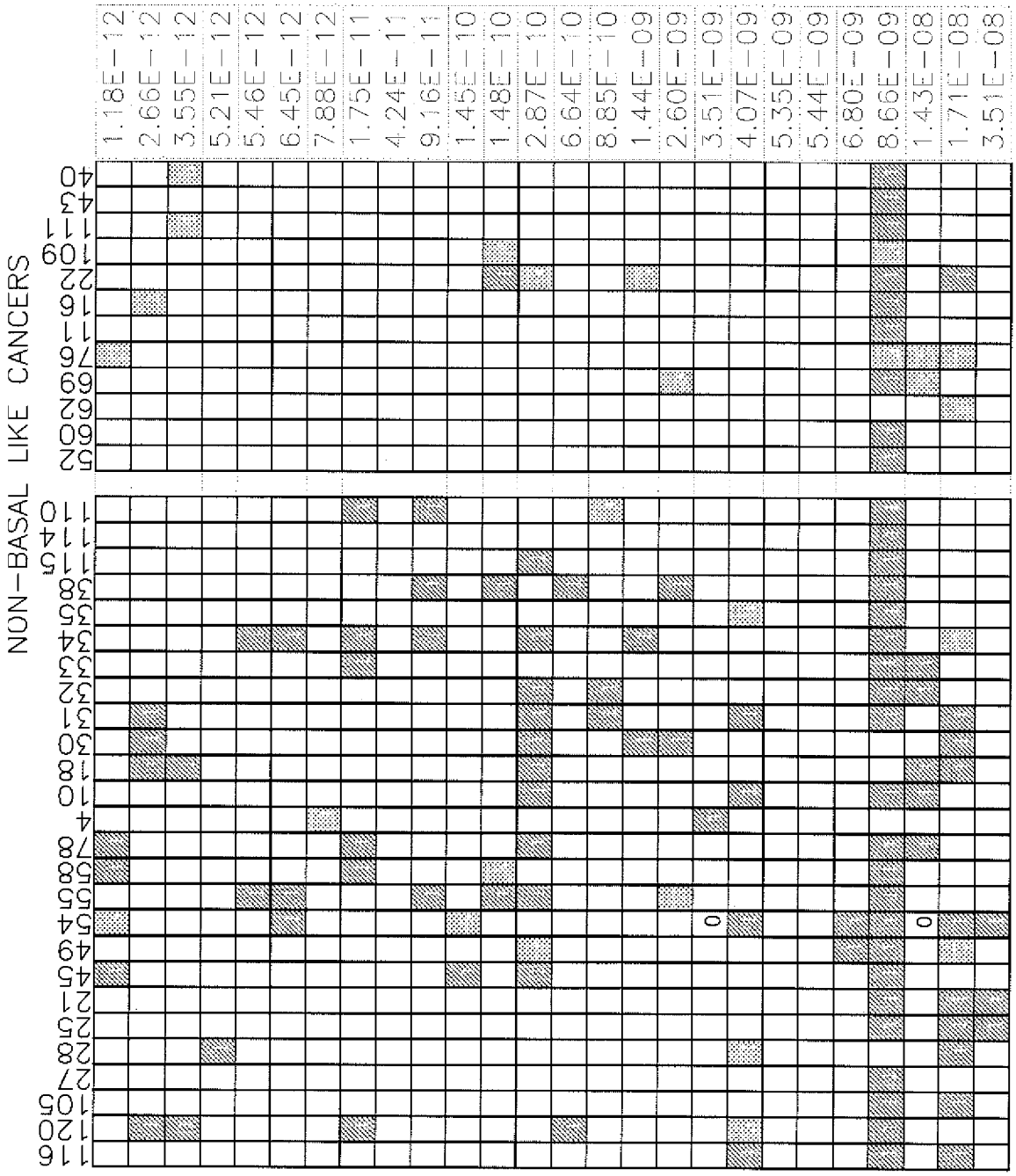

NON−BASAL LIKE CANCERS
1.18E−12
2.66E−12
3.55E−12
5.21E−12
5.46E−12
6.45E−12
7.88E−12
1.75E−11
4.24E−11
9.16E−11
1.45E−10
1.48E−10
2.87E−10
6.64E−10
8.85E−10
1.44E−09
2.60E−09
3.51E−09
4.07E−09
5.35E−09
5.44E−09
6.80E−09
8.66E−09
1.43E−08
1.71E−08
3.51E−08

FIG. 25

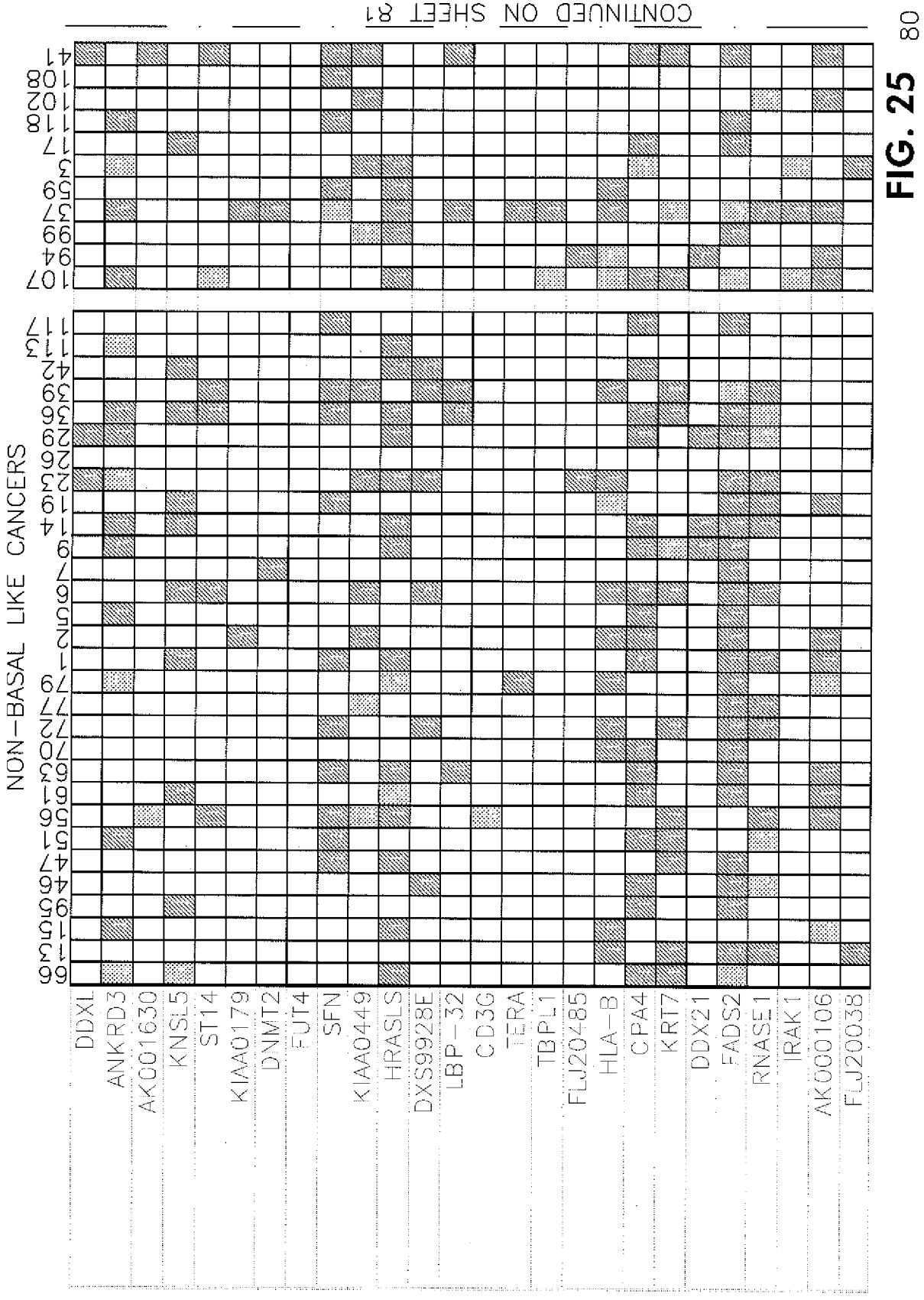

CONTINUED ON SHEET 81
NON-BASAL LIKE CANCERS
DDX1
ANKRD3
AK001630
KNSL5
ST14
KIAA0179
DNMT2
FUT4
SFN
KIAA0449
HRASLS
DXS9928E
LBP-32
CD3G
TERA
TBPL1
FLJ20485
HLA-B
CPA4
KRT7
DDX21
FADS2
RNASE1
IRAK1
AK000106
FLJ20038

FIG. 25 80

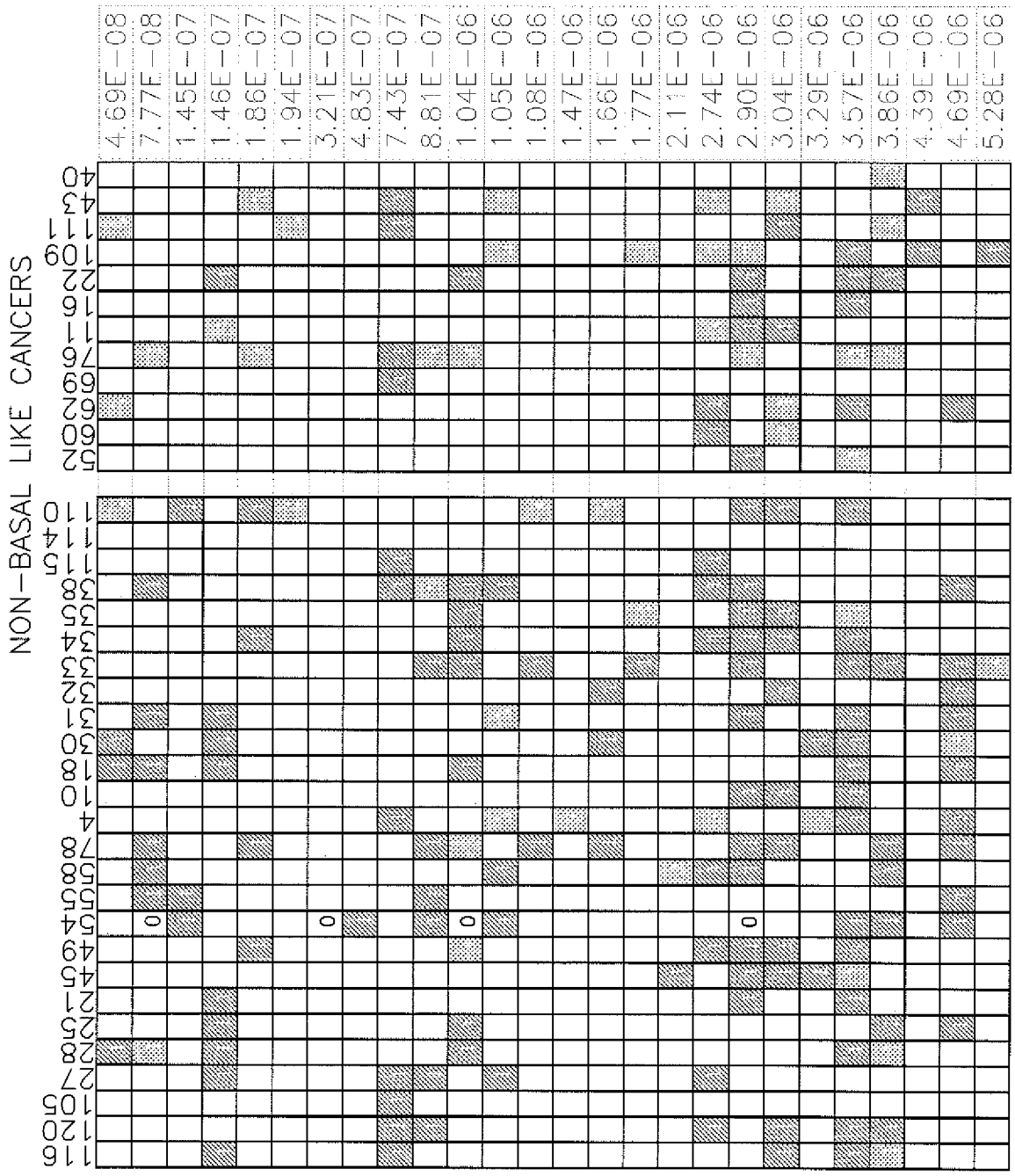

NON−BASAL LIKE CANCERS
4.69E−08
7.77E−08
1.45E−07
1.46E−07
1.86E−07
1.94E−07
3.21E−07
4.83E−07
7.43E−07
8.81E−07
1.04E−06
1.05E−06
1.08E−06
1.47E−06
1.66E−06
1.77E−06
2.11E−06
2.74E−06
2.90E−06
3.04E−06
3.29E−06
3.57E−06
3.86E−06
4.39E−06
4.69E−06
5.28E−06

FIG. 25 81

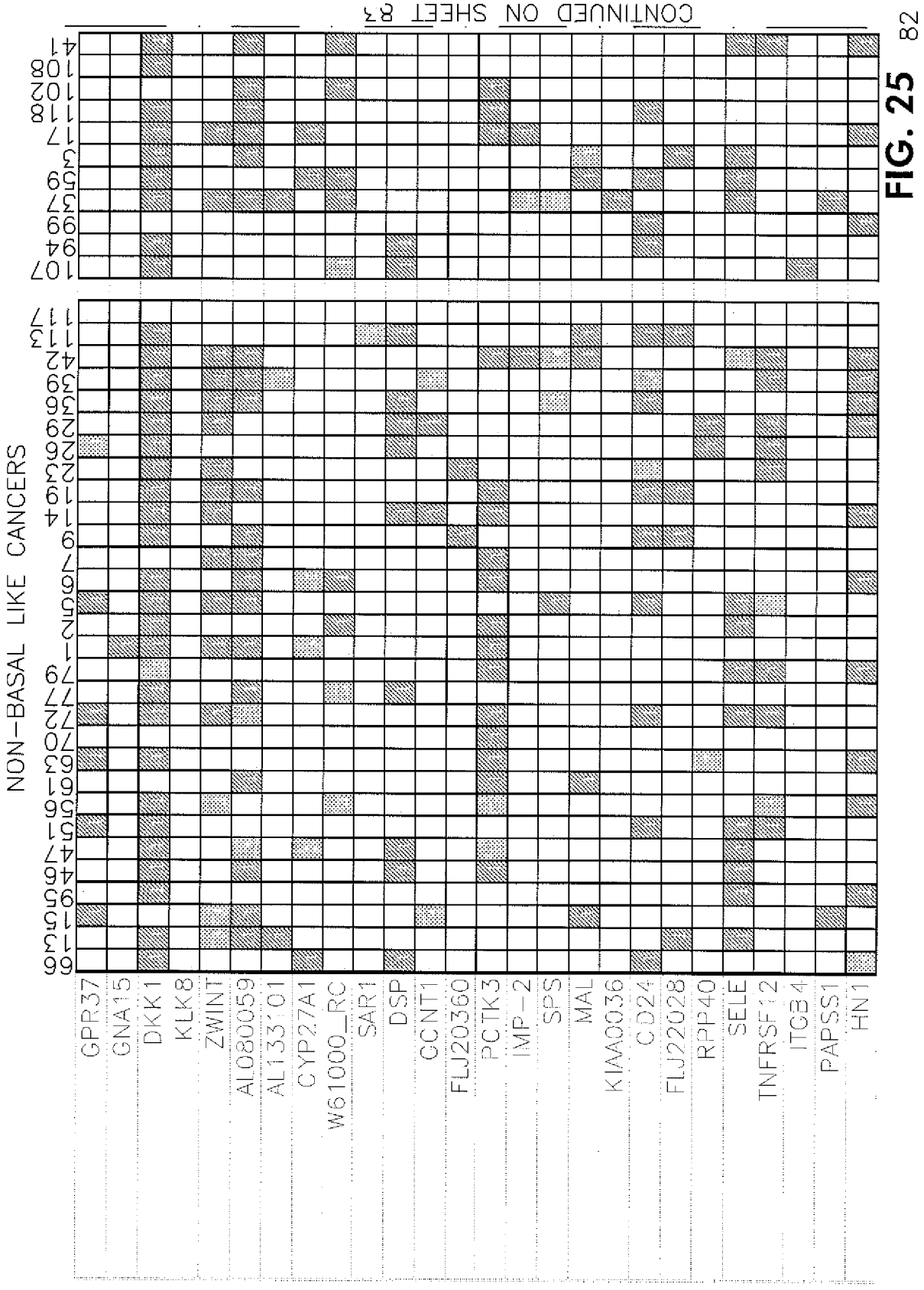

CONTINUED ON SHEET 83
NON-BASAL LIKE CANCERS
GPR37
GNA15
DKK1
KLK8
ZWINT
AL080059
AL133'01
CYP27A1
W61000_RC
SAR1
DSP
CCNT1
FLJ20360
PCTK3
IMP-2
SPS
MAL
KIAA0036
CD24
FLJ22028
RPP40
SELE
TNFRSF12
ITGB4
PAPSS1
HN1

FIG. 25 82

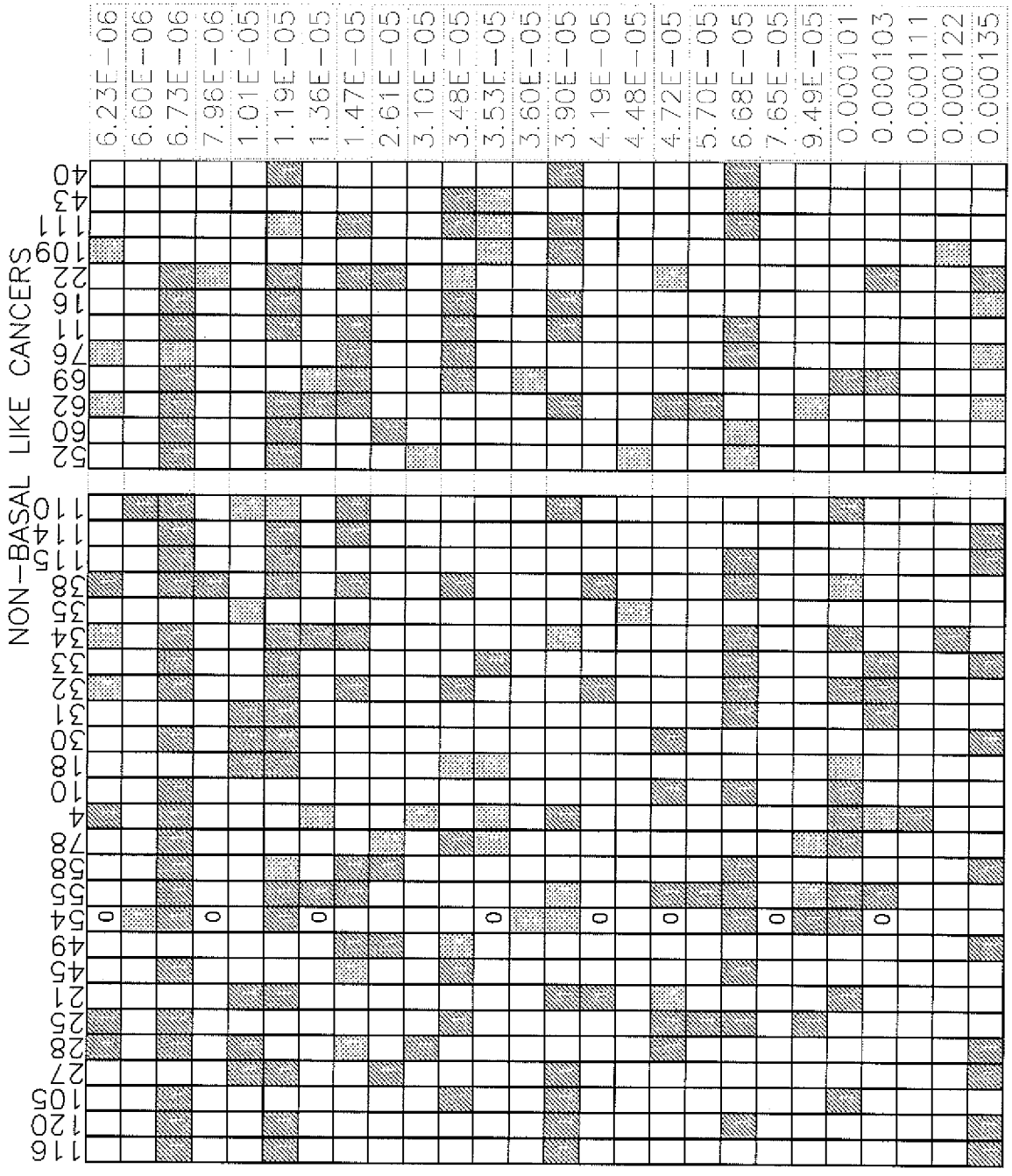

NON-BASAL LIKE CANCERS
116 120 105 27 228 225 21 245 249 254 255 258 78 4 210 230 231 232 234 235 238 115 114 110
52 60 62 69 76 11 16 22 109 111 43 40
6.23E-06
6.60E-06
6.73E-06
7.96E-06
1.01E-05
1.19E-05
1.36E-05
1.47E-05
2.61E-05
3.10E-05
3.48E-05
3.53E-05
3.60E-05
3.90E-05
4.19E-05
4.48E-05
4.72E-05
5.70E-05
6.68E-05
7.65E-05
9.49E-05
0.000101
0.000103
0.000111
0.000122
0.000135

FIG. 25 83

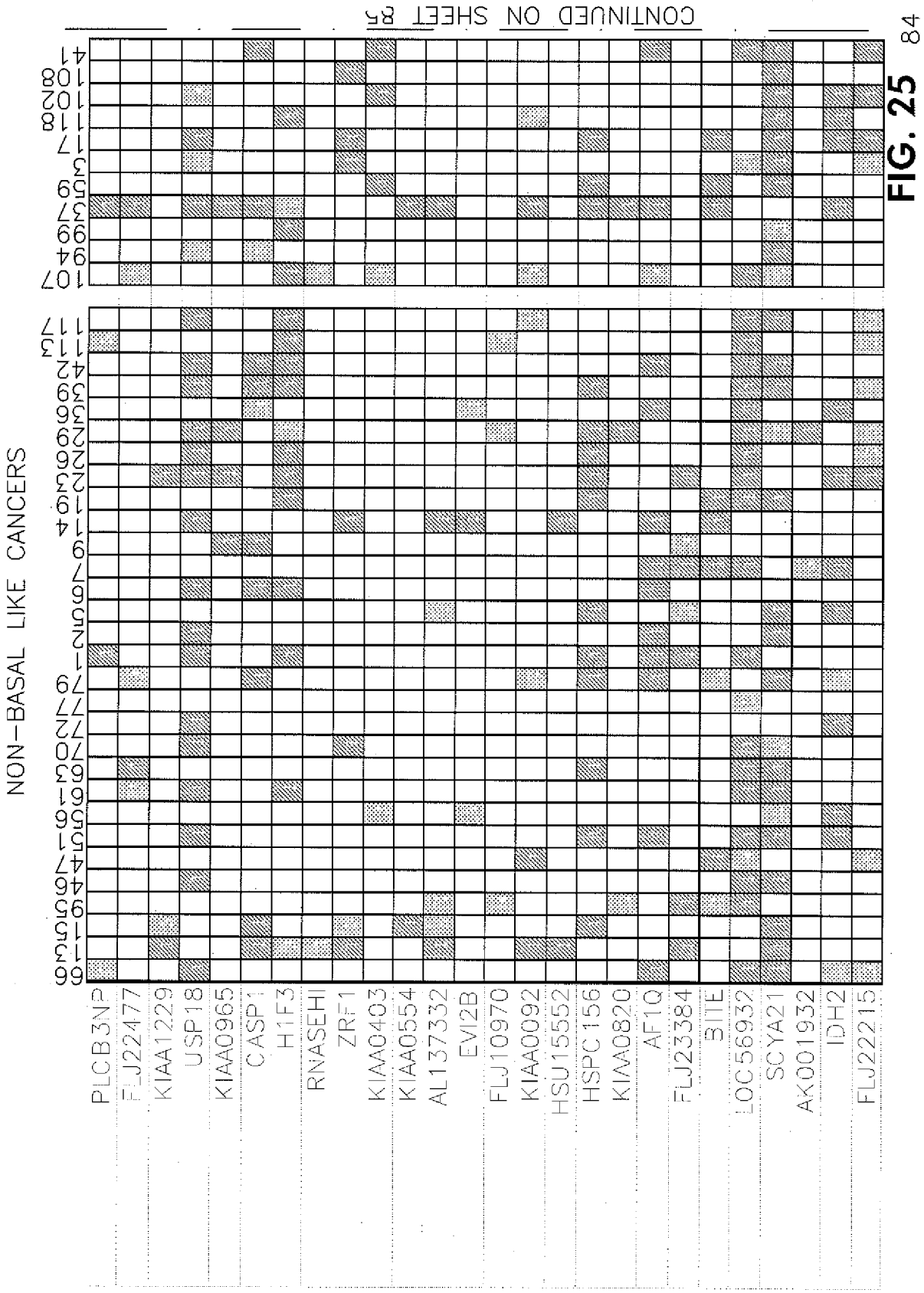

CONTINUED ON SHEET 85
NON-BASAL LIKE CANCERS
PLCB3NP
FLJ22477
KIAA1229
USP18
KIAA0965
CASP1
H1F3
RNASEHI
ZRF1
KIAA0403
KIAA0554
AL137332
EVI2B
FLJ10970
KIAA0092
HSU15552
HSPC156
KIAA0820
AF1Q
FLJ23384
BIIE
LOC56932
SCYA21
AK001932
IDH2
FLJ22215

FIG. 25

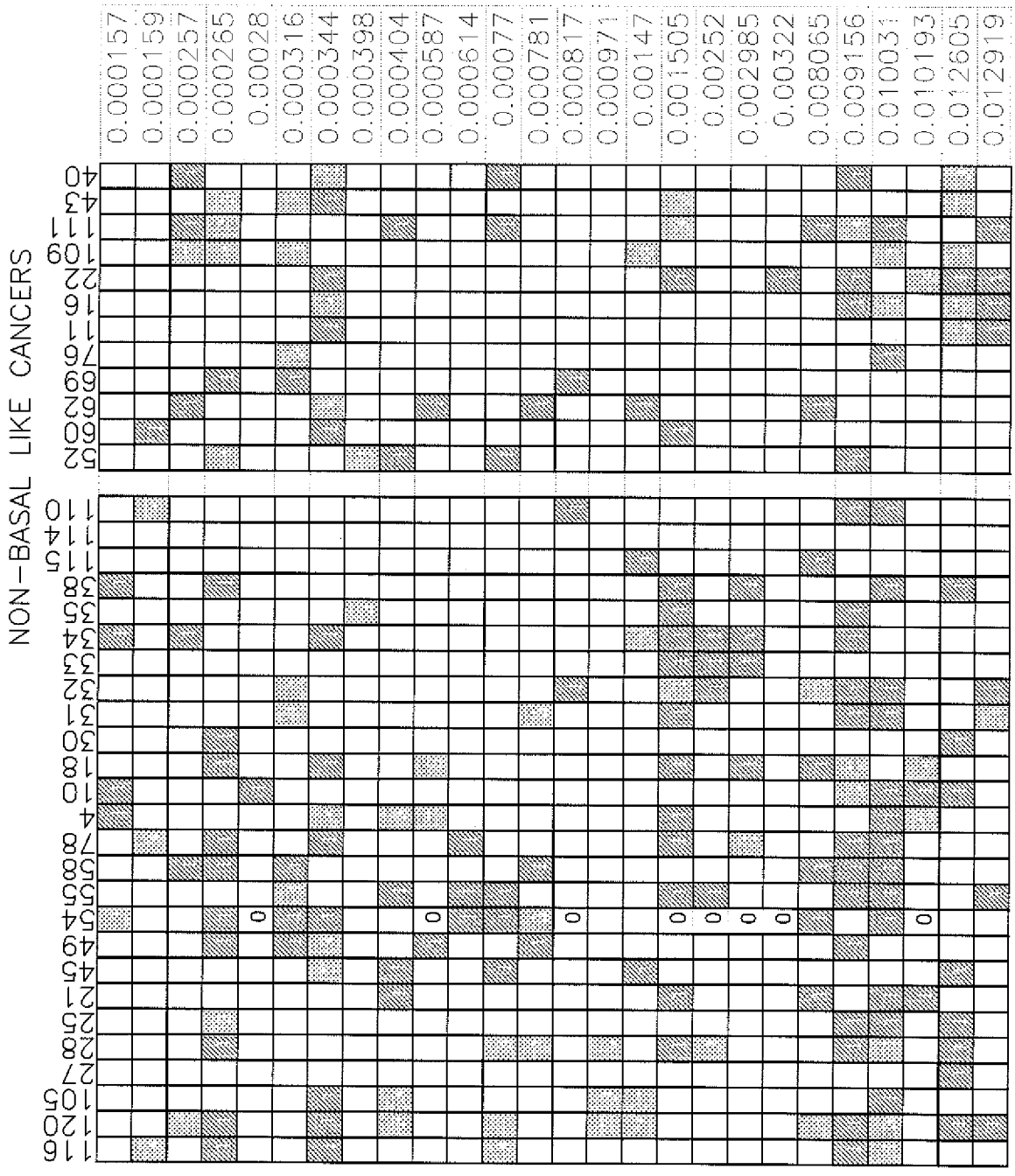

NON-BASAL LIKE CANCERS
0.000157
0.000159
0.000257
0.000265
0.00028
0.000316
0.000344
0.000398
0.000404
0.000587
0.000614
0.00077
0.000781
0.000817
0.000971
0.00147
0.001505
0.00252
0.002985
0.00322
0.008065
0.009156
0.010031
0.010193
0.012605
0.012919

FIG. 25

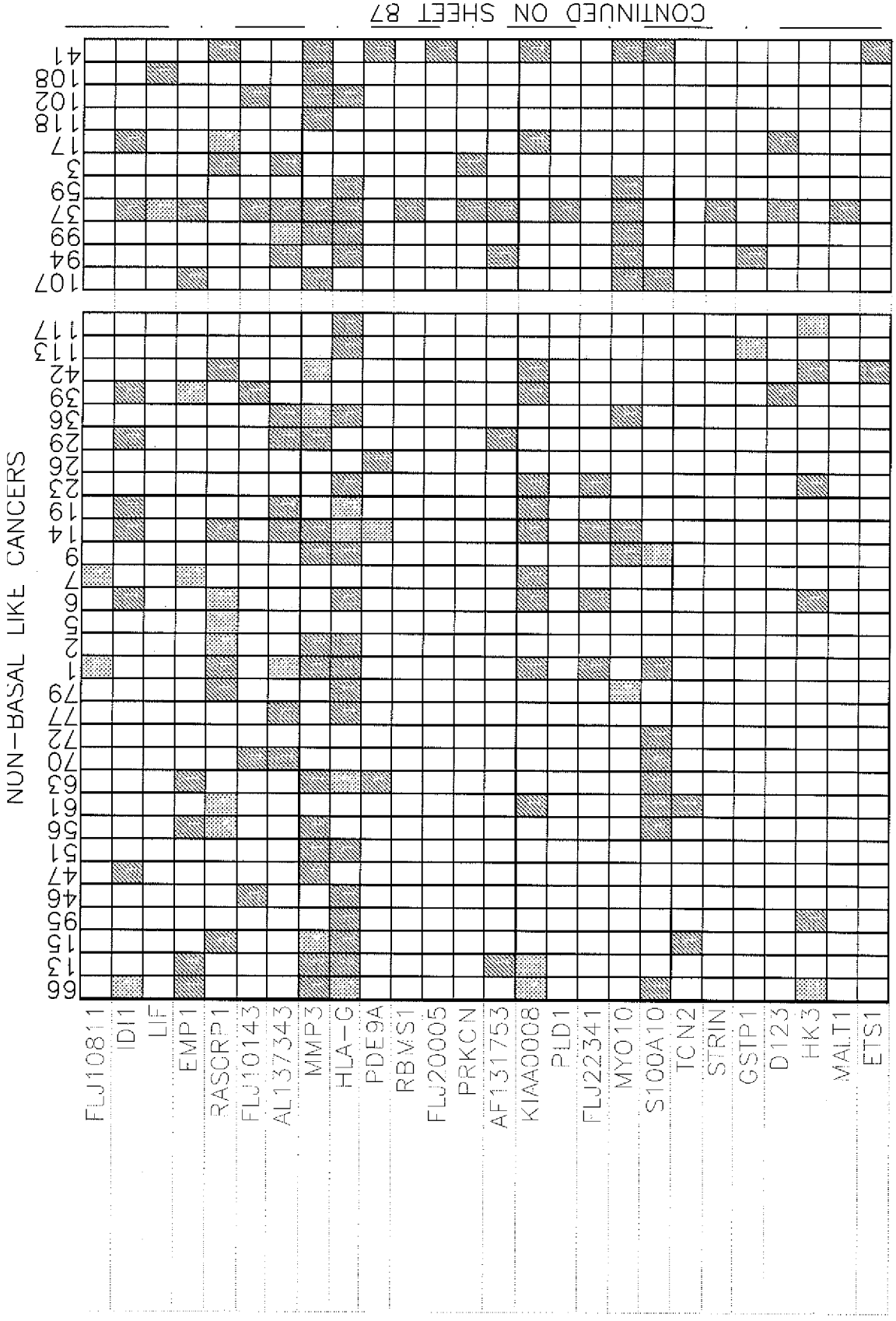

CONTINUED ON SHEET 87
NON-BASAL LIKE CANCERS
FLJ10811
IDI1
LIF
EMP1
RASGRP1
FLJ10143
AL137343
MMP3
HLA-G
PDE9A
RBMS1
FLJ20005
PRKCN
AF131753
KIAA0008
PLD1
FLJ22341
MYO10
S100A10
TCN2
STRN
GSTP1
D123
HK3
MALT1
ETS1

FIG. 25

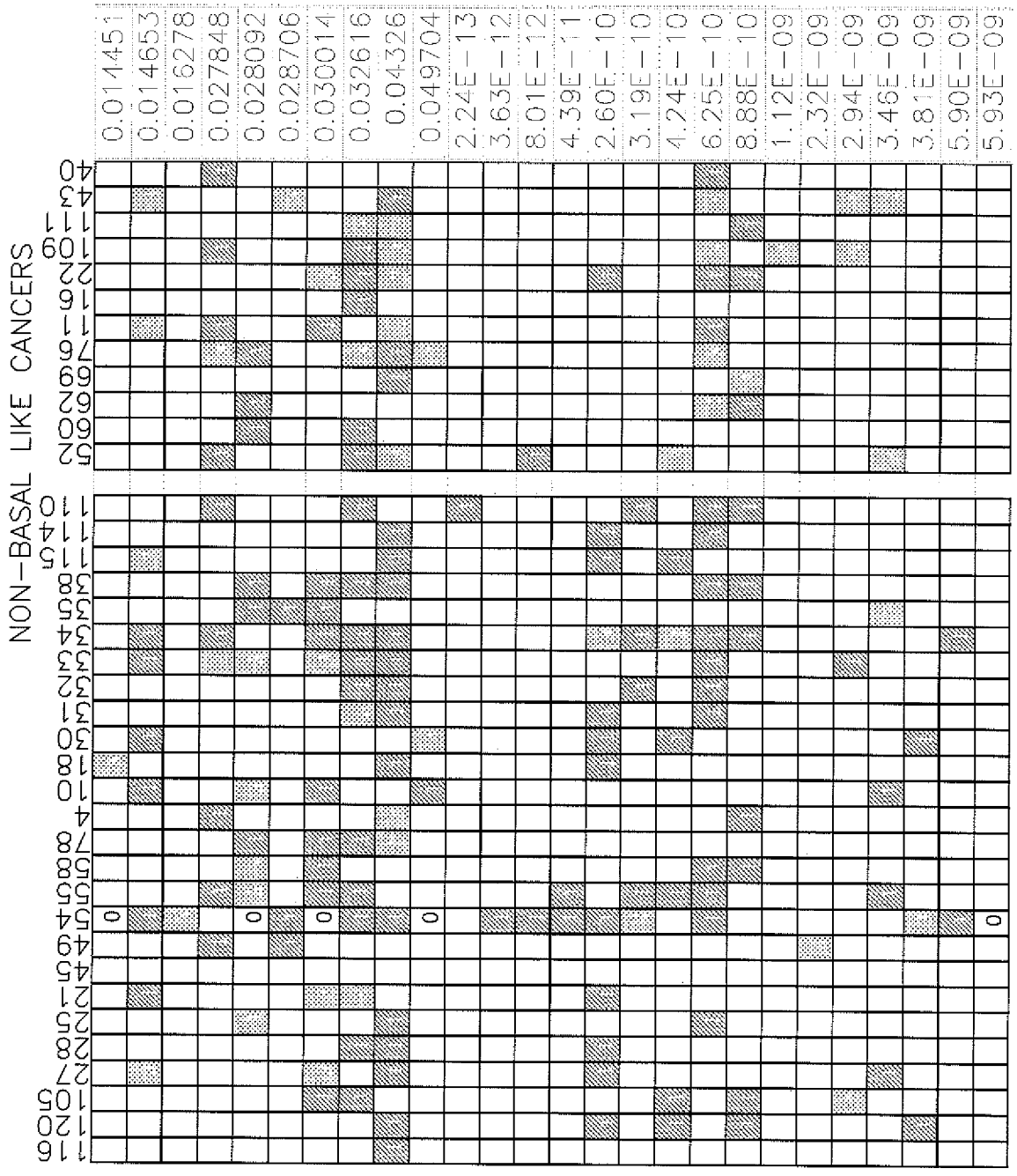

NON−BASAL LIKE CANCERS
0.014451
0.014653
0.016278
0.027848
0.028092
0.028706
0.030014
0.032616
0.04326
0.049704
2.24E−13
3.63E−12
8.01E−12
4.39E−11
2.60E−10
3.19E−10
4.24E−10
6.25E−10
8.88E−10
1.12E−09
2.32E−09
2.94E−09
3.46E−09
3.81E−09
5.90E−09
5.93E−09

FIG. 25 87

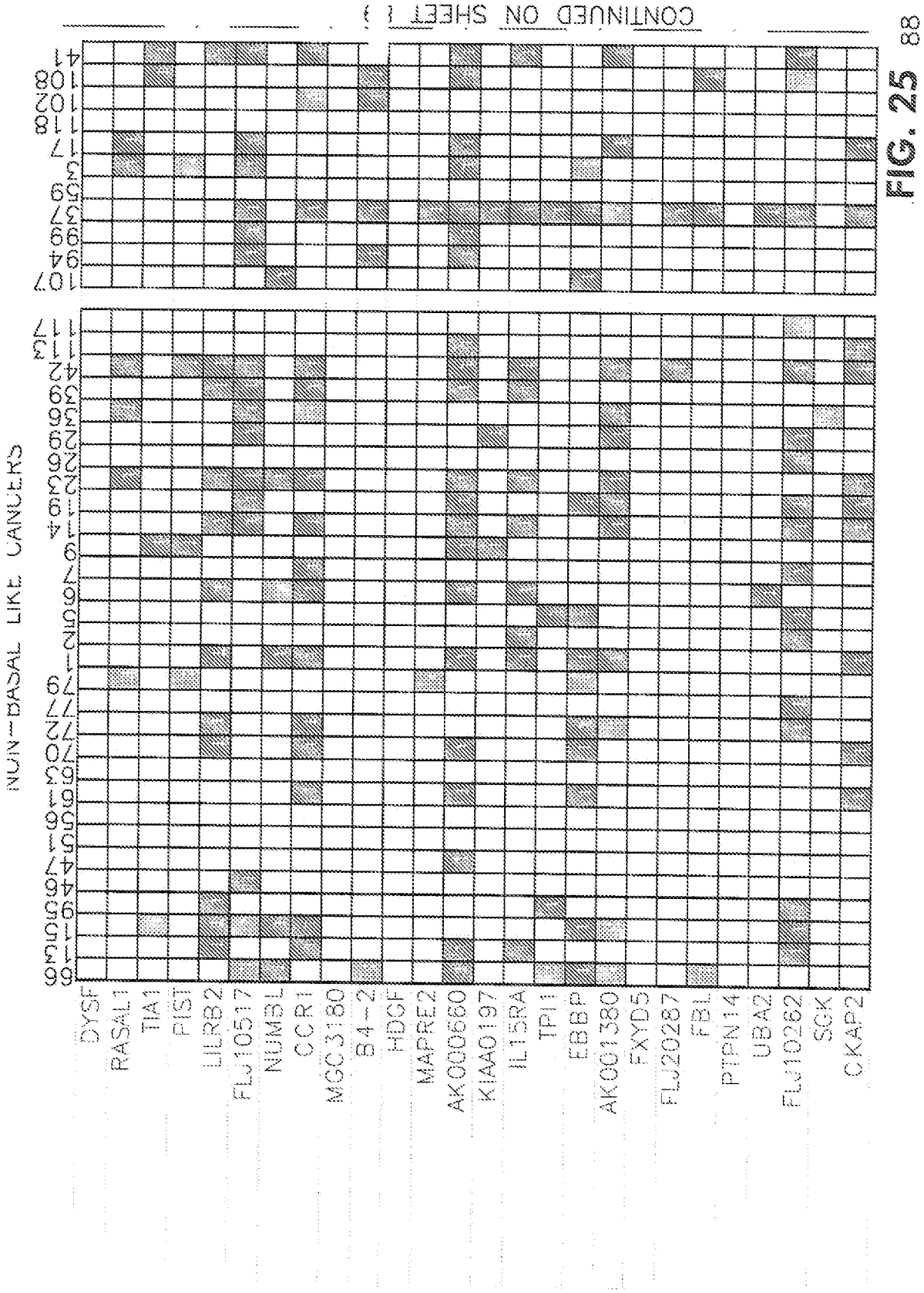

CONTINUED ON SHEET 89
NON-BASAL LIKE CANCERS
DYSF
RASAL1
TIA1
PIST
LILRB2
FLJ10517
NUMBL
CCR1
MGC3180
B4-2
HDGF
MAPRE2
AK000660
KIAA0197
IL15RA
TPI1
EBBP
AK001380
FXYD5
FLJ20287
FBL
PTPN14
UBA2
FLJ10262
SGK
CKAP2

FIG. 25 88

NON-BASAL LIKE CANCERS
6.07E-09
7.50E-09
7.84E-09
8.06E-09
9.91E-09
1.04E-08
1.17E-08
1.23E-08
1.36E-08
1.46E-08
1.52E-08
1.96E-08
2.70E-08
2.95E-08
2.95E-08
3.92E-08
4.26E-08
5.07E-08
5.33E-08
7.09E-08
7.11E-08
7.16E-08
7.76E-08
8.10E-08
1.06E-07
1.27E-07

FIG. 25

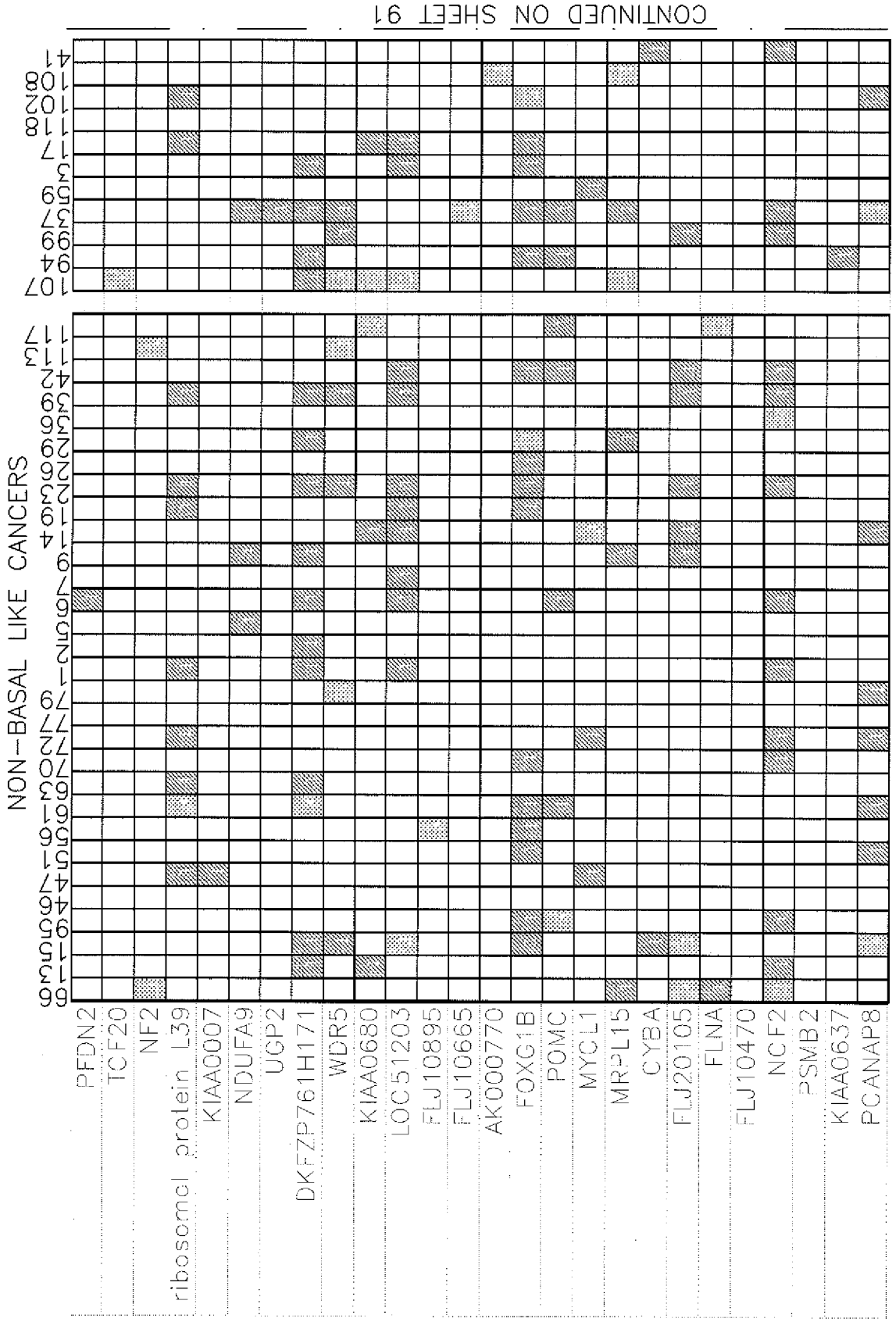

NON-BASAL LIKE CANCERS
PFDN2
TCF20
NF2
ribosomal protein L39
KIAA0007
NDUFA9
UGP2
DKFZP761H171
WDR5
KIAA0680
LOC51203
FLJ10895
FLJ10665
AK000770
FOXG1B
POMC
MYCL1
MRPL15
CYBA
FLJ20105
FLNA
FLJ10470
NCF2
PSMB2
KIAA0637
PCANAP8
CONTINUED ON SHEET 91

FIG. 25 90

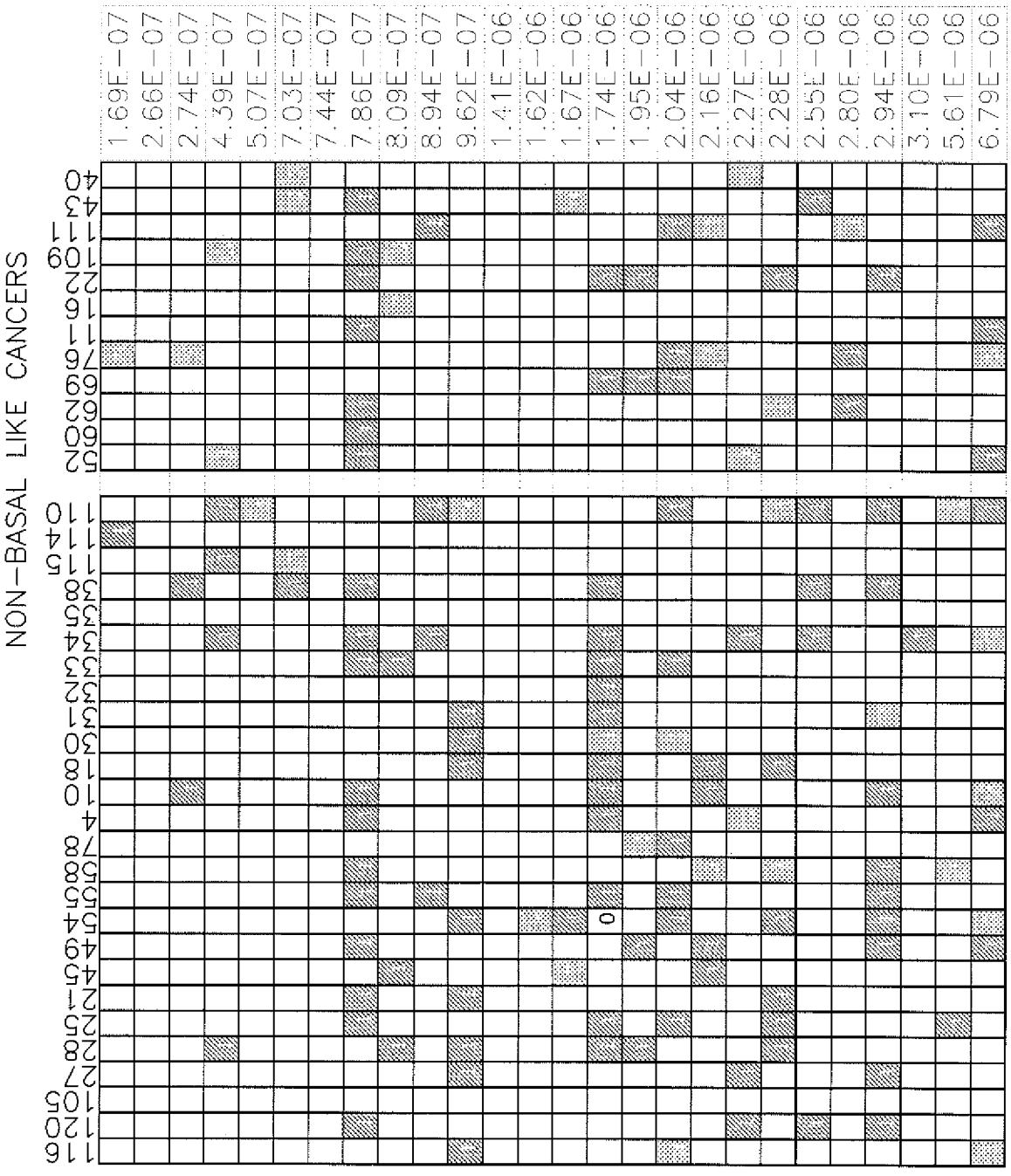

NON−BASAL LIKE CANCERS
1.69E−07
2.66E−07
2.74E−07
4.39E−07
5.07E−07
7.03E−07
7.44E−07
7.86E−07
8.09E−07
8.94E−07
9.62E−07
1.41E−06
1.62E−06
1.67E−06
1.74E−06
1.95E−06
2.04E−06
2.16E−06
2.27E−06
2.28E−06
2.55E−06
2.80E−06
2.94E−06
3.10E−06
5.61E−06
6.79E−06

FIG. 25 91

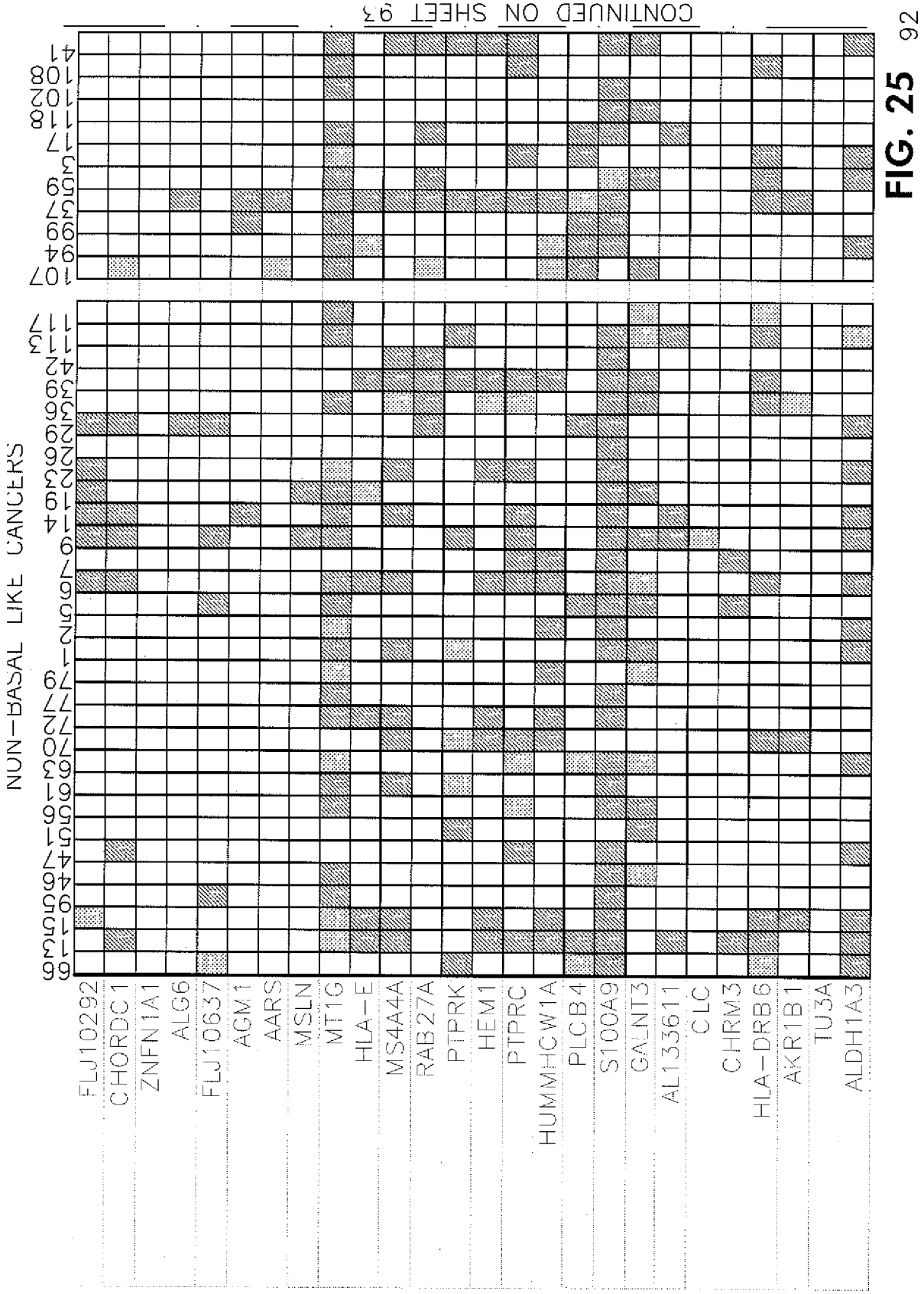

CONTINUED ON SHEET 93
NON-BASAL LIKE CANCERS
FLJ10292
CHORDC1
ZNFN1A1
ALG6
FLJ10637
AGM1
AARS
MSLN
MT1G
HLA-E
MS4A4A
RAB27A
PTPRK
HEM1
PTPRC
HUMMHCW1A
PLCB4
S100A9
GALNT3
AL133611
CLC
CHRM3
HLA-DRB6
AKR1B1
TU3A
ALDH1A3

FIG. 25 92

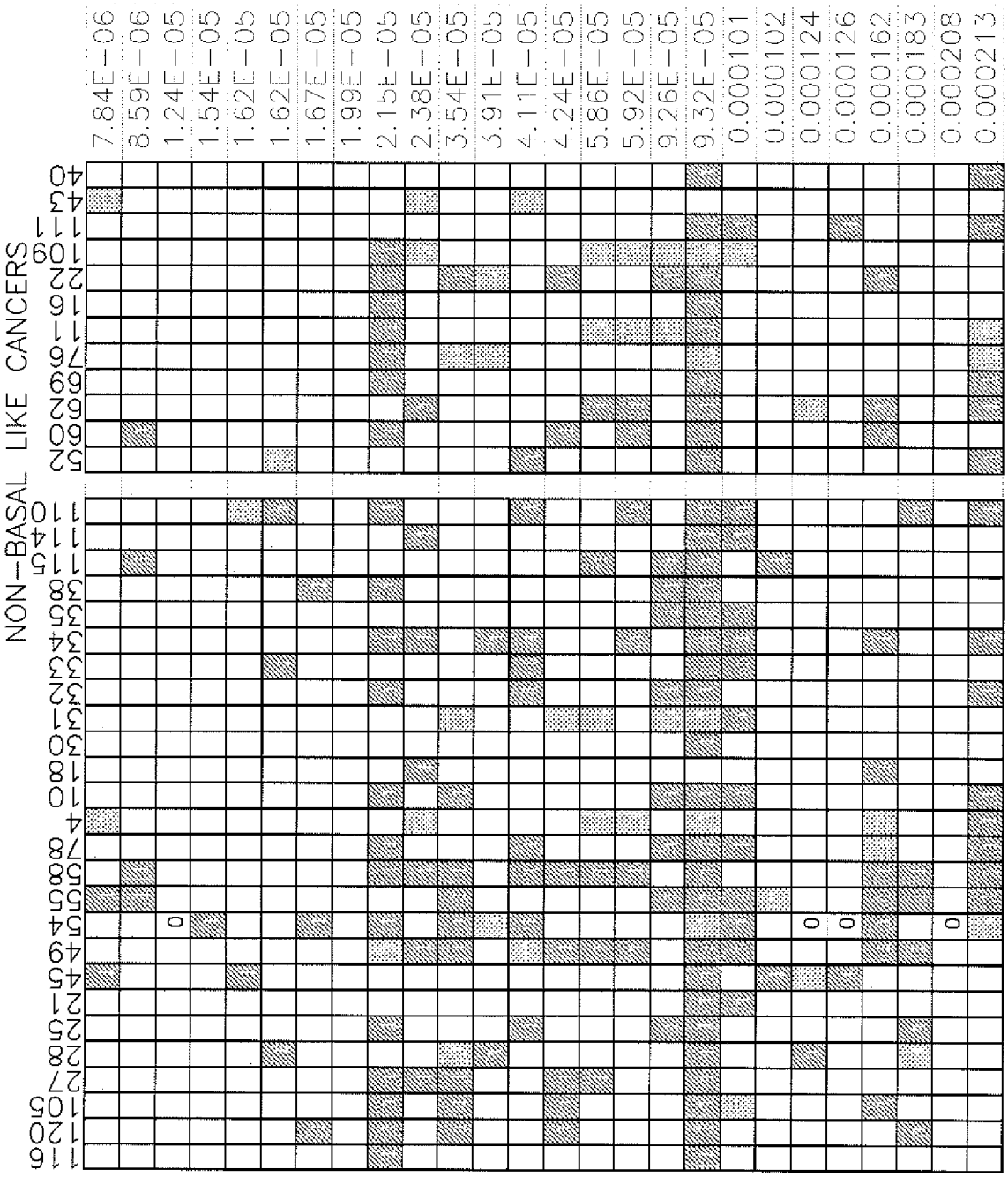

NON−BASAL LIKE CANCERS
7.84E−06
8.59E−06
1.24E−05
1.54E−05
1.62E−05
1.62E−05
1.67E−05
1.99E−05
2.15E−05
2.38E−05
3.54E−05
3.91E−05
4.11E−05
4.24E−05
5.86E−05
5.92E−05
9.26E−05
9.32E−05
0.000101
0.000102
0.000124
0.000126
0.000162
0.000183
0.000208
0.000213

FIG. 25 93

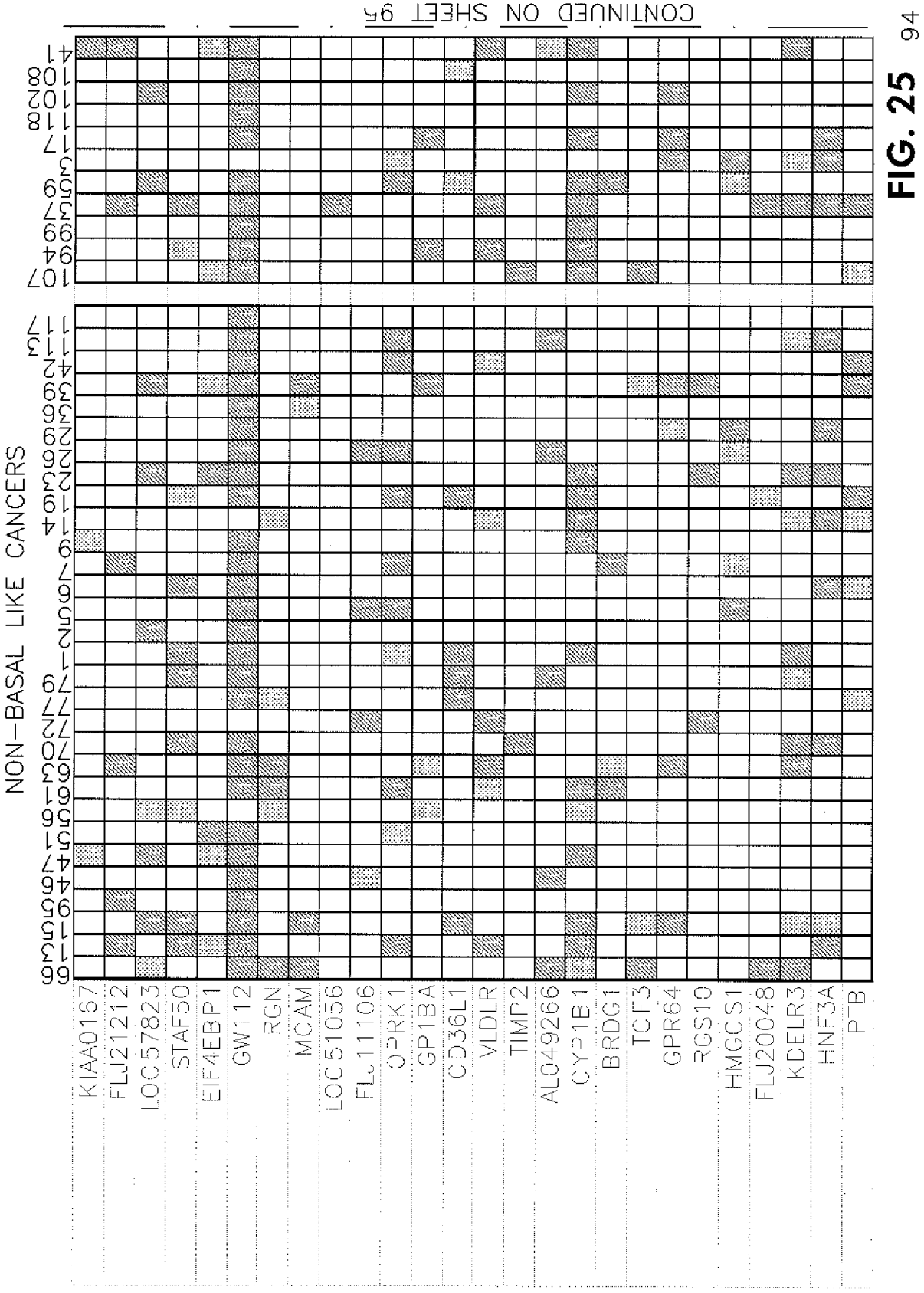

CONTINUED ON SHEET 95
NON-BASAL LIKE CANCERS
KIAA0167
FLJ21212
LOC57823
STAF50
EIF4EBP1
GW112
RGN
MCAM
LOC51056
FLJ11106
OPRK1
GP1BA
CD36L1
VLDLR
TIMP2
AL049266
CYP1B1
BRDG1
TCF3
GPR64
RGS10
HMGCS1
FLJ20048
KDELR3
HNF3A
PTB

FIG. 25 94

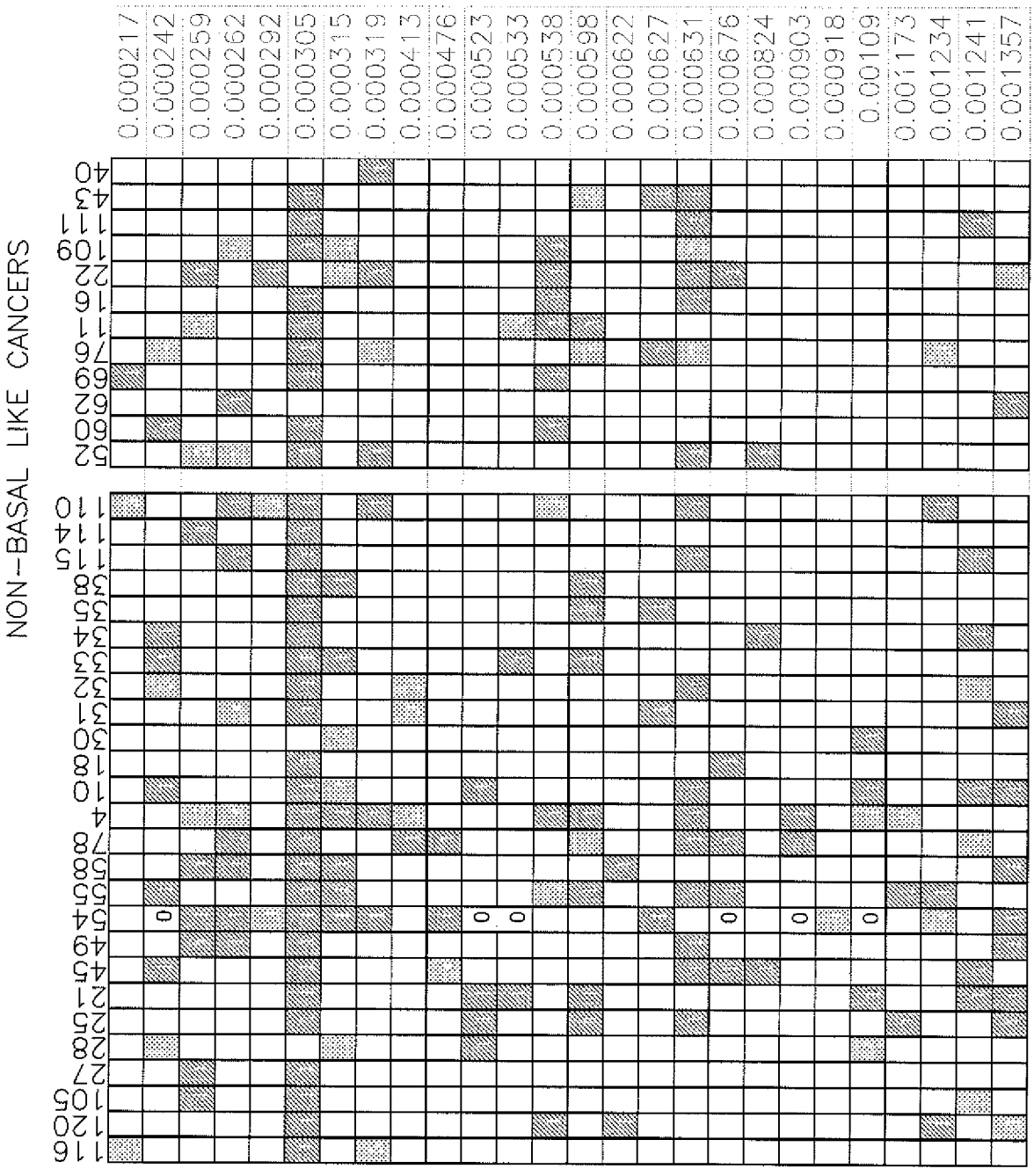

NON-BASAL LIKE CANCERS
0.000217
0.000242
0.000259
0.000262
0.000292
0.000305
0.000315
0.000319
0.000413
0.000476
0.000523
0.000533
0.000538
0.000598
0.000622
0.000627
0.000631
0.000676
0.000824
0.000903
0.000918
0.00109
0.001173
0.001234
0.001241
0.001357

FIG. 25 95

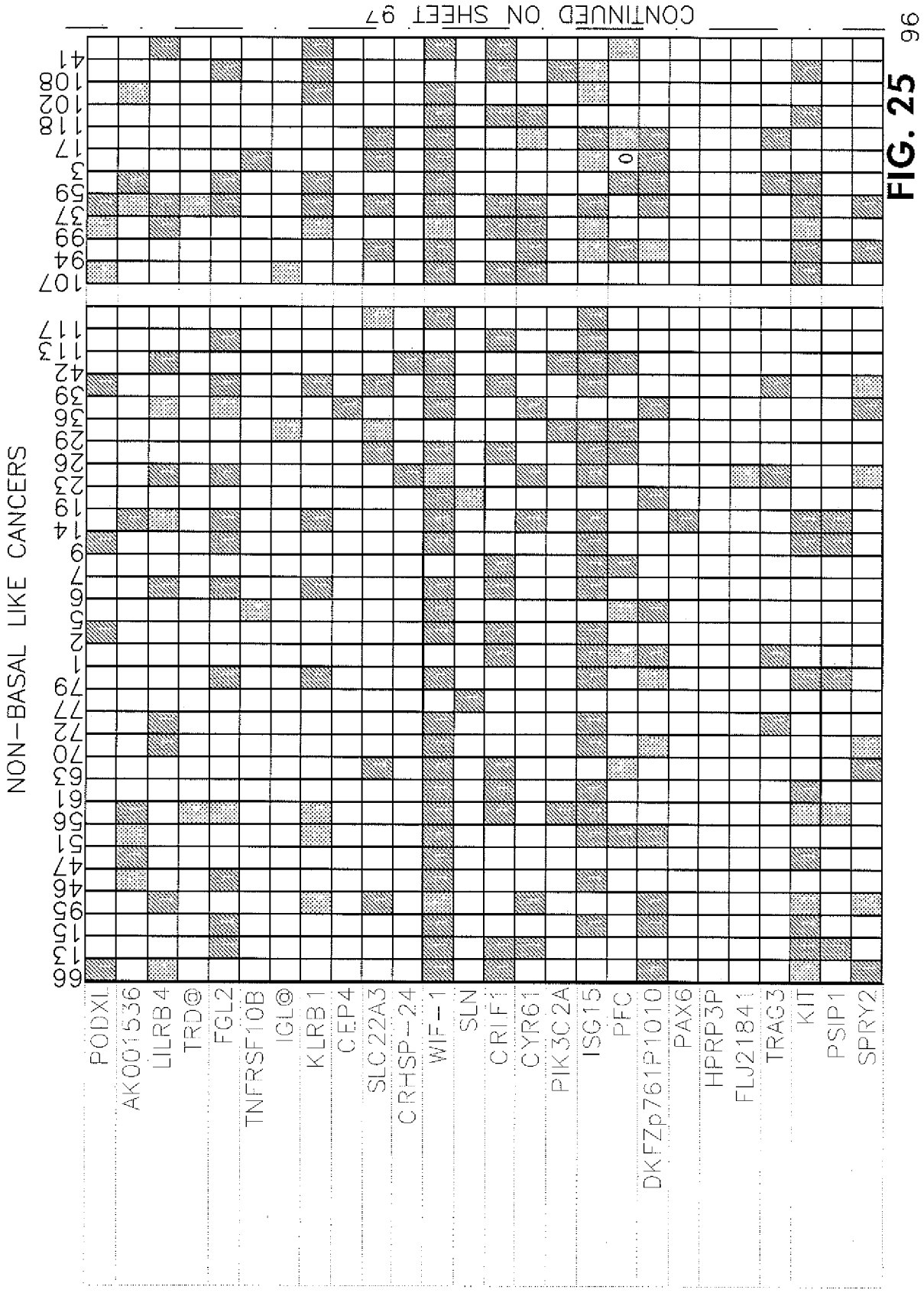

NON-BASAL LIKE CANCERS
PODXL
AK001536
LILRB4
TRD@
FGL2
TNFRSF10B
IGL@
KLRB1
CEP4
SLC22A3
CRHSP-24
WIF-1
SLN
CRIF1
CYR61
PIK3C2A
ISG15
PFC
DKFZp761P1010
PAX6
HPRP3P
FLJ21841
TRAG3
KIT
PSIP1
SPRY2
CONTINUED ON SHEET 97

FIG. 25

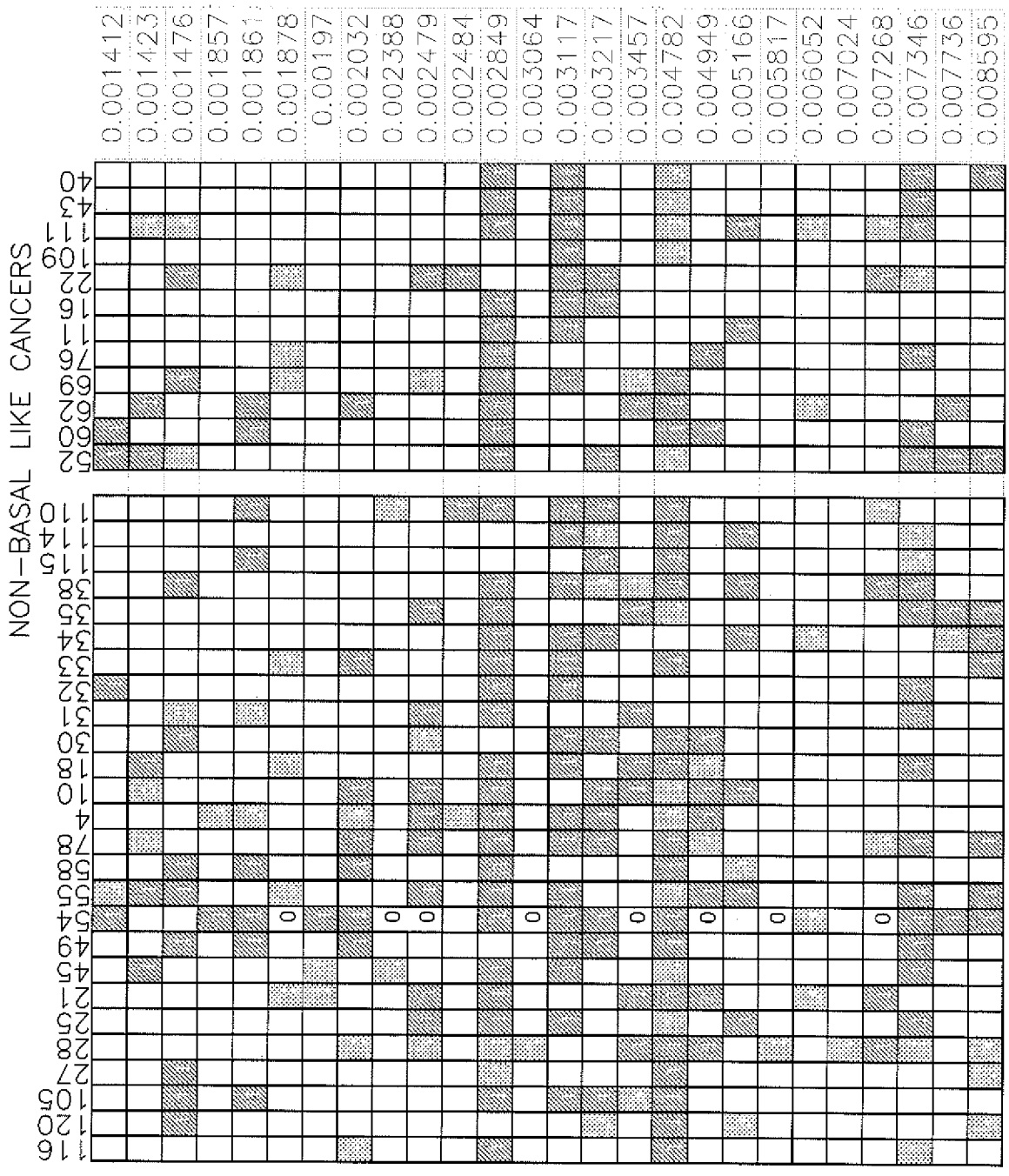

NON-BASAL LIKE CANCERS
0.001412
0.001423
0.001476
0.001857
0.001861
0.001878
0.00197
0.002032
0.002388
0.002479
0.002484
0.002849
0.003064
0.003117
0.003217
0.003457
0.004782
0.004949
0.005166
0.005817
0.006052
0.007024
0.007268
0.007346
0.007736
0.008595

FIG. 25 97

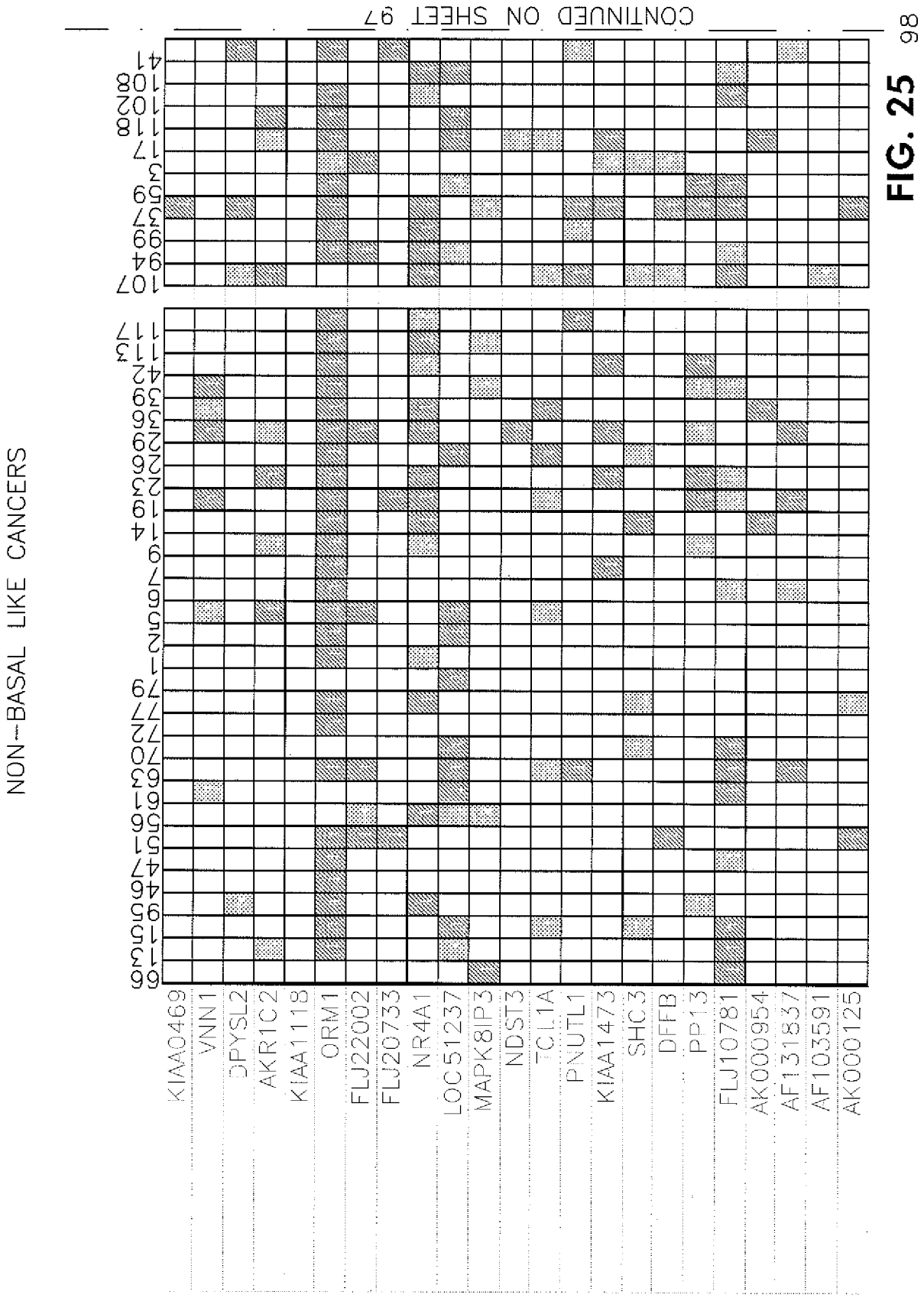

NON-BASAL LIKE CANCERS
CONTINUED ON SHEET 97
KIAA0469
VNN1
SPYSL2
AKR1C2
KIAA1118
ORM1
FLJ22002
FLJ20733
NR4A1
LOC51237
MAPK8IP3
NDST3
TCL1A
PNUTL1
KIAA1473
SHC3
DFFB
PP13
FLJ10781
AK000954
AF131837
AF103591
AK000125

FIG. 25 98

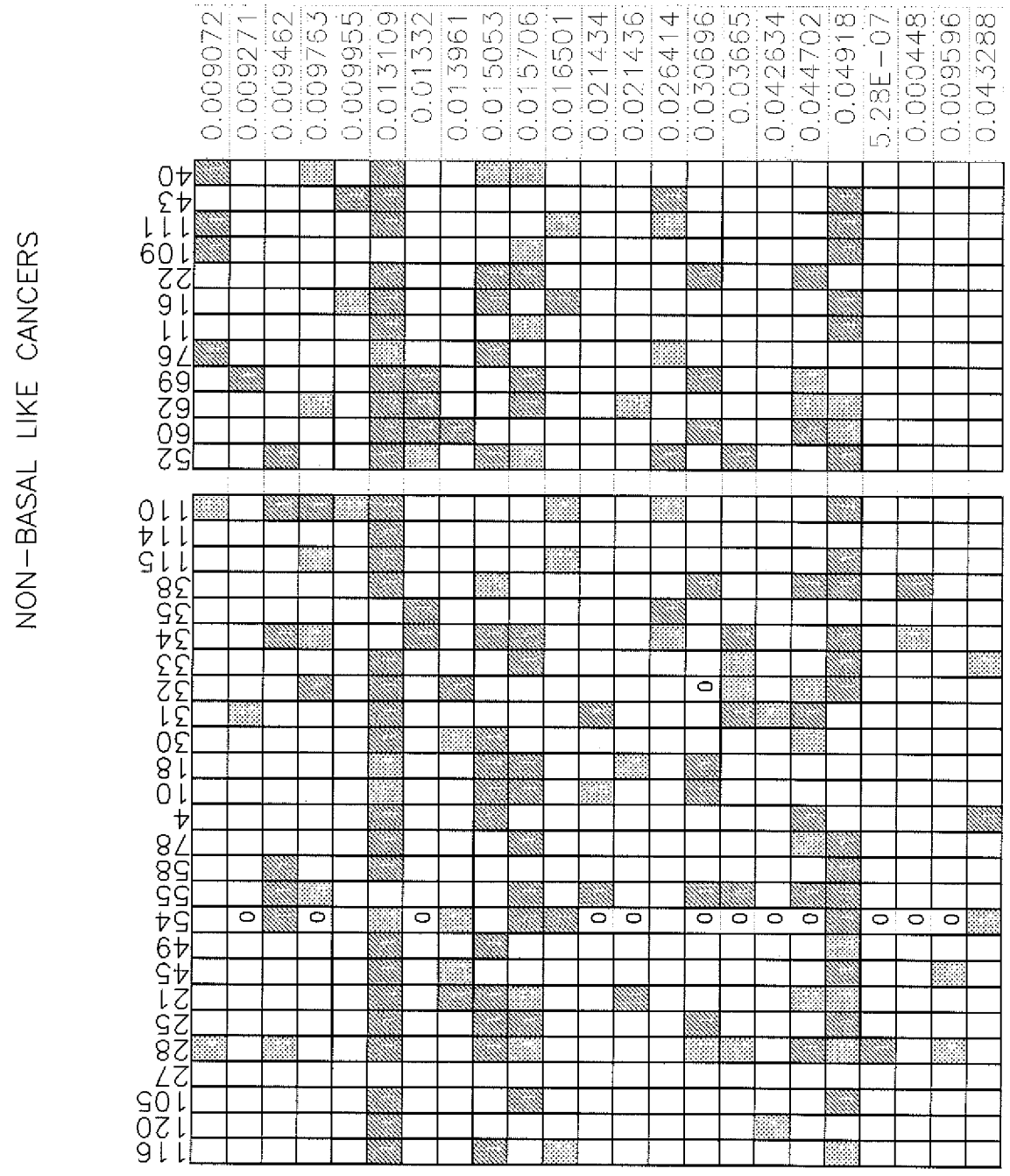

NON-BASAL LIKE CANCERS
0.009072
0.009271
0.009462
0.009763
0.009955
0.013109
0.01332
0.013961
0.015053
0.015706
0.016501
0.021434
0.021436
0.026414
0.030696
0.03665
0.042634
0.044702
0.04918
5.28E-07
0.000448
0.009596
0.043288

FIG. 25 99

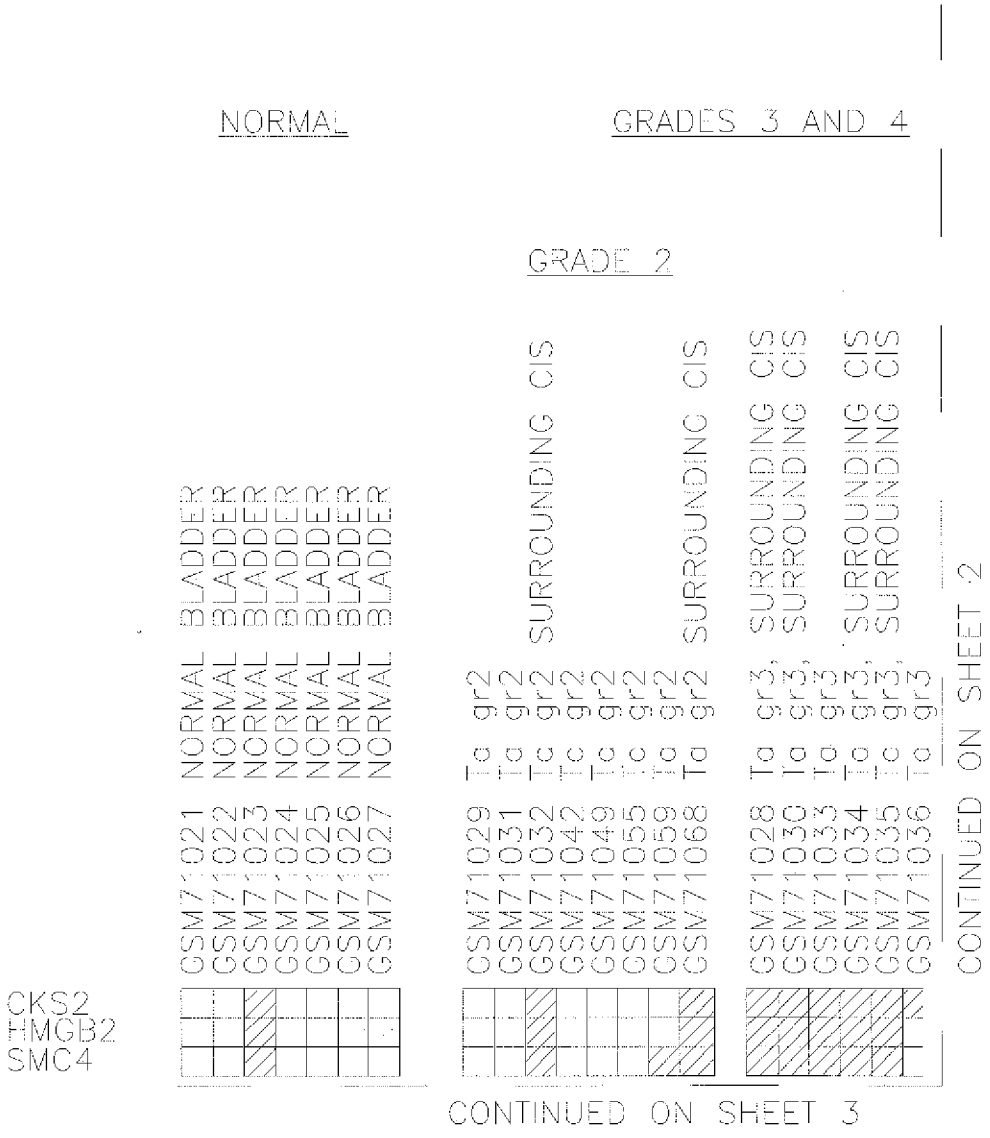

NORMAL
GRADES 3 AND 4
GRADE 2
GSM71021 NORMAL BLADDER
GSM71022 NORMAL BLADDER
GSM71023 NORMAL BLADDER
GSM71024 NORMAL BLADDER
GSM71025 NORMAL BLADDER
GSM71026 NORMAL BLADDER
GSM71027 NORMAL BLADDER
GSM71029 Ta gr2 SURROUNDING CIS
GSM71031 Ta gr2
GSM71032 Tc gr2
GSM71042 Tc gr2
GSM71049 Tc gr2
GSM71055 Ta gr2
GSM71059 Ta gr2 SURROUNDING CIS
GSM71068 Ta gr2
GSM71028 Ta gr3, SURROUNDING CIS
GSM71030 Ia gr3, SURROUNDING CIS
GSM71033 Ta gr3,
GSM71034 Ta gr3, SURROUNDING CIS
GSM71035 Tc gr3, SURROUNDING CIS
GSM71036 Ta gr3
CONTINUED ON SHEET 2
CKS2
HMGB2
SMC4
CONTINUED ON SHEET 3

FIG. 26

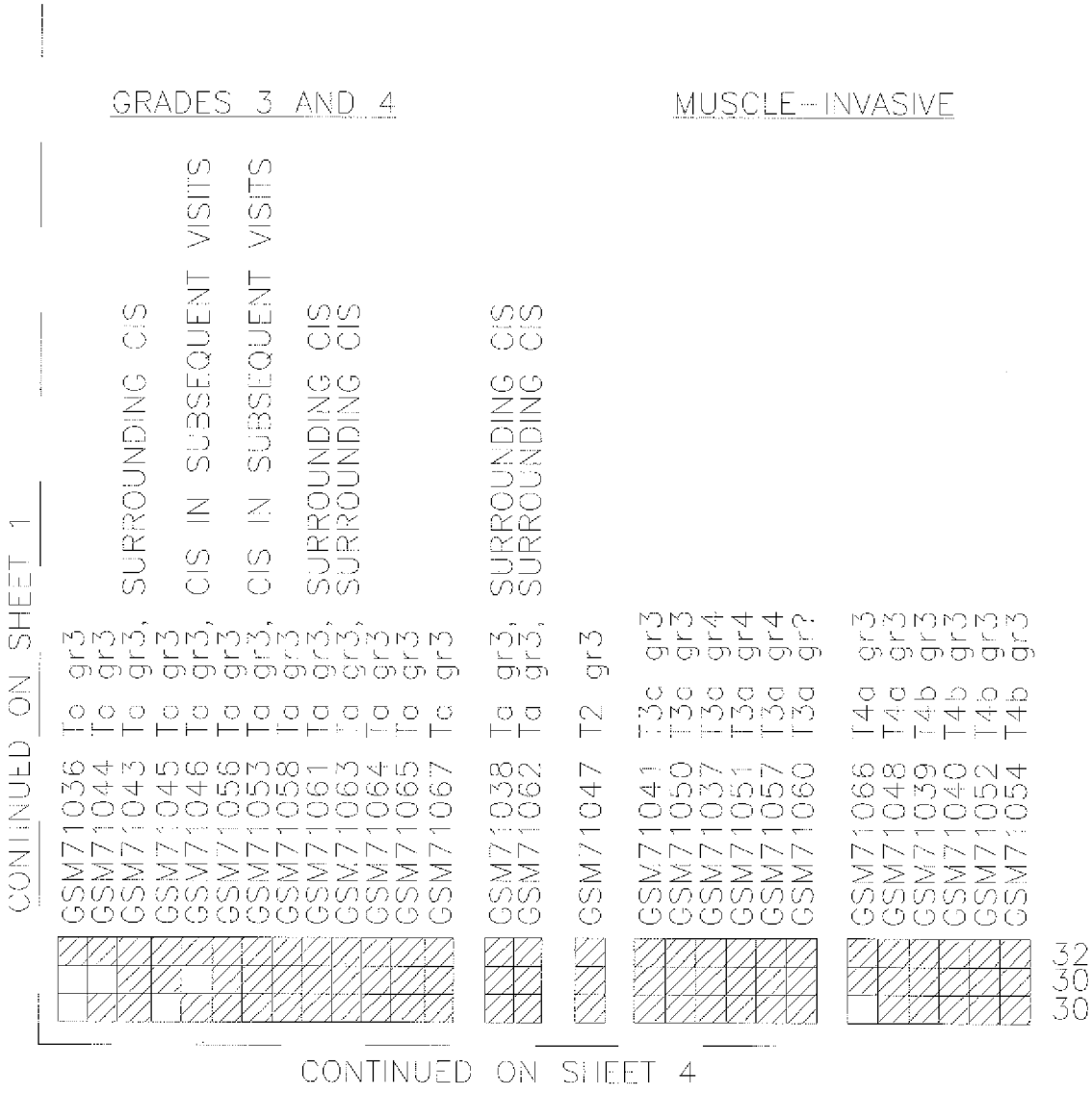

CONTINUED ON SHEET 1
GRADES 3 AND 4
MUSCLE-INVASIVE
SURROUNDING CIS
CIS IN SUBSEQUENT VISITS
CIS IN SUBSEQUENT VISITS
SURROUNDING CIS
SURROUNDING CIS
SURROUNDING CIS
SURROUNDING CIS
GSM71036 Ta gr3
GSM71044 Ta gr3
GSM71043 Ta gr3,
GSM71045 Ta gr3
GSM71046 Ta gr3,
GSM71056 Ta gr3,
GSM71053 Ta gr3,
GSM71058 Ta gr3
GSM71061 Ta gr3,
GSM71063 Ta gr3,
GSM71064 Ta gr3
GSM71065 Ta gr3
GSM71067 Ta gr3
GSM71038 Ta gr3,
GSM71062 Ta gr3,
GSM71047 T2 gr3
GSM71041 T3c gr3
GSM71050 T3c gr3
GSM71037 T3c gr4
GSM71051 T3a gr4
GSM71057 T3a gr4
GSM71060 T3a gr?
GSM71066 T4a gr3
GSM71048 T4c gr3
GSM71039 T4b gr3
GSM71040 T4b gr3
GSM71052 T4b gr3
GSM71054 T4b gr3
CONTINUED ON SHEET 4

FIG. 26

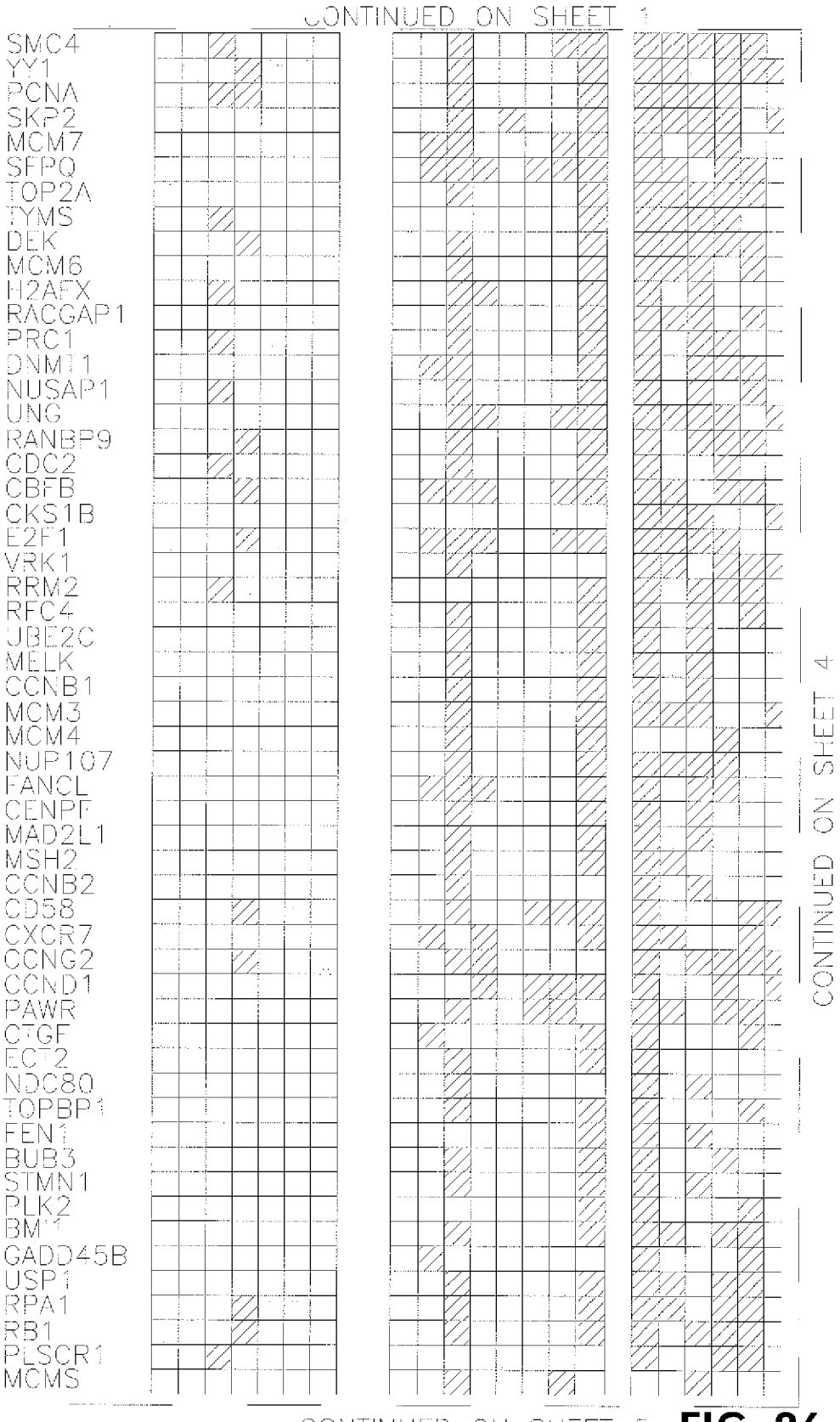

CONTINUED ON SHEET 1
SMC4
YY1
PCNA
SKP2
MCM7
SFPQ
TOP2A
TYMS
DEK
MCM6
H2AFX
RACGAP1
PRC1
DNMT1
NUSAP1
UNG
RANBP9
CDC2
CBFB
CKS1B
E2F1
VRK1
RRM2
RFC4
UBE2C
MELK
CCNB1
MCM3
MCM4
NUP107
FANCL
CENPF
MAD2L1
MSH2
CCNB2
CD58
CXCR7
CCNG2
CCND1
PAWR
CTGF
ECT2
NDC80
TOPBP1
FEN1
BUB3
STMN1
PLK2
BMI1
GADD45B
USP1
RPA1
RB1
PLSCR1
MCM5
CONTINUED ON SHEET 4
CONTINUED ON SHEET 5

FIG. 26

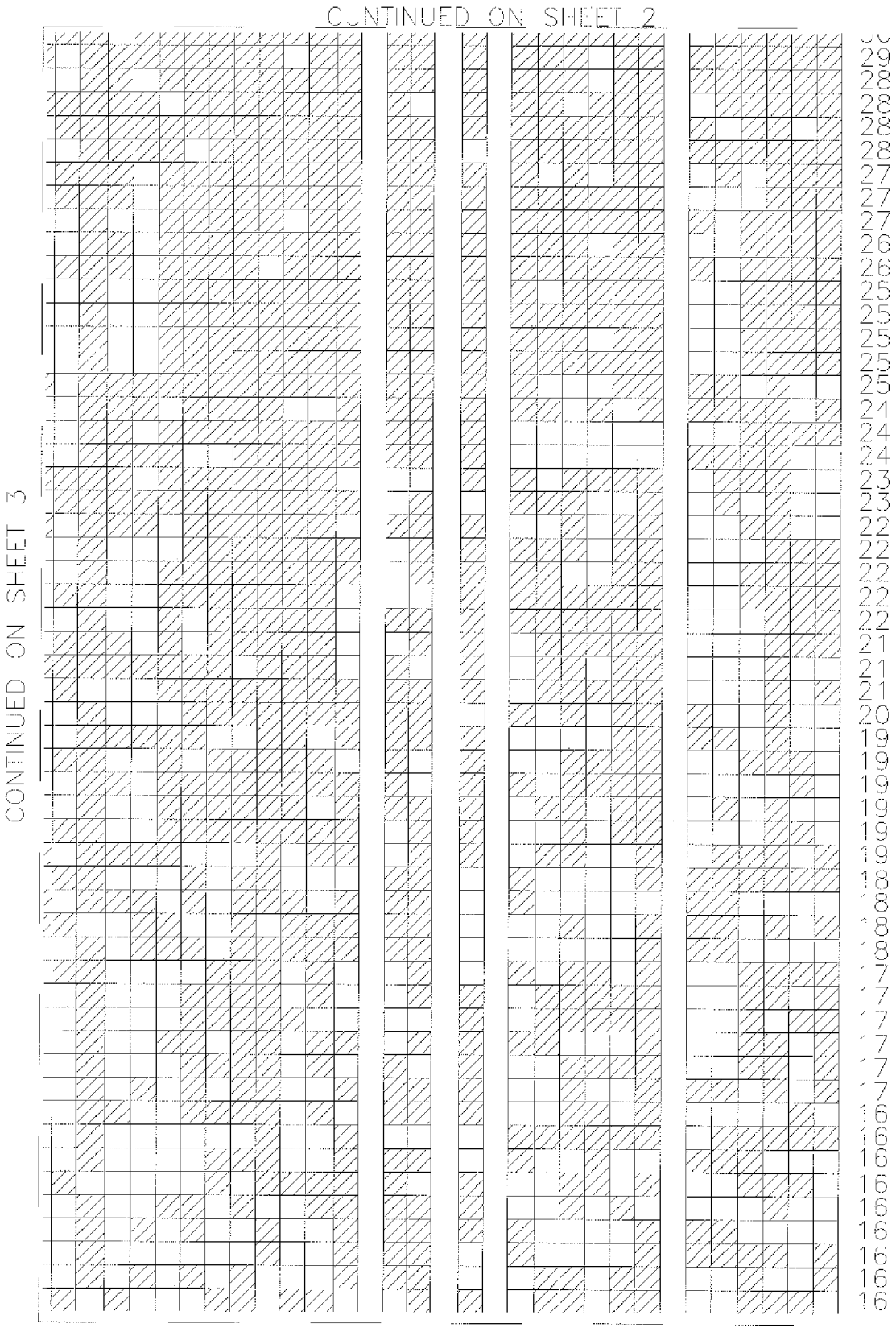

CONTINUED ON SHEET 2
CONTINUED ON SHEET 3
CONTINUED ON SHEET 6

FIG. 26

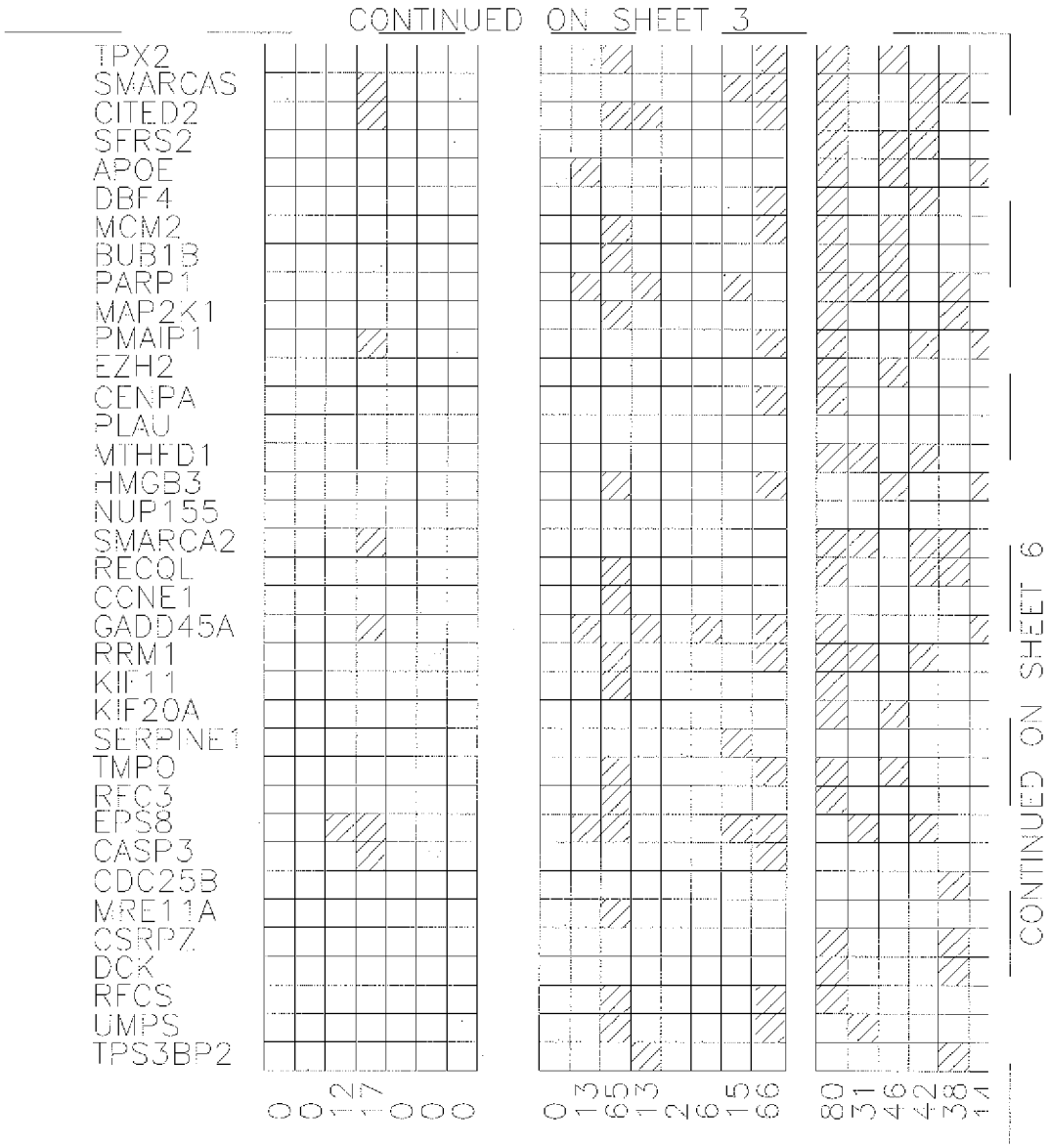

CONTINUED ON SHEET 3
TPX2
SMARCAS
CITED2
SFRS2
APOE
DBF4
MCM2
BUB1B
PARP1
MAP2K1
PMAIP1
EZH2
CENPA
PLAU
MTHFD1
HMGB3
NUP155
SMARCA2
RECQL
CCNE1
GADD45A
RRM1
KIF11
KIF20A
SERPINE1
TMPO
RFC3
EPS8
CASP3
CDC25B
MRE11A
CSRP2
DCK
RFC5
UMPS
TPS3BP2
CONTINUED ON SHEET 6

FIG. 26

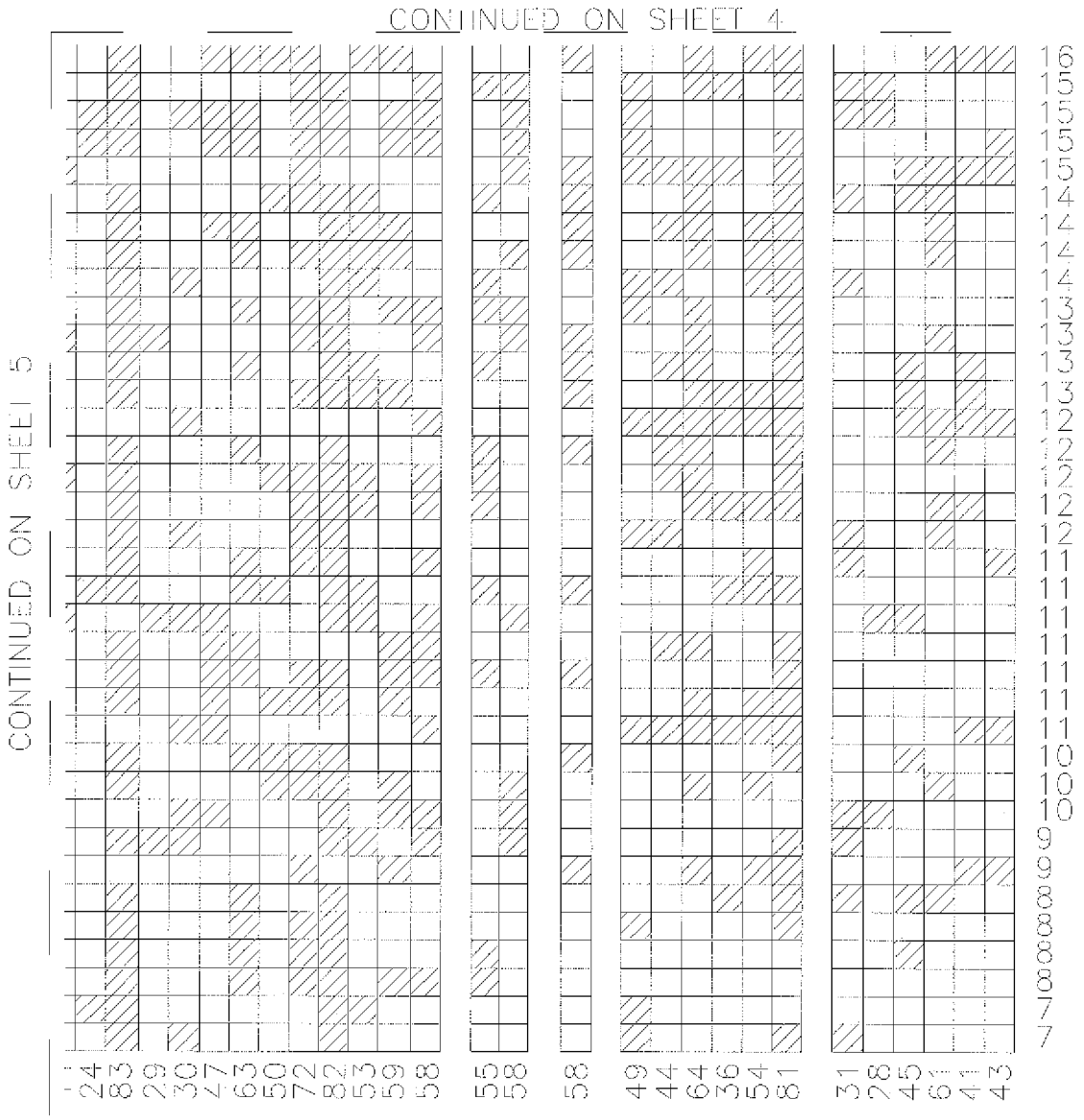


FIG. 26

HEPATOMA

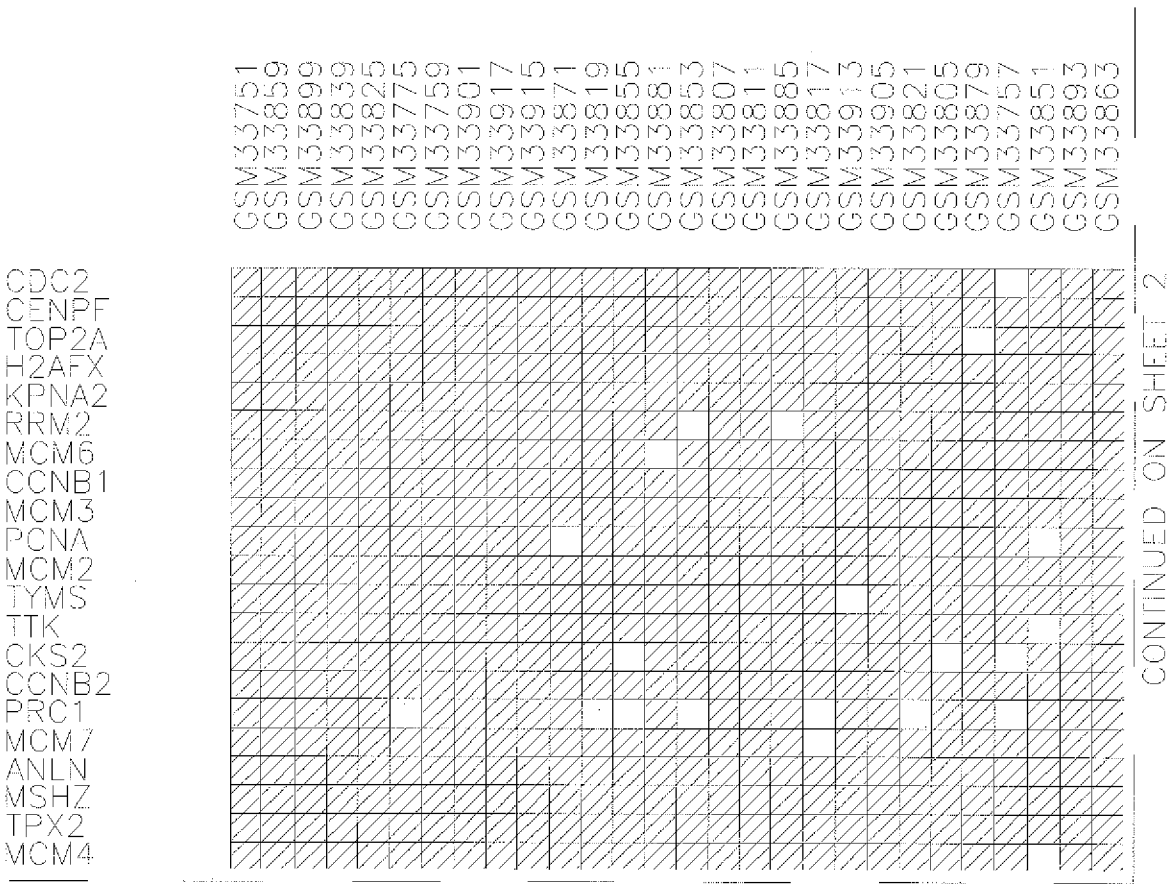


FIG. 27

HEPATOMA

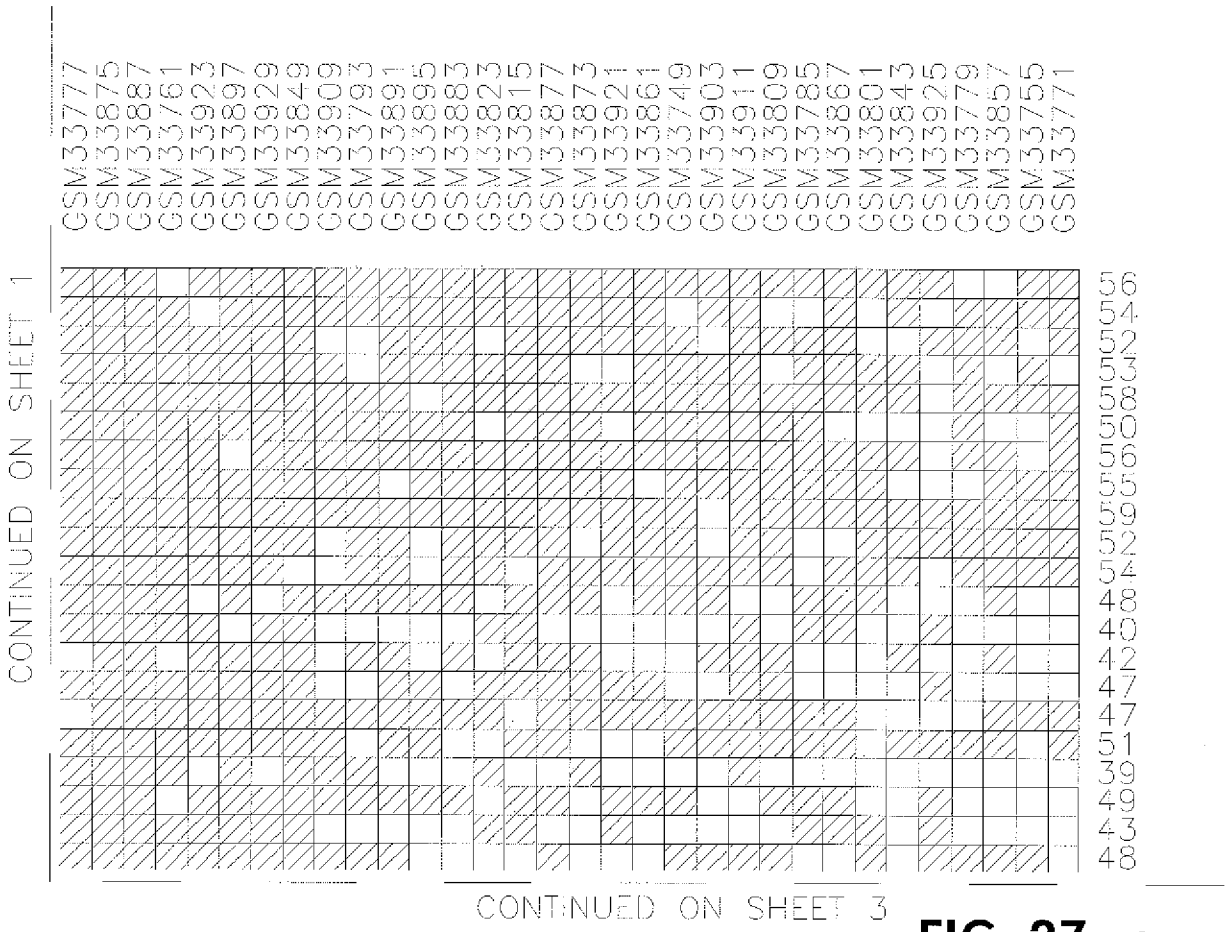


FIG. 27 2

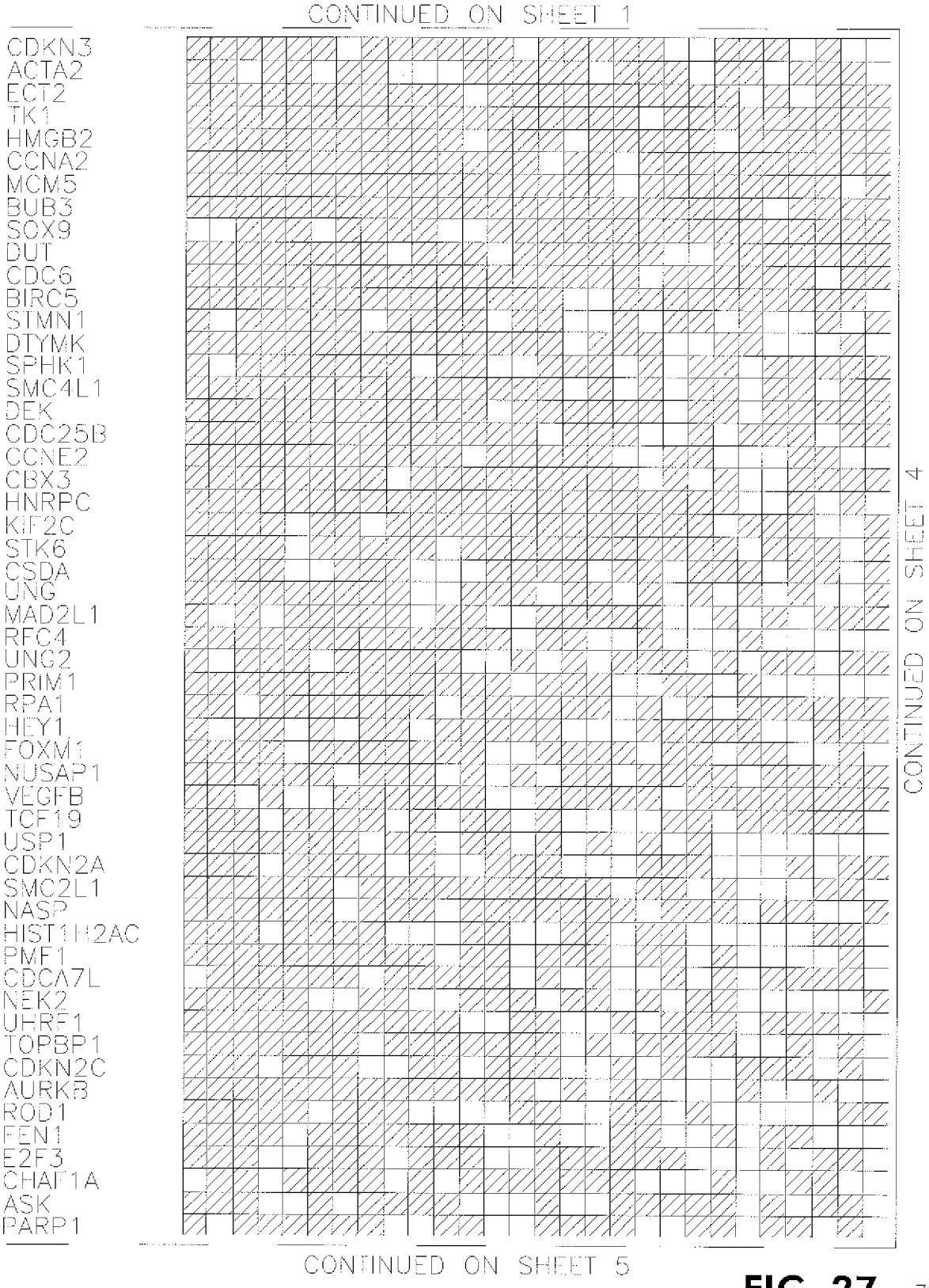
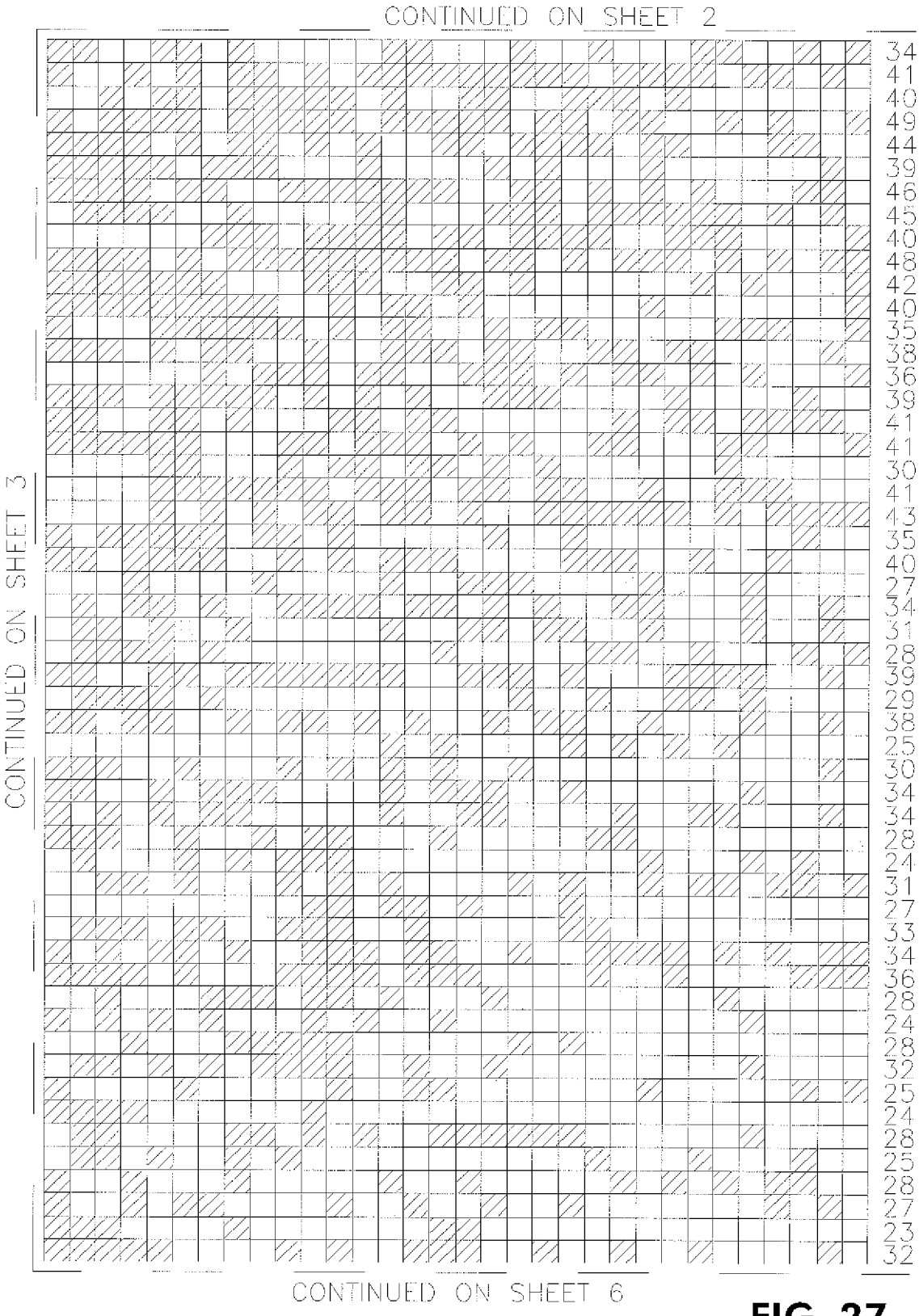

CONTINUED ON SHEET 1
CDKN3
ACTA2
ECT2
TK1
HMGB2
CCNA2
MCM5
BUB3
SOX9
DUT
CDC6
BIRC5
STMN1
DTYMK
SPHK1
SMC4L1
DEK
CDC25B
CCNE2
CBX3
HNRPC
KIF2C
STK6
CSDA
UNG
MAD2L1
RFC4
UNG2
PRIM1
RPA1
HEY1
FOXM1
NUSAP1
VEGFB
TCF19
USP1
CDKN2A
SMC2L1
NASP
HIST1H2AC
PMF1
CDCA7L
NEK2
UHRF1
TOPBP1
CDKN2C
AURKB
ROD1
FEN1
E2F3
CHAF1A
ASK
PARP1
CONTINUED ON SHEET 4
CONTINUED ON SHEET 5

FIG. 27


CONTINUED ON SHEET 2
CONTINUED ON SHEET 3
CONTINUED ON SHEET 6
34
41
40
49
44
39
46
45
40
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42
40
35
38
36
39
41
41
30
41
43
35
40
27
34
31
28
39
29
38
25
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FIG. 27

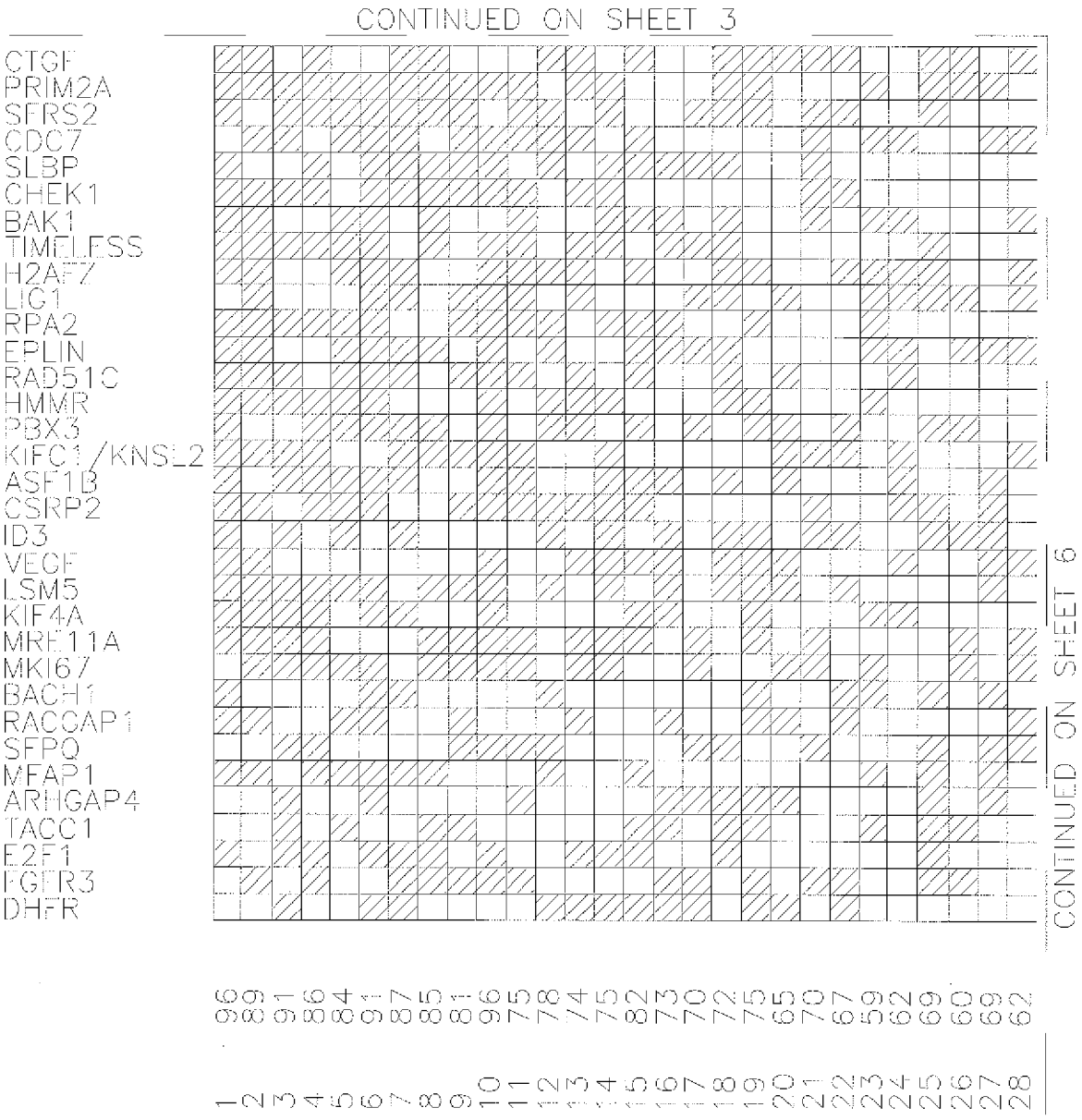
CONTINUED ON SHEET 3
CTGF
PRIM2A
SFRS2
CDC7
SLBP
CHEK1
BAK1
TIMELESS
H2AFZ
LIG1
RPA2
EPLIN
RAD51C
HMMR
PBX3
KIFC1/KNSL2
ASF1B
CSRP2
ID3
VEGF
LSM5
KIF4A
MRE11A
MKI67
BACH1
RACGAP1
SFPQ
MFAP1
ARHGAP4
TACC1
E2F1
FGFR3
DHFR
CONTINUED ON SHEET 6
99 98 91 86 84 91 87 85 81 96 75 78 74 75 82 73 70 72 75 65 70 67 59 62 69 60 69 62
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28

FIG. 27

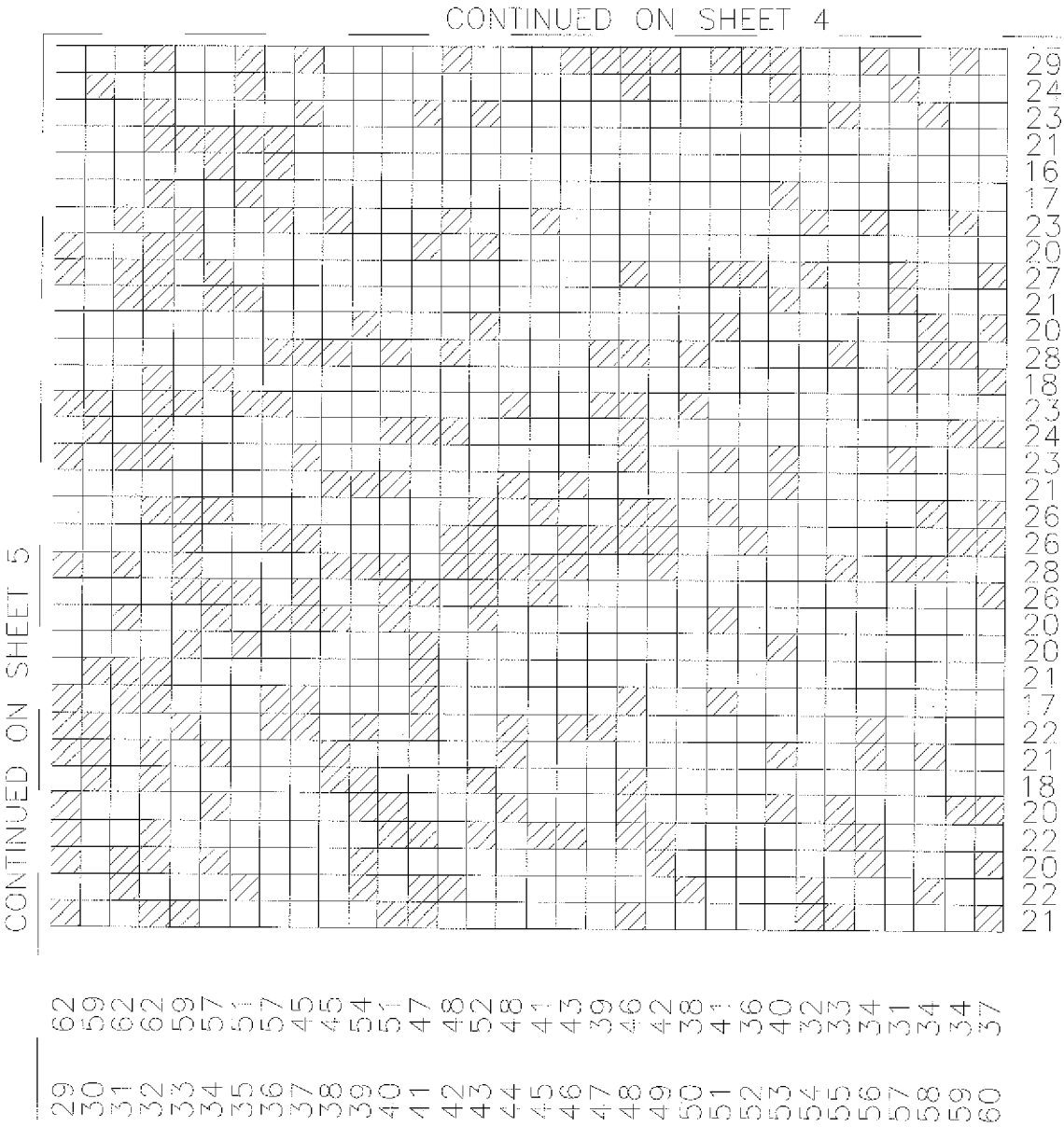
CONTINUED ON SHEET 4
CONTINUED ON SHEET 5
29 24 23 21 16 17 23 20 27 21 20 28 18 23 24 23 21 26 26 28 26 20 20 21 17 22 21 18 20 22 20 22 21
62 59 62 62 59 57 51 57 45 45 54 51 47 48 52 48 41 43 39 46 42 38 41 36 40 32 33 34 31 34 34 37
29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60

FIG. 27

INTERNATIONAL SEARCH REPORT

International application No
PCT/US2009/064294

A. CLASSIFICATION OF SUBJECT MATTER
INV. C12Q1/68

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)
C12Q

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 practical, search terms used)
EPO-Internal, BIOSIS, CHEM ABS Data, EMBASE, FSTA

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	VAN 'T VEER L J ET AL: "Gene expression profiling predicts clinical outcome of breast cancer" NATURE, NATURE PUBLISHING GROUP, LONDON, UK, vol. 415, 31 January 2002 (2002-01-31), pages 530-536, XP002967258 ISSN: 0028-0836 cited in the application the whole document	1-31, 46-52

-/--

[X] Further documents are listed in the continuation of Box C.

[ ] See patent family annex.

* Special categories of cited documents :

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

"E" earlier document 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	Date of mailing of the international search report
16 February 2010	08/03/2010

Name and mailing address of the ISA/	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL – 2280 HV Rijswijk Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016	Leber, Thomas

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2009/064294

Box No. I Nucleotide and/or amino acid sequence(s) (Continuation of item 1.b of the first sheet)

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application and necessary to the claimed invention, the international search was carried out on the basis of:

   a. (means)

   [ ] on paper

   [X] in electronic form

   b. (time)

   [X] in the international application as filed

   [ ] together with the international application in electronic form

   [ ] subsequently to this Authority for the purpose of search

2. [ ] In addition, in the case that more than one version or copy of a sequence listing and/or table relating thereto has been filed or furnished, the required statements that the information in the subsequent or additional copies is identical to that in the application as filed or does not go beyond the application as filed, as appropriate, were furnished.

3. Additional comments:

INTERNATIONAL SEARCH REPORT

International application No
PCT/US2009/064294

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	DAI H ET AL: "A cell proliferation signature is a marker of extremely poor outcome in a subpopulation of breast cancer patients" CANCER RESEARCH, AMERICAN ASSOCIATION FOR CANCER RESEARCH, BALTIMORE, MD., US, vol. 65, no. 10, 15 May 2005 (2005-05-15), pages 4059-4066, XP002521840 ISSN: 0008-5472 the whole document	1-31, 46-52
A	TSANTOULIS P K ET AL: "Involvement of E2F transcription factor family in cancer" EUROPEAN JOURNAL OF CANCER, PERGAMON PRESS, OXFORD, GB, vol. 41, no. 16, 1 November 2005 (2005-11-01), pages 2403-2414, XP025298206 ISSN: 0959-8049 [retrieved on 2005-11-01] the whole document	1-31, 46-52
T	YONGJIN PARK ET AL: "Network-Based Inference of Cancer Progression from Microarray Data" IEEE/ACM TRANSACTIONS ON COMPUTATIONAL BIOLOGY AND BIOINFORMATICS, IEEE SERVICE CENTER, NEW YORK, NY, US, vol. 6, no. 2, 1 April 2009 (2009-04-01), pages 200-212, XP011266959 ISSN: 1545-5963 the whole document	

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box II.2

Claims Nos.: 32-45

Claims 32-45 are formulated as second medical use claims whereby a particular compound is used in the manufacture of a medicament "for the treatment of an ERGO tumor identified according to the method of claim 1". This claim formulation permits to gain protection for a as such known compound through its use for a novel and inventive therapeutic application. It is evident that this novel and inventive therapeutic application must be clear (Art 6 PCT). In the present case, this therapeutic application is defined to be "an ERGO tumor identified according to the method of claim 1". Claim 1 refers to a method of "identifying a tumor as an ERGO tumor". The term "ERGO" stands thereby for "E2F-responsive gene over-expressing" (description, page 8, lines 8-9). The method of claim 1 is further characterised by determining the expression of approx. 350 genes in a tumor sample, by providing a reference and "measuring the reference" whereby a tumor is specified to be an ERGO-tumor if at least 21 of the said genes are over-expressed in comparison to the reference. As to the reference, claim 1 fails to specify any details. It remains, in particular, unclear what could represent such a reference and which parameters are actually measured. The description provides several options for a reference and the said parameters (description, page 12, line 32 - page 13, line 3). According to this section, the reference may be i) normal cells or tissues. Alternatively, the reference may be ii) the average of the signal intensity values from all sample-probed gene spots on a microarray set. Moreover, the reference may also be iii) a signal corresponding to one or more gene transcripts, such as housekeeping genes like GAPDH or others, which are assumed not to vary significantly in living cells. Considering these references, the International Authority notes the following: While the first option i) for the reference appears, prima facie, meaningful, it remains, however, unclear which parameters are actually measured. Such parameter could be an "internal calibration" of array data as indicated in second option ii) or a general reference such as a house keeping gene (option iii)). Evidently, the definition of what constitutes the reference will have an impact on what is subsequently recognised as ERGO-tumor. A study exclusively analysing the approx. 350 E2F-genes specified in claim 1 and using the "internal calibration" of option ii) as reference will obviously come to entirely different results as a study in which GAPDH of a normal cell is used as reference. Indeed, using as reference the average of the signal intensity values from all sample-probed gene spots on a microarray consisting of the above approx. 350 E2F-genes, i.e. option ii), will unavoidably result in each tumour being called an ERGO-tumour as the term "average" already implies that approx. 50% of the genes are higher expressed than the average (= over-expressed) and approx. 50% of the genes are lower expressed than the average (= under-expressed). Among the about 350 genes tested for each tumour will thus always be at least 21 that are over-expressed with regard to the said reference resulting in this tumour being an ERGO tumour. This applies, of course to ALL tumours. Taken together, the definition of claim 1 on how to recognise an ERGO tumor lacks clarity to such an extent that its subject-matter appears technically meaningless

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

(Art 6 PCT). As, moreover, also the application as filed fails to provides any other and clear definition what could constitute a ERGO tumour, it is presently not possibly to specify the subject-matter of claims 32-45, which aim to provide compound for use in the preparation of a medicament "for the treatment of an ERGO tumor" (Art 6 PCT). The International Authority is moreover of the opinion that this lack of clarity is such that presently no meaningful search can be carried out (Art 17(2)(a)(ii) PCT).

The applicant's attention is drawn to the fact that claims relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure. If the application proceeds into the regional phase before the EPO, the applicant is reminded that a search may be carried out during examination before the EPO (see EPO Guideline C-VI, 8.2), should the problems which led to the Article 17(2) declaration be overcome.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2009/064294

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.: 32-45
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:
see FURTHER INFORMATION sheet PCT/ISA/210

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

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

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

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional 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.