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(54) **ROBUST GENOMIC PREDICTOR OF BREAST AND LUNG CANCER METASTASIS**

(71) Applicants: **Harry Ostrer**, New York, NY (US); **Johnny C. Loke**, Valley Cottage, NY (US); **Alexander Pearlman**, New York, NY (US)

(72) Inventors: **Harry Ostrer**, New York, NY (US); **Johnny C. Loke**, Valley Cottage, NY (US); **Alexander Pearlman**, New York, NY (US)

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C12Q 1/6886 (2018.01)
G06F 17/18 (2006.01)

(52) **U.S. Cl.**
CPC ***C12Q 1/6886*** (2013.01); ***G06F 17/18*** (2013.01); *C12Q 2600/112* (2013.01); *C12Q 2600/118* (2013.01); *C12Q 2600/156* (2013.01); *C12Q 2600/16* (2013.01)

(58) **Field of Classification Search**
None
See application file for complete search history.

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Primary Examiner — Christian L Fronda
(74) *Attorney, Agent, or Firm* — Scully, Scott, Murphy & Presser, P.C.

(57) **ABSTRACT**

A method of determining the risk of metastasis of breast or lung cancer in a human subject who has or had breast or lung cancer is disclosed herein. The method is based on detecting in a sample from the subject the number of copies per cell of genes and/or genomic regions of a metastatic gene signature set disclosed herein, and determining alternations in the number of copies per cell of the genes and/or genomic regions in the signature set, as compared to the number of copies per cell in non-cancer cells, thereby determining the risk of breast/lung cancer metastasis.

6 Claims, 11 Drawing Sheets
(10 of 11 Drawing Sheet(s) Filed in Color)

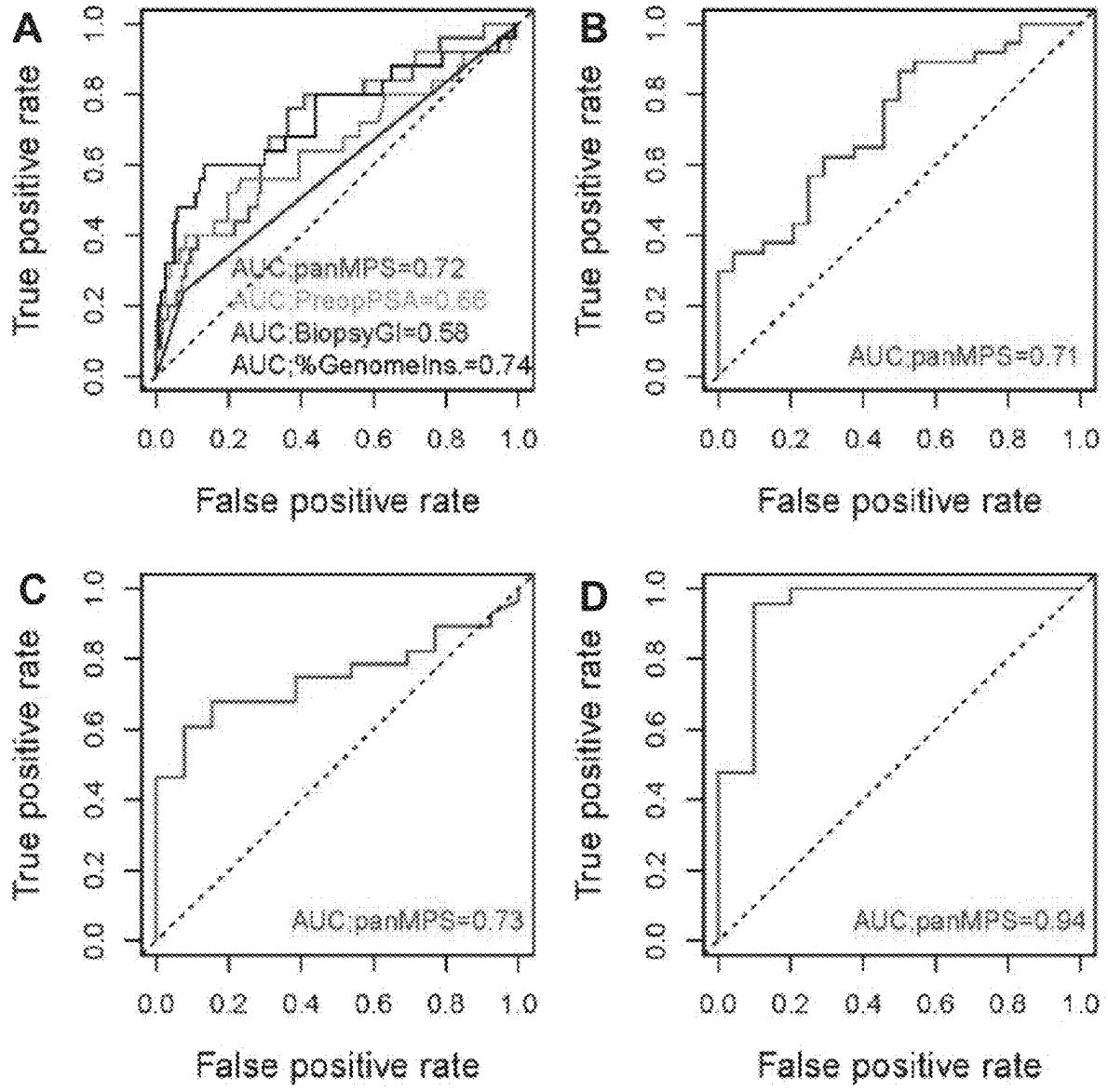

A
True positive rate
False positive rate
AUC:panMPS=0.72
AUC:PreopPSA=0.68
AUC:BiopsyGl=0.58
AUC:%GenomeIns.=0.74
B
True positive rate
False positive rate
AUC:panMPS=0.71
C
True positive rate
False positive rate
AUC:panMPS=0.73
D
True positive rate
False positive rate
AUC:panMPS=0.94

FIG. 1A – 1D

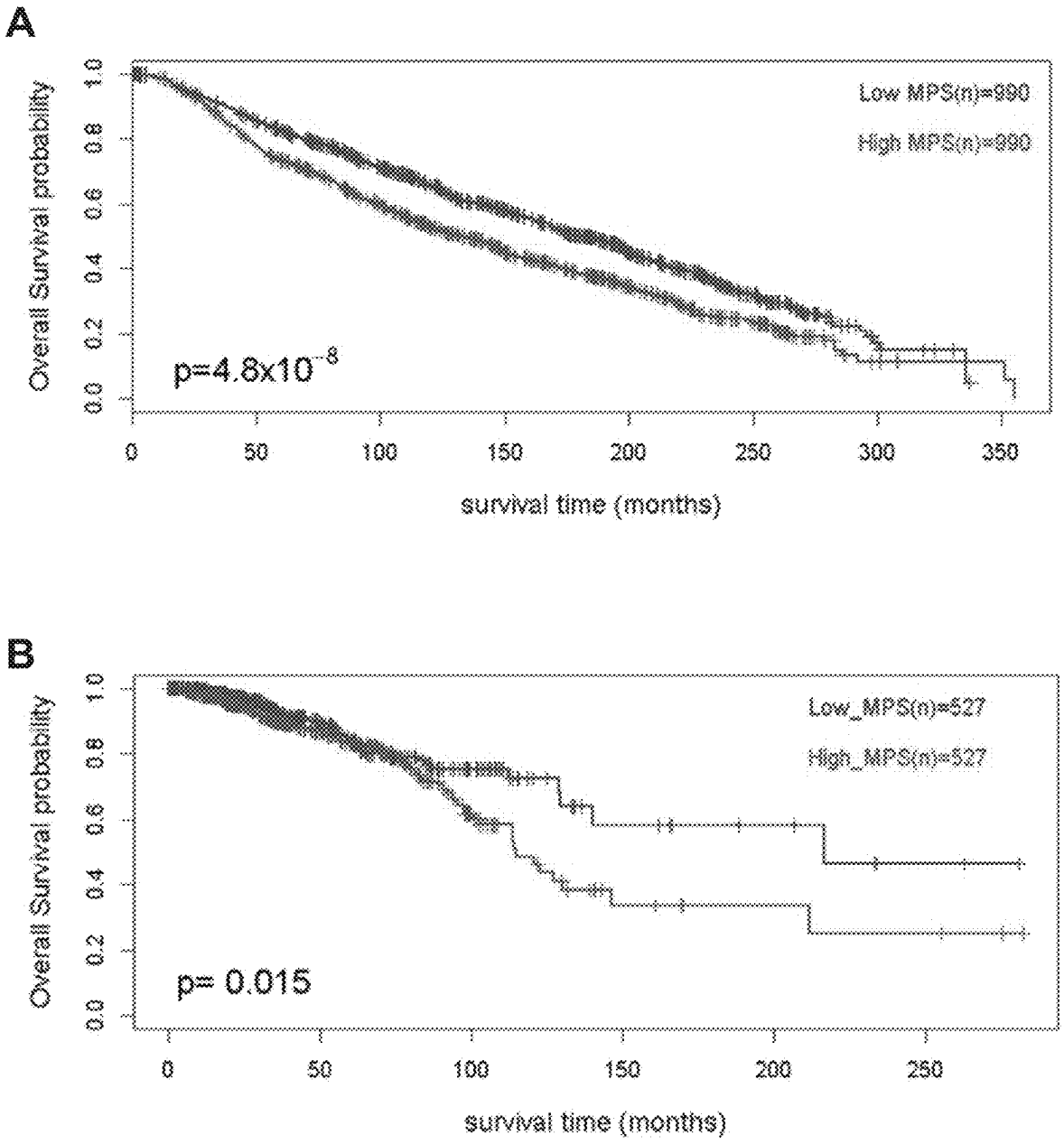
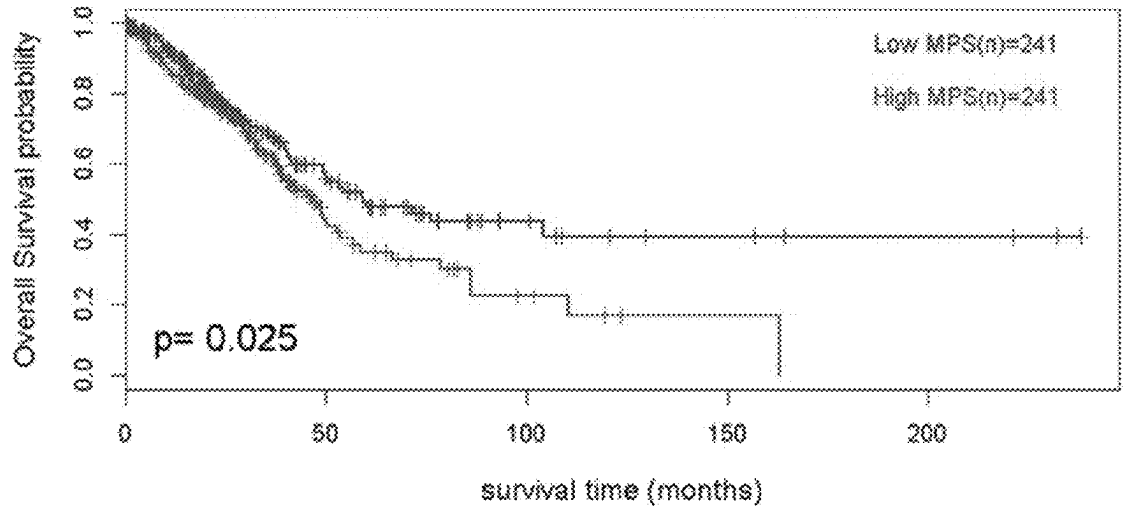

A
Overall Survival probability
0.0
0.2
0.4
0.6
0.8
1.0
Low MPS(n)=990
High MPS(n)=990
p=4.8x10^-8
0
50
100
150
200
250
300
350
survival time (months)
B
Overall Survival probability
0.0
0.2
0.4
0.6
0.8
1.0
Low_MPS(n)=527
High_MPS(n)=527
p= 0.015
0
50
100
150
200
250
survival time (months)

FIG. 2A – 2B

C


Overall Survival probability
0.0
0.2
0.4
0.6
0.8
1.0
Low MPS(n)=241
High MPS(n)=241
p= 0.025
0
50
100
150
200
survival time (months)

D

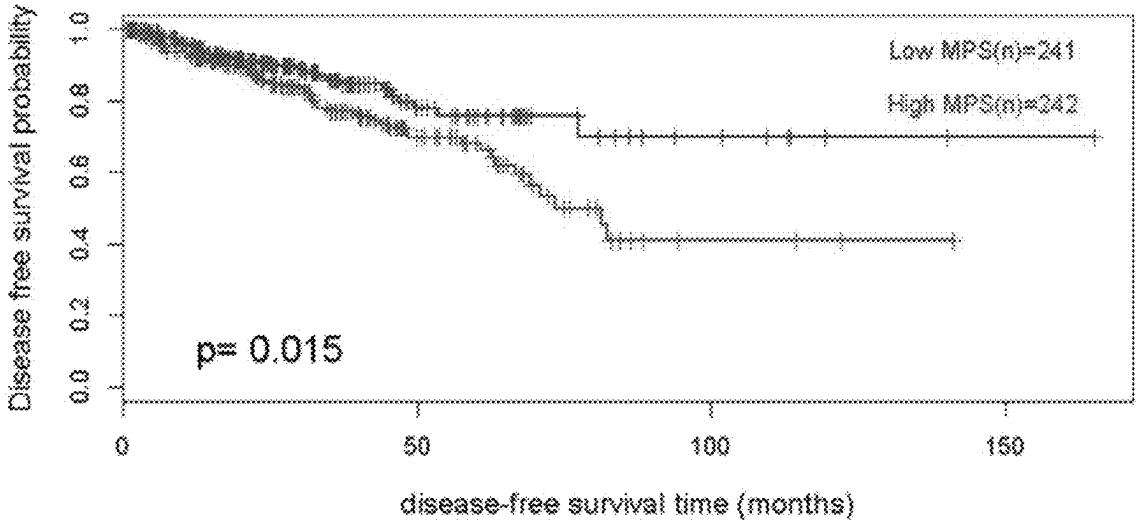

Disease free survival probability
0.0
0.2
0.4
0.6
0.8
1.0
Low MPS(n)=241
High MPS(n)=242
p= 0.015
0
50
100
150
disease-free survival time (months)

FIG. 2C – 2D

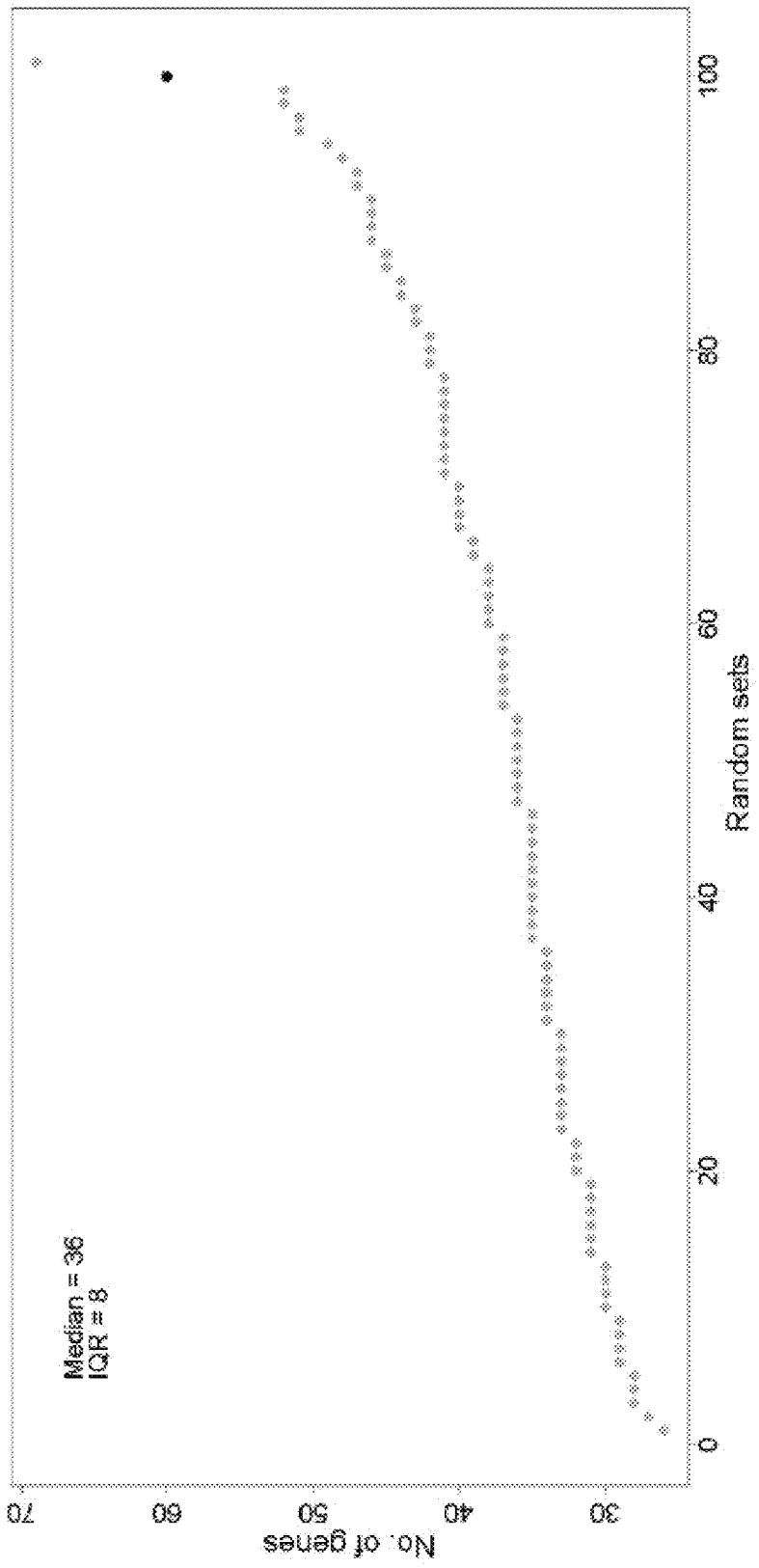

No. of genes
30
40
50
60
70
Random sets
0
20
40
60
80
100
Median = 36
IQR = 8

FIG. 3

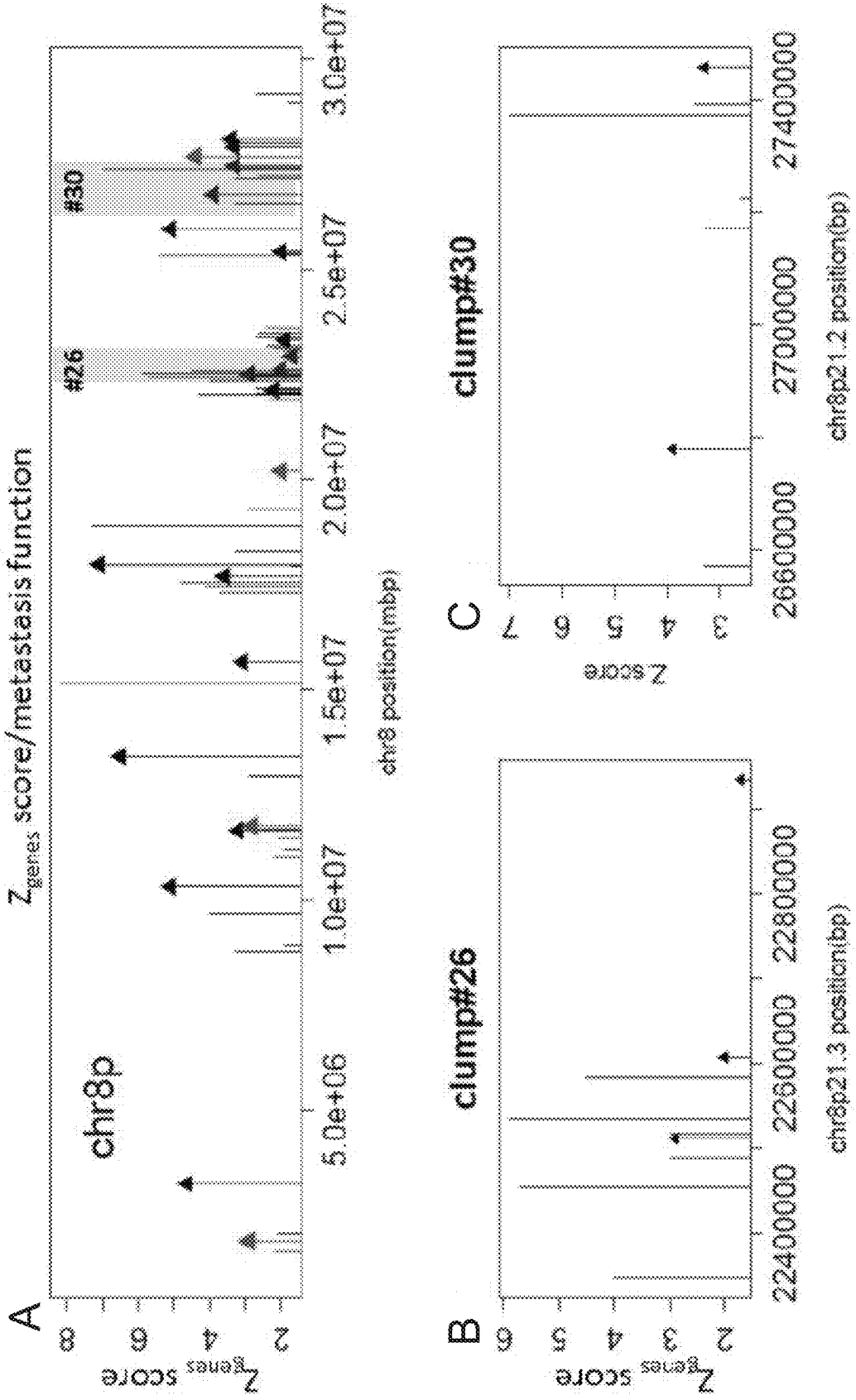

A
Z_{genes} score/metastasis function
chr8p
#26
#30
Z_{genes} score
2
4
6
8
5.0e+06
1.0e+07
1.5e+07
2.0e+07
2.5e+07
3.0e+07
chr8 position(mbp)
B
clump#26
Z_{genes} score
2
3
4
5
6
2400000
2600000
2800000
chr8p21.3 position(bp)
C
clump#30
Z score
3
4
5
6
7
26600000
27000000
27400000
chr8p21.2 position(bp)

FIG. 4A-4C

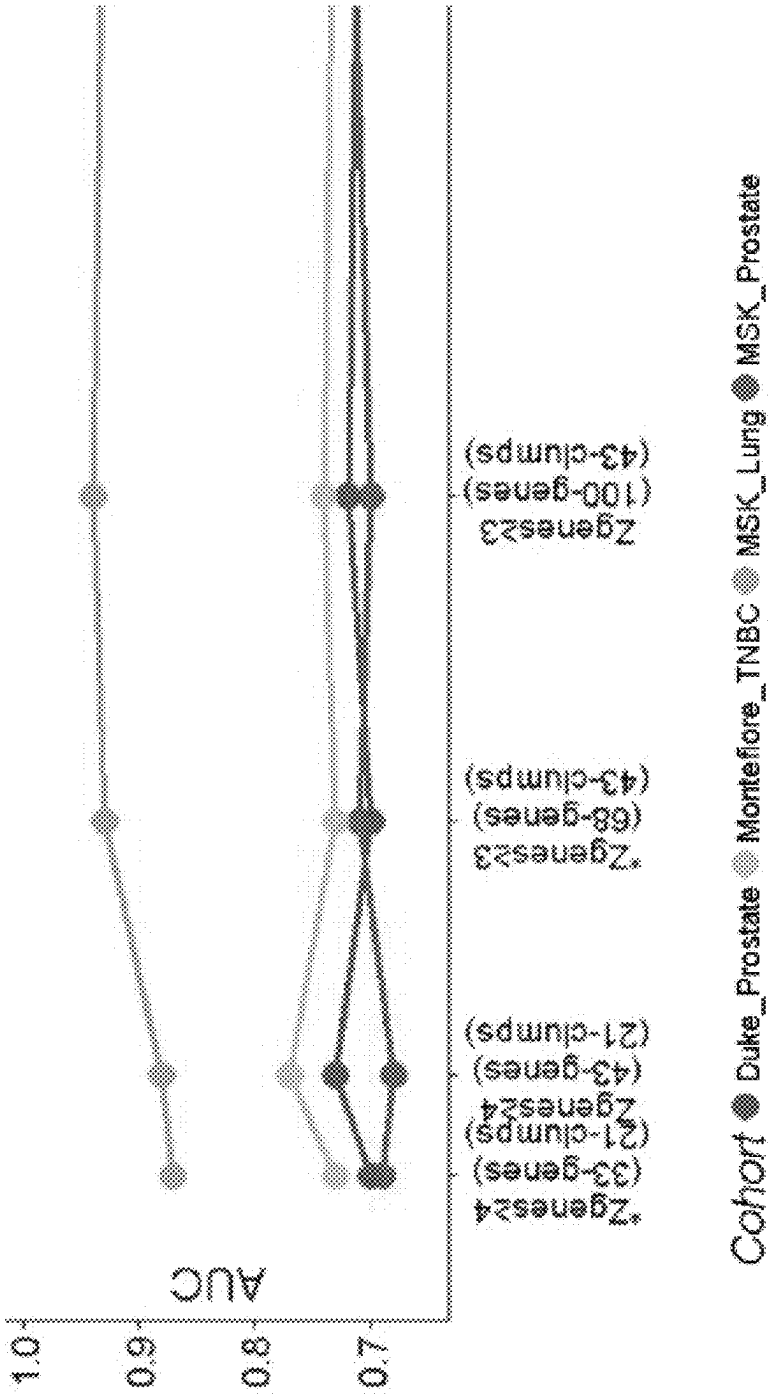

AUC
1.0
0.9
0.8
0.7
*Zgenes≥4 (33-genes) (21-clumps)
Zgenes≥4 (43-genes) (21-clumps)
*Zgenes≥3 (68-genes) (43-clumps)
Zgenes≥3 (100-genes) (43-clumps)
Cohort Duke_Prostate Montefiore_TNBC MSK_Lung MSK_Prostate

FIG. 5A

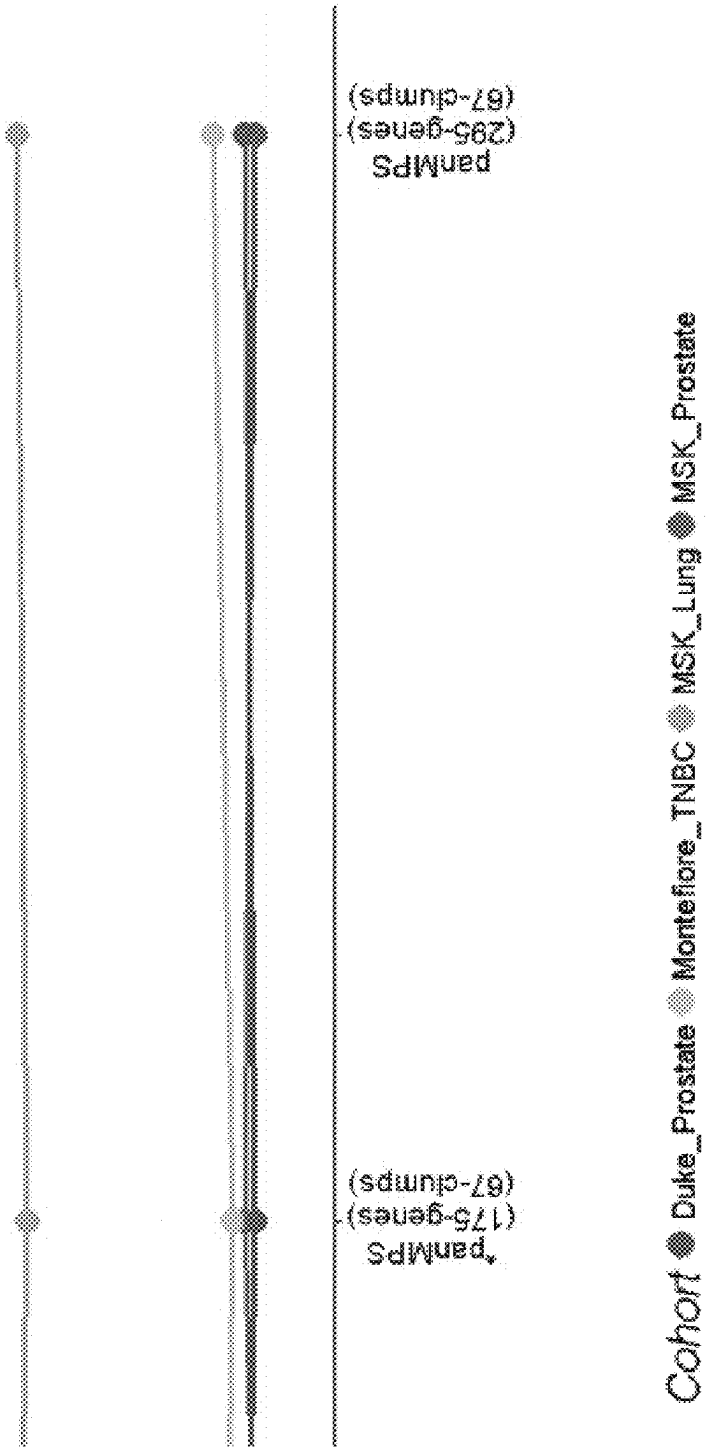

*panMPS
(175-genes)
(67-dumps)
panMPS
(285-genes)
(67-dumps)
Cohort
Duke_Prostate
Montefiore_TNBC
MSK_Lung
MSK_Prostate

FIG. 5A Cont'd

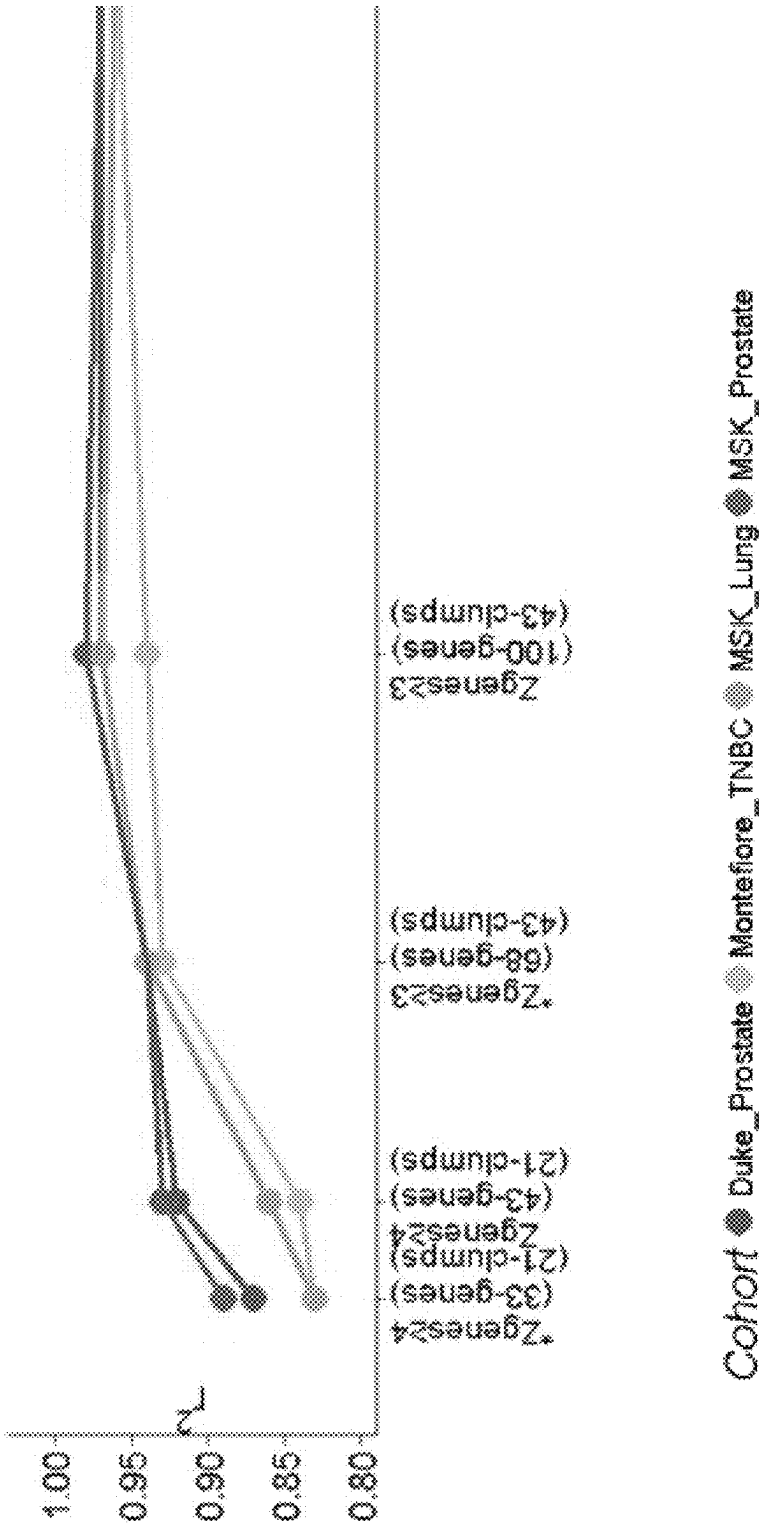

1.00
0.95
0.90
0.85
0.80
AUC
*Zgenes≥4 (33-genes) (21-clumps)
Zgenes≥4 (43-genes) (21-clumps)
*Zgenes≥3 (68-genes) (43-clumps)
Zgenes≥3 (100-genes) (43-clumps)
Cohort Duke_Prostate Montefiore_TNBC MSK_Lung MSK_Prostate

FIG. 5B

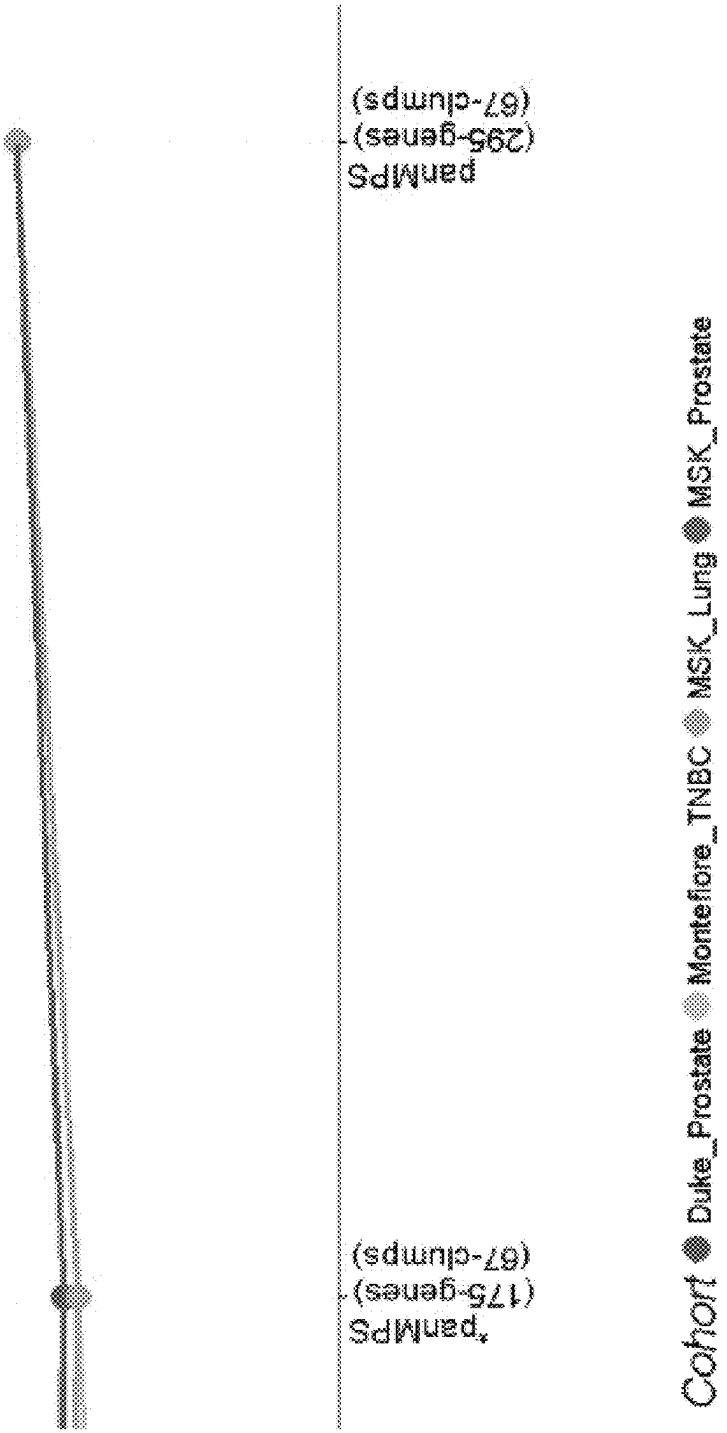

panMPS
(67-clumps)
(295-genes)
panMPS
(67-clumps)
(175-genes)
Cohort Duke_Prostate Montefiore_TNBC MSK_Lung MSK_Prostate

FIG. 5B Cont'd

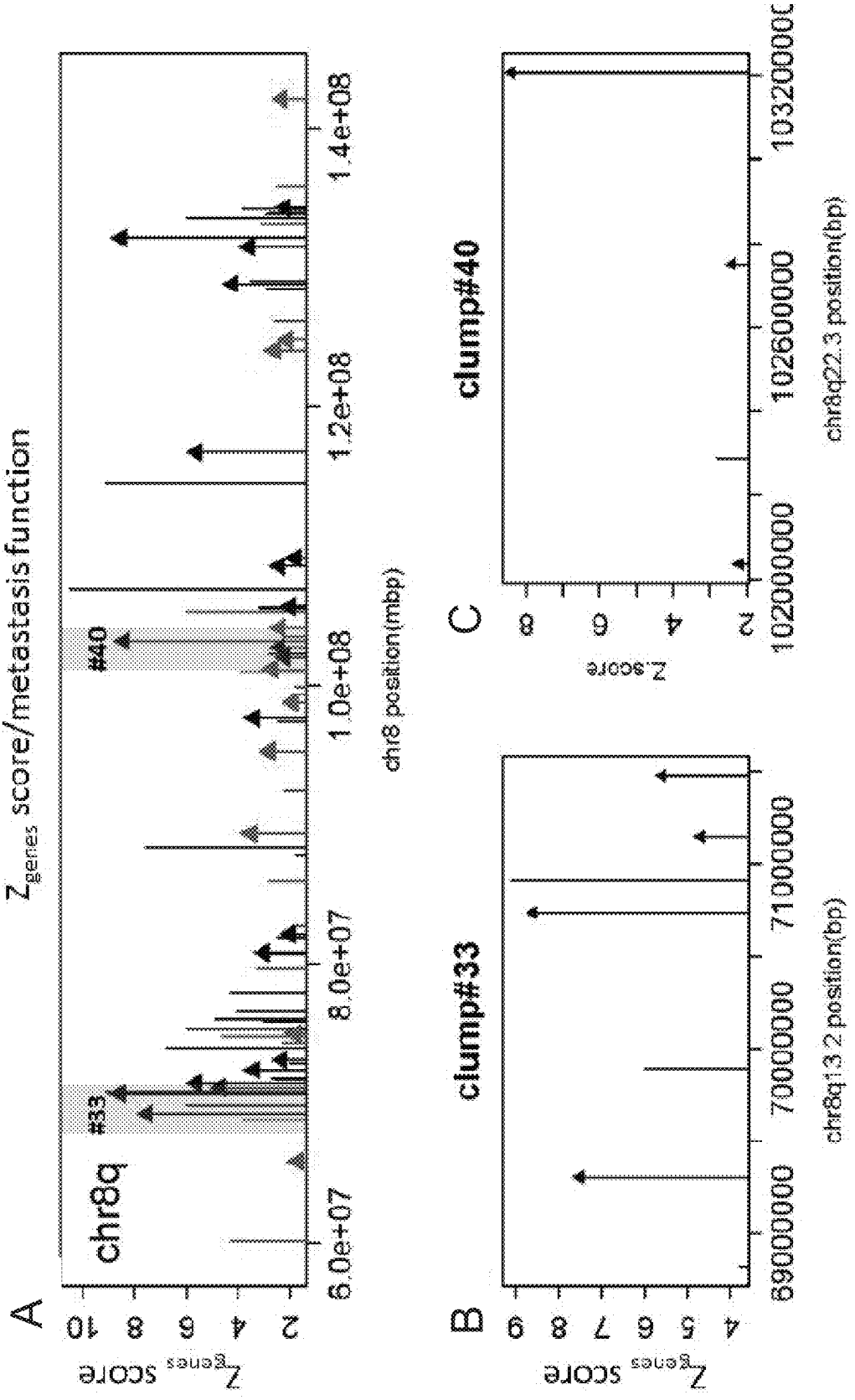

A
chr8q
#33
#40
Z_{genes} score/metastasis function
Z_{genes} score
chr8 position(mbp)
B
clump#33
chr8q13.2 position(bp)
C
clump#40
Z_score
chr8q22.3 position(bp)

FIG. 6A - 6C

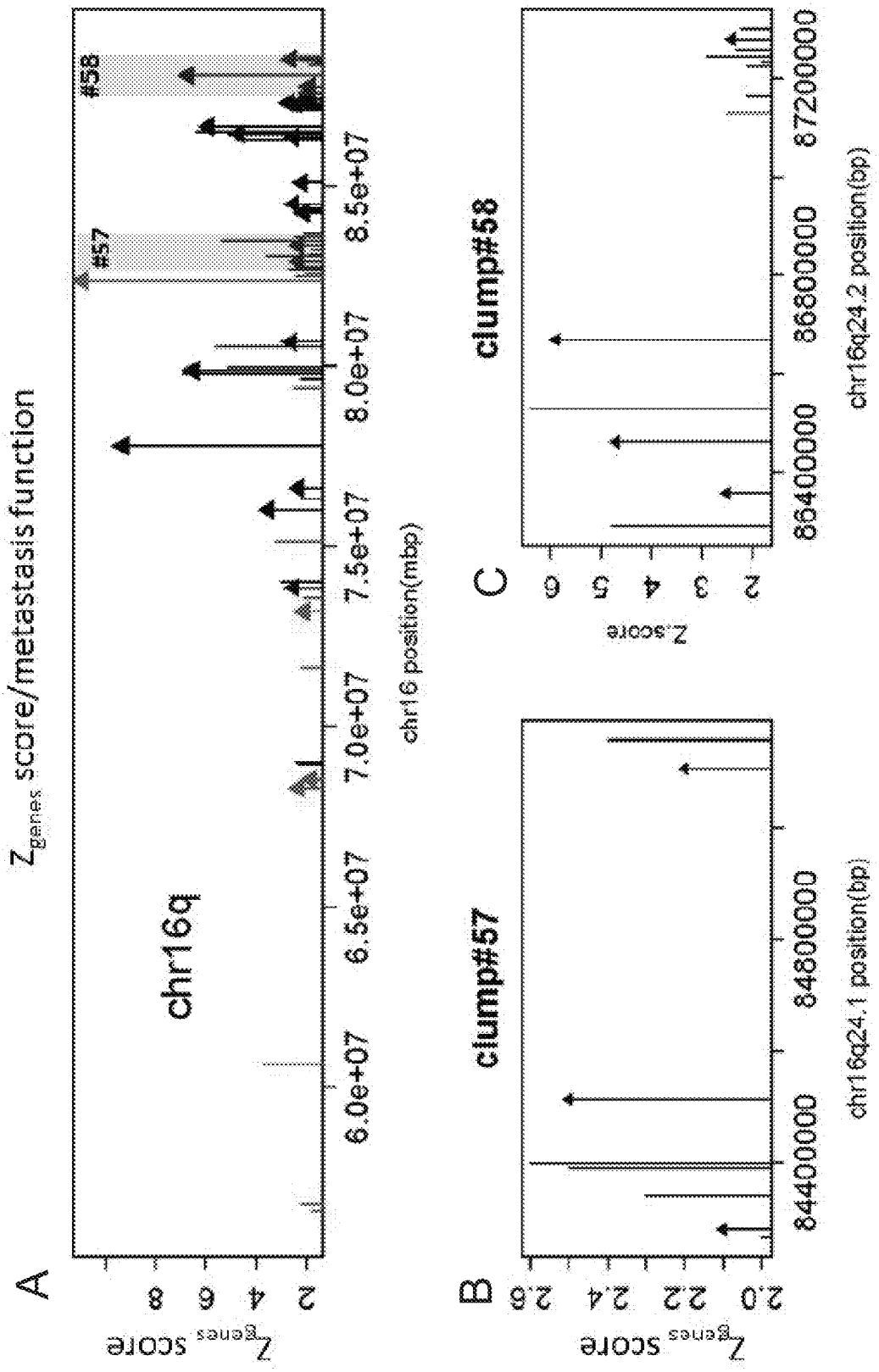

A
Z_{genes} score/metastasis function
chr16q
#57
#58
Z_{genes} score
2
4
6
8
6.0e+07
6.5e+07
7.0e+07
7.5e+07
8.0e+07
8.5e+07
chr16 position(mbp)
B
clump#57
Z_{genes} score
2.0
2.2
2.4
2.6
84400000
84800000
chr16q24.1 position(bp)
C
clump#58
Z_score
2
3
4
5
6
86400000
86800000
87200000
chr16q24.2 position(bp)

FIG 7A - 7C

ROBUST GENOMIC PREDICTOR OF BREAST AND LUNG CANCER METASTASIS

CROSS REFERENCE TO RELATED APPLICATION

This application is the continuation of PCT/US2019/016268 which claims the benefit of priority from U.S. Provisional Application No. 62/625,553, filed Feb. 2, 2018, the entire contents of which are incorporated herein by reference.

FIELD OF THE DISCLOSURE

This disclosure relates to metastatic gene signatures. More particularly, this disclosure has identified copy number alterations (CNAs) around genes that are over-represented in breast and lung cancer metastases, which serve as the basis for predicting whether a primary tumor will metastasize.

BACKGROUND OF THE DISCLOSURE

Tumor metastasis to distant sites results in 90% of solid tumor cancer deaths (Nguyen, D. X. et al., *Nat Rev Genet,* 8, 341-52 (2007)). The frequency with which metastasis occurs varies by tumor type and even within a tumor type the time to metastasis can be quite variable from the time at diagnosis to many years in the future. Nonetheless, many of the steps involved in the development of metastasis, invasion beyond the site of origin, escape from apoptosis when detached from the matrix of origin, and colonization of distant sites, are shared across tumor types. These steps are genetically encoded. Metastasis-promoting genes that alter cellular functions in cell lines and in animal models have been identified (Nguyen, D. X. et al., *Nat Rev Genet,* 8, 341-52 (2007); *Vogelstein, B. & Kinzler, K. W., Nat Med,* 10, 789-99 (2004); and Hunter, K. W., *Br J Cancer,* 752-5 (2004)).

Analysis of copy number alterations (CNAs) has proven to be fruitful for identifying recurrent events that are associated with metastasis within specific primary tumor types (Taylor, B. S. et al., *Cancer Cell,* 18, 11-22 (2010); Pearlman, A. et al., *J Probab Stat,* 2012, 873570 (2012) and US Patent Publication No. 2014/0221229). CNAs are the genetic changes most commonly observed in human cancers, reflecting the innate chromosomal instability of many tumors (Vogelstein, B. & Kinzler, K. W., *Nat Med,* 10, 789-99 (2004)). An average one-third of a cancer genome demonstrates CNAs with roughly equal distributions of copy number gains and losses (Beroukhim, R. et al., *Nature,* 463, 899-905 (2010).). CNAs are accentuated when mutations occur in stability genes that affect the repair of DNA, mitotic recombination or chromosomal segregation (Vogelstein, B. & Kinzler, K. W., *Nat Med,* 10, 789-99 (2004)). In a previous study, the inventors observed that despite the high frequency of these CNAs throughout the genome, 366 genes within these regions were commonly altered with similar patterns in prostate cancer metastases and primary tumors (Pearlman, A. et al., *J Probab Stat,* 2012, 873570 (2012)). Sixty-five percent of the genes (241 of 366) were structured on the genome as contiguous gene clumps of two through thirteen genes per clump. The remaining 35% of the genes (125 of 366) were observed as singletons.

Knowledge of these genes and their CNAs could have clinical utility for predicting who might have aggressive disease requiring treatment and whose disease might be indolent. To make such predictions, the inventors developed a metastatic potential score (MPS) that was based on the weighted frequency of specific CNAs overlapping 366 genes observed in prostate cancer metastases (Pearlman, A. et al., *J Probab. Stat.,* 2012, 873570 (2012)). In particular, metastases and metastasis-prone primary tumors all demonstrate enrichment of specific CNAs in one direction. This directionality provided a basis for calculating Z_{genes} scores for the specific genes within the CNAs that included a penalty when the CNA went against the grain of the directionality. The MPS score represented the sum of the Z_{genes} scores, divided by the number of genes being summed. When applied to a small cohort of 60 primary prostate tumors, of which 13 had metastasis outcome, MPS was predictive of the endpoint of metastasis-free survival using a Cox proportional hazards model (Pearlman, A. et al., *J Probab Stat,* 2012, 873570 (2012)).

In this disclosure, the inventors assessed the prevalence of these CNAs among large numbers of primary prostate cancers, triple negative breast cancers, other breast cancers and lung adenocarcinomas with known outcome. The inventors used a subset of the CNA genes to develop a predictive pan-cancer metastatic potential score (panMPS), because the four cohorts were assayed on different array platforms that represented different CNA genes. The panMPS was derived by using 295 of the 366 CNA genes that overlapped across all array platforms. Although 71 CNA genes were not represented in the panMPS, most of these were located in multi-gene clumps, thereby capturing the content of 67 of the 69 clumps, with no loss in the predictive accuracy for the panMPS relative to the MPS using 366 genes (Table 13, except the two pseudogenes (C8orf16 and ERW)). The inventors also observed high frequencies of these alterations in metastatic cell lines for tumors of eight different origins.

BRIEF DESCRIPTION OF THE DRAWINGS

The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawing(s) will be provided by the Office upon request and payment of the necessary fee

FIG. **1**A-**1**D. Receiver operating characteristic curves estimate the accuracy of the panMPS for predicting metastatic outcome for prostate cancer (A. MSK cohort, B. Duke cohort), triple negative breast cancer (C. Montefiore cohort) and lung adenocarcinoma (D. MSKCC cohort). For prostate cancer, panMPS was predictive of mPT and iPT status in both the MSK and Duke cohorts. In addition, preoperative PSA, biopsy Gleason score, and percent genomic instability were predictive of mPT and iPT status in the MSK cohort, only. The AUC is indicated for each curve.

FIG. **2**A-**2**D. Kaplan Meier analysis shows that MPS is associated with overall survival. A. Metabric breast cancer (N=1980); B. TCGA breast cancer (N=1054); C. TCGA prostate cancer (N=482); D. TCGA lung adenocarcinoma (N=483). Y-axis indicates overall survival probability and X axis indicates survival time. p-value calculated by log-rank test.

FIG. **3**. MPS genes show higher functional and biomarker annotations than 100 random sets of 366 genes. Number of genes found to have Pubmed citations for metastasis functions for random sets of genes (grey) and MPS genes (black). There were 2 outliers the exceeded the upper fence, the MPS genes (N=60) and one random set (N=69).

FIG. **4**A-**4**C. Chromosome 8p exhibiting 70 genes predictive of metastatic potential, including genes that occur in clumps (A). Each bar represents a gene as it is located on the chromosome (X-axis) whereas the height of the bar denotes

a Zgenes score (Y-axis) that measures the gene CNA profile's ability to predict the metastatic potential of a primary prostate cancer. Arrows on top of some of the bars indicate that the gene has been validated in prior metastasis studies as a biomarker or to have metastatic function. Clump region #26 (nine gene segment) and clump region #30 (seven gene segment) are highlighted in the top panel and zoomed in (B) (Clump region #26) and (C) (Clump region #30).

FIG. **5**A-**5**B. Small sets of high Zgenes score genes predict metastatic outcome and panMPS almost as well as all MPS genes for all four cohorts. ROC-AUCs estimating metastatic outcome and linear regression (r^2) estimating panMPS for all four cohorts demonstrate reduction of complexity for high Z_{genes} score genes. AUC (A) and r^2 (B) estimating metastatic outcome and panMPS, respectively, for simplified versions of MPS, including those with high Z_{genes} scores. Numbers of genes and clumps are indicated for different Z_{genes} scores. * one gene per clump.

FIG. **6**A-**6**C. Chromosome 8q exhibiting 75 genes predictive of metastatic potential, including genes that occur in clumps (A). Each bar represents a gene as it is located on the chromosome (X-axis) whereas the height of the bar denotes a Z_{genes} score (Y-axis) that measures the gene CNA profile's ability to predict the metastatic potential of a primary prostate cancer. Arrows on top of some of the bars indicate that the gene has been validated in prior metastasis studies as a biomarker or to have metastatic function. Red colored bars/arrows indicate a singleton gene or one member clump. Clump region #33 (six-gene segment) and clump region #40 (four-gene segment) are highlighted in (A) and zoomed in (B) (Clump region #33) and (C) (Clump region #40).

FIG. **7**A-**7**C. Chromosome 16q exhibiting 74 genes predictive of metastatic potential, including genes that occur in clumps (A). Each bar represents a gene as it is located on the chromosome (X-axis) while the height of the bar denotes a Z_{genes} score (Y-axis) that measures the gene CNA's ability to predict the metastatic potential of a primary prostate cancer tumor. Arrows on top of some of the bars indicate that the gene has been validated in prior metastasis studies as a biomarker or to have metastatic function. Red colored bars/arrows indicate a singleton gene or one member clump. Clump region #57 (8-gene segment) and clump region #58 (13-gene segment) are highlighted in (A) and zoomed in (B) (Clump region #57) and (C) (Clump region #58).

DETAILED DESCRIPTION

This disclosure provides a risk model that reliably predicts those tumors that are likely to metastasize, while minimizing the false positive rate and increasing the specificity of treatment decisions.

The risk model has been developed through the identification of copy number alterations (CNAs) around genes that were over-represented in metastases and primary tumors that later progressed to metastases. These CNAs are predictive of whether a primary tumor will metastasize. Cross-validation analysis has revealed a predictive accuracy of 80.5% and log rank analysis of the metastatic potential score has been shown to be significantly related to the endpoint of metastasis-free survival (p=0.014). In contrast to other reported risk models, the risk model disclosed herein based on the study of CNAs predicts distant metastasis progression as the clinical endpoint without the use of intermediate endpoints (such as biochemical markers of progression). The hierarchy of the genes and genomic regions that contribute to the prediction of metastatic potential has also been determined.

Accordingly, disclosed herein is a method for determining the risk of metastasis of breast or lung cancer in a human subject who has or had breast or lung cancer. This method is based on determining in a breast or lung sample from the subject, copy number alterations (CNAs) of genes and genomic regions of a metastatic gene signature set, and correlating the CNAs with a risk of breast or lung cancer metastasis.

The present method is useful for diagnosing breast and lung cancer in fluid aspirates or lavage or cell-free DNA in scrum, monitoring therapeutic response in tissue, fluid or blood samples, and monitoring disease recurrence or progression in tissue, fluid or blood samples.

Metastatic Gene Signature

Metastatic gene signatures have been developed by the present inventors as described in detail in U.S. patent application Ser. No. 14/114,057 and hereinbelow. Accordingly, in one embodiment, this disclosure provides a metastatic gene signature set which includes the 366 genes identified herein, set forth in Table 13 (Table 13 has 368 genes, but the two pseudogenes C8orf16 and ERW are excluded from the gene signature set).

As displayed in Table 3, the 366 genes include a number of "clumps", each clump identified by a "Clump Index Number". A "clump", as used herein, refers to a group of genes that are adjacent to one another on the chromosome, and copy number alterations are detected for the genomic region which includes this group of genes in connection with prostate cancer metastasis. A multi-member clump may include both drivers (genes that cause or more directly associate with metastasis) and passengers (genes that indirectly associate with metastasis because of its close proximity of a metastasis driver gene).

The term "genomic region" is used herein interchangeably with the term "clump", and is typically used herein in conjunction with the name of a member gene within the genomic region or clump. For example, the PPP3CC gene listed in the first row of Table 14 belongs to Clump Index 26, which also includes the genes KIAA1967, BIN3, SORBS3, PDLIM2, RHOBTB2, SLC39A14, EGR3, and C8orf58. Therefore, Clump Index 26 is also referred to herein as "the PPP3CC genomic region".

While many of the 366 genes belong to clumps, some of the genes do not belong to any clump and copy number alterations have been identified specifically around each of these genes in connection with metastasis of prostate cancer. For example, as shown in Table 14 (with "NA" in the Clump Index column), CDH13, CDH8, CDH2 CTD8, COL19A1, YWHAG, and ENOX1, among many others, are genes which do not belong to any clump.

In other embodiments, this disclosure provides smaller metastatic gene signature sets which include at least 80, at least 40, at least 20, or at least 12, non-overlapping genes and/or genomic regions listed in Table 14.

By "non-overlapping" it is meant that the genes selected to constitute a smaller signature set do not belong to the same genomic region or clump.

Accordingly, in one embodiment, a metastatic gene signature set includes at least the top 80 genes and genomic regions shown in Table 14.

In another embodiment, a metastatic gene signature set includes at least the top 40 genes and genomic regions shown in Table 14.

In still another embodiment, a metastatic gene signature set includes at least the top 20 genes and genomic regions shown in Table 14.

In yet another embodiment, a metastatic gene signature set includes at least the top 12 genes and genomic regions shown in Table 14.

Determination of Copy Number Alterations (CNAs)

A copy number alteration is a variation in the number of copies of a gene or genomic region present in the genome of a cell. A normal diploid cell typically has two copies of each chromosome and the genes contained therein. Copy number alterations may increase the number of copies, or decrease the number of copies.

To determine whether there is any copy number alteration for a given gene or genomic region, a sample is obtained from a subject of interest, wherein the sample can be from lung or breast tissue. A breast sample refers to a cell or tissue sample taken from the breast of a subject of interest which sample contains genomic DNA to be analyzed for CNAs. A lung sample refers to a cell or tissue sample taken from the lung of a subject of interest which sample contains genomic DNA to be analyzed for CNAs. Methods of procuring cell and tissue samples are well known to those skilled in the art, including, for example, tissue sections, needle biopsy, surgical biopsy, and the like. For a cancer patient, cells and tissue can be obtained from a tumor. A cell or tissue sample can be processed to extract, purify or partially purify, or enrich or amplify the nucleic acids in the sample for further analysis.

Nucleic acid probes are designed based on the genes and genomic regions of a metastatic signature gene set which permit detection and quantification of CNAs in the genes and genomic regions.

In one embodiment, the probes are composed of a collection of nucleic acids that specifically hybridize to the full set of 366 genes of the metastatic signature gene set.

In another embodiment, the probes are composed of a collection of nucleic acids that specifically hybridize to the top 80 genes and genomic regions shown in Table 14.

In still another embodiment, the probes are composed of a collection of nucleic acids that specifically hybridize to the top 40 genes and genomic regions shown in Table 14.

In yet another embodiment, the probes are composed of a collection of nucleic acids that specifically hybridize to the top 20 genes and genomic regions shown in Table 14.

In a further embodiment, the probes are composed of a collection of nucleic acids that specifically hybridize to the top 12 genes and genomic regions shown in Table 14.

By "specifically hybridize" it is meant that a nucleic acid probe binds preferentially to a target gene or genomic region under stringent conditions, and to a lesser extent or not at all to other genes or genomic regions.

"Stringent conditions" in the context of nucleic acid hybridization are known in the art, e.g., as described in Sambrook, *Molecular Cloning: A Laboratory Manual* (2^{nd} ed.) vol. 1-3, Cold Spring Harbor Laboratory, Cold Spring Harbor Press, New York (1989). Generally, highly stringent hybridization and wash conditions are selected to be about 5° C. lower than the thermal melting point for a specific sequence at a defined ionic strength and pH. An example of highly stringent hybridization conditions is 42° C. in standard hybridization solutions. An example of highly stringent wash conditions include 0.2×SSC at 65° C. for 15 minutes. An example of medium stringent wash conditions is 1×SSC at 45° C. for 15 minutes. An example of a low stringency wash is 4×-6×SSC at room temperature to 40° C. for 15 minutes.

Nucleic acid probes for purposes of this invention should be at least 15 nucleotides in length to permit specific hybridization to a target gene or genomic region, and can be 50, 100, 200, 400, 600, 800, 1000, or more nucleotides in length, or of a length ranging between any of the two above-listed values. A nucleic acid probe designed to specifically hybridize to a target gene can include the full length sequence or a fragment of the gene. A nucleic acid probe designed to specifically hybridize to a specific target genomic region can include at least a fragment of the genomic region, e.g., at least the full length sequence or a fragment of a gene (any gene) within the genomic region. Alternatively, a nucleic acid probe shares at least 80%, 85%, 90%, 95%, 98%, 99% or greater sequence identity with the target gene to permit specific hybridization.

The hybridized nucleic acids can be detected by detecting one or more labels attached to the sample or probe nucleic acids. The labels can be incorporated by a variety of methods known in the art, and include detectable labels such as magnetic beads, a fluorescent compound (e.g., Texas red, rhodamine, green fluorescent protein and the like), radio isotope, enzymes, colorimetric labels (e.g., colloidal gold particles). In other embodiments, the sample or probe nucleic acids can be conjugated with one member of a binding pair, and the other member of the binding pair is conjugated with a detectable label. Binding pairs suitable for use herein include biotin and avidin, and hapten and a hapten-specific antibody.

A number of techniques for analyzing chromosomal alterations are well known in the art. For example, fluorescence in-situ hybridization (FISH) can be used to study copy numbers of individual genetic loci or regions on a chromosome. See, e.g., Pinkel et al., Proc. Natl. Acad. Sci. USA 85: 9138-9142 (1988). Comparative genomic hybridization (CGH) can also be used to detect copy number alterations of chromosomal regions. See, e.g., U.S. Pat. No. 7,638,278.

In some embodiments, hybridization is performed on a solid support. For example, probes that specifically hybridize to signature genes and genomic regions can be spotted or immobilized on a surface, e.g., in an array format, and subsequently samples containing genomic DNA are added to the array to permit specific hybridization.

Immobilization of nucleic acid probes on various solid surfaces and at desired densities (e.g., high densities with each probe concentrated in a small area) can be achieved by using methods and techniques known in the art. See, e.g., U.S. Pat. No. 7,482,123 B2. Examples of solid surfaces include nitrocellulose, nylon, glass, quartz, silicones, polyformaldehyde, cellulose, cellulose acetate; and plastics such as polyethylene, polypropylene, polystyrene, and the like; gelatins, agarose and silicates, among others. High density immobilization of nucleic acid probes are used for high complexity comparative hybridizations which will reduce the total amount of sample nucleic acids required for binding to each immobilized probe.

In some embodiments, the arrays of nucleic acid probes can be hybridized with one population of samples, or can be used with two populations of samples (one test sample and one reference sample). For example, in a comparative genomic hybridization assay, a first collection of nucleic acids (e.g., sample from a possible tumor) is labeled with a first label, while a second collection of nucleic acids (e.g., control from a healthy cell or tissue) is labeled with a second label. The ratio of hybridization of the nucleic acids is determined by the ratio of the two labels binding to each member in the array. Where there are genomic deletions or amplifications, differences in the ratio of the signals from the two labels will be detected and provide a measure of the copy number.

The calculated metastatic potential score is compared to a reference distribution of samples (the metastatic potential score determined from a population of men with prostate cancer with metastasis-free survival clinical outcome information). Such reference distributions can be predetermined or calculated side-by-side in the same experiment as the sample being investigated. Therefore, an increase in the metastatic potential score as compared to the reference distributions is correlated with an increased risk of metastasis of prostate cancer. According to this disclosure, a one-point increase in the metastatic potential score corresponds to an odds ratio of 6.3 for progression to metastasis (p=0.01).

Determination of Risk

Once copy number alterations for each of a metastatic signature gene set have been determined, the risk for metastasis can be correlated with the copy number alterations detected. An increase in the copy number per cell of the sample for one or more of the genes or genomic regions of a metastatic signature gene set disclosed herein, whose amplifications have been associated with metastatic prostate cancer, will indicate a higher risk of metastasis as compared to a control (e.g., a sample obtained from a healthy individual) in which no increase in the copy number occurs. On the other hand, a decrease in the sample in the copy number for one or more of the genes or genomic regions of a metastatic signature gene set disclosed herein, whose deletions have been associated with metastatic prostate cancer, will indicate a higher risk of metastasis as compared to a control in which no decrease in the copy number is observed.

For example, for a metastatic signature gene set composed of the top 20 genes and genomic regions listed in Table 6, an increase in the copy number per cell of the sample for all of the SLCOSA1 genomic region, the KCNB2 genomic region, the KCNH4 genomic region, the JPH1 genomic region, the NCALD genomic region, and the YWHAG gene, and a decrease in the sample in the copy number per cell of the sample for all of the PPP3CC genomic region, the SLC7A5 genomic region, the SLC7A2 genomic region, the CRISPLD2 genomic region, the CDH13 gene, the CDH8 gene, the CDH2 gene, the ASAH1 genomic region, the CTD8 gene, the MEST genomic region, the COL19A1 gene, the MAP3K7 genomic region, the NOL4 genomic region, and the ENOX1 gene, correlate with an increased risk of breast cancer or lung cancer metastasis. However, it is not necessary for all the genes and genomic regions within a signature set to change in the same direction as set forth in Table 6 in order to have a reasonably reliable prediction of the risk. That is, an increased risk can be predicted based on an increase in the copy number per cell of the sample for one or more, preferably a plurality of, the SLCO5A1 genomic region, the KCNB2 genomic region, the KCNH4 genomic region, the JPH1 genomic region, the NCALD genomic region, and the YWHAG gene, and/or a decrease in the sample in the copy number per cell of the sample for one or more, preferably a plurality of, the PPP3CC genomic region, the SLC7A5 genomic region, the SLC7A2 genomic region, the CRISPLD2 genomic region, the CDH13 gene, the CDH8 gene, the CDH2 gene, the ASAH1 genomic region, the CTD8 gene, the MEST genomic region, the COL19A1 gene, the MAP3K7 genomic region, the NOL4 genomic region, or the ENOX1 gene. By "plurality" it is meant at least 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 of the top 20 genes and gene regions listed in Table 14.

This disclosure also provides a quantitative measure of the risk based on the copy number alterations of a signature gene set disclosed herein. More specifically, the risk of metastasis has been found to correlate with a metastatic potential score calculated based on the formula:

$$M(SM) = \sum_{i}^{n} Zadjust_i * Dir_{sig}(i) * Dir_{samp}(i)$$

That is, for a particular gene or genomic region, if the CNA of the signature and the sample are in the same direction (amplified or deleted), the coefficient (coefficient is shown as Dir, wherein Dir (i)=Dir_{sig} (i)*Dir_{samp} (i) in the formula above) will be 1, the logistic adjusted Z-score (Zadjust) for this gene or genomic region will be added; if in opposing directions, the coefficient will be −1, the logistic adjusted Z-score (Zadjust) for the gene or genomic region will be substracted; and if Dir_{samp}(i)=0, then the entire term will not count towards the score. Thus, essentially, the logistic adjusted Z-scores from genes (i . . . n) that match the metastasis signature are added, whereas from genes that mismatch the signature are subtracted. The logistic adjusted Z-scores (Zadjust) for each of the 366 genes of the full metastatic signature set are found in Table 14.

The calculated metastatic potential score is compared to a reference distribution of samples (the metastatic potential score determined from a population of patients with breast or lung cancer with metastasis-free survival clinical outcome information, also called herein "the reference metastatic potential score"). Such reference distributions can be predetermined or calculated side-by-side in the same experiment as the sample being investigated. In many of the embodiments, the reference metastatic potential score equals to or is approximately 1.0. Therefore, an increase in the metastatic potential score of a test subject as compared to the control score from the reference distributions is correlated with an increased risk of metastasis of breast or lung cancer. According to this disclosure, a one-point increase in the metastatic potential score corresponds to an odds ratio of 6.3 for progression to metastasis (p=0.01). In some embodiments, an increase in the metastatic potential score as compared to a reference score by at least about 0.5, 0.53, 0.56, 0.58, 0.6, 0.65, 0.7 or greater, is considered to represent a significantly high risk of metastasis.

The disclosed method for predicting the likelihood of distant metastases represents a significant advancement in the diagnosis and treatment of breast and lung cancer. This predictor may be important for correctly categorizing patients at the time of diagnosis and can lead to a choice of therapy that would maximize their chances of survival and minimize adverse side effects if aggressive treatment can be avoided. Thus, both treatment outcomes and quality of life could be improved. In addition, because the proposed tool, tumor genomic analysis, is comprehensive for identifying the genetic changes that are associated with pathogenesis and metastases, there is a greater likelihood of selecting a sufficient number of markers that are both sensitive and specific predictors. Furthermore, because these genomic alterations are themselves susceptible to manipulation with drugs, radiation or other therapies, they could provide a basis for assessing intermediate endpoints, such as androgen sensitivity and response to radiation. Ultimately, copy number alterations could guide the development of individually tailored therapies, including for cancers other than prostate, breast or lung.

Methods for Detecting Copy Number Alterations (CNAs)

The following methods can be utilized in detection of copy number alterations.

Multiplex Ligation-dependent Probe Amplification (MLPA)

Multiplex Ligation-dependent Probe Amplification (MLPA®) is a high-throughput method developed to determine the copy number of up to 50 genomic DNA sequences in a single multiplex PCR-based reaction. MLPA is easy to perform, requires only 20 ng of sample DNA and can distinguish sequences differing in only a single nucleotide. The MLPA reaction results in a mixture of amplification fragments ranging between 100 and 500 nt in length which can be separated and quantified by capillary electrophoresis. The equipment necessary for MLPA is identical to that for performing standard sequencing reactions: a thermocycler and a fluorescent capillary electrophoresis system. Comparison of the peak pattern obtained on a DNA sample to that of a reference sample indicates which sequences show aberrant copy numbers.

Fundamental for the MLPA technique is that it is not the sample DNA that is amplified during the PCR reaction, but MLPA probes that hybridise to the sample DNA. Each MLPA probe consists of two probe oligonucleotides, which should hybridise adjacent to the target DNA for a successful ligation. Only ligated probes can be exponentially amplified by PCR. In contrast to standard multiplex PCR, only one pair of PCR primers is used for the MLPA PCR reaction, resulting in a more robust system. This way, the relative number of fragments present after the PCR reaction depends on the relative amount of the target sequence present in a DNA sample. MLPA protocol is described in detail in Eijk-Van Os PG. et al. (*Methods Mol Biol.* 2011; 688:97-126).

Quantitative Polymerase Chain Reaction (qPCR)

Quantitative real-time PCR (qPCR) is PCR visualized in real time by the use of fluorescent or intercalating dyes used to measure gene expression or gene quantification including including contiguous gene deletions or duplications. A simple method is described to quantify DNA copy number from human samples in Lijiang et al. (*Curr Protoc Hum Genet.* 2014 Jan. 21; 80:7.21.1-7.21.8).

PCR-Based Detection of DNA Copy Number Variation (dPCR)

A method for PCR-based detection of copy number of target genes in human genome using TaqMan copy number assay is described in MehrotraM. (Methods Mol Biol. 2016; 1392:27-32. doi: 10.1007/978-1-4939-3360-0_3).

Genomic Sequencing

Whole genome copy number alteration analyses and the computational approaches that can be utilized are discussed in Pirooznia et al. (*Front Genet.,* 2015; 6:138). In some embodiments, the whole genome analysis is a Next Generation (NextGen) sequencing based assay. Next-generation sequencing refers to non-Sanger-based high-throughput DNA sequencing technologies. Millions or billions of DNA strands can be sequenced in parallel, yielding substantially more throughput and minimizing the need for the fragment-cloning methods that are often used in Sanger sequencing of genomes. Next Generation Sequencing is described in Behjati et al. (*Arch Dis Child Educ Pract Ed.* 2013 December; 98 (6): 236-238).

The present description is further illustrated by the following examples, which should not be construed as limiting in any way. The contents of all cited references (including literature references, issued patents, and published patent applications as cited throughout this application) are hereby expressly incorporated by reference.

EXAMPLES

Example 1: Materials and Methods

Predictive CNAs, MPS and panMPS.

This disclosure provides an in-depth comparison of a set of 366 genes whose CNAs are predictive of breast or lung cancer metastasis. The contributions of these genes to MPS as Z_{genes} scores were reported previously (Pearlman, A. et al., *J Probab Stat,* 2012, 873570 (2012) and US Patent Publication No. 2014/0221229). These are calculated by assigning each probe on the array to a gene, provided it falls within 10,000 bp upstream or downstream of the transcription start or stop site.$z=(X-\mu)/\sigma$ as described previously (4). The score for a gene, X, is subtracted by the mean, μ, of the background distribution of selection model scores and divided by the standard deviation, σ, of the background distribution of selection model scores. A conservative background distribution of selection model scores was calculated by sampling the top 5th percentile of amplified or deleted probes from all genes on the array with the same number of probes as the gene in question. The result is a Z_{genes} score for each gene in the genome that is represented on the array. Alternatively, the complete set of genomic CNAs was used to calculate percent genomic instability. The CNA methodology is assay platform-independent, but requires that genomic DNA signal intensities are measured within the regions of the metastasis signature. In this study, the analysis was conducted on primary data sets reported here utilizing the Affymetrix Oncoscan FFPE V3 array (Foster, J. M. et al., *BMC Med Genomics* 8, 5 406 (2015)), and on previously generated data sets assayed on Agilent 240K and other arrays (Hieronymus, H. et al., *Proc Natl Acad Sci USA* 111, 11139-44 (2014)). For comparison of cohorts from different platforms, the corresponding numbers of the MPS genes were reduced to include only those that overlapped (366 to 295 genes), representing the panMPS.

Cohorts, Tissue and Sample Processing

A prostate cancer radical prostatectomy cohort of 37 men that progressed to metastasis (mPTs) and 24 men that were free from biochemical recurrence and metastases (iPTs) after at least five years of follow up was collected at Duke University (Duke cohort-Table 10A). The Duke cohort had a case-control design that matched mPTs and iPTs for age, race, pathological stage, margin status, Gleason score, and surgery year. Tumor regions were microdissected, extracted for DNA, and assayed on the Oncoscan FFPE V3 array (Affymetrix Oncoscan Service, Santa Clara, California).

A second prostate cancer cohort, comprised of 25 mPTs along with 157 iPTs was collected at Memorial Sloan-Kettering Cancer Center (MSK cohort—Table 10A). The collection, extraction and data generation for the second cohort has been described previously (Hieronymus, H. et al., *Proc Natl Acad Sci USA* 111, 11139-44 (2014)). The MSK cohort represented a consecutive case-cohort design with non-recurrent, non-metastatic outcome samples making up a disproportionate number. Unlike the Duke samples, these samples were not matched on any criteria. The MSK cohort was comprised of fresh frozen radical prostatectomies. The Duke and MSK cohorts differed in their length of follow-up, clinical and pathologic attributes and biochemical recurrence and metastasis outcomes (Table 10A). The Duke cohort was collected for individuals with greater than five years follow-up since the majority of prostate cancers recur or metastasize within this timeframe. To achieve parity for prediction modeling and maximizing the metastasis informativeness of each patient, the MSK cohort was filtered for

subjects that had at least five years of follow-up. Also, for both cohorts, metastasis negative subjects treated with radical prostatectomy and adjuvant radiation and/or hormonal therapy were excluded from analysis to provide a more homogeneous iPT group.

A triple negative breast cancer radical surgical cohort of 28 women that progressed to metastasis (mBCs) and 13 women that were free from local recurrence and metastasis (iBCs) after at least five years of follow up was collected at Montefiore Medical Center (Montefiore cohort—Table 10B). The Montefiore cohort had a case-control design that matched mBCs and iBCs for age, race, pathological stage, margin status, and surgery year. The breast cancer tumor blocks from each patient were handled in a fashion similar to the prostate cancer tumor blocks and reviewed by a single pathologist and shown to be negative for expression of the estrogen receptor, progresterone receptor and HER2/NEU protein, as judged by immunohistochemistry. Tumor regions were microdissected, extracted for DNA, and assayed on the Oncoscan FFPE V2 array (Affymetrix Oncoscan Service, Santa Clara, California).

Tumor tissue from 199 primary lung adenocarcinomas was collected at the time of resection between 1996 and 2006 at MSKCC and analyzed for CNAs on Agilent 44K CGH arrays, as described previously (Chitale, D. et al., *Oncogene* 28, 2773-83 (2009)). From this cohort, all available early stage (1A, B and 2A,B) samples that progressed to mortality (mLA, n=23) and late stage (3B and 4) samples that remained alive for greater than one year of follow up (iLA, n=10) (Table 10C) were selected.

This study was reviewed and approved by the Institutional Review Boards at Albert Einstein College of Medicine, New York University School of Medicine, and Duke University.

The copy number alterations (CNAs) level 3 data from cBioPortal for cancer genomics for 3998 patients with three tumor types (Gao J. et al., *Sci Signal* 6: pl1, 2013, Cerami E. et al., *Cancer Discov,* 2:401-4, 2012) were downloaded. Metabric and TCGA provisional study were selected for breast invasive carcinoma, TCGA provisional study was selected for Lung adenocarcinoma and TCGA provisional study was selected for prostate adenocarcinoma (Milioli H H. Et al., *PLOS One,* 10: e0129711, 2015, Pereira B. et al., *Nat Commun,* 7:11479, 2016). panMPS score was calculated based on CNAs for these studies. Univariate Cox proportional hazards model was used to examine the association between MPS and survival. Overall survival was used as the endpoint.

Cell Lines.

CNA data from 183 human cell lines of metastatic origin were available from the Cancer Cell Line Encyclopedia (CCLE). These cell lines included breast, lung adeno, pancreas, large intestine, lymphoid, melanoma, lung small cell and stomach cancers. The data were generated using the Affymetrix SNP 6.0 arrays, as described previously (Beroukhim R. et al., *Nature,* 463:899-905, 2010).

MPS and panMPS

MPS was calculated based on genomic CNAs overlapping 366 genes with a higher score indicating a greater likelihood of metastasis, as described previously (Pearlman, A. et al., *J Probab Stat,* 2012, 873570 (2012)). The pan cancer MPS or panMPS was derived from the MPS by using a subset of 295 genes from the MPS. Univariate and multivariate logistic regression and Cox proportional hazards survival models for prostate cancer were evaluated for panMPS, pre-surgery predictors (PSA, clinical stage, biopsy Gleason), demographic variables (age at diagnosis and race), and percent genomic instability, as described previously (Hieronymus, H. et al., *Proc Natl Acad Sci USA* 111, 11139-44 (2014)). The logistic regression and Cox models were also tested for triple negative breast cancer and lung adenocarcinoma. AUC and concordance index were calculated for the logistic and Cox models, respectively.

Functions of MPS Genes in Driving Metastases

To gauge whether the MPS genes played a role in metastasis, we performed in-silico analysis by running three comprehensive queries with the RISmed package from R. First we performed a general Pubmed citation query by searching for the 366 gene IDs and the terms "metastasis", "metastases" or "metastatic" in the title or abstract of the publication ("metastasis IDs"). Next, we appended this query to capture metastasis functions by adding search terms, "apoptosis assay", "TUNEL", "Matrigel", "invasion assay", "wound healing assay", "migration assay", "MTT", "BrDU", "proliferation assay", "SiRNA" and "xenograft" ("metastasis functions"). Then, the title query was appended to capture predictive biomarkers of metastasis by adding search terms, "Cox", "Kaplan-Meier" and "hazard ratio" ("metastasis biomarkers"). The MPS gene queries were manually curated and confirmed for accuracy by two reviewers. The annotation frequency was computed for each query type. To assess the significance of these annotations for the MPS genes compared to the remaining, non-overlapping 18,638 protein coding genes an enrichment analysis based on the hypergeometric distribution was performed for the MPS genes versus all 19,004 protein coding genes annotated using the same query search terms to create expanded gene sets for metastasis ID, metastasis functions, metastasis biomarkers and chemokine ID.

Reduction of Complexity

To determine whether the genes with the highest Z_{genes} score among the clumps could predict outcomes as well as the full set of panMPS genes, we calculated AUC and r^2 for simplified MPS versions by using genes with Z_{genes} score≥3, Z_{genes} score≥4, or highest Z_{genes} score within a clump.

Example 2. panMPS Predicts Risk of Metastasis Outcome for Prostate and Triple Negative Breast Cancers and Lung Adenocarcinomas.

The clinical validity of panMPS as a predictor of metastasis outcome was tested in studies of prostate and triple negative breast cancers and lung adenocarcinomas. For the outcome of prostate cancer metastasis, univariate logistic regression of panMPS resulted in significant odds ratios and areas under receiver-operator curves (AUCs) for the MSK (OR 6.01, AUC 0.71, p=0.001) and the Duke cohorts (OR 11.39, AUC 0.72, p=0.004) (Table 1A and FIG. **1**). Preoperative PSA and pathology stage improved the AUC in logistic regression analysis of the MSK cohort, but, because of matching between mPTs and iPTs, did not lead to improvement in the Duke cohort (Table 5). In univariate logistic regression analysis of the MSK cohort, percent genomic instability as a predictor had an OR 1.17, AUC=0.74, $p=1.4\times10^{-5}$; however, this predictor did not reach statistical significance in the Duke cohort (OR 1.04, AUC=0.80, p=0.12) (Table 5). This indicates that percent genomic instability, while useful in the MSK cohort, was not an independent and robust predictor of metastasis. Thus, the subset of genes comprised by panMPS contributes to prostate cancer metastasis formation when copy numbers are altered.

For the outcome of triple negative breast cancer metastasis, univariate logistic regression of panMPS resulted in a significant odds ratio and AUC for the Montefiore cohort (OR 44.74, AUC 0.75, p=0.02) (Table 1B and FIG. **1**). Percent genomic instability was not an independent predic-

tor of metastasis. Because matching had been performed for the triple negative breast cancers, stage was also not a predictor of outcome.

For the outcome of lung adenocarcinoma metastasis, univariate logistic regression of panMPS resulted in a significant AUC for the MSKCC cohort (OR 3.45×10^{3}, AUC 0.94, p=0.006) (Table 1C and FIG. **1**). Because cases with advanced stage were selected for favorable outcome and cases with early stage were selected for unfavorable outcome, stage is thus not a valid predictor of metastasis.

Example 3. panMPS Predicts Metastasis-Free Survival for Prostate Cancer, Triple Negative Breast Cancer and Lung Adenocarcinomas

As a continuous univariate predictor through a Cox model, panMPS was associated with prostate cancer metastasis-free survival in both the MSK (HR=5.4, p=0.0003, concordance index 0.74) and Duke (HR=3.4, p=0.03, concordance index 0.62) cohorts (Table 2A). In univariate Cox analysis of the MSK cohort, percent genomic instability was associated with metastasis-free survival (HR=1.11, $p=3.3\times10^{-2}$, concordance index=0.67), as previously reported for this cohort (Hieronymus, H. et al., *Proc Natl Acad Sci USA* 111, 11139-44 (2014)); however, this variable did not reach statistical significance in the Duke cohort. Biopsy and pathological Gleason scores, preoperative PSA and pathological stage and combinations of these with panMPS were predictors of metastasis-free survival in Cox analysis of the MSK cohort only (Table 6).

As a continuous univariate predictor in a Cox model, panMPS was associated with triple negative breast cancer metastasis-free survival in the Montefiore cohort (HR=4.1, p=0.05, concordance index 0.60) (Table 2B). Stage was also an independent predictor (HR=3.2, p=0.03), whereas percent genomic instability was not.

As a continuous Cox model univariate predictor, panMPS was associated with lung adenocarcinoma metastasis-free survival in the MSKCC cohort (HR=6.6, p=0.02, concordance index 0.67) (Table 2C). Stage cannot be used as a predictor as explained above.

Example 4. panMPS is Associated with Overall Survival in Breast Cancer, Prostate Cancer and Lung Adenocarcinoma.

Data about CNAs in primary cancers and their survival outcomes are available for a variety of cancer types from publically available datasets, including The Cancer Genome Atlas (TCGA) (Gao J. et al., *Sci Signal* 6: pl1, 2013, Cerami E. et al., *Cancer Discov,* 2:401-4, 2012) and Metabric (Milioli H H. Et al., *PLOS One,* 10: e0129711, 2015). To examine general utility as a predictor of survival outcome, Kaplan Meier analysis of panMPS was applied to the TGCA prostate cancer, breast cancer, and lung adenocarcinoma cohorts and the Metabric breast cancer cohort. panMPS (median cut point) was observed to be significantly associated with overall survival in the Metabric breast cancer cohort (n=1,980, $p=4.8\times10^{-08}$) and in three TCGA cohorts (breast: n=1054, p=0.015, prostate: n=483, p=0.015, and lung adenocarcinoma: n=482, p=0.025; FIG. **2**), providing evidence that panMPS is a predictor not only of metastasis, but also survival. Metastasis-free survival data were not available for these cohorts.

Example 5. panMPS is Elevated in Many Metastatic Cancer Cell Lines of Epithelial Origin.

To test applicability in other cancer types, genomic instability and panMPS were evaluated in a set of 133 cell lines of different tissue origins from the Cancer Cell Line Encyclopedia (CCLE). All cell lines were reported to be from metastatic tumors. The median number of protein coding genes demonstrating CNAs ranged from 2091 for lymphoma to 6805 for pancreatic carcinoma and 6916 for stomach carcinoma, thereby confirming the high frequency of CNAs in metastases. By way of reference, the median number of genes demonstrating CNAs in a sample of clinical prostate cancer metastases was 3731. For metastatic cancer cell lines of epithelial origin, including breast, lung adenocarcinoma, pancreas and stomach, the frequency of CNAs was higher than those observed in prostate cancer metastases (p=0.04, 0.002, 3×10^{-4}, 0.005, respectively), whereas for metastatic cell lines of non-epithelial origin, including lymphoid tissue, melanoma, and lung small cell, the frequency of unstable genes was similar to that observed for prostate cancer metastases. Despite the higher frequencies of CNAs among metastatic cells lines of epithelial origin, the MPS of these cell lines, including breast, lung adenocarcinoma, pancreas, large intestine and stomach, was similar to that observed in prostate cancer metastasis. Cell lines of non-epithelial origin had either comparable (melanoma) or lower MPS (lymphoid—$p=8\times10^{-4}$, lung small cell—p=0.01) to those observed in clinical prostate cancer metastases. These findings extend the previous observation that the CNAs of cancer cell lines of a variety of origins display a specific CNA pattern (Pearlman A. et al., *J Probab Stat,* 2012: 873570, 2012), suggesting that panMPS might serve as a predictor of metastatic outcome across multiple cancer types.

Example 6. MPS Genes are More Likely to have Known Roles in Promoting Metastasis or Predicting Metastatic Outcomes than Randomly Selected Genes.

One way of gauging whether the MPS genes played a role in cancer metastasis beyond prostate and triple-negative breast cancers and lung adenocarcinomas was to identify Pubmed citations for these genes (Table 7). Further refinement of this search included metastatic functions such as cell viability, proliferation, invasion, and escape from apoptosis and for biomarker genes predictive of metastasis outcome when their copy number or expression is altered. Following guidelines for the functional interpretation of genes and their variants provided by the American College of Medical Genetics and Genomics (Richards S. et al., *Genet Med,* 17:405-24, 2015), the Association for Molecular Pathology (Rehm H L. Et al., *N Engl J Med,* 372:2235-42, 2015), and codified by the NIH-supported, Clinical Genome Resource (Strande N T., *Am J Hum Genet,* 100:895-906, 2017), each of the 366 MPS genes were annotated for literature reports. Statistical tests were then performed, first to compare MPS genes to random gene sets for metastatic functions and the second of protein coding gene sets that have known associations with metastasis functions, such as invasion, motility and escape from apoptosis when detached from matrix of origin, and chemokine activity, and for biomarker genes predictive of metastasis outcome when their copy number or expression is altered. The frequency of these citations was compared to the frequencies with which citations were observed for 100 random sets of 366 genes from the 18,638 protein coding genes that excluded overlapping MPS genes. Among the 366 MPS genes, 60 were found to have Pubmed citations for the search terms related to metastasis functions and metastasis biomarkers, whereas the range for the random sets was 26 to 69 (FIG. **2**). In fact, only one random set had a larger number of genes cited (N=69) than the observed 60, indicating that both represented outliers of non-random gene sets based on current knowledge of annotated metastasis genes. In an alternative approach the 19,004 protein coding genes were annotated for whether they had known metastasis associations ("Metastasis ID," Table 3, Table 8A), metastasis functions ("Metastasis functions," Table 3,

Table 8B) or whether they have been identified as biomarkers that were predictive of metastasis ("Metastasis biomarkers," Table 3, Table 8C). Of 2463 metastasis ID genes, 112 overlapped with MPS genes ($p=2.42\times10^{-20}$). Of 929 metastasis function genes, 40 overlapped with MPS genes ($p=1.18\times10^{-6}$). Of the 687 metastasis biomarker genes, 28 overlapped with MPS genes (p=0.0001). Thus, the MPS genes were enriched among gene sets with terms for metastasis function or metastasis biomarkers in the article.

Example 7. Elevated Z_{genes} Scores Provide Evidence for Potential Metastasis-Driver Genes.

The MPS genes occur as singleton CNAs as well as in clumps that are distributed over 15 chromosomal arms (Table 7). The genes within a clump are likely to include both drivers that are directly associated with metastasis function and passengers that are indirectly associated with metastasis function, because of their proximity to a metastasis driver gene. For example, a clump index 26 on chromosome 8p21.3 includes the nine genes, PPP3CC, KIAA1967, BIN3, SORBS3, PDLIM2, RHOBTB2, SLC39A14, EGR3, and C8orf58 (Table 7). In this clump three of the 9 genes (EGR3, PDILMS, and RHOBTB2) overlapped with the gene sets, metastasis ID, metastasis functions and metastasis biomarkers. In addition to annotations, another way of gauging whether some of the MPS genes play a role as metastasis drivers is to compare the Z_{genes} scores within clumps (Pearlman, A. et al., *J Probab Stat,* 2012, 873570 (2012) and US Patent Publication No. 2014/0221229). The clumps of genes vary by breakpoints in individual cancer genomes and the CNAs of some genes in a clump will yield higher Z_{genes} scores by being overrepresented and in the right direction expected for metastasis, compared to cancer genomes that are not metastasis-prone. The range of Z_{genes} scores within a clump varied from 1.7 to over 10 with no apparent pattern of decay for the highest Z_{genes} score gene adjacent to those with the lowest Z_{genes} score (FIG. **3**). Multiple genes within a clump had Pubmed annotations, which were not necessarily those with the highest Z_{genes} score. Some of the unannotated MPS genes with high Z_{genes} scores may also act as drivers of metastasis, but may not have been studied yet for functional roles (FIG. **5**).

Other genes, including CDH13, CDH8, CDH2, CTD8, COL19A1, YWHAG, and ENOX1, do not belong to any clump. Both the Z_{genes} scores and the annotations of these genes suggest that they may act as drivers (Table 7). However, the functions of some of these genes may overlap with each other (e.g., the cadherin genes, CDH13, CDH8, CDH2). Thus, there may be some functional redundancy among the MPS genes and, as judged by Z_{genes} scores, genes are not equally predictive of the predisposition to metastasis. Yet, some of these genes have higher Z_{genes} scores suggesting that their contributions to metastasis are observed more frequently.

Example 8. High Z_{genes} Score Genes within Clumps Predict Outcomes.

To test whether a reduced set of clumps could predict outcomes and produce similar values to those observed with panMPS, AUC and r^2 were calculated for simplified MPS versions that included genes with Z_{genes} score≥4 (21 clumps) and Z_{genes} score≥3 (43 clumps) or the highest Z_{genes} score gene within a clump. The results were compared to all 295 panMPS genes. The 21 and 43 clumps predicted AUC and r^2 almost as well panMPS, whether calculated for all genes exceeding the threshold or for only the gene with the highest Z_{genes} score (Table 9A and 9B). This result indicated that there was a hierarchy of clumps with 21 clumps (Z_{genes} score≥4) performing as well as 43 clumps (Z_{genes} score≥3) capturing almost all of the contribution of the clump to AUC and r^2. These result also indicated a lead gene within a clump could capture almost all of the contribution of the clump to AUC and panMPS r^2.

CNAs are the result of chromosomal instability and are far more common than mutations in human cancers, including prostate, triple negative breast cancer and lung adenocarcinoma (Vogelstein. B. & Kinzler, K. W., *Nat Med,* 10, 789-99 (2004), Kandoth et al., *Nature,* 502:333-9, 2013). CNAs may occur randomly across the genome or may be favored by repeated structural elements, including Alu or LINE sequences (Aguilera et al., *Annu Rev Genet.,* 47:1-32, 2013). Amplifications or deletions of genes may occur repeatedly within the same regions of genomes in populations of cancer cells within a tumor (Pearlman, A. et al., *J Probab Stat,* 2012, 873570 (2012), Shah et al., *Nature,* 486:395-9, 2012). This observation of specific CNA pattern enrichment is the basis for calculating Zgenes scores for specific genes within CNAs. In turn, MPS represents the sum of Zgenes scores, divided by the number of genes being summed. CNA burden alone (i.e. the frequency of chromosomal instability) was not an accurate predictor of outcome in most cohorts because it did not consider specific pattern nor functional contributions by specific metastatic genes.

This disclosure provides evidence that panMPS can be used as a predictor of metastasis and metastasis-free survival, not only in prostate cancer, as we have shown before (Pearlman, A. et al., *J Probab Stat,* 2012, 873570 (2012)), but also for triple negative breast cancer, other breast cancers, and lung adenocarcinoma and 133 CCLE metastasis cell lines of 8 different cancer origins. A panMPS was also able to predict overall survival in Metabric cohort of breast cancer and several large TCGA cohorts of prostate cancer, breast cancer and lung adenocarcinoma.

These observations fit a model of chromosomal rearrangements occurring in early tumorigenesis by punctuated bursts (Gao R. et al., *Nat Genet* 48:1119-30, 2016). Metastasis is driven by selection for rearrangements that promote invasion, escape from apoptosis and growth at distant sites (Nyugen D X. et al., *Nat Rev Genet* 8:341-52, 2007 PMID: 17440531). A study of mutated genes in multiple cancer types drew a similar conclusion that genes under positive selection, either in individual or multiple tumor sites, tend to display higher mutation frequencies above background (Kandoth et al., *Nature,* 502:333-9, 2013). However, large-scale targeted and whole genome sequence efforts have identified single nucleotide variants and short indels in a set of overlapping or related genes that account for carcinogenesis, but have not identified genes involved in metastasis (Kan Z. et al., *Nature* 466:869-73, 2010).

These CNAs occur on a segmental basis with multiple genes within a segment or clump being amplified or deleted. Within a clump, one or more genes could be drivers of metastasis (Kandoth et al., *Nature,* 502:333-9, 2013). The drivers showed elevated Zgenes scores and were annotated in the literature as having metastatic functions, including invasion, motility, escape from apoptosis when detached from matrix of origin, and chemokine activity. Other genes with elevated Zgenes scores, but no annotations, may also represent drivers whose functions have not yet been identified. However, the remainder of the genes may be passengers that are carried along with the CNA events. Not all of the drivers are required for predicting risk of metastasis. Testing only genes with the highest Zgenes score within a clump may capture most, if not all of the metastatic risk,

reflected by the panMPS. These genes with high Zgenes score may act as proxies for all of the genes within the clump.

Based on the hypergeometric analysis, the MPS genes indeed represent a subset of all metastatic genes, specifically those that can be readily identified by CNA analysis. Other metastatic genes would not be readily detected as they are not subject to CNA events and may need to be detected by other molecular methods, such as sequencing.

Analyzing these genes in patient samples may be required to improve the accuracy of predicting metastasis—although the current study suggests that as few as 33 genes with high Zgenes score may be sufficient for many clinical applications.

The availability of a panMPS-based diagnostic tool may contribute to clinical care. Collectively, lung, breast and prostate cancer account for ~676,000 or 40% of newly diagnosed cancer cases and ~226,000 or 39% of cancer deaths in the United States each year (Siegel R L. et al., *CA Cancer J Clin,* 65:5-29, 2015). Currently, there are no clinical tests in common use for prediction of outcomes in triple negative breast cancer or lung adenocarcinoma. Future studies will assess the accuracy of panMPS derived from surgical specimens and biopsies for predicting outcomes of these diseases.

Having a test that would accurately predict across cancer-types which patients are likely to develop metastases would be extremely useful. For example, panMPS could improve the clinical management of men with prostate cancer. Men with early-stage disease and low-risk profiles would be candidates for active surveillance that might safely preserve quality of life by helping them to avoid erectile dysfunction and urinary incontinence that may occur in up to 50% of treated patients (Cooperberg et al., *J Natl Cancer Inst* 101:878-87, 2009, Paris P L. et al., *Clinical cancer research,* 16:195-202, 2010). Men with early-stage disease and high-risk profiles might benefit from aggressive treatment (Pound C R. et al., *The Urologic clinics of North America* 24:395-406, 1997). Men with higher-risk disease who underwent initial surgery might benefit from adjuvant radiation therapy (Thompson I M., *The Journal of urology* 181:956-62, 2009). Notably, the accuracy of combined panMPS and pre-operative PSA appears to be similar to the various RNA expression profile tests plus clinical predictors for use as a post-surgical tool (Table10A-10C). These tests, Genomic Prostate Score (GPS) (Cullen J. et al., *European Urology,* 68:123-31, 2015 PMID: 25465337., Klein E A. et al., *European Urology,* 66:550-60, 2014), Cell Cycle Progression Score (CCPS) (Cuzick J. et al., *The Lancet Oncology* 12:245-55, 2011), and Genomic Classifier (GC) (Ross A E et al., *Prostate Cancer Prostatic Dis.,* 17:64-9, 2014; Cooperberg M R et al. *European Urology* 67:326-33, 2015; Erho N et al., *PLOS One,* 8: e66855, 2013; Karnes R J. et al., *J Urol,* 190:2047-53, 2013; 4097302; Den R B et al., *Int J Radiat Oncol Biol Phys,* 89:1038-46, 2014), measure the altered expression of mostly non-overlapping sets of genes that have not been demonstrated to play a direct role with the biological events of prostate cancer progression and metastasis. As with panMPS, the accuracy of these tests was improved by the addition of clinical and pathological predictors, both as univariate predictors or as captured by the Cancer of the Prostate Risk Assessment (CAPRA-S) score (Cooperberg M R et al., *Cancer,* 117:5039-46, 2011; 3170662; Greene K L et al., *The Journal of Urology* 171: 2255-9, 2004), and the Stephenson nomogram (Brockman J A. et al., *Eur Urol,* 67:1160-7, 2015). Although Oncotype DX and Prosigna are two RNA expression profile tests in common use for prognostic prediction of breast cancer, their use is limited to estrogen receptor positive breast cancer (Nielsen T. et al., *BMC Cancer,* 14:177, 2014; Kaklamani V., *Expert Rev Mol Diagn.,* 6:803-9, 2006).

TABLE 1A

Univariate logistic regression model of panMPS predicts progression to metastasis for prostate cancer

	Cohort							
	MSK prostate cancer (n = 182, mPT = 25, iPT = 157)				Duke prostate cancer (n = 61, mPT = 37, iPT = 24)			
Variable	Odds Ratio	P	95% CI	AUC	Odds Ratio	P	95% CI	AUC
panMPS	6.01	0.001	2.21 to 17.89	0.71	11.39	0.004	2.39 to 70.36	0.72

TABLE 1B

Univariate logistic regression model of panMPS predicts progression to metastasis for triple negative breast cancer Montefiore triple negative breast cancer cohort (n = 41, mBC = 28, iBC = 13)

Variable	Odds Ratio	P	95% CI	AUC
panMPS	44.74	0.02	2.91 to 1927.9	0.75

TABLE 1C

Univariate logistic regression model of panMPS predicts progression to metastasis for lung adenocarcinoma MSK lung adenocarcinoma cohort (n = 33, mLA = 23, iLA = 10)

Variable	Odds Ratio	P	95% CI	AUC
panMPS	3.45×10^3	0.006	41.5 to 1.26×10^7	0.94

TABLE 2A

Univariate Cox proportional hazards model of panMPS predicts metastasis-free survival for prostate cancer

	Cohort							
	MSK prostate cancer (n = 222, mPT = 25, iPT = 197)				Duke prostate cancer (n = 76, mPT = 37, iPT = 39)			
	Variable							
	Hazard Ratio	95% CI	Conc-indx	P	Hazard Ratio	95% CI	Conc-indx	P
panMPS	5.42	2.18 to 13.49	0.74	0.0003	3.4	1.15 to 10.12	0.62	0.03

TABLE 2B

Univariate Cox proportional hazards model of panMPS predicts metastasis-free survival for triple negative breast cancer Montefiore triple negative breast cancer cohort (n = 41, mBC = 28, iBC = 13)

Variable	Hazard Ratio	95% CI	Conc-indx	P
panMPS	4.1	1.03 to 16.04	0.60	0.05

TABLE 2C

Cox proportional hazards model of panMPS predicts metastasis-free survival for lung adenocarcinoma MSK lung adenocarcinoma (n = 33, mLA = 23, iLA = 10)

Variable	Hazard Ratio	95% CI	Conc-indx	P
panMPS	6.57	1.31 to 33.04	0.67	0.02

TABLE 3

Hypergeometric analysis of MPS genes versus in silico gene sets for metastasis biomarker and metastasis function reviewed by cellular assays. Metastasis ID and chemokine ID terms in article title or abstract.

Gene Set	Overlap	Gene set size	Overlap %	P
Metastasis biomarkers	28	687	4.08	0.0001
Metastasis function	40	929	4.31	1.18×10^{-6}
Metasiasis ID	112	2463	4.55	2.42×10^{-20}
Chemokine ID	65	3126	2.08	0.04

TABLE 4

Left and Center: Logistic regression and Cox proportional hazards models predict progression to metastasis for full set (variable number by cohort) and panMPS (295) genes. Right: Linear regression model predicting correlation (r^2) between MPS and panMPS.

		Logistic Regression				Cox Regression				Linear Regression
Cohort	Variables	Odds Ratio	P	95% CI	AUC	Hazard Ratio	95% CI	Conc-Index	P	r^2
MSK_Prostate	MPS (320 genes)	5.39	0.001	2.03 to 15.49	0.69	4.85	2.00 to 11.77	0.72	0.0005	0.97
	panMPS	6.01	0.001	2.21 to 17.69	0.71	5.42	2.18 to 13.49	0.74	0.0003	0.97

TABLE 4-continued

Left and Center: Logistic regression and Cox proportional hazards models predict progression to metastasis for full set (variable number by cohort) and panMPS (295) genes. Right: Linear regression model predicting correlation (r^2) between MPS and panMPS.

		Logistic Regression				Cox Regression				Linear Regression
Cohort	Variables	Odds Ratio	P	95% CI	AUC	Hazard Ratio	95% CI	Conc-Index	P	r^2
Duke_Prostate	MPS (351 genes)	10.99	0.004	2.36 to 65.88	0.72	3.54	1.20 to 10.44	0.62	0.02	0.99
	panMPS	11.39	0.004	2.39 to 70.36	0.72	3.41	1.15 to 10.12	0.62	0.03	0.97
Montefiore_TNBC	MPS (352 genes)	44.36	0.02	2.87 to 2005.4	0.75	4.01	1.04 to 15.44	0.59	0.04	0.99
	panMPS	44.74	0.02	2.91 to 1927.9	0.75	4.06	1.03 to 16.04	0.59	0.05	0.96
MSK_Lung	MPS (353 genes)	3.78×10^3	0.006	42.79 to 1.04×10^7	0.94	4.55	1.04 to 20.63	0.65	0.04	0.96
	panMPS	3.45×10^3	0.006	41.5 to1.25×10^7	0.94	6.57	1.31 to 33.04	0.67	0.02	0.96

TABLE 5

Logistic regression models predicting progression to metastasis for prostate cancer based on panMPS and clinical variables

	Cohort							
	MSK Prostate CA (n = 182, mPT = 25, iPT = 157)				Duke Prostate CA (n = 61, mPT = 37, iPT = 24)			
	Variable							
	Odds Ratio	P	95% CI	AUC	Odds Ratio	P	95% CI	AUC
Univariate								
panMPS	5.98	0.001	2.12 to 18.57	0.7	11.84	0.002	2.78 to 67.71	0.75
Preop PSA	1.06	0.02	1.02 to 1.11	0.66	1.1	0.08	1.01 to 1.21	0.61
Biopsy Gleason	3.82	0.02	1.21 to 11.10	0.59	3.86	0.08	0.89 to 27.84	0.59
Clinical Stage	2.3	0.06	0.98 to 5.59	0.6	4	0.1	0.86 to 28.88	0.61
Path Gleason	68	1.3×10^{-10}	20.51 to 280.1	0.81	7.5	0.01	1.83 to 51.3	0.66
Path Stage	5.19	0.001	2.12 to 14.08	0.7	0.47	0.23	0.13 to 1.63	0.57
% Genome Inst.	1.17	1.4×10^{-5}	1.09 to 1.26	0.74	1.04	0.12	1.00 to 1.12	0.8
Multivariate								
panMPS	4.09	0.01	1.38 to 13.19	0.75	14.32	0.003	2.7 to 103.6	0.78
Preop PSA	1.04	0.05	1.01 to 1.1		1.1	0.06	1.01 to 1.24	
panMPS	5.09	0.003	1.6 to 15.54	0.73	6.06	0.06	2.4 to 70.4	0.68
Biopsy Gleason	2.32	0.15	0.69 to 7.17		1.18	0.88	1.03 to 47.04	
panMPS	5.51	0.001	1.99 to 16.59	0.73	4.42	0.13	0.71 to 34.06	0.72
Clinical Stage	1.93	0.15	0.79 to 4.83		2.76	0.26	0.52 to 21.2	
panMPS	1.5	0.55	0.39 to 5.88	0.86	7.45	0.03	1.4 to 49.38	0.77
Path Gleason	56.8	1.21×10^{-8}	15.57 to 263.14		4.83	0.06	1.1 to 34.44	
panMPS	3.93	0.01	1.43 to 11.94	0.77	10.59	0.01	2.18 to 65.6	0.73
Path Stage	3.83	0.006	1.49 to 10.74		0.59	0.45	0.15 to 2.32	
panMPS	1.79	0.32	0.59 to 5.97	0.75	8.45	0.03	1.41 to 62.2	0.73
% Genome Inst.	1.15	0.001	1.06 to 1.25		1.01	0.53	0.98 to 1.07	
panMPS	1.49	0.52	0.45 to 5.39	0.8	9.93	0.02	1.47 to 85.45	0.78
Preop PSA	1.03	0.21	1.00 to 1.09		1.1	0.06	1.01 to 1.24	
% Genome Inst.	1.14	0.004	1.05 to 1.25		1.02	0.5	0.98 to 1.08	
panMPS	3.7	0.03	1.2 to 11.93	0.76	8.6	0.04	1.25 to 90.53	0.74
Biopsy Gleason	2.2	0.21	0.59 to 7.1		1.35	0.78	0.17 to 13.8	
Preop PSA	1.04	0.05	1.01 to 1.09		1.11	0.09	1.01 to 1.28	
panMPS	4.71	0.01	1.66 to 14.48	0.75	4.47	0.13	0.70 to 36.93	0.71
Biopsy Gleason	2.24	0.17	0.66 to 6.97		0.93	0.95	0.12 to 8.55	
Clinical Stage	1.88	0.17	0.77 to 4.76		2.8	0.26	0.51 to 22.16	
panMPS	1.29	0.71	0.34 to 4.99	0.85	6.88	0.03	1.27 to 45.95	0.77
Path Gleason	47.21	8.69×10^{-8}	12.71 to 224.2		4.91	0.06	1.08 to 35.13	
Path Stage	2.87	0.08	0.87 to 9.88		0.56	0.42	1.13 to 2.31	
panMPS	3.56	0.03	1.16 to 11.62	0.78	6.97	0.04	0.94 to 77.9	0.76
Biopsy Gleason	2.15	0.22	0.59 to 6.97		1.07	0.08	0.11 to 11.94	
Clinical Stage	1.41	0.48	0.54 to 3.71		2.73	0.46	0.46 to 22.54	
Preop PSA	1.04	0.07	1.01 to 1.08		1.11	0.29	1.01 to 1.29	
panMPS	3.5	0.03	1.16 to 11.2	0.79	5.68	0.13	0.66 to 68.5	0.76
Biopsy Gleason	2.2	0.22	0.60 to 7.51		1.34	0.82	0.12 to 31.9	

TABLE 5-continued

Logistic regression models predicting progression to metastasis for prostate cancer based on panMPS and clinical variables

	Cohort							
	MSK Prostate CA (n = 182, mPT = 25, iPT = 157)				Duke Prostate CA (n = 61, mPT = 37, iPT = 24)			
	Variable							
	Odds Ratio	P	95% CI	AUC	Odds Ratio	P	95% CI	AUC
Clinical Stage	1.37	0.52	0.52 to 3.61		2.39	0.37	0.38 to 20.3	
Preop PSA	1.04	0.06	1.01 to 1.09		1.1	0.13	0.99 to 1.27	
Age	0.51	0.35	0.13 to 2.49		7.85×10^{5}	0.99	$3.85 \times 10^{-10.4}$ to NA	

Table 5 Continued

TABLE 6

Cox proportional hazards model of panMPS and its association with metastasis-free survival for prostate cancer based on panMPS and clinical variables

	Cohort							
	MSK Prostate CA (n = 222, mPT = 25, iPT = 197)				Duke Prostate CA (n = 76, mPT = 37, iPT = 39)			
	Variables							
	Hazard Ratio	95% CI	Conc-indx	P	Hazard Ratio	95% CI	Conc-indx	P
	Univariate							
panMPS	4.2	1.67 to 10.4	0.7	0.002	3.9	1.48 to 10.4	0.63	0.01
Preop PSA	1.01	1.00 to 1.01	0.63	7.60×10^{-5}	1	0.97 to 1.03	0.51	0.96
Biopsy Gleason	3.11	1.24 to 7.83	0.73	0.02	1.63	0.71 to 3.72	0.65	0.25
Clinical Stage	1.75	0.78 to 3.91	0.65	0.17	0.48	0.21 to 1.09	0.64	0.06
Path Gleason	17.34	7.63 to 39.4	0.97	9.90×10^{-12}	1.67	0.84 to 3.34	0.71	0.14
Path Stage	3.99	1.67 to 9.58	0.82	0.002	0.61	0.23 to 1.57	0.57	0.3
% Genome Inst.	1.11	1.07 to 1.16	0.67	3.30×10^{-7}	1.01	0.99 to 1.02	0.66	0.2
	Multivariate							
panMPS	4.31	1.72 to 10.8	0.74	0.002	3.52	1.18 to 10.5	0.71	0.02
Preop PSA	1.01	1.00 to 1.01		0.0002	0.99	1.02 to 1.12		0.7
panMPS	3.77	1.49 to 9.51	0.72	0.005	3.13	1.06 to 9.29	0.66	0.04
Biopsy Gleason	2.18	0.83 to 5.69		0.1	1.86	0.88 to 3.93		0.1
panMPS	4.59	1.83 to 11.6	0.71	0.001	2.25	0.62 to 8.17	0.6	0.22
Clinical Stage	1.81	0.81 to 4.03		0.15	1.86	0.79 to 4.34		0.15
panMPS	1.79	0.69 to 4.65	0.86	0.23	2.97	0.94 to 9.41	0.64	0.06
Path Gleason	14.34	5.96 to 34.5		2.74×10^{-9}	1.29	0.62 to 2.69		0.5
panMPS	2.96	1.19 to 7.33	0.76	0.02	3.19	1.05 to 9.64	0.62	0.04
Path Stage	3.03	1.22 to 7.55		0.02	0.73	0.27 to 1.91		0.5
panMPS	1.37	0.47 to 3.97	0.71	0.56	3.26	1.08 to 9.8	0.62	0.04
% Genome Inst.	1.1	1.04 to 1.16		0.001	1.01	0.99 to 1.02		0.32
panMPS	1.29	0.44 to 3.85	0.73	0.64	3.35	1.1 to 10.17	0.62	0.03
Preop PSA	1.01	1.00 to 1.01		0.0001	0.99	0.97 to 1.02		0.77
% Genome Inst.	1.09	1.04 to 1.16		0.001	1.01	0.99 to 1.02		0.35
panMPS	3.69	1.44 to 9.47	0.76	0.01	2.75	0.78 to 9.64	0.67	0.11
Biopsy Gleason	2.3	0.86 to 5.94		0.09	1.19	0.49 to 2.92		0.69
Prep PSA	1.01	1.00 to 1.01		0.0001	1.06	1.01 to 1.11		0.03
panMPS	4.07	1.58 to 10.5	0.74	0.01	1.96	0.53 to 7.23	0.6	0.31
Biopsy Gleason	2.09	0.81 to 5.42		0.13	1.69	0.72 to 3.97		0.23
Clinical Stage	1.76	0.78 to 3.94		0.17	2.02	0.84 to 4.85		0.11
panMPS	1.79	0.71 to 4.51	0.86	0.22	2.67	0.56 to 7.6	0.64	0.1
Path Gleason	11.98	4.98 to 28.8		2.91×10^{-8}	1.35	0.49 to 3.14		0.44
Path Stage	2.04	0.83 to 5.06		0.12	1.91	0.78 to 4.64		0.46
panMPS	3.95	1.51 to 10.3	0.76	0.01	2.06	0.56 to 7.61	0.65	0.28
Biopsy Gleason	2.19	0.84 to 5.72		0.11	1.25	0.49 to 3.14		0.63
Clinical Stage	1.57	0.68 to 3.58		0.29	1.91	0.78 to 4.64		0.15
Preop PSA	1.01	1.00 to 1.01		0.001	1.05	1.01 to 1.11		0.04
panMPS	3.95	1.49 to 10.5	0.76	0.01	1.73	0.46 to 6.55	0.66	0.42
Biopsy Gleason	2.21	0.84 to 5.76		0.11	1.58	0.59 to 3.92		0.37
Clinical Stage	1.56	0.68 to 3.6		0.29	1.68	0.66 to 4.29		0.27
Preop PSA	1.01	1.00 to 1.01		0.001	1.04	0.99 to 1.11		0.13
Age	0.89	0.26 to 3.09		0.86	8.31×10^{7}	0 to Inf		0.99

Table 6 Continued

TABLE 7

Clump analysis of genes, including Z_{genes} score, clump index, number of genes in clump and PubMed ID for metastasis function annotations, metastasis predictive biomarkers and metastasis in the article

Gene	Z_{genes} score	clump index	No. of genes in clump	Metastasis Function PubMed ID	Metastasis Predictive Biomarkers PubMed ID	Metastasis PubMed ID
ACTL8	1.9	1	2			23592437
ARHGEF10L	2.1	1	2			
LEPREL1	2.6	2	2	24319452		
TP63	3.0	2	2	21760596, 24488880	15761962, 23913939	19142959, 26208975
GLRB	2.7	3	2			
GRIA2	2.3	3	2		16953328	
CCDC125	2.0	4	7			
CDK7	2.7	4	7	23393140, 25490451, 25820824		25117707
CENPH	1.9	4	7		22999412	
MARVELD2	3.0	4	7			
MRPS36	2.6	4	7			
RAD17	2.6	4	7			
TAF9	2.6	4	7			
EPHA7	1.8	5	2			16007213
MAP3K7	3.2	5	2	23370768, 25770290		17785553
ASCC3	1.8	6	2			
SIM1	2.2	6	2			
EPM2A	2.4	7	2			18824542
UTRN	2.3	7	2			
C6orf118	2.8	8	2			
PDE10A	4.7	8	2			
CLIP2	3.1	9	4			
EIF4H	2.0	9	4			
LAT2	2.0	9	4			
RFC2	1.8	9	4			
MDH2	2.0	10	3			
STYXL1	2.3	10	3			
TMEM120A	1.7	10	3			
PILRA	1.9	11	2			
PILRB	2.9	11	2			
ACTL6B	1.7	12	9			21136596
AGFG2	2.3	12	9			
C7orf51	2.2	12	9			
FBXO24	2.5	12	9			
LRCH4	2.2	12	9			
MOSPD3	2.3	12	9			
PCOLCE	1.8	12	9			
TFR2	2.6	12	9			
TSC22D4	2.1	12	9			
COPG2	3.1	13	7			
CPA1	2.1	13	7			
CPA2	2.1	13	7			
CPA4	1.9	13	7			27073726
CPA5	2.8	13	7			
MEST	3.2	13	7		23229728	
TSGA14	9.4	13	7			
CSMD1	4.6	14	2	18614856		
MYOM2	2.1	14	2			
ERI1	1.9	15	2			
MFHAS1	3.3	15	2			
MSRA	5.1	16	2			17784942
TNKS	4.0	16	2			
C8orf16	2.2	17	2			
MTMR9	1.9	17	2			
GATA4	3.2	18	2	19509152	20222162	23239811, 24862985
NEIL2	2.7	18	2			
C8orf79	2.9	19	2			
DLC1	6.5	19	2	11118037		
SGCZ	8.2	20	2			
TUSC3	3.1	20	2	23404293, 24096664, 24435307, 25735931	23096450	

TABLE 7-continued

Clump analysis of genes, including Z_{genes} score, clump index, number of genes in clump and PubMed ID for metastasis function annotations, metastasis predictive biomarkers and metastasis in the article

Gene	Z_{genes} score	clump index	No. of genes in clump	Metastasis Function PubMed ID	Metastasis Predictive Biomarkers PubMed ID	Metastasis PubMed ID
MTMR7	3.7	21	4			
MTUS1	3.6	21	4	19794912, 24299308, 25885343		16650523
PDGFRL	4.8	21	4			
SLC7A2	4.1	21	4			
ASAH1	7.1	22	2	23423838		
PCM1	1.7	22	2			
NAT2	3.3	23	3			
PSD3	7.3	23	3			
SH2D4A	2.9	23	3			
FAM160B2	4.3	24	5			
HR	2.7	24	5			
LGI3	2.0	24	5			
NUDT18	2.3	24	5			
REEP4	2.5	24	5			
BMP1	2.2	25	3		19723875	23584484
PHYHIP	2.2	25	3			
POLR3D	2.7	25	3			
BIN3	4.5	26	9			
C8orf58	3.0	26	9			
EGR3	2.0	26	9			23342064
KIAA1967	5.9	26	9			
PDLIM2	2.9	26	9	23584482		24196835
PPP3CC	5.7	26	9			
RHOBTB2	1.7	26	9	20930524, 21801820	15922864, 19173804, 19937980	
SLC39A14	4.0	26	9			
SORBS3	3.0	26	9			
CHMP7	2.4	27	3			
TNFRSF10A	2.2	27	3			
TNFRSF10D	1.9	27	3			
ENTPD4	2.7	28	2			
LOXL2	1.9	28	2	25128648, 24014025, 24008674, 23971878, 23933800	27008697	23030485
CDCA2	2.0	29	3	23418564		17611626
EBF2	5.1	29	3			19671856
KCTD9	2.0	29	3			
ADRA1A	3.9	30	7		21360568	24607827, 26276037
CHRNA2	3.5	30	7			
DPYSL2	3.3	30	7			
EPHX2	3.3	30	7			16456776
PTK2B	7.0	30	7			
STMN4	3.3	30	7			
TRIM35	2.6	30	7			
C8orf80	3.6	31	3			
ELP3	3.4	31	3		22740850	
SCARA5	3.3	31	3	20038795, 24061576	22642751	
HMBOX1	1.8	32	2			
KIF13B	2.7	32	2			
C8orf34	6.0	33	7			
CPA6	3.8	33	7			
NCOA2	5.6	33	7			25295534
PRDM14	4.7	33	7	21339739, 25233927, 25635424	17942894, 23690269	
PREX2	7.5	33	7		22622578, 25151370, 25829446	
SLCO5A1	9.1	33	7			
SULF1	8.6	33	7		19780053, 21228115, 22653794	19373441
EYA1	3.4	34	6			24729159
KCNB2	6.8	34	6			

TABLE 7-continued

Clump analysis of genes, including Z_{genes} score, clump index, number of genes in clump and PubMed ID for metastasis function annotations, metastasis predictive biomarkers and metastasis in the article

Gene	Z_{genes} score	clump index	No. of genes in clump	Metastasis Function PubMed ID	Metastasis Predictive Biomarkers PubMed ID	Metastasis PubMed ID
LACTB2	2.6	34	6			
MSC	2.0	34	6			
TRPA1	2.3	34	6	24037916		
XKR9	2.7	34	6			
CRISPLD1	4.9	35	6			
GDAP1	2.0	35	6			
HNF4G	4.1	35	6			
JPH1	6.0	35	6			
PI15	3.0	35	6			
ZFHX4	4.3	35	6			
HEY1	3.0	36	2		23226563	
STMN2	2.8	36	2			
PAG1	2.0	37	2	21092590, 21156787		20388373, 21388951, 24675741
ZNF704	2.5	37	2			
CNBD1	7.6	38	2			
CNGB3	1.8	38	2			
PTDSS1	2.5	39	2			
SDC2	3.4	39	2	20863401, 22745764	19288017, 20683009	
GRHL2	2.4	40	4	18752864, 20938050, 23284647, 23814079, 24756056	23441166, 26355710	
NCALD	8.4	40	4			27027352
YWHAZ	2.2	40	4	20098429, 22912335		
ZNF706	2.8	40	4			
DPYS	3.2	41	3			
LRP12	2.0	41	3		22138261, 14676824	
ZFPM2	10.5	41	3			
ANGPT1	2.4	42	2			20651738
RSPO2	1.8	42	2	21732367, 25769727	26416247	24476626
CSMD3	9.1	43	2			
TRPS1	5.6	43	2	24709795, 26183398	16043716, 23762646, 26377811	
MYC	4.2	44	3	20133671		15810077, 9012485
POU5F1B	2.9	44	3			
TMEM75	3.5	44	3			
ADCY8	8.5	45	5			19082487, 22419659
ASAP1	3.6	45	5	18519696, 20154719	24427349, 24788532	
EFR3A	3.1	45	5			
KCNQ3	6.0	45	5			
OC90	1.9	45	5			
PHF20L1	2.8	46	5			
SLA	2.2	46	5			
TG	3.8	46	5			
TMEM71	2.9	46	5			
WISP1	2.2	46	5	19078974, 21109017, 21453685, 12865923	175787808, 20372786	
CDC42BPG	2.3	47	2			
MEN1	2.1	47	2			
ESD	2.6	48	3	21596165		
HTR2A	3.3	48	3			
LRCH1	2.4	48	3			
DACH1	1.9	49	3	16980615		
KLHL1	1.9	49	3			
PCDH9	4.5	49	3	25172662	22300792, 25869928, 25979483	
DDX19A	2.3	50	2			

TABLE 7-continued

Clump analysis of genes, including Z_{genes} score, clump index, number of genes in clump and PubMed ID for metastasis function annotations, metastasis predictive biomarkers and metastasis in the article

Gene	Z_{genes} score	clump index	No. of genes in clump	Metastasis Function PubMed ID	Metastasis Predictive Biomarkers PubMed ID	Metastasis PubMed ID
ST3GAL2	2.4	50	2			
BCAR1	2.5	51	2	22476538	10539513, 15448007, 17192874, 23904007	15972849, 21765937, 22241677
CFDP1	3.0	51	2			
ADAMTS18	3.5	52	4	18449690	25569086	21196270, 21047771, 24896365
CLEC3A	2.3	52	4			19173304
NUDT7	2.2	52	4			
WWOX	9.3	52	4	14695174, 18487009, 23824713	15073846, 16360296, 17289881, 21731849	
BCMO1	6.5	53	7	23803888		
C16orf46	2.2	53	7			
GAN	5.1	53	7			
GCSH	1.9	53	7			
HSD17B2	2.6	53	7		25929810	
PKD1L2	6.9	53	7			
PLCG2	5.6	53	7			
HSDL1	2.0	54	3			
LRRC50	2.4	54	3			
MBTPS1	2.7	54	3			
ATP2C2	3.6	55	3			
KIAA1609	1.9	55	3			
WFDC1	2.3	55	3	18842679, 19468830	10967136, 12032731, 15305341	
CRISPLD2	5.4	56	5			
KIAA0513	2.1	56	5			
KLHL36	1.8	56	5			
USP10	2.3	56	5	24332849, 25168367	16773218	24343337
ZDHHC7	2.5	56	5			
C16orf74	2.3	57	8		21203532	
COX4I1	2.6	57	8			
COX4NB	2.5	57	8			
FOXF1	2.2	57	8	24186199	23103611	20145151, 20587515, 23864317
GINS2	2.1	57	8	21082043, 24273454	24137407, 25348432	
IRF8	2.5	57	8	23308054	24091328	17409439, 19074829, 24175153
KIAA0182	2.0	57	8			
MTHFSD	2.4	57	8			
BANP	5.9	58	13	17668048, 25086032		20709157, 18981184, 18822384
C16ORF85	2.1	58	13			
CA5A	6.4	58	13			
CYBA	2.9	58	13			
IL17C	1.8	58	13			
JPH3	4.8	58	13			
KLHDC4	2.5	58	13	27030985		
MVD	2.3	58	13			
RNF166	2.2	58	13			
SLC7A5	4.7	58	13	21439283	23981989, 26244545	
SNAI3	2.4	58	13			
ZC3H18	2.1	58	13			
ZFPM1	2.5	58	13			
CDT1	2.0	59	2		26408331	21159650
FAM38A	2.7	59	2	22792288		
CBFA2T3	1.9	60	3	12183414		25749032
GALNS	2.3	60	3			
TRAPPC2L	1.9	60	3			
ANKRD11	6.7	61	2	18840648		21986947

TABLE 7-continued

Clump analysis of genes, including Z_{genes} score, clump index, number of genes in clump and PubMed ID for metastasis function annotations, metastasis predictive biomarkers and metastasis in the article

Gene	Z_{genes} score	clump index	No. of genes in clump	Metastasis Function PubMed ID	Metastasis Predictive Biomarkers PubMed ID	Metastasis PubMed ID
CDH15	1.9	61	2			9615235
FANCA	1.9	62	4			
SPIRE2	1.7	62	4			
TCF25	2.1	62	4			
TUBB3	2.6	62	4	25414139	24928347	20534991, 24053422
AFG3L1	2.3	63	2			
DEF8	1.9	63	2			
DHX58	6.9	64	5			
HSPB9	2.9	64	5			
KAT2A	3.2	64	5			
KCNH4	3.8	64	5			
RAB5C	3.5	64	5			
ASPSCR1	1.8	65	2			
NOTUM	2.7	65	2			
DUS1L	2.3	66	2			
FASN	3.0	66	2	18770866, 22266115, 22892389		17882277
DTNA	2.2	67	2			
NOL4	3.9	67	2			
C19orf57	2.8	68	2			
CC2D1A	4.0	68	2			
AR	4.9	69	4		7541709, 8604394	7723794, 11325816,
EDA2R	2.0	69	4			
HEPH	1.8	69	4			
OPHN1	5.8	69	4			
ALCAM	2.5	NA	1	16204050, 15140234	15509676, 10702391	9502422, 15986133, 16024937, 11206637, 18202807
ANXA13	2.1	NA	1		22294041	22559327
ARHGEF10	2.9	NA	1			21412932
ARHGEF5	2.7	NA	1			21525037
ATP6V1C1	2.4	NA	1	24155651, 24454753	20404513	15558013, 19885577, 18638373, 19424568, 17467328
BFSP2	2.4	NA	1			
BLK	2.1	NA	1			
BOD1L	2.4	NA	1			
C13orf23	2.2	NA	1			
C16orf80	2.2	NA	1			
CCDC25	4.4	NA	1		22202459	
CD226	3.3	NA	1	24468679		20008292
CDH13	10.9	NA	1			11389090, 12067979, 16807071, 15245595, 20642860
CDH17	2.8	NA	1	19676131, 20568120, 23298905, 23604127, 23554857	23326130, 22904132	
CDH2	3.4	NA	1	19190132		20848731
CDH8	3.7	NA	1			
CDYL2	2.5	NA	1			
CLCNKB	2.0	NA	1			
CLDN3	2.6	NA	1	19208807		
CNGB1	1.8	NA	1			
CNTNAP4	3.2	NA	1			
COL11A1	1.9	NA	1			11375892, 19112599, 21047417
COL12A1	1.8	NA	1	21462330		
COL19A1	3.4	NA	1			
COL21A1	1.8	NA	1			

TABLE 7-continued

Clump analysis of genes, including Z_{genes} score, clump index, number of genes in clump and PubMed ID for metastasis function annotations, metastasis predictive biomarkers and metastasis in the article

Gene	Z_{genes} score	clump index	No. of genes in clump	Metastasis Function PubMed ID	Metastasis Predictive Biomarkers PubMed ID	Metastasis PubMed ID
CTNNA2	1.8	NA	1			24100690
CTSB	2.8	NA	1	16707449, 20133781		
CYP7B1	1.7	NA	1		17639508	
DCC	6.6	NA	1	26345965		9387266
DCHS2	2.8	NA	1			24898286
DGKG	1.9	NA	1			
DIAPH3	3.3	NA	1	22593025		
DLGAP2	2.2	NA	1			
DNAH2	1.8	NA	1			
DOCK5	5.4	NA	1			
DPYD	2.9	NA	1			
ENOX1	5.6	NA	1			21055930
EPO	2.0	NA	1			24497137
FBXL18	1.9	NA	1			
FBXL4	1.7	NA	1			
FSTL5	2.2	NA	1			
GABRA2	2.3	NA	1			
GAS8	2.9	NA	1			
GHDC	1.8	NA	1			
GIGYF1	2.7	NA	1			
GLG1	2.1	NA	1	25301730	19148506	
GPC5	2.1	NA	1	23962560	26631038	24260047, 25093697, 25818666, 26098560
GRID2	5.1	NA	1			
GRK5	2.4	NA	1	22099983, 24755472		
GRM1	1.9	NA	1	18435704, 23065756, 24491800, 16040064		
GYS2	2.8	NA	1			
HIP1	4.4	NA	1	12163454	21697888	26595459
IMPA1	1.9	NA	1			
IQCE	1.8	NA	1			
KALRN	2.4	NA	1			
KCNAB1	5.8	NA	1			
KCTD8	2.8	NA	1			
KIAA0196	2.6	NA	1		16130124	
LPHN3	2.5	NA	1		23317273	
LZTS1	2.0	NA	1	18559591	18686028, 24466374	11410489, 23695671, 24525428
MACROD1	4.8	NA	1			
MDGA2	2.8	NA	1			
ME1	2.5	NA	1	25753478		
MECOM	2.0	NA	1			
MEF2C	2.3	NA	1	19584403		
MEIS2	3.9	NA	1			
MEPCE	2.1	NA	1			
MLYCD	2.4	NA	1			
MMP16	3.5	NA	1			21600596
MTDH	1.9	NA	1	19111877, 21976539, 21371176, 24099913		19723648, 22031094, 23851509
MTMR9	1.9	NA	1			
MYLK	2.8	NA	1		15970650, 25179839	
NALCN	2.2	NA	1			
NECAB2	2.0	NA	1			
NFAT5	2.3	NA	1			19011242, 22266867, 25152734, 25311085, 26299924
NIPAL2	1.9	NA	1			
NKIRAS2	2.0	NA	1			
NKX2-6	2.4	NA	1			

TABLE 7-continued

Clump analysis of genes, including Z_{genes} score, clump index, number of genes in clump and PubMed ID for metastasis function annotations, metastasis predictive biomarkers and metastasis in the article

Gene	Z_{genes} score	clump index	No. of genes in clump	Metastasis Function PubMed ID	Metastasis Predictive Biomarkers PubMed ID	Metastasis PubMed ID
NLGN4Y	2.4	NA	1			
NRXN1	3.2	NA	1			
NUS1	2.2	NA	1			
PDS5B	2.0	NA	1		23850494	
PKIA	3.3	NA	1			
PLCB1	1.9	NA	1		26620550	
PPM1L	2.0	NA	1			
PPP2R5B	1.8	NA	1			
PTK2	2.3	NA	1	14578863		
RAB9A	3.7	NA	1			
RALYL	2.8	NA	1			
RCOR2	1.7	NA	1			
RFX1	2.2	NA	1			
RGS22	2.7	NA	1	21533872		26323264
RIMS2	6.0	NA	1			
RNF40	2.1	NA	1		22155569	
RPL7	2.3	NA	1			
SF1	2.5	NA	1		18824866	
SLC26A7	2.2	NA	1			
SLC9A9	2.7	NA	1		25835977	
SMARCB1	1.8	NA	1		15899790, 16528370, 17040295, 21057957, 24503755	
STAG3	2.4	NA	1			
STAU2	4.6	NA	1			
STIP1	1.8	NA	1		24163084, 24488757	
STK3	1.8	NA	1			
STX1A	2.2	NA	1			
TBC1D10B	1.8	NA	1			
TBC1D22A	4.6	NA	1			
TCEB1	1.8	NA	1	18844214		25676555
TFDP1	2.3	NA	1	14618416	26684807	19995430
TFE3	2.1	NA	1		11438465, 12459622, 19606011, 20154303, 20871214	
TICAM2	1.8	NA	1			
TOX	4.3	NA	1			
TRDN	3.0	NA	1			
UBE2CBP	2.8	NA	1			
UBR5	2.2	NA	1			
VPS13B	3.9	NA	1			
VPS13C	1.8	NA	1			
WDR59	2.1	NA	1			
WDR7	2.0	NA	1			
WWP2	1.8	NA	1	26662306		23938591, 26783238
XPO7	2.3	NA	1			
YWHAG	2.7	NA	1			
ZBTB20	1.8	NA	1	25311537	21702992	
ZFAT	2.5	NA	1			
ZFHX3	2.2	NA	1			
ZHX2	2.6	NA	1		17447851	
ZSWIM4	2.8	NA	1			

Table 7 Continued

Table 7 Continued

Table 7 Continued

Table 7 Continued

Table 7 Continued

Table 7 Continued

Table 7 Continued

Table 7 Continued

Table 7 Continued . . .

TABLE 8A

Genes in gene set for Metastasis ID
SEPT9, DEC1, ABAT, ABCA13, ABCA2, ABCA3, ABCB1, ABCB11, ABCB5, ABCC10, ABCC2, ABCC3, ABCC5, ABCD1, ABCD3, ABCE1, ABCG1, ABCG2, ABCG4, ABHD11, ABHD4, ABI1, ABI2, ABL1, ABL2, ABR, ACACA, ACCS, ACE, ACE2, ACHE, ACP1, ACP5, ACP6, ACPT, ACR, ACRBP, ACSS2, ACTB, ACTG2, ACTN4, ADAM10, ADAM19, ADAM29, ADAM33, ADAM7, ADAM8, ADAM9, ADAMTS1, ADAMTS12, ADAMTS13, ADAMTS18, ADAMTS19, ADAMTS5, ADAMTS8, ADIPOQ, ADIPOR1, ADIPOR2, ADM, ADO, ADORA2B, ADRA2A, ADRB2, ADRBK2, ADRM1, AES, AFAP1, AFAP1L1, AFM, AFP, AGA, AGBL2, AGK, AGR2, AGR3, AGXT, AHNAK, AHR, AHSG, AIM1, AIM2, AKAP12, AKAP13, AKIRIN2, AKR1B10, AKR1C1, AKR1C3, AKT1, AKT2, AKT3, ALDH1A1, ALDH1A3, ALDH3A1, ALK, ALCAM, ALKBH5, ALOX5, AMN, AMOTL1, AMOTL2, ANG, ANGPT2, ANGPTL2, ANGPTL3, ANLN, ANKRD11, ANO1, ANO9, ANP32A, ANTXR1, ANXA1, ANXA11, ANXA2, ANXA5, ANXA7, APAF1, APC, APCS, API5, APLP2, APOA1, APOBEC3G, APOH, APP, APPL1, AQP1, AQP3, AQP5, AQP6, AQP9, AR, ARAF, AREG, ARF1, ARF6, ARFGAP1, ARG1, ARHGAP21, ARHGAP5, ARHGAP6, ARHGEF3, ARHGEF5, ARHGEF7, ARID1A, ARID2, ARID3B, ARID4A, ARID4B, ARL4C, ARMC3, ARNT, ARPC1B, ARRB1, ARRDC3, ASAP1, ASCL2, ASIP, ASL, ASPM, ASS1, ATAD2, ATF1, ATF3, ATF4, ATF5, ATF6, ATG10, ATG16L1, ATG4A, ATG5, ATIC, ATM, ATOH1, ATOH8, ATP11A, ATP4A, ATP5J, ATP6AP2, ATP6V1C1, ATP7B, ATR, ATRX, AURKA, AUTS2, AVEN, AXIN2, AZGP1, B3GALNT1, B3GNT3, B3GNT7, B4GALNT2, BACE1, BACH1, BAD, BAG1, BAG2, BAG3, BAIAP2L1, BAMBI, BARD1, BARX2, BATF2, BAX, BAZ2A, BCAM, BCAR1, BCAR3, BCAS2, BCAS3, BCAT1, BCL10, BCL2, BCL2L12, BCL2L2, BCL3, BCL6, BCL9, BCL9L, BCOR, BCORL1, BCR, BDKRB2, BDNF, BET1, BHMT, BID, BIK, BIN1, BIRC3, BIRC5, BIRC6, BLCAP, BLID, BMF, BMP1, BMP10, BMP3, BMP4, BMP6, BMP7, BMPER, BMPR1A, BNC1, BNIP3L, BOLL, BOP1, BPI, BPTF, BRCA1, BRCA2, BRCC3, BRD4, BRD8, BRE, BRF2, BRIP1, BRMS1, BRMS1L, BRSK2, BST2, BTBD7, BTC, BTG1, BTG2, BTG3, BTK, BTLA, BTRC, BUB1, BUB1B, BVES, C10orf10, C19orf48, C1orf61, C2orf40, C3, C5, C6, C6orf106, C7, C8orf4, C9, CA2, CA9, CACNA2D3, CACYBP, CAD, CADM1, CALU, CAMK2N1, CAMP, CAMSAP1, CANT1, CAPZA1, CARD10, CARM1, CARS, CASK, CASP4, CASP6, CASP8, CASR, CASS4, CAV1, CBL, CBX2, CBX4, CBX5, CBX7, CBX8, CCDC34, CDC6, CCDC67, CCDC8, CCL1, CCL11, CCL13, CCL14, CCL17, CCL18, CCL19, CCL2, CCL20, CCL21, CCL22, CCL4, CCL5, CCL7, CCL8, CCNA2, CCNB1, CCNE1, CCNG2, CCNH, CCNY, CCR1, CCR3, CCR4, CCR6, CCR7, CCR9, CCRL2, CCT2, CD109, CD14, CD163, CD163L1, CD164, CD1A, CD1C, CD1D, CD2, CD200, CD226, CD244, CD248, CD27, CD274, CD33, CD36, CD38, CD4, CD40, CD46, CD47, CD48, CD53, CD55, CD58, CD63, CD69, CD70, CD74, CD81, CD82, CD86, CD9, CD93, CD96, CD99, CDA, CDC14A, CDC20, CDC25A, CDC25B, CDC25C, CDC37, CDC42, CDC6, CDC7, CDC73, CDCA5, CDCA7L, CDCA8, CDCP1, CDH1, CDH13, CDH17, CDH2, CDH22, CDK2AP1, CDK3, CDK4, CDK5, CDK5RAP3, CDK6, CDK7, CDK8, CDKN1A, CDKN1C, CDKN2A, CDKN2B, CDKN3, CDT1, CDX1, CDX2, CEACAM1, CEACAM5, CEP55, CEP70, CES2, CFL1, CFTR, CGA, CHAD, CHAT, CHD1, CHD1L, CHD5, CHD8, CHEK1, CHEK2, CHGB, CHI3L1, CHL1, CHML, CHRM3, CHRNA1, CHRNA3, CHST11, CIAPIN1, CIITA, CISD2, CISH, CITED1, CITED2, CIZ1, CKAP2, CKAP4, CKB, CLC, CLCA1, CLCA2, CLCA4, CLDN10, CLDN11, CLDN16, CLDN3, CLEC3A, CLEC3B, CLEC5A, CLIC4, CLOCK, CLPTM1L, CLU, CMTM3, CMTM8, CNN3, CNOT7, CNTF, CNTN1, COIL, COL11A1, COL18A1, COL1A1, COL1A2, COL3A1, COL4A2, COL5A1, COL5A2, COL6A1, COMMD1, COMT, CORT, COTL1, COX7A2, CP, CPA4, CPE, CPEB4, CPM, CPNE3, CPOX, CPS1, CPSF2, CPT1A, CPZ, CR1, CRABP1, CRCT1, CREB1, CREB3, CREB3L1, CREB3L2, CREB5, CREBBP, CREBZF, CRH, CRHR1, CRHR2, CRIM1, CRISP3, CRK, CRKL, CRNN, CRP, CRTC1, CRTC3, CRX, CS, CSE1L, CSF1, CSF2, CSK, CSMD1, CSNK1A1, CSPG4, CST6, CST7, CTAG2, CTBP1, CTBP2, CTCF, CTCFL, CTGF, CTHRC1, CTLA4, CTNNA1, CTNNB1, CTNND1, CTTN, CUEDC2, UL4A, CUX1, CX3CL1, CX3CR1, CXCL1, CXCL10, CXCL11, CXCL12, CXCL13, CXCL14, CXCL17, CXCL2, CXCL3, CXCL5, CXCL6, CXCL9, CXCR4, CXCR5, CXCR6, CXXC4, CXXC5, CYB5A, CYB5D2, CYFIP1, CYHR1, CYLD, CYP17A1, CYP19A1, CYP1A1, CYP1B1, CYP24A1, CYP26A1, CYP27A1, CYP27B1, CYP2A6, CYP2B6, CYP2C8, CYP2E1, CYP2J2, CYP2R1, CYP39A1, CYP3A4, CYP3A43, CYP3A5, CYP4F8, CYR61, DAB1, DAB2, DAB2IP, DACH1, DACH2, DACT1, DACT2, DAND5, DAP, DAP3, DBF4, DBN1, DCC, DCK, DCLK1, DCN, DCT, DCTN1, DCUN1D1, DCX, DCXR, DDB2, DDC, DDIT3, DDR2, DDT, DDX1, DDX11, DDX20, DDX27, DDX43, DEDD, DEK, DEPDC1B, DES, DFNA5, DGCR6, DGCR6L, DGCR8, DHCR24, DHFR, DHRS7, DHX32, DIAPH1, DIAPH3, DICER1, DIO3, DIRAS1, DIRAS3, DIS3, DIXDC1, DKK1, DKK2, DLC1, DLD, DLEC1, DLG5, DLK1, DLK2, DLL4, DLX2, DLX5, DMGDH, DMP1, DNAJA1, DNAJB1, DNAJC13, DNM3, DNMT1, DNMT3A, DOCK1, DOCK2, DOCK3, DOCK4, DOCK5, DOCK8, DOT1L, DPF3, DPH3, DPP4, DPPA2, DPYD, DR1, DRD2, DSC1, DSG1, DSG3, DTX3L, DUOX2, DUSP1, DUSP4, DUSP6, DYRK1B, DYRK2, E2F1, E2F2, E2F3, E2F4, E2F5, E2F6, EBAG9, EBF2, EBP, ECD, ECH1, ECM1, ECT2, EDIL3, EDNRA, EDNRB, EEF1A2, EFEMP1, EFHD2, EFNA1, EFNA3, EFNB2, EGF, EGFL7, EGFR, EGR1, EGR3, EHD1, EHMT1, EI24, EIF3A, EIF3E, EIF3H, EIF3I, EIF4E, EIF5A2, EIF6, ELAC2, ELAVL1, ELF3, ELF5, ELMO2, ELP3, ELOVL6, EMILIN1, EMP2, EMX2, ENAH, ENG, ENO1, ENPP2, ENTPD5, EP300, EPAS1, EPB41L3, EPC1, EPCAM, EPHA1, EPHA2, EPHA3, EPHA4, EPHA6, EPHA7, EPHA8, EPHB2, EPHB3, EPHB4, EPHB6, EPHX2, EPO, EPS15, EPS8, EPSTI1, ERBB3, ERBB4, ERC1, ERCC1, ERCC2, ERCC3, ERCC5, ERG, ERGIC1, ERGIC3, ERP29, ESD, ESPL1, ESPN, ESR1, ESR2, ESRP1, ETS1, ETV1, ETV4, ETV5, ETV6, EVI5, EVL, EVX1, EWSR1, EXO1, EXT1, EXTL3, EYA1, EYA2, EYA4, EZH2, EZR, F10, F11, F2, F5, F8, F9, FABP1, FABP4, FABP5, FABP7, FADD, FAF1, FAIM2, FAM107A, FAM120A, FAM129B, FAM134B, FAM20C, FAM3B, FAM3C, FAM83D, FANCA, FANCC, FANCD2, FANCF, FAP, FAS, FASN, FASTKD2, FAT4, FBN1, FBN2, FBXL5, FBXO11, FBXO32, FBXO4, FBXO45, FBXW7, FCN2, FDPS, FECH, FEM1A, FER, FEV, FEZ1, FEZF1, FGD4, FGF1, FGF10, FGF14, FGF18, FGF2, FGF23, FGF3, FGF4, FGF5, FGF7, FGF8, FGF9, FGFBP1, FGFR1, FGFR2, FGFR3, FGFR4, FGG, FGR, FH,

TABLE 8A-continued

Genes in gene set for Metastasis ID
FHIT, FHL1, FHL2, FHOD1, FHOD3, FJX1, FKBP14, FKBPL, FLI1, FLNA, FLOT2, FLT1, FLT3, FLT4, FMNL2, FMNL3, FN1, FNDC3B, FOSB, FOXA1, FOXA2, FOXC1, FOXC2, FOXD3, FOXE1, FOXF1, FOXF2, FOXG1, FOXH1, FOXJ1, FOXJ3, FOXL1, FOXL2, FOXM1, FOXO1, FOXO3, FOXO4, FOXP1, FOXP2, FOXP3, FOXQ1, FOXR2, FRAS1, FRAT1, FRMD4A, FRY, FRYL, FSCN1, FSHR, FST, FSTL1, FURIN, FUS, FUT3, FUT4, FUT5, FUT8, FXYD3, FXYD5, FXYD6, FYN, FZD1, FZD2, FZD5, FZD8, G3BP1, GAB1, GAB2, GABARAPL1, GABRP, GADD45A, GADD45G, GAK, GAL, GAL3ST2, GALC, GALNT14, GALNT2, GALNT3, GALNT9, GAN, GAS1, GAS6, GAS8, GAST, GATA2, GATA4, GATA5, GATA6, GBP1, GBP2, GBX2, GC, GCG, GCKR, GDF15, GDF2, GDF3, GDNF, GEM, GEMIN5, GFAP, GFI1, GGH, GHRH, GIP, GIPC1, GIT1, GJA3, GJB5, GKN1, GLA, GLB1, GLE1, GLI1, GLI2, GLIPR1, GLO1, GMDS, GNA13, GNA15, GNAI2, GNAI3, GNAQ, GNAS, GNE, GNG2, GNRH1, GOLPH3, GP2, GPC5, GPI, GPNMB, GPR171, GPR18, GPR32, GPR34, GPR39, GPR55, GPR87, GPRC5A, GPX2, GPX3, GRB14, GRB2, GRHL2, GRHL3, GRIN2A, GRK5, GRK6, GRM1, GRM4, GRM5, GRPR, GSC, GSN, GSPT1, GSTM3, GSTP1, GTSE1, GUCY2C, GUK1, H3F3A, HABP2, HACE1, HADHA, HAO2, HAPLN3, HAS1, HAS2, HAX1, HBD, HBEGF, HBP1, HCCS, HDAC1, HDAC2, HDAC4, HDAC6, HDAC7, HDAC8, HDGF, HECTD1, HECTD2, HELLS, HEPACAM, HERC5, HES1, HES5, HEXA, HEXIM1, HEY1, HFE, HGS, HHIP, HIF1A, HINT1, HIP1, HIPK1, HIPK2, HIRA, HJURP, HK1, HK3, HLTF, HMGA1, HMGA2, HMGB3, HMGCR, HMGCS2, HMGN1, HMGN5, HMMR, HN1, HNF1A, HNF4A, HNRNPA2B1, HOMER1, HOOK1, HOPX, HOXA1, HOXA11, HOXA13, HOXA5, HOXA9, HOXB2, HOXB9, HOXC11, HPD, HPGD, HPR, HPSE, HR, HRG, HS3ST2, HSD17B2, HSD3B1, HSF1, HSP90B1, HSPA14, HSPA2, HSPA9, HSPB8, HTATIP2, HTRA1, HTRA2, HTRA3, HTT, HUNK, HUWE1, HYOU1, IAPP, ICMT, ID1, ID2, ID3, ID4, IDH1, IDH2, IDO1, IER2, IFI27, IFIT2, IFIT3, IFNG, IGF1R, IGF2, IGF2BP1, IGF2BP2, IGF2BP3, IGFBP1, IGFBP2, IGFBP3, IGFBP5, IGFBP7, IGFBPL1, IKBKB, IKZF1, IL10, IL13, IL17A, IL17F, IL18, IL1A, IL1R1, IL23R, IL24, IL33, IL4, IL6R, IL7, ILK, IMP3, IMPACT, INA, ING1, ING2, ING3, ING5, INHBA, INSIG2, INSM1, IQGAP1, IQGAP2, IRAK1, IRF8, IRX2, IRX5, ITGA2, ITGA3, ITGA5, ITGA7, ITGA8, ITGA9, ITGAV, ITGB1, ITGB3, ITGB4, ITGB8, ITGBL1, ITIH5, JAG1, JAG2, JAK1, JAK2, JAK3, JAZF1, JMJD6, JUN, KAT2A, KCNJ1, KCNK9, KCNMA1, KCNQ1, KCNRG, KDM1A, KDM2A, KDM3A, KDM4A, KDM4B, KDM4C, KDM5B, KDM5C, KDM6A, KDR, KEAP1, KIAA0101, KIF11, KIF14, KIF15, KIF18A, KIF1B, KIF26B, KIF2A, KIF3A, KIF3C, KIF5B, KIFC1, KIN, KIR2DL4, KISS1, KIT, KITLG, KL, KLB, KLF12, KLF15, KLF17, KLF2, KLF4, KLF5, KLF6, KLHDC4, KLK10, KLK14, KLK15, KLK3, KLK7, KLK8, KLRG1, KMO, KPNA2, KPNB1, KRAS, KRT19, KRT20, KRT7, KY, LAMA4, LAMA5, LAMB1, LAMB3, LAMB4, LAMC1, LAMC2, LAMP1, LAMP2, LAMP3, LAP3, LAPTM4B, LARP1, LARP7, LARS, LASP1, LAT, LATS1, LATS2, LBH, LBX1, LCK, LCT, LDB1, LEMD3, LEP, LEPREL1, LETM1, LFNG, LGALS3, LGALS3BP, LGALS9, LGI4, LGR5, LHCGR, LIF, LIFR, LIG4, LILRB1, LILRB2, LIMD2, LIMK2, LIN28B, LMNA, LMO2, LMO4, LMO7, LMX1B, LOX, LOXL2, LPAR1, LPCAT1, LPHN3, LPIN2, LPP, LRG1, LRP1, LRP1B, LRP5, LRP6, LRP8, LRPPRC, LRRC3B, LRRC4, LRRFIP1, LSAMP, LSM1, LSP1, LTBP4, LXN, LY75, LYAR, LYN, LZTFL1, LZTS1, MACROD2, MADD, MAGEA1, MAGEC2, MAGED4B, MAGI1, MAK, MAL, MAL2, MALL, MALT1, MAML1, MAML2, MAOA, MAP1B, MAP1S, MAP2, MAP2K1, MAP2K4, MAP3K1, MAP3K2, MAP3K7, MAP3K8, MAP3K9, MAP4K3, MAP4K4, MAPK1, MAPK8, MAPKAPK2, MAPT, MARCKS, MARCO, MARK4, MARVELD3, MAS1, MAT2A, MAT2B, MAX, MB, MBD1, MBD2, MBD4, MBP, MCC, MCM2, MCM4, MCRS1, MDM4, ME1, MED1, MED12, MED19, MED27, MEF2C, MEF2D, MEIS1, MEMO1, MEN1, MEST, MET, METTL13, MFAP3L, MFSD2A, MGA, MGAT1, MGAT3, MGMT, MGST1, MIA, MIB1, MICAL2, MIF, MINA, MIP, MITF, MKL1, MLF2, MLN, MME, MMP10, MMP11, MMP12, MMP13, MMP14, MMP16, MMP28, MMP7, MMP9, MNT, MOBP, MOS, MOV10, MPI, MPL, MPO, MPZL1, MRC2, MSC, MSH3, MSH6, MSMB, MSN, MSRA, MST1R, MSX2, MT3, MT4, MTA1, MTA2, MTA3, MTAP, MTBP, MTDH, MTHFD2, MTHFR, MTMR3, MTOR, MTRR, MTSS1, MTUS1, MUC13, MUC16, MUC17, MUC2, MUC20, MUC4, MUC7, MUM1, MUSK, MUT, MUTYH, MVD, MVP, MX1, MX2, MXD1, MXI1, MXRA5, MYBL2, MYC, MYCN, MYD88, MYEOV, MYH9, MYL9, MYLK, MYO5B, MYO9B, MZF1, NAB2, NAMPT, NAP1L1, NAT1, NAT2, NAV1, NBN, NCALD, NCK1, NCK2, NCL, NCOA1, NCOA2, NCOA3, NCOA5, NCOR1, NCOR2, NCSTN, NDC80, NDP, NDRG2, NDRG3, NDRG4, NDUFB6, NDUFB9, NDUFS6, NEB, NEDD1, NEDD4, NEDD4L, NEDD8, NEFL, NEIL1, NEIL2, NEK2, NEK6, NEK7, NES, NET1, NETO2, NEU3, NEUROD1, NF1, NFAT5, NFATC2, NFIB, NFKB1, NFKBIA, NGF, NGFR, NHS, NIPSNAP1, NISCH, NKD1, NKD2, NKTR, NLK, NLRP1, NLRP3, NME1, NME4, NME6, NMI, NMU, NNAT, NNT, NOB1, NOD1, NOD2, NODAL, NOG, NOP14, NOS1, NOS2, NOS3, NOTCH1, NOTCH3, NOTCH4, NOV, NOX1, NOX4, NPAS2, NPC1, NPL, NPM1, NPS, NPY, NPY1R, NQO2, NR0B1, NR1D1, NR1I2, NR1I3, NR2F1, NR2F2, NR3C2, NR4A2, NR4A3, NR5A2, NR6A1, NRAS, NRK, NRL, NT5E, NTRK1, NTRK3, NTS, NTSR1, NUAK1, NUCB2, NUCKS1, NUMB, NUP88, NUSAP1, OAT, ODAM, ODF4, OLA1, OLFM4, OLIG1, OLIG2, ONECUT2, ORAI1, ORAOV1, OSM, OSMR, OTC, OTP, OTUB1, OTUD3, P4HA1, P4HA2, PABPC1, PACRG, PADI4, PAFAH1B1, PAH, PAK2, PAK3, PAK4, PAK6, PALB2, PAM, PARD3, PARG, PARP1, PARVA, PARVB, PAX3, PAX4, PAX5, PAX6, PAX7, PAX8, PBK, PBRM1, PBX3, PC, PCBP1, PCBP2, PCDH10, PCDH9, PCK2, PCNA, PDC, PDCD4, PDCD5, PDCD6, PDCL3, PDF, PDGFB, PDGFRA, PDGFRB, PDIA3, PDK3, PDLIM2, PDLIM5, PDPN, PDSS2, PDX1, PEBP1, PEG10, PELP1, PER1, PER2, PERP, PFKFB2, PFKFB3, PFN2, PGC, PGF, PGK1, PGRMC2, PHF10, PHF20, PHF8, PHIP, PHLDA1, PHLPP1, PHLPP2, PHOX2B, PIAS1, PICK1, PIGF, PIGR, PIGS, PIEZO1, PIK3C2G, PIK3CA, PIK3CB, PIK3CD, PIK3CG, PIK3R1, PIK3R3, PIKFYVE, PIN1, PINK1, PIP4K2B, PIR, PITPNC1, PITX1, PITX2, PIWIL1, PIWIL2, PIWIL4, PKN1, PKP1, PKP2, PLA2G16, PLA2G7, PLAC1, PLAG1, PLAGL1, PLAU, PLAUR, PLCE1, PLCG1, PLD2, PLEKHA5, PLK1, PLOD2, PLS3, PLXDC1, PLXNA2, PMAIP1, PMEPA1, PML, PMP22, PMS2, PNLIPRP3, POLB, POLE, POLI, POLR2A, POMC, PON1, POSTN, POT1, POU2F1, POU3F2, POU3F3, PPA1, PPARG, PPM1A, PPM1B, PPM1D, PPM1F, PPM1H, PPP1CA, PPP1R13L, PPP1R3B, PPP2CA, PPP2R2C, PRAME, PRC1, PRDM10, PRDM14, PRDM5, PRDX1, PRDX4, PRDX6, PREP, PAG1, PTK2B, PREX2, PRICKLE1, PRKAA1, PRKAR1A, PRKCD, PRKCDBP, PRKCI, PRKCZ, PRKD1, PRKD2, PRKX, PRL, PRMT1, PRMT2, PRMT5, PRMT6, PRMT7, PRNP, PROK1, PROM1, PROX1, PRR15, PRSS3, PRUNE, PRUNE2, PRX, PSAT1, PSCA, PTBP2, PTCH1, PTEN, PTER, PTGIS, PTGS2, PTH, PTH1R, PTHLH, PTK6, PTK7, PTOV1, PTP4A1, PTP4A3, PTPN12, PTPN13, PTPN14, PTPN4, PTPRF, PTPRG, PTPRT, PTS, PTTG1IP, PTX3, PVR, PYY, QKI, QRFP, RAB11A, RAB14, RAB17, RAB1A, RAB22A, RAB25, RAB27B, RAB32, RAB3D, RAB40B,

TABLE 8A-continued

Genes in gene set for Metastasis ID
RAB40C, RAB5C, RABL3, RAC1, RAC2, RACGAP1, RAD18, RAD21, RAD50, RAD51, RAD52, RAD54B, RAF1, RAI2, RALA, RALB, RALBP1, RALY, RAMP3, RAN, RANGAP1, RAP1A, RAP1B, RAP1GAP, RAP2A, RAP2B, RAPGEF2, RAPH1, RARB, RARRES1, RASA1, RASAL1, RASAL2, RASGRF1, RASGRF2, RASGRP1, RASGRP3, RASSF1, RASSF3, RASSF7, RASSF8, RB1, RB1CC1, RBBP4, RBBP6, RBBP8, RBM3, RBM47, RBM5, RBP1, RBP2, RBX1, RCAN3, RD3, REG4, RELA, REPS2, RERG, RET, REV3L, RFC1, RFX6, RFXAP, RGMB, RGS1, RGS16, RGS17, RGS2, RGS22, RGS6, RGSL1, RHBDD2, RHO, RHOB, RHOBTB2, RHOC, RHOD, RHOG, RHOJ, RHOT1, RHOU, RIN1, RIOK3, RIPK1, RIPK2, RIPK3, RLF, RNASEL, RND3, RNF111, RNF13, RNF180, RNF2, RNF4, RNF40, RNF43, RNH1, ROBO1, ROBO3, ROBO4, ROCK1, ROCK2, ROR1, ROR2, RORA, RP1, RPA1, RPE, RPL15, RPL26, RPL39, RPL41, RPL7, RPN2, RPS12, RPS3, RPS6KB1, RPSA, RRBP1, RRM1, RRM2, RRP1B, RSPO2, RTKN, RUFY3, RUNX1, RUNX1T1, RUNX2, RUNX3, RXFP1, RXRA, RYBP, S100A11, S100A2, S100A6, S100A7, S100A8, S100A9, S100B, S100P, S100PBP, S100Z, S1PR3, SAA2, SACS, SALL4, SAMD9, SARS, SART1, SART3, SASH1, SATB2, SCAI, SCAMP1, SCARA5, SCGB2A2, SCN7A, SCRIB, SCUBE2, SCUBE3, SDC1, SDC2, SDC4, SDCBP, SDHA, SDHC, SDPR, SEC14L2, SEC23A, SEC62, SEL1L, SELP, SEMA3E, SEMA3F, SEMA4C, SEMA6D, SENP1, SENP2, SENP3, SERPINA1, SERPINA3, SERPINA5, SERPINB13, SERPINB2, SERPINB3, SERPINB5, SETD2, SETDB1, SF3B1, SFPQ, SFRP1, SFRP2, SFRP4, SGPP1, SGPP2, SGTA, SH2B1, SH3BGRL, SH3GL2, SH3GLB2, SH3PXD2B, SHB, SHE, SHH, SHISA3, SHMT1, SHOC2, SHOX2, SI, SIAH2, SIN3A, SIPA1, SIRT1, SIRT2, SIRT3, SIX2, SIX3, SIX4, SKA3, SKAP2, SKI, SKP1, SKP2, SLC19A1, SLC19A3, SLC22A17, SLC22A18, SLC25A1, SLC28A3, SLC29A1, SLC29A3, SLC2A1, SLC38A1, SLC39A14, SLC5A8, SLC6A14, SLC7A11, SLC7A5, SLCO1B1, SLCO1B3, SLIT3, SLITRK3, SLITRK6, SLK, SLN, SMAD1, SMAD2, SMAD3, SMAD4, SMAD5, SMAD7, SMAP1, SMARCA4, SMARCA5, SMARCB1, SMARCC1, SMARCD1, SMC4, SMO, SMR3A, SMS, SMURF1, SMURF2, SMYD2, SMYD3, SNAI2, SNAI3, SNAPIN, SND1, SNTB2, SNX6, SNX9, SOCS1, SOCS2, SOCS3, SOD2, SOD3, SOHLH2, SOS1, SOST, SOX10, SOX11, SOX12, SOX17, SOX2, SOX3, SOX4, SOX6, SOX7, SOX8, SOX9, SP1, SP100, SP3, SP6, SPAG5, SPAG9, SPARC, SPARCL1, SPDEF, SPIN1, SPINT2, SPOCK1, SPOP, SPR, SPRED1, SPRR2A, SPRR3, SPRY1, SPRY2, SPRY4, SPTAN1, SQLE, SQSTM1, SRC, SRD5A1, SRD5A2, SRF, SRPK1, SRRM4, SSBP1, SSRP1, SST, SSTR2, SSTR3, SSTR5, SSX1, SSX2IP, ST13, SLC9A9, ST3GAL6, ST6GALNAC2, STAG2, STARD10, STARD13, STAT1, STAT3, STAT4, STAT5B, STAT6, STC2, STEAP1, STEAP2, STIM2, STIP1, STK33, STK39, STK4, STMN1, STRAP, STRN, STS, STX6, STYK1, SUDS3, SUFU, SULF1, SULF2, SULT1E1, SUMO1, SUMO3, SUSD2, SUZ12, SVEP1, SYK, TAC1, TACC2, TACC3, TACSTD2, TAGLN, TAGLN2, TANK, TARBP2, TAT, TBC1D16, TBK1, TBP, TBX2, TBX21, TBX3, TBX4, TBX5, TBXAS1, TCEB1, TCF12, TCF21, TCF3, TCF4, TCF7, TCF7L2, TDGF1, TDO2, TDP1, TDRD1, TEAD4, TEC, TEF, TEK, TERT, TES, TET1, TET2, TEX101, TF, TFAP2A, TFAP2C, TFAP2E, TFCP2, TFEB, TFF1, TFF2, TFF3, TFG, TFPI, TFPI2, TG, TGFA, TGFB1, TGFBI, TGFBR2, TGFBR3, TGIF1, TGM2, TGM3, THBS1, THBS4, THOC1, THRSP, THY1, TIAF1, TIAM2, TIMELESS, TIMM17A, TIMP2, TIMP3, TIMP4, TJP1, TKTL1, TLE1, TLE4, TLN1, TLR3, TLR4, TLR5, TLR7, TLR8, TLR9, TM4SF1, TM4SF5, TM9SF4, TMED3, TMEM100, TMEM127, TMEM14A, TMEM174, TMEM207, TMEM25, TMEM33, TMEM45B, TMEM97, TMOD1, TMPRSS2, TMPRSS3, TMPRSS4, TNFAIP1, TNFRSF10A, TNFRSF10B, TNFRSF1B, TNK2, TNS1, TNS3, TNS4, TOB1, TOB2, TOM1, TOM1L1, TOMM34, TOP1, TOPBP1, TOX, TP53, TP53BP2, TP53INP1, TP63, TP73, TPD52, TPM3, TPO, TPR, TRAF2, TRAF4, TRAF6, TREM2, TRH, TRIB1, TRIB2, TRIB3, TRIM16, TRIM31, TRIM33, TRIM37, TRIM44, TRIM59, TRIM66, TRIM9, TRIT1, TRPA1, TRPC1, TRPC6, TRPM2, TRPM7, TRPM8, TRPV1, TRPV5, TRPV6, TSC1, TSC2, TSG101, TSLP, TSPAN1, TSPAN12, TSPAN7, TSPAN8, TSPAN9, TSPYL5, TSSC1, TTC4, TTF1, TTK, TTYH2, TUSC1, TWIST1, TXN, TFE3, TRPS1, TUBB3, TUSC3, TYK2, TYMS, TYR, TYRO3, TYRP1, U2AF2, UBE2C, UBE2D3, UBE2Q1, UBIAD1, UCHL1, UCN, UGT2B17, ULBP2, UNC5B, UPF1, USF1, USP10, USP14, USP15, USP18, USP22, USP28, USP37, USP4, USP9X, UVRAG, VANGL2, VAPB, VASP, VAV2, VAV3, VCAM1, VCP, VDAC1, VDR, VEGFC, VEZT, VGLL2, VHL, VIM, VIP, VPS25, VRK1, VTCN1, VTI1A, VWF, WASF2, WBSCR22, WDR26, WEE1, WIF1, WIPI1, WIPI2, WISP1, WISP2, WISP3, WNT10A, WNT10B, WNT11, WNT2, WNT3, WNT3A, WNT4, WNT5B, WNT6, WNT7A, WRN, WT1, WTAP, WWP1, WWP2, WWTR1, XAF1, XBP1, XCR1, XG, XPA, XPO1, XPO5, XPO6, YBX1, YTHDC2, YWHAG, YWHAH, YWHAZ, YY1, ZAP70, ZBED3, ZBTB16, ZBTB20, ZBTB7A, ZBTB8A, ZEB2, ZFX, ZIC1, ZKSCAN3, ZMAT1, ZNF165, ZNF217, ZNF281, ZNF300, ZNF304, ZNF331, ZNF395, ZNF419, ZNF444, ZNF488, WWOX

Table 8A Continued . . .
Table 8A Continued . . .
Table 8A Continued . . .
Table 8A Continued . . .

TABLE 8B

Genes in gene set for metastasis function
ABCB1, ABCB5, ABCC3, ABCE1, ABCG2, ABL2, ABR, ACE2, ADAM10, ADAM19, ADAM8, ADAM9, ADAMTS1, ADAMTS5, ADIPOR1, ADIPOR2, ADM, ADO, ADORA2B, ADRB2, AFAP1, AFAP1L1, AFP, AGR2, AHNAK, AIM1, AKAP12, AKAP13, AKR1C3, AKT2, AKT3, ALDH1A1, ALDH1A3, ALK, AMOTL2, ANG, ANGPTL2, AKT1ANO1, ANO9, ANXA1, ANXA11, ANXA7, APC, APLP2, AQP3, AQP5, AQP9, ARF6, ARID1A, ARID2, ARID3B, ARID4A, ARRDC3, ATAD2, ATF3, AIF4, ATG4A, ATG5, ATM, ATOH1, ATOH8, ATP6AP2, ATP6V1C1, ATR, AURKA, AXIN2, B3GNT7, B4GALNT2, BACE1, BAD, BAG3, BAMBI, BATF2, BAX, BCAR1, BCAS3, BCAT1, BCL2, BCL2L2, BCL3, BCL6, BCL9, BDNFBIK, BIN1, BIRC5, BIRC6, BMP4, BMP7, BOLL, BPTF, BRCA1, BRCA2, BRD4, BRD8, BRMS1, BTBD7, BTG1, BTG2, BTG3, BTK, BVES, C3, C5, C6, C8orf4, C9, CA2, CA9, CACNA2D3, CACBP, CADM1, CALU, CAMP, CASP6, CBL, CBX7, CBX8, CCDC34, CCL17, CCL18, CCL19,

TABLE 8B-continued

Genes in gene set for metastasis function
CCL2, CCL20, CCL21, CCL22, CCL5, CCL7, CCNE1, CCNG2, CCR1, CCR4, CCR6, CCR7, CCR9, CD164, CD36, CD38, CD4, CD40, CD47, CD55, CD63, CD70, CD74, CD81, CD82, CD86, CD9, CD99, CDA, CDC20, CDC25A, CDC25B, CDC25C, CDC37, C42, CDCP1, CDH1, CDH17, CDH22, CDK4, CDK5, CDK5RAP3, CDK6, CDK8, CDKN1A, CDKN2A, CDX2, CEACAM1, CEACAM5, CFL1, CHD1L, CHEK1, CHI3L1, CHST11, CIAPIN1, CLCA1, CLCA2, CLDN10, CLOCK, CLU, CMTM3, CNTN1, COIL, COMMD1, CP, CPE, CPT1A, CRCT1, CRHR2, CRK, CRKL, CRP, CS, CSE1L, CSF1, CSK, CSPG4, CST6, CTBP1, CTBP2, CTGF, CTHRC1, CTLA4, CTTN, CUL4A, CUX1, CX3CR1, CXCL1, CXCL10, CXCL12, CXCL13, CXCL14, CXCL17, CXCL3, CXCL5, CXCL6, CXCL9, CXCR4, CXCR5, CXCR6, CYB5D2, CYLD, CYP1B1, CYP2E1, CYP2J2, CYP3A4, CYR61, DAB2IP, DACT2, DAND5, DAP, DCC, DCLK1, DDR2, DDX11, DDX20, DEK, DES, DHRS7, DKK1, DKK2, DLL4, DNM3, DNMT1, DNMT3A, DOCK1, DOT1L, DPH3, DPP4, DUSP1, DUSP6, DYRK1B, DYRK2, E2F1, E2F3, ECD, ECM1, ECT2, EDIL3, EEF1A2, EFEMP1, EGF, EGFL7, EGFR, EGR1, EIF3I, EIF4E, EIF5A2, EIF6, EMILIN1, EMP2, ENAH, ENG, ENO1, EPB41L3, EPCAM, EPHA2, EPHB2, EPHB4, EPHB6, ERBB3, ERBB4, ERCC1, ERCC2, ERCC3, ERG, ERGIC1, ESR1, ETS1, ETV1, EXT1, EYA2, EZH2, F11, F6, F8, FABP7, FADD, FANCA, FANCC, FANCD2, FAP, FAS, FASTKD2, FAT4, FBXL5, FBXO11, FBXW7, FGF10, FGF18, FGF2, FGFR1, FGFR2, FGFR3, FGFR4, FH, FHIT, FHL1, FHL2, FJX1, FLI1, FLNA, FLOT2, FLT1, FN1, FOSB, FOXA1, FOXA2, FOXC1, FOXC2, FOXD3, FOXL1, FOXM1, FOXO1, FOXO3, FOXO4, FOXP1, FOXP2, FOXP3, FOXO1, FRAT1, FSCN1, FSHR, FURIN, FUS, FUT3, FUT4, FYN, FZD5, FZD8, GAB1, GAB2, GADD45A, GAL, GALNT14, GALNT2, GAS6, GATA6, GC, GDNF, GEMIN5, GJA3, GKN1, GLB1, GLI1, GLI2, GLIPR1, GLO1, GNA13, GNAQ, GOLPH3, GPC5, GPI, GPNMB, GPR171, GPR3P, GPR55, GPR87, GPX3, GRB14, GRB2, GRK6, GRM1, HABP2, HAS2, HBD, HBP1, HDAC1, HDAC2, HDAC4, HDAC6, HES1, HES5, HEXA, HIF1A, HIPK2, HJURP, HMGA1, HMGA2, HMGB3, HMMR, HNRNPA2B1, HOOK1, HOXA1, HOXA5, HOXA9, HOXB2, HOXB9, HPR, HRG, HS3ST2, HSPA14, HTATIP2, HTRA1, HYOU1, ICMT, ID1, ID2, ID3, IDH2, IFIT2, IGF1R, IGF2, IGF2BP1, IGFBP1, IGFBP3, IGFBP5, IGFBP7, IL13, ILK, IMP3, IMPACT, ING1, ING2, ING3, ING5, IQGAP1, IRAK1, IRX2, ITGA2, ITGA3, ITGA5, ITGAV, ITGB1, ITGB3, JAG1, JAG2, JAK1, JAK2, JAK3, JMJD6, JUN, KCNJ1, KCNMA1, KDM2A, KDM4B, KDM5B, KDR, KEAP1, KIF11, KIF14, KIF15, KIF2A, KIF3C, KISS1, KIT, KITLG, KL, KLF17, XLF2, KLF4, XLF5, KLF6, KPNA2, KRAS, KRT19, KRT7, LAMB3, LAMC2, LAMP1, LAMP3, LAP3, LAPTM4B, LASP1, LATS1, LATS2, LIF, LIMK2, LIN28B, LMX1B, LOX, LOXL2, LRP1, LRP1B, LRP5, LRPPRC, LRRC4, LSM1, LYN, LZTS1, MACROD2, MADD, MAP2K4, MAP3K2, MAP3K9, MAP4K4, MAPK1, MAPKAPK2, MARCKS, MAX, MB, MBD2, MBP, MCM2, MDM4, MED1, MED12, MED27, MEF2C, MEIS1, MET, MFAP3L, MGAT1, MGMT, MIA, MIB1, MIF, MIP, MITF, MKL1, MLF2, MME, MMP10, MMP12, MMP13, MMP14, MMP28, MMP7, MMP9, MSC, MT3, MTA1, MTA2, MTA3, MTBP, MTDH, MTMR3, MTOR, MTSS1, MTUS1, MUC16, MUC4, MUSK, MVD, MVP, MX1, MYC, MYCN, MYD88, MYH9, MYD5B, NAP1L1, NAV1, NCK2, NCOA1, NDC80, NDRG2, NEDD1, NEDD4, NEDD4L, NET1, NF1, NFAT5, NGF, NHS, NKD1, NKD2, NLK, NLRP3, NME1, NOB1, NODAL, NOG, NOTCH1, NOTCH3, NOV, NOX1, NOX4, NPM1, NPS, NTSR1, NUAK1, NUMB, NUP88, OLA1, ORAI1, OSM, OTUB1, P4HA1, PAK2, PAK4, PALB2, PARP1, PAX3, PAX7, RAX8, PBK, PC, PCBP1, PCNA, PDC, PDCD4, PDCD5. PDGFRA, PDK3, PDPN, PEG10. PELP1,, PER2, PFKFB3, PGC, PHF8, PHLDA1, PIAS1, PICK1, PIGS, PIK3CA, PIKFYVE, PIN1, PIP4K2B, PIR, PIWIL1, PIWIL2, PKN1, PLA2G16, PLAUR, PLD2, PLK1, PMAIP1, PMEPA1, PMP22, POLB, PPARG, PPP1CA, PRAME, PRC1, PRDM14, PREX2, PRKCZ, PRXD1, PRL, PRMT1, PRMT5, PROK1, PROX1, PRSS3, PRUNE, PSCA, PTEN, PTER, PTG82, PTH, PTK6, PTK7, PTP4A3, PTPN13, PVR, QKI, RAB17, RAB22A, RAB25, RAB27B, RAB3D, RAB40B, RAB40C, RABL3, RAC1, RAC2, RACGAP1, RALA, RALB, RAMP3, RAN, RAP1A, RAP1B, RAP1GAP, RAP2B, RASAL2, RASSF3, RB1, RBP2, RBX1, RCAN3, RET, RGMB, RGS16, RHBDD2, RHO, RHOB, RHOBTB2, RHOC, RHOJ, RIN1, RIPK1, RIPK3, RNF111, RNF43, ROBO1, ROBO3, ROCK1, ROCK2, ROR1, ROR2, RPA1, RPL39, RPS12, RPS3, RPS6KB1, RREB1, RRM1, RRM2, RRP1B, RSPO2, RUNX2, RUNX3, RXFP1, S100A11, S100A2, S100A6, S100A7, S100A8, S100A9, S100B, S100P, S1PR3, SALL4, SART1, SASH1, SATB2, SCAI, SCAMP1, SCRIB, SDC1, SERPINB2, SETDB1, SFRP1, SFRP2, SH3GL2, SHH, SHMT1, SI, SIAH2, SIRT1, SIRT2, SKI, SKP2, SLC9A3, SLC38A1, SMAD1, SMAD2, SMAD3, SMAD4, SMAD7, SMO, SMYD3, SNAI2, SND1, SNTB2, SOCS3, SOD2, SOD3, SOX10, SOX12, SOX17, SOX2, SOX4, SOX6, SOX7, SOX9, SP1, SP3, SPAG5, SPAG9, SPARC, SPARCL1, SPDEF, SPOCK1, SPOP, SPRY1, SPRY4, SPTAN1, SQLE, SQSTM1, SRC, SRD5A2, SRF, SRPK1, SRRM4, SSTR2, SSX2IP, STARD13, STAT1, STAT3, STAT5B, STIP1, STMN1, STS, SULF1, SULF2, SUZ12, SYK, TACC3, TAGLN, TAT, TBK1,TBX2, TCEB1, TCF4, TCF7, TCF7L2, TDGF1, TEAD4, TERT, TET1, TF, TFF1, TFF3, TFPI, TG, TGFB1, TGFBI, TGIF1, TGM2, THY1, TIMM17A, TIMP2, TKTL1, TLR3; TLR4, TLR9, TM4SF1, TMED3, TMPRSS2, TMPRSS4, TNFAIP1, TNK2, TOB1, TOP1, TOPBP1, TP53, TRAF2, TRAF4, TRAF6, TRIB3, TRIM59, TRPA1, TRPM7, TRPM8, TRPV6, TSC2, TSG101, TSPAN12, TSPAN8, TSPAN9. TTYH2, TWIST1, TXN, TYR, UBE2Q1, UCHL1, UCN, UNC5B, USP10, USP15, USP18, USP22, USP37, USP9X, UVRAG, VASP, VAV2, VAV3, VCP, VEGFC, VEZT, VHL, VIP, VRK1, VTCN1, WBSCR22, WDR26, WEE1, WISP1, WNT10A, WNT10B, WNT3A, WNT5B, WT1, WTAP, WWP1, XAF1, XCR1, χPO1, YWHAZ, YY1, ZBED3, ZBTB7A, ZEB2, ZFX, ZKSCAN3, ZNF217, ZNF300, ZNF304, ZNF488, ALCAM, AR, ASAP1, DACH1, DLC1, PIEZO1, MMP16, PAG1, TUPS1, TUSC3, WWOX

Table 8B Continued . . .

TABLE 8C

Genes in gene set for biomarker analysis
ABAT, ABCA13, ABCB1, ABCC2, ABCG2, ACE2, ACP1, ACTN4 ADAM10, ADAM8, ADAM9, ADAMTS1, ADAMTS5, ADO, AFAP1, AFP, AGBL2, AGR2, AIM1, AKR1B10, AKT1, AKT2, ALDH1A1, ALDH1A3, ALK, ALCAM, ANG, ANLN, ANXA1, ANXA2, APC, APOA1, APOBEC3G, AQP1, AQP3, AQP5, AR, ARG1, ARHGEF7, ARID1A, ARPC1B, ASAP1, ASCL2, ASPM, ATAD2, ATF3, ATF5, ATM, ATOH8, BAD, BAMBI, BARX2, BATF2, BAX, BCL10, BCL2, BCL2L12, BCL6, BCOR, BCORL1, BDNF, BID, BIRC5, BMP4, BMP7, BMPR1A, BRCA1, BRCA2, BRE, BRMS1, BTBD7, BTC, BTG1, BTG3, BVES, C10orf10, C3, C6orf106, CA9, CACBP, CAD, CADM1, CAMP, CASK, CASP8, CASR, CBX7, CCL17, CCL19, CCL2, CCL20, CCL21, CCL4, CCL5, CCL7, CCNB1, CCNE1, CCNG2, CCNY, CCR6,, CCR7, CCT2, CD109, CD14, CD163, CD1A, CD4, CD40, CD47, CD55, CD74, CD82, CD9, CDC20, CDC25B, CDC25C, CDC42, CDC6, CDCP1, CDH1, CDH13, CDK4, CDK5, CDK8, CDKN2A, CDX2, CEACAM1, CES2, CFL1, CHD1L, CHEK1, CHEK2, CHRM3, CHRNA3, CIAPIN1, CISH, CLDN16,

TABLE 8C-continued

Genes in gene set for biomarker analysis
CLIC4, CLOCK, CLPTM1L, COIL, COL1A1, COL1A2, COMT, CP, CPE, CRK, CRKL, CRNN, CRP, CRTC1, CRTC3, CSE1L, CSNK1A1, CSPG4, CTBP2, CTGF, CTHRC1, CTNNB1, CTTN, CX3CL1, CX3CR1, CXCL1, CXCL10, CXCL12, CXCL14, CXCL5, CXCL9, CXCR4, CXCR6, CYB5A, CYP17A1, CYP19A1, CYP1A1, CYP24A1, CYP2B6, CYP3A4, CYP3A5, CYR61, DAB2, DACH1, DACH2, DACT2, DAND5, DAP, DCC, DCX, DDC, DDX1, DEC1, DEX, DES, DICER1, DIXDC1, DLC1, DLG5, DLK1, DLL4, DLX2, DLX5, DPP4, E2F1, EBP, ECD, ECM1, ECT2, EDIL3, EEF1A2, EFEMP1, EGF, EGR3, EGFL7, EGFR, EIF3E, EIF3I, EIF4E, EIF5A2, ENO1, EPAS1, EPCAM, EPHA2, EPHA3, EPHA7, EPHB4, EPHB6, EPO, EPS15, EPS8, ERBB3, ERBB4, ERCC1, ERG, ERP29, ESR1, ESR2, EVA2, EZH2, F2, FABP1, FABP4, FADD, FAM3C, FANCF, FAP, FAS, FBXO11, FBXW7, FER, FGF14, FGF2, FGFBP1, FGFR1, FGFR2, FGFR3, FGFR4, FHIT, FHL1, FHL2, FKBPL, FLNA, FLT1, FLT3, FLT4, FN1, FOXA1, FOXC1, FOXC2, FOXD3, FOXF2, FOXL1, FOXM1, FOXO3, FOXO4, FOXP1, FOXP3, FOXQ1, FRAT1, FSCN1, FURIN, FZD1, GAB2, GAL, GALNT9, GAS6, GATA2, GATA5, GATA6, GBP2, GC, GCG, GDF15, GGH, GIP, GIPC1, GLA, GLI1, GNAQ, GOLPH3, GPRC5A, GPX3, GRB2, GRM4, GSTP1, GTSE1, HAPLN3, HDAC1, HDAC2, HDAC6, HDGF, HES1, HIF1A, HK1, HMGA1, HMGA2, HMGB3, HNF1A, HOMER1, HOXA13, HOXA9, HOXB9, HPSE, HR, HSD3B1, HSPA2, HTATIP2, HTR42, HTRA3, HUWE1, HYOU1, ID2, ID3, IGF1R, IGFBP7, IL10, IL13, ILK, IMP3, IMPACT, ING3, IQGAP1, IQGAP2, IRX5, ITGA3, ITGA8, ITGB1, ITGB3, ITGB4, ITGBL1, JAK2, JMJD6, JUN, KCNJ1, KDM3A, KDM5C, KDR, KEAP1, KIAA0101, KIF14, KIF18A, KIF26B, KIF2A, KISS1, KIT, KLF17, KLF4, KLF6, KLK10, KLK3, KPNA2, KRAS, KRT7, LAMP3, LAPTM4B, LAT, LEP, LETM1, LIFR, LIG4, LIN28B, LMO7, LOX, LOXL2, LRG1, LYN, LZTS1, MAGEC2, MAGI1, MAML2, MAP4K3, MAP4K4, MARCKS, MAX, MB, MBP, MCM2, MET, MGMT, MGST1, MIA, MIB1, MIF, MIP, MITF, MMP11, MMP13, MMP16, MMP14, MMP7, MMP9, MMPO, MSX2, MTA1, MTA2, MTA3, MTBP, MTDH, MTHFD2, MTOR, MTSS1, MTUS1, MUC16, MUC2, MUC4, MVD, MVP, MYC, MYCN, MYD88, MYH9, MZF1, NAT1, NCK1, NCK2, NCOA2, NCDA5, NCOR1, NCOR2, NCSTN, NDRG2, NDRG3, NDRG4, NEDD4L, NEK2, NETO2, NEU3, NKD1, NKTR, NLK, NME1, NOB1, NOD2, NODAL, NOTCH1, NOTCH3, NOTCH4, NOV, NPM1, NQD2, NR2F2, NR4A2, NRAS, NUCB2, NUCKS1, OAT, OLA1, OLIG1, ORAI1, OTP, OTUB1, P4HA2, PAFAH1B1, PAK4, PARP1, PARVB, PAX3, PAX6, PAX8, PBK, PBRM1, PBX3, PC, PCDH10, PCDH9, PCNA, PDCD4, PDCD6, PDGFRA, PEG10, PER1, PER2, PFKPB2, PFN2PHIP, PHLDA1, PHLPP1, PHLPP2, PIGR, PIK3CA, PIK3CB, PIK3R1, PIP4K2B, PITX2, PIWIL2, PLA2G16, PLAGL1, PLAUR, PML, POLE, POMC, PPARG, PPM1D, PRAME, PRDX1, PRDX4, PRL, PROK1, PROM1, PROX1, PRSS3, PRUNE, PSCA, PTEN, PTGIS, PTGS2, PTK7, PTOV1, PTP4A3, RAB25, RAB27B, RAC1, RACGAP1, RAD50, RAD51, RALBP1, RALY, RAN, RASGRP3, RBM3, RBX1, REG4, RELA, REPS2, RET, RGS1, RGS6, RHO, RHOC, RIPK2, ROBO1, ROCK1, ROCK2, ROR1, ROR2, RRM1, RUNX2, RUNX3, S100A11, S100A2, S100A6, S100A9, S100B, S100P, SATB2, SCRIB, SCUBE2, SDC1, SDC2, SDHA, SELP, SEMA3F, SERPINB2, SETDB1, SF3B1, SFRP1, SGTA, SH2B1, SIAH2, SIPA1, SIRT1, SIX3, SIX4, SKI, SKP2, SLC19A1, SLC9A9, SLC22A18, SLC25A1, SLC29A3, SLCO1B1, SLCO1B3, SLN, SMAD1, SMAD2, SMAD3, SMAD4, SMAD7, SMYD2, SMYD3, SNAI2, SOCS3, SOD2, SOX10, SOX11, SOX17, SOX2, SOX4, SOX7, SOX8, SOX9, SP1, SPAG5, SPARC, SPARCL1, SRC, SRPK1, SST, STAG2, STARD10, STARD13, STAT1, STAT3, STAT6, STC2, STIP1, ST8, STYK1, SULT1E1, SUZ12, SYK, TACC2, TACSTD2, TAT, TBX2, TCF3, TEK, TFE3, TERT, TET1, TF, TFF3, TFPI, TGF81, TGFBI, TGM2, TGM3, THY1, TIMM17A, TKTL1, TLR4, TMPRSS2, TMPRSS3, TMPRSS4, TP53, TPD52, TRAF2, TRAF6, TRPM7, TRPS1, TSG101, TSPYL5, TUBB3, TWIST1, TYMS, UBE2C, UCN, USP10, USP14, USP22, USP9X, VAV3, VDAC1, VHL, VIP, WNT10A, WNT10B, WNT11, WNT2, WNT7A, WWOX, WWP1, XPA, XPO5, YY1, ZEB2, ZFX, ZMAT1, ZNF217

Table 8C Continued . . .

TABLE 9A

ROC-AUC comparisons of panMPS and other MPS versions developed by using subsets of genes based on Z_{genes} score thresholds and clump representations.

Distribution	No. of genes	No. of clumps	MSK_Prostate	Duke_Prostate	Montefiore_TNBC	MSK_Lung
*Z_{genes} score ≥ 4	33	21	0.69	0.70	0.73	0.87
Z_{genes} score ≥ 4	43	21	0.68	0.73	0.77	0.88
*Z_{genes} score ≥ 3	68	43	0.71	0.70	0.73	0.93
Z_{genes} score ≥ 3	100	43	0.70	0.72	0.74	0.94
panMPS	295	67	0.71	0.72	0.75	0.94

*Only highest Zgenes-score gene in clump

TABLE 9B

Linear regression model (r^2) between panMPS and other MPS versions developed by using subsets of genes based on Z_{genes} score thresholds and clump representations.

Distribution	No. of genes	No. of clumps	MSK_Prostate	Duke_Prostate	Montefiore_TNBC	MSK_Lung
*Z_{genes} score ≥ 4	33	21	0.89	0.87	0.83	0.83
Z_{genes} score ≥ 4	43	21	0.93	0.92	0.84	0.86
*Z_{genes} score ≥ 3	68	43	0.94	0.94	0.93	0.94
Z_{genes} score ≥ 3	100	43	0.97	0.97	0.94	0.96
panMPS	295	67	1	1	1	1

*Only highest Z_{genes} score gene in clump

TABLE 10A

Clinical and histological characteristics of samples used to validate the panMPS model for metastatic outcome for prostate cancer

	Cohort				
	MSK Prostate CA		Duke Prostate CA		
	mPT	iPT	mPT	iPT	P
Outcome					
n	25	260	37	39	
Age					
Mean	58.93	58.15	64.19	61.82	0.5
Median	59.47	58.13	64	62	
Standard deviation	7.23	6.82	6.48	8.41	
Range	46-71	37-75	47-77	46-77	
Clinical stage					
T1C	10 (3.51%)	146 (51.22%)	18 (23.68%)	24 (31.57%)	7.56×18^{-8}
T2	11 (3.86%)	106 (37.19%)	9 (11.84%)	4 (5.26%)	3.86×10^{-5}
T3	4 (1.40%)	8 (2.81%)	0 (0%)	0 (0%)	
Path stage					
T2	7 (2.46%)	156 (54.74%)	6 (7.89%)	9 (11.84%)	1.53×10^{-4}
T3	13 (4.56%)	92 (32.28%)	24 (31.57%)	26 (34.21%)	3.85×10^{-6}
T4	5 (1.75%)	12 (4.21%)	7 (9.21%)	4 (5.26%)	0.12
Biopsy Gleason score					
3	0 (0%)	0 (0%)	0 (0%)	1 (1.31%)	
4	0 (0%)	0 (0%)	1 (1.31%)	0 (0%)	
5	0 (0%)	2 (0.70%)	0 (0%)	4 (5.26%)	
6	7 (2.46%)	142 (49.82%)	10 (13.51%)	18 (23.68%)	1.91×10^{-5}
7	12 (4.21%)	92 (32.28%)	14 (18.42%)	12 (15.78%)	1.19×10^{-5}
8	5 (1.75%)	15 (5.26%)	5 (6.57%)	0 (0%)	0.01
9	0 (0%)	9 (3.16%)	3 (3.94%)	4 (5.26%)	0.06
10	0 (0%)	0 (0%)	1 (1.31%)	0 (0%)	
Path Gleason score					
6	1 (0.35%)	68 (23.86%)	2 (2.63%)	2 (2.63%)	0.01
7	8 (2.81%)	173 (60.70%)	20 (26.31%)	29 (38.16%)	9.27×10^{-10}
8	6 (2.11%)	10 (3.51%)	2 (2.63%)	3 (3.95%)	
9	19 (6.66%)	8 (2.81%)	12 (15.785)	5 (6.58%)	
10	0 (0%)	0 (0%)	1 (1.31%)	0 (0%)	
Preop PSA (ng/mL)					
Median	8.49	5.6	7.5	7.3	
<4	4 (1.40%)	46 (16.14%)	4 (5.26%)	4 (5.26%)	
4-10	10 (3.51%)	163 (57.19%)	16 (21.05%)	27 (35.52%)	
>10	11 (3.86%)	50 (17.54%)	17 (22.36%)	8 (10.52%)	

P-values were determined by Wilcoxon Rank Sum Test and Fisher's Exact Test respectively for continuous and categorical variables for inter cohort significance.

TABLE 10B

Clinical and histological characteristics of samples used to validate the panMPS model for metastasis outcome for TNBC

	Cohort Montefiore TNBC	
	mBC	iBC
Outcome		
n	28	13
Age		
Mean	58.3	53
Median	61.5	49
Standard deviation	11.57	11.7
Range	35-82	34-74
TNM Stage		
T1	4 (9.75%)	5 (12.19%)
T2	7 (17.07%)	5 (12.19%)
T3	4 (9.75%)	0 (0%)
T4	2 (4.88%)	0 (0%)

TABLE 10C

Clinical and histological characteristics of samples used to validate the panMPS model for metastasis outcome for TNBC

	Cohort MSK Lung Adeno CA	
	mLA	iLA
Outcome		
n	23	10
Sex		
Male	11 (26.83%)	4 (9.76%)
Female	12 (29.27%)	6 (14.63%)
TNM Stage		
1B	6 (14.63%)	0 (0%)
2	7 (17.07%)	1 (2.44%)
3	10 (24.39%)	5 (12.20%)
4	2 (4.88%)	4 (9.76%)

TABLE 11

AUC of Distribution of MPS genes based on lowest Z_{genes} scores in clumps

Distribution	No. of genes	No. of clumps	MSK_Prostate	Duke_Prostate	Montefiore_TNBC	MSK_Lung
	33	21	0.67	0.67	0.78	0.87
Z_{genes} score ≥ 4	43	21	0.68	0.73	0.77	0.88
	68	43	0.69	0.69	0.75	0.93
Z_{genes} score ≥ 3	100	43	0.7	0.72	0.74	0.94
*panMPS	175	67	0.7	0.72	0.76	0.97
panMPS	295	67	0.71	0.72	0.75	0.94

*Only lowest Zgenes-score gene in clump

TABLE 12

r^2 of Distribution of MPS genes based on lowest Zgenes scores in clumps

Distribution	No. of genes	No. of clumps	MSK_Prostate	Duke_Prostate	Montefiore_TNBC	MSK_Lung
	33	21	0.75	0.57	0.67	0.59
Z_{genes} score ≥ 4	43	21	0.93	0.92	0.84	0.86
	68	43	0.81	0.64	0.73	0.71
Z_{genes} score ≥ 3	100	43	0.97	0.97	0.94	0.96
*panMPS	175	67	0.89	0.75	0.84	0.84
panMPS	295	67	1	1	1	1

*Only lowest Z_{genes} score gene in clump

TABLE 13

MPS Genes

index	gene	NYU_Z	NYU_dir	MSKs1_Z	MSKs1_dir	MSKs2_Z	MSKs2_dir
1	CLCNKB	NA	NA	NA	NA	2.0	1
2	ARHGEF10L	NA	NA	2.1	−1	NA	NA
3	ACTL8	NA	NA	1.9	−1	NA	NA
4	DPYD	NA	NA	NA	NA	2.9	−1
5	COL11A1	NA	NA	NA	NA	1.9	−1
6	NRXN1	NA	NA	NA	NA	3.2	−1
7	CTNNA2	NA	NA	NA	NA	1.8	−1
8	ALCAM	NA	NA	NA	NA	2.5	1
9	ZBTB20	NA	NA	1.8	1	NA	NA
10	MYLK	NA	NA	2.8	1	NA	NA
11	KALRN	NA	NA	2.4	1	NA	NA

TABLE 13-continued

	MPS Genes						
12	BFSP2	NA	NA	2.4	1	NA	NA
13	SLC9A9	NA	NA	2.7	1	NA	NA
14	KCNAB1	NA	NA	5.8	1	NA	NA
15	PPM1L	NA	NA	2	1	NA	NA
16	MECOM	NA	NA	2	1	NA	NA
17	DGKG	NA	NA	1.9	1	NA	NA
18	TP63	NA	NA	3	1	NA	NA
19	LEPREL1	NA	NA	2.6	1	NA	NA
20	BOD1L	NA	NA	NA	NA	2.4	−1
21	KCTD8	NA	NA	NA	NA	2.8	−1
22	GABRA2	NA	NA	NA	NA	2.3	−1
23	LPHN3	NA	NA	NA	NA	2.5	−1
24	GRID2	NA	NA	NA	NA	5.1	−1
25	DCHS2	NA	NA	NA	NA	2.6	−1
26	GLRB	NA	NA	NA	NA	2.7	−1
27	GRIA2	NA	NA	NA	NA	2.3	−1
28	FSTL5	NA	NA	NA	NA	2.2	−1
29	CENPH	NA	NA	1.9	−1	NA	NA
30	MRPS36	NA	NA	2.6	−1	NA	NA
31	CDK7	NA	NA	2.7	−1	NA	NA
32	CCDC125	NA	NA	2	−1	NA	NA
33	TAF9	NA	NA	2.6	−1	NA	NA
34	RAD17	NA	NA	2.6	−1	NA	NA
35	MARVELD2	NA	NA	3	−1	NA	NA
36	MEF2C	NA	NA	NA	NA	2.3	−1
37	TICAM2	NA	NA	NA	NA	1.8	−1
38	COL21A1	NA	NA	NA	NA	1.8	−1
39	COL19A1	NA	NA	NA	NA	3.4	−1
40	COL12A1	NA	NA	NA	NA	1.6	−1
41	UBE2CBP	2.8	−1	NA	NA	NA	NA
42	ME1	2.5	−1	NA	NA	NA	NA
43	MAP3K7	NA	NA	NA	NA	3.2	−1
44	EPHA7	NA	NA	NA	NA	1.8	−1
45	FBXL4	NA	NA	NA	NA	1.7	−1
46	SIM1	NA	NA	NA	NA	2.2	−1
47	ASCC3	NA	NA	NA	NA	1.8	−1
48	NUS1	NA	NA	NA	NA	2.2	−1
49	TRDN	NA	NA	NA	NA	3.0	−1
50	UTRN	NA	NA	NA	NA	2.3	−1
51	EPM2A	NA	NA	NA	NA	2.4	−1
52	GRM1	NA	NA	NA	NA	1.9	−1
53	C6orf118	NA	NA	NA	NA	2.8	−1
54	PDE10A	NA	NA	NA	NA	4.7	−1
55	IQCE	NA	NA	NA	NA	1.8	1
56	FBXL18	NA	NA	NA	NA	1.9	1
57	STX1A	NA	NA	NA	NA	2.2	1
58	CLDN3	NA	NA	NA	NA	2.6	1
59	EIF4H	NA	NA	NA	NA	2.0	1
60	LAT2	NA	NA	NA	NA	2.0	1
61	RFC2	NA	NA	NA	NA	1.8	1
62	CLIP2	NA	NA	NA	NA	3.1	1
63	HIP1	NA	NA	NA	NA	4.4	1
64	TMEM120A	NA	NA	NA	NA	1.7	1
65	STYXL1	NA	NA	NA	NA	2.3	1
66	MDH2	NA	NA	NA	NA	2.0	1
67	YWHAG	NA	NA	NA	NA	2.7	1
68	STAG3	NA	NA	NA	NA	2.4	1
69	PILRB	NA	NA	NA	NA	2.9	1
70	PILRA	NA	NA	NA	NA	1.9	1
71	MEPCE	NA	NA	NA	NA	2.1	1
72	TSC22D4	NA	NA	NA	NA	2.1	1
73	C7orf51	NA	NA	NA	NA	2.2	1
74	AGFG2	NA	NA	NA	NA	2.3	1
75	LRCH4	NA	NA	NA	NA	2.2	1
76	FBXO24	NA	NA	NA	NA	2.5	1
77	PCOLCE	NA	NA	NA	NA	1.8	1
78	MOSPD3	NA	NA	NA	NA	2.3	1
79	TFR2	NA	NA	NA	NA	2.6	1
80	ACTL6B	NA	NA	NA	NA	1.7	1
81	GIGYF1	NA	NA	NA	NA	2.7	1
82	EPO	NA	NA	NA	NA	2.0	1
83	CPA2	NA	NA	NA	NA	2.1	1
84	CPA4	NA	NA	NA	NA	1.9	1
85	CPA5	NA	NA	NA	NA	2.8	1
86	CPA1	NA	NA	NA	NA	2.1	1
87	TSGA14	NA	NA	NA	NA	9.4	1
88	MEST	NA	NA	NA	NA	3.2	1
89	COPG2	NA	NA	NA	NA	3.1	1

TABLE 13-continued

	MPS Genes						
90	ARHGEF5	NA	NA	NA	NA	2.7	1
91	DLGAP2	NA	NA	2.2	−1	NA	NA
92	ARHGEF10	NA	NA	2.9	−1	NA	NA
93	MYOM2	2.1	−1	NA	NA	NA	NA
94	CSMD1	NA	NA	NA	NA	4.6	−1
95	MFHAS1	3.3	−1	NA	NA	NA	NA
96	ERI1	1.9	−1	NA	NA	NA	NA
97	TNKS	4	−1	NA	NA	NA	NA
98	MSRA	5.1	−1	NA	NA	NA	NA
99	C8orf16	2.2	−1	NA	NA	NA	NA
100	MTMR9	1.9	−1	NA	NA	NA	NA
101	BLK	2.1	−1	NA	NA	NA	NA
102	GATA4	3.2	−1	NA	NA	NA	NA
103	NEIL2	2.7	−1	NA	NA	NA	NA
104	CTSB	2.8	−1	NA	NA	NA	NA
105	C8orf79	2.9	−1	NA	NA	NA	NA
106	DLC1	6.5	−1	NA	NA	NA	NA
107	SGCZ	4.7	−1	NA	NA	3.5	−1
108	TUSC3	3.1	−1	NA	NA	NA	NA
109	MTMR7	3.7	−1	NA	NA	NA	NA
110	SLC7A2	4.1	−1	NA	NA	NA	NA
111	PDGFRL	4.8	−1	NA	NA	NA	NA
112	MTUS1	3.6	−1	NA	NA	NA	NA
113	PCM1	1.7	−1	NA	NA	NA	NA
114	ASAH1	7.1	−1	NA	NA	NA	NA
115	NAT2	3.3	−1	NA	NA	NA	NA
116	PSD3	7.3	−1	NA	NA	NA	NA
117	SH2D4A	2.9	−1	NA	NA	NA	NA
118	LZTS1	2	−1	NA	NA	NA	NA
119	XPO7	2.3	−1	NA	NA	NA	NA
120	FAM160B2	2.5	−1	1.8	−1	NA	NA
121	NUDT18	NA	NA	2.3	−1	NA	NA
122	HR	NA	NA	2.7	−1	NA	NA
123	REEP4	NA	NA	2.5	−1	NA	NA
124	LGI3	NA	NA	2	−1	NA	NA
125	BMP1	NA	NA	2.2	−1	NA	NA
126	PHYHIP	NA	NA	2.2	−1	NA	NA
127	POLR3D	NA	NA	2.7	−1	NA	NA
128	SLC39A14	1.8	−1	2.2	−1	NA	NA
129	PPP3CC	3.1	−1	2.6	−1	NA	NA
130	SORBS3	NA	NA	3	−1	NA	NA
131	PDLIM2	NA	NA	2.9	−1	NA	NA
132	C8orf58	NA	NA	3	−1	NA	NA
133	KIAA1967	2.8	−1	3.1	−1	NA	NA
134	BIN3	1.7	−1	2.8	−1	NA	NA
135	EGR3	NA	NA	2	−1	NA	NA
136	RHOBTB2	NA	NA	1.7	−1	NA	NA
137	TNFRSF10D	1.9	−1	NA	NA	NA	NA
138	TNFRSF10A	NA	NA	2.2	−1	NA	NA
139	CHMP7	NA	NA	2.4	−1	NA	NA
140	LOXL2	NA	NA	1.9	−1	NA	NA
141	ENTPD4	2.7	−1	NA	NA	NA	NA
142	erw	2.6	−1	NA	NA	NA	NA
143	NKX2-6	2.4	−1	NA	NA	NA	NA
144	DOCK5	5.4	−1	NA	NA	NA	NA
145	KCTD9	2	−1	NA	NA	NA	NA
146	CDCA2	2	−1	NA	NA	NA	NA
147	EBF2	5.1	−1	NA	NA	NA	NA
148	DPYSL2	3.3	−1	NA	NA	NA	NA
149	ADRA1A	3.9	−1	NA	NA	NA	NA
150	STMN4	3.3	−1	NA	NA	NA	NA
151	TRIM35	2.6	−1	NA	NA	NA	NA
152	PTK2B	7	−1	NA	NA	NA	NA
153	CHRNA2	3.5	−1	NA	NA	NA	NA
154	EPHX2	3.3	−1	NA	NA	NA	NA
155	CCDC25	4.4	−1	NA	NA	NA	NA
156	SCARA5	3.3	−1	NA	NA	NA	NA
157	C8orf80	3.6	−1	NA	NA	NA	NA
158	ELP3	3.4	−1	NA	NA	NA	NA
159	HMBOX1	1.8	−1	NA	NA	NA	NA
160	KIF13B	2.7	−1	NA	NA	NA	NA
161	TOX	4.3	1	NA	NA	NA	NA
162	CYP7B1	NA	NA	1.7	1	NA	NA
163	CPA6	3.8	1	NA	NA	NA	NA
164	PREX2	7.5	1	NA	NA	NA	NA
165	C8orf34	6	1	NA	NA	NA	NA
166	SULF1	5.2	1	3.4	1	NA	NA
167	SLCO5A1	4.9	1	4.2	1	NA	NA

TABLE 13-continued

		MPS Genes					
168	PRDM14	4.7	1	NA	NA	NA	NA
169	NCOA2	3.2	1	2.4	1	NA	NA
170	LACTB2	2.6	1	NA	NA	NA	NA
171	XKR9	2.7	1	NA	NA	NA	NA
172	EYA1	3.4	1	NA	NA	NA	NA
173	MSC	2	1	NA	NA	NA	NA
174	TRPA1	2.3	1	NA	NA	NA	NA
175	KCNB2	6.8	1	NA	NA	NA	NA
176	RPL7	2.3	1	NA	NA	NA	NA
177	STAU2	4.6	1	NA	NA	NA	NA
178	TCEB1	1.8	1	NA	NA	NA	NA
179	JPH1	6	1	NA	NA	NA	NA
180	GDAP1	2	1	NA	NA	NA	NA
181	PI15	3	1	NA	NA	NA	NA
182	CRISPLD1	4.9	1	NA	NA	NA	NA
183	HNF4G	4.1	1	NA	NA	NA	NA
184	ZFHX4	4.3	1	NA	NA	NA	NA
185	PKIA	3.3	1	NA	NA	NA	NA
186	STMN2	2.8	1	NA	NA	NA	NA
187	HEY1	3	1	NA	NA	NA	NA
188	ZNF704	NA	NA	2.5	1	NA	NA
189	PAG1	NA	NA	2	1	NA	NA
190	IMPA1	NA	NA	1.9	1	NA	NA
191	RALYL	2.8	1	NA	NA	NA	NA
192	CNGB3	1.8	1	NA	NA	NA	NA
193	CNBD1	3.8	1	3.8	1	NA	NA
194	MMP16	NA	NA	3.5	1	NA	NA
195	SLC26A7	NA	NA	2.2	1	NA	NA
196	CDH17	2.8	1	NA	NA	NA	NA
197	PTDSS1	2.5	1	NA	NA	NA	NA
198	SDC2	3.4	1	NA	NA	NA	NA
199	MTDH	NA	NA	1.9	1	NA	NA
200	NIPAL2	1.9	1	NA	NA	NA	NA
201	STK3	1.8	1	NA	NA	NA	NA
202	VPS13B	3.9	1	NA	NA	NA	NA
203	RGS22	2.7	1	NA	NA	NA	NA
204	YWHAZ	NA	NA	2.2	1	NA	NA
205	ZNF706	NA	NA	2.8	1	NA	NA
206	GRHL2	NA	NA	2.4	1	NA	NA
207	NCALD	5.5	1	2.9	1	NA	NA
208	UBR5	NA	NA	2.2	1	NA	NA
209	ATP6V1C1	NA	NA	2.4	1	NA	NA
210	RIMS2	2	1	4	1	NA	NA
211	DPYS	3.2	1	NA	NA	NA	NA
212	LRP12	NA	NA	2	1	NA	NA
213	ZFPM2	4.2	1	6.3	1	NA	NA
214	ANGPT1	2.4	1	NA	NA	NA	NA
215	RSPO2	1.8	1	NA	NA	NA	NA
216	CSMD3	4.9	1	4.2	1	NA	NA
217	TRPS1	2.9	1	2.7	1	NA	NA
218	ZHX2	NA	NA	2.6	1	NA	NA
219	ANXA13	2.1	1	NA	NA	NA	NA
220	KIAA0196	2.6	1	NA	NA	NA	NA
221	POU5F1B	2.9	1	NA	NA	NA	NA
222	MYC	4.2	1	NA	NA	NA	NA
223	TMEM75	3.5	1	NA	NA	NA	NA
224	ASAP1	NA	NA	3.6	1	NA	NA
225	ADCY8	3.1	1	5.4	1	NA	NA
226	EFR3A	3.1	1	NA	NA	NA	NA
227	OC90	1.9	1	NA	NA	NA	NA
228	KCNQ3	6	1	NA	NA	NA	NA
229	TMEM71	2.9	1	NA	NA	NA	NA
230	PHF20L1	2.8	1	NA	NA	NA	NA
231	TG	3.8	1	NA	NA	NA	NA
232	SLA	2.2	1	NA	NA	NA	NA
233	WISP1	2.2	1	NA	NA	NA	NA
234	ZFAT	2.5	1	NA	NA	NA	NA
235	PTK2	NA	NA	2.3	1	NA	NA
236	GRK5	NA	NA	2.4	−1	NA	NA
237	RCOR2	NA	NA	NA	NA	1.7	1
238	MACROD1	NA	NA	1.9	1	2.9	1
239	STIP1	NA	NA	NA	NA	1.8	1
240	SF1	NA	NA	NA	NA	2.5	1
241	MEN1	NA	NA	NA	NA	2.1	1
242	CDC42BPG	NA	NA	NA	NA	2.3	1
243	PPP2R5B	NA	NA	NA	NA	1.8	1
244	GYS2	NA	NA	NA	NA	2.8	−1
245	PDS5B	NA	NA	NA	NA	2.0	−1

TABLE 13-continued

		MPS Genes					
246	C13orf23	NA	NA	NA	NA	2.2	−1
247	ENOX1	NA	NA	NA	NA	5.6	−1
248	LRCH1	NA	NA	NA	NA	2.4	−1
249	ESD	NA	NA	NA	NA	2.6	−1
250	HTR2A	NA	NA	NA	NA	3.3	−1
251	DIAPH3	NA	NA	NA	NA	3.3	−1
252	PCDH9	NA	NA	NA	NA	4.5	−1
253	KLHL1	NA	NA	NA	NA	1.9	−1
254	DACH1	NA	NA	NA	NA	1.9	−1
255	GPC5	NA	NA	NA	NA	2.1	−1
256	NALCN	NA	NA	NA	NA	2.2	−1
257	TFDP1	NA	NA	2.3	−1	NA	NA
258	MDGA2	NA	NA	NA	NA	2.8	−1
259	MEIS2	NA	NA	NA	NA	3.9	−1
260	VPS13C	NA	NA	NA	NA	1.8	−1
261	TBC1D10B	NA	NA	NA	NA	1.8	1
262	RNF40	NA	NA	NA	NA	2.1	1
263	CNGB1	1.8	−1	NA	NA	NA	NA
264	C16orf80	2.2	−1	NA	NA	NA	NA
265	CDH8	NA	NA	NA	NA	3.7	−1
266	NFAT5	2.3	−1	NA	NA	NA	NA
267	WWP2	1.8	−1	NA	NA	NA	NA
268	DDX19A	2.3	−1	NA	NA	NA	NA
269	ST3GAL2	2.4	−1	NA	NA	NA	NA
270	ZFHX3	2.2	−1	NA	NA	NA	NA
271	GLG1	2.1	−1	NA	NA	NA	NA
272	WDR59	2.1	−1	NA	NA	NA	NA
273	BCAR1	2.5	−1	NA	NA	NA	NA
274	CFDP1	3	−1	NA	NA	NA	NA
275	CNTNAP4	3.2	−1	NA	NA	NA	NA
276	ADAMTS18	3.5	−1	NA	NA	NA	NA
277	NUDT7	2.2	−1	NA	NA	NA	NA
278	CLEC3A	2.3	−1	NA	NA	NA	NA
279	WWOX	9.3	−1	NA	NA	NA	NA
280	CDYL2	2.5	−1	NA	NA	NA	NA
281	C16orf46	NA	NA	2.2	−1	NA	NA
282	GCSH	NA	NA	1.9	−1	NA	NA
283	PKD1L2	4.9	−1	2	−1	NA	NA
284	BCMO1	2.9	−1	3.6	−1	NA	NA
285	GAN	2.7	−1	2.4	−1	NA	NA
286	PLCG2	2.9	−1	2.7	−1	NA	NA
287	HSD17B2	2.6	−1	NA	NA	NA	NA
288	CDH13	8	−1	2.9	−1	NA	NA
289	MLYCD	2.4	−1	NA	NA	NA	NA
290	NECAB2	NA	NA	2	−1	NA	NA
291	MBTPS1	2.7	−1	NA	NA	NA	NA
292	HSDL1	NA	NA	2	−1	NA	NA
293	LRRC50	2.4	−1	NA	NA	NA	NA
294	WFDC1	2.3	−1	NA	NA	NA	NA
295	ATP2C2	3.6	−1	NA	NA	NA	NA
296	KIAA1609	NA	NA	1.9	−1	NA	NA
297	KLHL36	NA	NA	1.8	−1	NA	NA
298	USP10	2.3	−1	NA	NA	NA	NA
299	CRISPLD2	2.5	−1	2.9	−1	NA	NA
300	ZDHHC7	NA	NA	2.5	−1	NA	NA
301	KIAA0513	NA	NA	2.1	−1	NA	NA
302	KIAA0182	NA	NA	2	−1	NA	NA
303	GINS2	NA	NA	2.1	−1	NA	NA
304	C16orf74	NA	NA	2.3	−1	NA	NA
305	COX4NB	NA	NA	2.5	−1	NA	NA
306	COX4I1	NA	NA	2.6	−1	NA	NA
307	IRF8	NA	NA	2.5	−1	NA	NA
308	FOXF1	NA	NA	2.2	−1	NA	NA
309	MTHFSD	NA	NA	2.4	−1	NA	NA
310	JPH3	2.4	−1	2.4	−1	NA	NA
311	KLHDC4	NA	NA	2.5	−1	NA	NA
312	SLC7A5	1.7	−1	3	−1	NA	NA
313	CA5A	2.6	−1	3.8	−1	NA	NA
314	BANP	2.6	−1	3.3	−1	NA	NA
315	ZFPM1	NA	NA	2.5	−1	NA	NA
316	C16orf85	NA	NA	2.1	−1	NA	NA
317	ZC3H18	NA	NA	2.1	−1	NA	NA
318	IL17C	NA	NA	1.8	−1	NA	NA
319	CYBA	NA	NA	2.9	−1	NA	NA
320	MVD	NA	NA	2.3	−1	NA	NA
321	SNAI3	NA	NA	2.4	−1	NA	NA
322	RNF166	NA	NA	2.2	−1	NA	NA
323	FAM38A	NA	NA	2.7	−1	NA	NA

TABLE 13-continued

MPS Genes

324	CDT1	NA	NA	2	−1	NA	NA
325	GALNS	NA	NA	2.3	−1	NA	NA
326	TRAPPC2L	NA	NA	1.9	−1	NA	NA
327	CBFA2T3	NA	NA	1.9	−1	NA	NA
328	CDH15	NA	NA	1.9	−1	NA	NA
329	ANKRD11	3	−1	3.7	−1	NA	NA
330	FANCA	NA	NA	1.9	−1	NA	NA
331	SPIRE2	NA	NA	1.7	−1	NA	NA
332	TCF25	NA	NA	2.1	−1	NA	NA
333	TUBB3	NA	NA	2.6	−1	NA	NA
334	DEF8	NA	NA	1.9	−1	NA	NA
335	AFG3L1	NA	NA	2.3	−1	NA	NA
336	GAS8	NA	NA	2.9	−1	NA	NA
337	DNAH2	1.8	−1	NA	NA	NA	NA
338	NKIRAS2	NA	NA	NA	NA	2.0	1
339	DHX58	NA	NA	NA	NA	8.9	1
340	KAT2A	NA	NA	NA	NA	3.2	1
341	HSPB9	NA	NA	NA	NA	2.9	1
342	RAB5C	NA	NA	NA	NA	3.5	1
343	KCNH4	NA	NA	NA	NA	3.8	1
344	GHDC	NA	NA	NA	NA	1.8	1
345	NOTUM	NA	NA	NA	NA	2.7	1
346	ASPSCR1	NA	NA	NA	NA	1.8	1
347	DUS1L	NA	NA	NA	NA	2.3	1
348	FASN	NA	NA	NA	NA	3.0	1
349	CDH2	NA	NA	NA	NA	3.4	−1
350	NOL4	NA	NA	NA	NA	3.9	−1
351	DTNA	NA	NA	NA	NA	2.2	−1
352	DCC	NA	NA	NA	NA	6.6	−1
353	WDR7	NA	NA	NA	NA	2.0	−1
354	CD226	NA	NA	NA	NA	3.3	−1
355	ZSWIM4	NA	NA	NA	NA	2.8	1
356	C19orf57	NA	NA	NA	NA	2.8	1
357	CC2D1A	NA	NA	NA	NA	4.0	1
358	RFX1	NA	NA	NA	NA	2.2	1
359	PLCB1	NA	NA	NA	NA	1.9	−1
360	SMARCB1	NA	NA	1.8	−1	NA	NA
361	TBC1D22A	NA	NA	4.6	−1	NA	NA
362	RAB9A	NA	NA	3.7	1	NA	NA
363	TFE3	NA	NA	2.1	1	NA	NA
364	HEPH	1.8	1	NA	NA	NA	NA
365	EDA2R	2	1	NA	NA	NA	NA
366	AR	2.3	1	2.6	1	NA	NA
367	OPHN1	5.8	1	NA	NA	NA	NA
368	NLGN4Y	NA	NA	NA	NA	2.4	−1

index	gene	gene_Chr	gene_Cytoband	gene_start	gene_end
1	CLCNKB	1	p36.13	16242834	16256390
2	ARHGEF10L	1	p36.13	17738917	17896956
3	ACTL8	1	p36.13	17954395	18026145
4	DPYD	1	p21.3	97315890	98159203
5	COL11A1	1	p21.1	1.03E+08	1.03E+08
6	NRXN1	2	p16.3	49999148	51113178
7	CTNNA2	2	p12	79732191	80729415
8	ALCAM	3	q13.11	1.07E+08	
9	ZBTB20	3	q13.31	1.18E+08	
10	MYLK	3	q21.1	124811586	125085868
11	KALRN	3	q21.1	125296275	125922726
12	BFSP2	3	q22.1	134601480	134676746
13	SLC9A9	3	q24	144466755	145049979
14	KCNAB1	3	q25.31	157321095	157739621
15	PPM1L	3	q26.1	161956791	162271511
16	MECOM	3	q26.2	170283981	170347054
17	DGKG	3	q27.3	187347686	187562717
18	TP63	3	q28	190831910	191107935
19	LEPREL1	3	q28	191157213	191321407
20	BOD1L	4	p15.33	13179464	13238426
21	KCTD8	4	p13	43870683	44145581
22	GABRA2	4	p12	45946341	46086561
23	LPHN3	4	q13.1	62045434	62620762
24	GRID2	4	q22.1	93444831	94914730
25	DCHS2	4	q32.1	155375138	155632318
26	GLRB	4	q32.1	158216788	158312299
27	GRIA2	4	q32.1	158361186	158506677
28	FSTL5	4	q32.2	162524501	163304636
29	CENPH	5	q13.2	68521131	68541939
30	MRPS36	5	q13.2	68549329	68577710

TABLE 13-continued

MPS Genes					
31	CDK7	5	q13.2	68566471	68609004
32	CCDC125	5	q13.2	68612278	68664392
33	TAF9	5	q13.2	68696327	68701596
34	RAD17	5	q13.2	68700880	68746384
35	MARVELD2	5	q13.2	68746699	68773646
36	MEF2C	5	q14.3	88051922	88214780
37	TICAM2	5	q22.3	114942247	114989610
38	COL21A1	6	p12.1	56029347	56366851
39	COL19A1	6	q13	70633169	70978878
40	COL12A1	6	q14.1	75850762	75972343
41	UBE2CBP	6	q14.1	83658836	83832269
42	ME1	6	q14.2	83976827	84197498
43	MAP3K7	6	q15	91282074	91353628
44	EPHA7	6	q16.1	94007864	94185993
45	FBXL4	6	q16.2	99428055	99502570
46	SIM1	6	q16.3	100939606	101019494
47	ASCC3	6	q16.3	101062791	101435961
48	NUS1	6	q22.2	118103310	118138577
49	TRDN	6	q22.31	123579182	123999937
50	UTRN	6	q24.2	144654566	145215859
51	EPM2A	6	q24.3	145988141	146098684
52	GRM1	6	q24.3	146390611	146800427
53	C6orf118	6	q27	165613148	165643101
54	PDE10A	6	q27	165660766	165995578
55	IQCE	7	p22.2	2565158	2620893
56	FBXL18	7	p22.1	5481955	5523646
57	STX1A	7	q11.23	72751472	72771925
58	CLDN3	7	q11.23	72821263	72822536
59	EIF4H	7	q11.23	73226625	73249358
60	LAT2	7	q11.23	73261662	73282099
61	RFC2	7	q11.23	73283770	73306674
62	CLIP2	7	q11.23	73341739	73458196
63	HIP1	7	q11.23	75001345	75206215
64	TMEM120A	7	q11.23	75454238	75461913
65	STYXL1	7	q11.23	75463592	75515257
66	MDH2	7	q11.23	75515329	75533864
67	YWHAG	7	q11.23	75794053	75826252
68	STAG3	7	q22.1	99613474	99659778
69	PILRB	7	q22.1	99771673	99803388
70	PILRA	7	q22.1	99809004	99835650
71	MEPCE	7	q22.1	99865190	99869676
72	TSC22D4	7	q22.1	99902080	99914838
73	C7orf51	7	q22.1	99919486	99930358
74	AGFG2	7	q22.1	99974770	100003778
75	LRCH4	7	q22.1	100009570	100021712
76	FBXO24	7	q22.1	100021892	100036674
77	PCOLCE	7	q22.1	100037818	100043732
78	MOSPD3	7	q22.1	100047661	100050932
79	TFR2	7	q22.1	100055975	100077109
80	ACTL6B	7	q22.1	100078678	100092007
81	GIGYF1	7	q22.1	100115066	100124806
82	EPO	7	q22.1	100156359	100159257
83	CPA2	7	q32.2	129693939	129716870
84	CPA4	7	q32.2	129720230	129751249
85	CPA5	7	q32.2	129771892	129795807
86	CPA1	7	q32.2	129807468	129815165
87	TSGA14	7	q32.2	129823611	129868133
88	MEST	7	q32.2	129913282	129933363
89	COPG2	7	q32.2	129933404	129935887
90	ARHGEF5	7	q35	143683366	143708657
91	DLGAP2	8	p23.3	1436939	1644048
92	ARHGEF10	8	p23.3	1759549	1894206
93	MYOM2	8	p23.3	1980565	2080779
94	CSMD1	8	p23.2	2780282	3258996
95	MFHAS1	8	p23.1	8679409	8788541
96	ERI1	8	p23.1	8897856	8928139
97	TNKS	8	p23.1	9450855	9677266
98	MSRA	8	p23.1	9949189	10323803
99	C8orf16	8	p23.1	11021390	11025155
100	MTMR9	8	p23.1	11179410	11223062
101	BLK	8	p23.1	11388930	11459516
102	GATA4	8	p23.1	11599162	11654918
103	NEIL2	8	p23.1	11664627	11682263
104	CTSB	8	p23.1	11737442	11763055
105	C8orf79	8	p22	12847554	12931653
106	DLC1	8	p22	12985243	13416766
107	SGCZ	8	p22	13991744	15140219
108	TUSC3	8	p22	15442101	15666366

TABLE 13-continued

MPS Genes					
109	MTMR7	8	p22	17199923	17315207
110	SLC7A2	8	p22	17398975	17472357
111	PDGFRL	8	p22	17478443	17545655
112	MTUS1	8	p22	17545584	17702666
113	PCM1	8	p22	17824646	17935562
114	ASAH1	8	p22	17958214	17986787
115	NAT2	8	p22	18293035	18303003
116	PSD3	8	p22	18429093	18915476
117	SH2D4A	8	p21.3	19215483	19297594
118	LZTS1	8	p21.3	20147956	20205754
119	XPO7	8	p21.3	21833126	21920041
120	FAM160B2	8	p21.3	22002660	22017835
121	NUDT18	8	p21.3	22020328	22023403
122	HR	8	p21.3	22027877	22045326
123	REEP4	8	p21.3	22051478	22055393
124	LGI3	8	p21.3	22060290	22070290
125	BMP1	8	p21.3	22078645	22125782
126	PHYHIP	8	p21.3	22133162	22145796
127	POLR3D	8	p21.3	22158564	22164624
128	SLC39A14	8	p21.3	22280737	22347462
129	PPP3CC	8	p21.3	22354541	22454580
130	SORBS3	8	p21.3	22465196	22488952
131	PDLIM2	8	p21.3	22492199	22511483
132	C8orf58	8	p21.3	22513067	22517605
133	KIAA1967	8	p21.3	22518202	22533920
134	BIN3	8	p21.3	22533906	22582553
135	EGR3	8	p21.3	22601119	22606760
136	RHOBTB2	8	p21.3	22913059	22933655
137	TNFRSF10D	8	p21.3	23049051	23077485
138	TNFRSF10A	8	p21.3	23104916	23138584
139	CHMP7	8	p21.3	23157095	23175450
140	LOXL2	8	p21.3	23210097	23317667
141	ENTPD4	8	p21.3	23299386	23371081
142	erw	8	p21.2	23442308	23486008
143	NKX2-6	8	p21.2	23615909	23620056
144	DOCK5	8	p21.2	25098204	25326536
145	KCTD9	8	p21.2	25341283	25371837
146	CDCA2	8	p21.2	25372428	25421353
147	EBF2	8	p21.2	25758042	25958292
148	DPYSL2	8	p21.2	26491327	26571607
149	ADRA1A	8	p21.2	26661584	26778839
150	STMN4	8	p21.2	27149738	27171843
151	TRIM35	8	p21.2	27198321	27224751
152	PTK2B	8	p21.2	27224916	27372820
153	CHRNA2	8	p21.2	27373196	27392730
154	EPHX2	8	p21.1	27404562	27458403
155	CCDC25	8	p21.1	27646756	27686089
156	SCARA5	8	p21.1	27783672	27906117
157	C8orf80	8	p21.1	27935607	27997307
158	ELP3	8	p21.1	27999759	28104584
159	HMBOX1	8	p21.1	28803830	28966706
160	KIF13B	8	p21.1	28980715	29176529
161	TOX	8	q12.1	59880531	60194321
162	CYP7B1	8	q12.3	65671246	65873902
163	CPA6	8	q13.2	68496963	68821134
164	PREX2	8	q13.2	69026907	69306451
165	C8orf34	8	q13.2	69405511	69893810
166	SULF1	8	q13.2	70541427	70735701
167	SLCO5A1	8	q13.3	70747129	70909762
168	PRDM14	8	q13.3	71126574	71146116
169	NCOA2	8	q13.3	71178380	71478574
170	LACTB2	8	q13.3	71712045	71743946
171	XKR9	8	q13.3	71755848	71809213
172	EYA1	8	q13.3	72272222	72437021
173	MSC	8	q13.3	72916332	72919285
174	TRPA1	8	q13.3	73096040	73150373
175	KCNB2	8	q13.3	73642524	74012880
176	RPL7	8	q21.11	74365073	74375857
177	STAU2	8	q21.11	74495160	74821629
178	TCEB1	8	q21.11	75021184	75046959
179	JPH1	8	q21.11	75309493	75396117
180	GDAP1	8	q21.11	75425173	75441888
181	PI15	8	q21.11	75899327	75929819
182	CRISPLD1	8	q21.11	76059531	76109346
183	HNF4G	8	q21.11	76482732	76641600
184	ZFHX4	8	q21.11	77756078	77942076
185	PKIA	8	q21.12	79590891	79678040
186	STMN2	8	q21.13	80685916	80740868

TABLE 13-continued

MPS Genes					
187	HEY1	8	q21.13	80838801	80842653
188	ZNF704	8	q21.13	81713324	81949571
189	PAG1	8	q21.13	82042605	82186858
190	IMPA1	8	q21.13	82732751	82761115
191	RALYL	8	q21.2	85604112	85963979
192	CNGB3	8	q21.3	87655277	87825017
193	CNBD1	8	q21.3	87947840	88435220
194	MMP16	8	q21.3	89118580	89408833
195	SLC26A7	8	q21.3	92330692	92479554
196	CDH17	8	q22.1	95208566	95289986
197	PTDSS1	8	q22.1	97343340	97415950
198	SDC2	8	q22.1	97575058	97693213
199	MTDH	8	q22.1	98725583	98807711
200	NIPAL2	8	q22.2	99273563	99375797
201	STK3	8	q22.2	99536037	99907074
202	VPS13B	8	q22.2	100094670	100958983
203	RGS22	8	q22.2	101042452	101187520
204	YWHAZ	8	q22.3	101999980	102034745
205	ZNF706	8	q22.3	102278444	102287136
206	GRHL2	8	q22.3	102574162	102750995
207	NCALD	8	q22.3	102767947	103206311
208	UBR5	8	q22.3	103334748	103493671
209	ATP6V1C1	8	q22.3	104102424	104154461
210	RIMS2	8	q22.3	104582291	105333263
211	DPYS	8	q22.3	105460829	105548453
212	LRP12	8	q22.3	105570643	105670344
213	ZFPM2	8	q23.1	106400323	106885939
214	ANGPT1	8	q23.1	108330899	108579459
215	RSPO2	8	q23.1	108980721	109165052
216	CSMD3	8	q23.3	113304337	114518418
217	TRPS1	8	q23.3	116489900	116750429
218	ZHX2	8	q24.13	123863082	124055936
219	ANXA13	8	q24.13	124762216	124818828
220	KIAA0196	8	q24.13	126105691	126173191
221	POU5F1B	8	q24.21	128497039	128498621
222	MYC	8	q24.21	128816862	128822853
223	TMEM75	8	q24.21	129029046	129029462
224	ASAP1	8	q24.21	131133535	131483399
225	ADCY8	8	q24.22	131861736	132123854
226	EFR3A	8	q24.22	132985517	133095071
227	OC90	8	q24.22	133105667	133167084
228	KCNQ3	8	q24.22	133210438	133561961
229	TMEM71	8	q24.22	133779633	133842010
230	PHF20L1	8	q24.22	133856786	133930234
231	TG	8	q24.22	133948387	134216325
232	SLA	8	q24.22	134118155	134184479
233	WISP1	8	q24.22	134272494	134310751
234	ZFAT	8	q24.22	135559215	135794463
235	PTK2	8	q24.3	141737683	142080514
236	GRK5	10	q26.11	120957091	121205118
237	RCOR2	11	q13.1	63435303	63440892
238	MACROD1	11	q13.1	63522607	63690109
239	STIP1	11	q13.1	63709873	63728596
240	SF1	11	q13.1	64288654	64302817
241	MEN1	11	q13.1	64327564	64335342
242	CDC42BPG	11	q13.1	64348240	64368617
243	PPP2R5B	11	q13.1	64448756	64458523
244	GYS2	12	p12.1	21580390	21649048
245	PDS5B	13	q13.1	32058564	32250157
246	C13orf23	13	q13.3	38482003	38510252
247	ENOX1	13	q14.11	42685704	43259044
248	LRCH1	13	q14.13	46025304	46222786
249	ESD	13	q14.2	46243393	46269368
250	HTR2A	13	q14.2	46305514	46368176
251	DIAPH3	13	q21.2	59137718	59636120
252	PCDH9	13	q21.32	65774970	66702578
253	KLHL1	13	q21.33	69172727	69580592
254	DACH1	13	q21.33	70910099	71339331
255	GPC5	13	q31.3	90848919	92316693
256	NALCN	13	q33.1	100504131	100866814
257	TFDP1	13	q34	113287057	113343500
258	MDGA2	14	q21.3	46379045	47213703
259	MEIS2	15	q14	34970519	35189740
260	VPS13C	15	q22.2	59931884	60139939
261	TBC1D10B	16	p11.2	30275925	30288587
262	RNF40	16	p11.2	30681100	30695129
263	CNGB1	16	q13	56475004	56562513
264	C16orf80	16	q21	56705000	56720797

TABLE 13-continued

MPS Genes					
265	CDH8	16	q21	60244866	60628240
266	NFAT5	16	q22.1	68156498	68296054
267	WWP2	16	q22.1	68353710	68533145
268	DDX19A	16	q22.1	68938322	68964780
269	ST3GAL2	16	q22.1	68970839	69030492
270	ZFHX3	16	q22.3	71374285	71639775
271	GLG1	16	q22.3	73043357	73198518
272	WDR59	16	q23.1	73464975	73576518
273	BCAR1	16	q23.1	73820429	73859452
274	CFDP1	16	q23.1	73885109	74024888
275	CNTNAP4	16	q23.1	74868677	75150636
276	ADAMTS18	16	q23.1	75873527	76026512
277	NUDT7	16	q23.1	76313912	76333652
278	CLEC3A	16	q23.1	76613944	76623495
279	WWOX	16	q23.1	76691052	77803532
280	CDYL2	16	q23.2	79195176	79395680
281	C16orf46	16	q23.2	79644603	79668373
282	GCSH	16	q23.2	79673430	79687481
283	PKD1L2	16	q23.2	79691985	79811477
284	BCMO1	16	q23.2	79829797	79882248
285	GAN	16	q23.2	79906076	79971441
286	PLCG2	16	q23.2	80370408	80549399
287	HSD17B2	16	q23.3	80626364	80689638
288	CDH13	16	q23.3	81439761	82387705
289	MLYCD	16	q23.3	82490231	82507286
290	NECAB2	16	q23.3	82559738	82593878
291	MBTPS1	16	q24.1	82644872	82708018
292	HSDL1	16	q24.1	82713389	82736265
293	LRRC50	16	q24.1	82736366	82769024
294	WFDC1	16	q24.1	82885822	82920888
295	ATP2C2	16	q24.1	82959634	83055293
296	KIAA1609	16	q24.1	83068608	83095794
297	KLHL36	16	q24.1	83239632	83253416
298	USP10	16	q24.1	83291050	83371026
299	CRISPLD2	16	q24.1	83411113	83500614
300	ZDHHC7	16	q24.1	83565573	83602642
301	KIAA0513	16	q24.1	83618911	83685327
302	KIAA0182	16	q24.1	84202524	84267311
303	GINS2	16	q24.1	84268782	84280089
304	C16orf74	16	q24.1	84298624	84342190
305	COX4NB	16	q24.1	84369737	84390601
306	COX4I1	16	q24.1	84390697	84398109
307	IRF8	16	q24.1	84490275	84513710
308	FOXF1	16	q24.1	85101634	85105570
309	MTHFSD	16	q24.1	85121284	85157509
310	JPH3	16	q24.2	86194000	86289263
311	KLHDC4	16	q24.2	86298920	86357056
312	SLC7A5	16	q24.2	86421131	86460615
313	CA5A	16	q24.2	86479126	86527613
314	BANP	16	q24.2	86542539	86668425
315	ZFPM1	16	q24.2	87047226	87128890
316	C16orf85	16	q24.2	87147613	87164049
317	ZC3H18	16	q24.2	87164343	87225756
318	IL17C	16	q24.3	87232502	87234385
319	CYBA	16	q24.3	87237199	87244958
320	MVD	16	q24.3	87245849	87257019
321	SNAI3	16	q24.3	87271591	87280383
322	RNF166	16	q24.3	87290411	87300312
323	FAM38A	16	q24.3	87302916	87330317
324	CDT1	16	q24.3	87397687	87403166
325	GALNS	16	q24.3	87407644	87450885
326	TRAPPC2L	16	q24.3	87451007	87455020
327	CBFA2T3	16	q24.3	87468768	87570902
328	CDH15	16	q24.3	87765664	87789400
329	ANKRD11	16	q24.3	87861536	88084470
330	FANCA	16	q24.3	88331460	88410566
331	SPIRE2	16	q24.3	88422408	88465228
332	TCF25	16	q24.3	88467520	88505287
333	TUBB3	16	q24.3	88513168	88530006
334	DEF8	16	q24.3	88542684	88561968
335	AFG3L1	16	q24.3	88566489	88594696
336	GAS8	16	q24.3	88616509	88638880
337	DNAH2	17	p13.1	7562746	7677783
338	NKIRAS2	17	q21.2	37422564	37431180
339	DHX58	17	q21.2	37506979	37518277
340	KAT2A	17	q21.2	37518657	37526872
341	HSPB9	17	q21.2	37528361	37528897
342	RAB5C	17	q21.2	37530524	37560548

TABLE 13-continued

MPS Genes					
343	KCNH4	17	q21.2	37562439	37586822
344	GHDC	17	q21.2	37594632	37599722
345	NOTUM	17	q25.3	77503689	77512353
346	ASPSCR1	17	q25.3	77528715	77568569
347	DUS1L	17	q25.3	77609043	77629242
348	FASN	17	q25.3	77629504	77649395
349	CDH2	18	q12.1	23784934	24011189
350	NOL4	18	q12.1	29685062	30057513
351	DTNA	18	q12.1	30327279	30725806
352	DCC	18	q21.2	48121156	49311780
353	WDR7	18	q21.31	52469614	52848040
354	CD226	18	q22.2	65681175	65775140
355	ZSWIM4	19	p13.13	13767274	13804044
356	C19orf57	19	p13.12	13854168	13877909
357	CC2D1A	19	p13.12	13878014	13902691
358	RFX1	19	p13.12	13933353	13978097
359	PLCB1	20	p12.3	8061296	8813547
360	SMARCB1	22	q11.23	22459150	22506703
361	TBC1D22A	22	q13.31	45537193	45948399
362	RAB9A	23	p22.2	13617262	13637681
363	TFE3	23	p11.23	48772613	48787722
364	HEPH	23	q12	65299388	65403956
365	EDA2R	23	q12	65732204	65775608
366	AR	23	q12	66680599	66860844
367	OPHN1	23	q12	67179440	67570372
368	NLGN4Y	24	q11.221	15144026	15466924

Table 13 Cont'd . . .
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TABLE 14

Table14-1a

Final-RANK	gene	index	NYU-2	NYU-dir	NYU-count	MSKs1-Z	MSKs1-dir	MSKs2-count	MSKs2-Z	MSKs2-dir	MSKs2 count	logrank-n52random	logank-n271random	logrank-composite	gene-Chr	gene-Cytoband
1	PPP3CC	129	3.1	−1	958	2.6	−1	965	NA	NA	NA	48	41	45	8	p21.3
2	SLCO5A1	167	4.9	1	1000	4.2	1	982	NA	NA	NA	31	13	19	8	q13.3
5	SLC7A5	312	1.7	−1	508	3	−1	980	NA	NA	NA	43	37	40	18	q24.2
4	SLC7A2	110	4.1	−1	1000	NA	NA	NA	NA	NA	NA	44	43	44	8	p22
5	CRISPLD2	299	2.5	−1	735	2.9	−1	939	NA	NA	NA	54	67	61	16	q24.1
6	CDH13	288	8	−1	984	2.9	−1	767	NA	NA	NA	46	86	63	16	q23.3
7	CDH8	265	NA	NA	NA	NA	NA	NA	3.7344	−1	989	15	10	11	16	q21
8	CDH2	348	NA	NA	NA	NA	NA	NA	3.4486	−1	967	16	15	17	18	q12.1
9	ASAH1	114	7.1	−1	1000	NA	NA	NA	NA	NA	NA	105	64	80	8	p22
10	KCNB2	175	8.8	1	1000	NA	NA	NA	NA	NA	NA	59	74	66	8	q13.3
11	KCNH4	343	NA	NA	NA	NA	NA	NA	3.7501	1	983	1	1	1	17	q21.2
12	KCTD8	21	NA	NA	NA	NA	NA	NA	2.8192	−1	921	30	24	29	4	p13
13	JPH1	179	6.8	1	1000	NA	NA	NA	NA	NA	NA	29	35	31	8	q21.11
14	MEST	88	NA	NA	NA	NA	NA	NA	3.2232	1	940	32	32	32	7	q32.2
15	NCALD	200	5.5	1	1000	2.9	1	953	NA	NA	NA	13	12	13	8	q22.3
16	COL19A1	39	NA	NA	NA	NA	NA	NA	3.4333	−1	936	27	20	21.5	6	q13
17	MAP3K7	43	NA	NA	NA	NA	NA	NA	3.1873	−1	929	47	54	49	6	q15
18	YWHAG	67	NA	NA	NA	NA	NA	NA	2.7386	1	951	40	62	47	7	q11.23
19	NOL4	350	NA	NA	NA	NA	NA	NA	3.9113	−1	993	4	2	2	18	q12.1
20	ENOX1	247	NA	NA	NA	NA	NA	NA	5.6235	−1	1000	2	8	4	13	q14.11
21	CSMD1	94	NA	NA	NA	NA	NA	NA	4.6280	−1	971	7	6	6	8	p23.2
22	SGCZ	107	4.7	−1	926	NA	NA	NA	3.5107	−1	861	9	5	7	8	p22
23	PDE10A	54	NA	NA	NA	NA	NA	NA	4.5945	−1	999	8	7	8	5	q27
24	PCDH9	252	NA	NA	NA	NA	NA	NA	4.5416	−1	962	5	19	9	13	q21.32
25	HTR2A	250	NA	NA	NA	NA	NA	NA	3.2974	−1	966	10	11	10	13	q14.2
26	HIP1	63	NA	NA	NA	NA	NA	NA	4.4416	1	1000	11	14	12	7	q11.23
27	CD226	354	NA	NA	NA	NA	NA	NA	3.3032	−1	1000	18	9	14	18	q22.2
28	DCC	352	NA	NA	NA	NA	NA	NA	6.6211	−1	1000	12	17	15	18	q21.2
29	CC2D1A	357	NA	NA	NA	NA	NA	NA	3.9705	1	996	17	18	18	19	p1312
30	PT K2B	152	7	−1	1000	NA	NA	NA	NA	NA	NA	20	27	21.5	8	p21.2
31	BCMO1	284	2.9	−1	943	3.6	−1	957	NA	NA	NA	26	21	23	16	q23.2
32	MACROD1	233	NA	NA	NA	1.9	1	533	2.8909	1	973	25	22	24	11	q13.1
33	GRID2	24	NA	NA	NA	NA	NA	NA	5.1108	−1	983	22	25	25	4	q22.1
34	DIAPH3	251	NA	NA	NA	NA	NA	NA	3.2653	−1	982	24	29	27	13	q21.2
35	PILRB	69	NA	NA	NA	NA	NA	NA	2.9352	1	996	25	25	28	7	q22.1
36	MEIS2	259	NA	NA	NA	NA	NA	NA	3.9428	−1	999	19	39	30	15	q14
37	MSRA	98	5.1	−1	999	NA	NA	NA	NA	NA	NA	34	31	33	8	p23.1
38	DPYD	4	NA	NA	NA	NA	NA	NA	2.8861	−1	847	33	34	34	1	p21.3

Table 14-1b

Final-RANK	gene	gene-start	gene-end	genesBtwn	contg	clump-index	dstprev	dstnext	min-disto-ROL	IndexO-Proxy1	NYU-Zadjust	MSKs1-Zadust	MSKS2-Zadjust
1	PPP3CC	22354541	22454580	0	1	26	10616	−7079	−7079	1	0.52	0.29	NA
2	SLCO5A1	70747129	70909762	0	1	33	216812	−11428	−11428	1	1.63	1.16	NA

TABLE 14-continued

3	SLC7A5	86421131	86460815	0	1	58	18511	−84075	18511	1	0.00	0.47	NA	
4	SLC7A2	17398975	17472357	0	1	21	6086	−83768	6086	1	1.10	NA	NA	
5	CRISPLD2	83411113	83500814	0	1	56	64959	−40087	−40087	1	0.25	0.42	NA	
6	CDH13	81439751	82387705	1	0	NA	102526	−750123	102526	1	3.67	0.42	NA	
7	CDH8	60244866	60626240	82	0	NA	7528258	−3524069	−3524069	1	NA	NA	0.87	
8	CDH2	23784934	24011189	19	0	NA	5673873	NA	5673873	1	NA	NA	0.70	
9	ASAH1	17958214	17986787	1	1	22	306248	−22652	−22652	1	3.10	NA	NA	
10	KCNB2	73642524	74012880	1	1	34	352193	492151	352193	1	2.91	NA	NA	
11	KCNH4	37582439	37586822	1	1	6.4	7810	−1891	−1891	1	NA	NA	0.88	
12	KCTD8	43870883	44145681	3	0	NA	1800760	−30632257	1800760	1	NA	NA	0.38	
13	JPH1	75308493	75396117	0	1	35	29056	−262534	29058	1	227	NA	NA	
14	MEST	129913282	129933363	0	1	13	41	−45149	41	1	NA	NA	0.56	
15	NCALD	102767947	103206311	1	1	40	128437	−16952	−16962	1	2.03	0.42	NA	
16	COL19A1	70833169	70978878	20	0	NA	4871884	NA	4871884	1	NA	NA	0.70	
17	MAP3K7	91282074	91353828	0	1	5	2654236	−7084576	2654236	1	NA	NA	0.58	
18	YWHAG	75794053	75828252	126	0	NA	23787222	−260189	−260189	1	NA	NA	0.34	
19	NOL4	29686062	30057513	0	1	67	269766	−5673873	269766	1	NA	NA	0.98	
20	ENOX1	42886704	43259044	18	0	NA	2766260	−4175452	2766260	1	NA	NA	2.12	
21	CSMD1	2780262	3258996	46	1	14	5420413	699503	−699503	1	NA	NA	1.44	
22	SGCZ	13991744	15140219	0	1	20	301882	−574978	301882	1	1.49	NA	0.74	
23	PDE10A	165560755	166995578	NA	1	8	NA	−17665	−17655	1	NA	NA	1.49	
24	PCDH9	65774970	66702579	0	1	49	2470149	−6138850	2470149	1	NA	NA	1.38	
25	HTR2A	46305514	46368175	44	1	48	12769542	−36146	−36145	1	NA	NA	0.62	
26	HIP1	75001345	75206215	5	0	NA	248023	−1543149	248023	1	NA	NA	1.32	
25	CD226	65881175	65775140	NA	0	NA	NA	−12833135	−12033135	1	NA	NA	0.63	
26	DCC	48121155	49311780	10	0	NA	3157834	−17395350	3157834	1	NA	NA	2.79	
29	CC2D1A	13878014	13902691	1	1	68	30662	−105	−105	1	NA	NA	1.02	
30	PT K2B	27224915	27372820	0	1	30	376	−165	−165	1	3.04	NA	NA	
31	BCMO1	79829797	79882248	0	1	53	23828	−18320	−18320	1	0.42	0.80	NA	
32	MACROD1	63522607	63690109	1	0	NA	19764	−81715	19784	1	NA	0.05	0.41	
33	GRID2	93444831	94914730	186	0	NA	60460408	−3624009	−30824089	1	NA	NA	1.77	
34	DIAPH3	59137718	59636120	2	0	NA	6138850	−12769542	6138850	1	NA	NA	0.60	
35	PILRB	99771673	99803388	0	1	11	5616	−111895	5615	1	NA	NA	0.44	
36	MEIS2	34970519	35189740	193	0	NA	24742144	NA	24742144	1	NA	NA	1.00	
37	MSRA	9949189	10323803	4	1	16	897587	−271923	−271923	1	1.76	NA	NA	
38	DPYD	97315890	98159203	19	0	NA	4955408	−79289745	4955408	1	NA	NA	0.41	

Table 14-2a

Final-RANK	gene	index	NYU-2	NYU-dir	NYU-count	MSKs1-Z	MSKs1-dir	MSKs2-count	MSKs2-Z	MSKs2-dir	MSKs2 count	logrank-n52random	logank-n271random	logrank-composite	gene-Chr	gene-Cytoband
39	ANKRD11	329	3	−1	948	3.7	−1	988	NA	NA	NA	37	33	35	18	q24.3
40	NRXN1	6	NA	NA	NA	NA	NA	NA	3.2327	−1	840	39	38	38	2	p16.3
41	ADCY8	225	3.1	1	980	5.4	1	1000	NA	NA	NA	52	30	39	8	q24.22
42	TRDN	49	NA	NA	NA	NA	NA	NA	3.0342	−1	898	38	44	41	6	q22.31
43	STAU2	177	4.6	1	1000	NA	NA	NA	NA	NA	NA	45	42	43	8	q21.11
44	SF1	240	NA	NA	NA	NA	NA	NA	2.4710	1	888	56	48	48	11	q13.1
45	CLIP2	62	NA	NA	NA	NA	NA	NA	3.0945	1	998	57	47	50	7	q11.23
46	CLDN3	58	NA	NA	NA	NA	NA	NA	2.6179	1	984	51	53	51	7	q11.23
47	ZSWIM4	355	NA	NA	NA	NA	NA	NA	2.8120	1	975	60	51	57	19	p13.13
48	GLRB	26	NA	NA	NA	NA	NA	NA	2.6600	−1	963	64	48	58	4	q32.1
49	DCHS2	25	NA	NA	NA	NA	NA	NA	2.7883	−1	954	68	80	84	4	q32.1

TABLE 14-continued

50	TRPS1	217	2.9	1	814	2.7	1	751	NA	NA	NA	63	65	65	8	q23.3
51	MDGA2	258	NA	NA	NA	NA	NA	NA	2.8345	−1	823	69	66	68	14	q21.3
52	CNBD1	193	38	1	999	3.8	1	940	NA	NA	NA	57	70	69	8	q21.3
53	STAG3	68	NA	NA	NA	NA	NA	NA	2.416	1	967	78	68	71	7	q22.1
54	GATA4	102	3.2	1	979	NA	NA	NA		NA	NA	72	77	72	8	p23.1
55	VPS13B	202	3.9	1	999	NA	NA	NA	NA	NA	NA	85	69	74	8	q22.2
56	DOCK5	144	5.4	−1	1000	NA	NA	NA	NA	NA	NA	81	78	76	8	p21.2
57	ZHX2	218	NA	NA	NA	2.6	1	771	NA	NA	NA	82	80	78	8	q24.13
58	ARHGEF5	90	NA	NA	NA	NA	NA	NA	2.7472	1	760	66	102	81	7	q35
59	SDC2	198	3.4	1	991	NA	NA	NA	NA	NA	NA	75	90	82	8	q22.1
60	MYLK	10	NA	NA	NA	2.8	1	842	NA	NA	NA	93	75	83	3	q21.1
61	LPHN3	23	NA	NA	NA	NA	NA	NA	2.4808	1	794	80	92	85	4	q13.1
62	MOSPD3	78	NA	NA	NA	NA	NA	NA	2.3144	1	904	90	82	86	7	q22.1
63	GYS2	244	NA	NA	NA	NA	NA	NA	2.7616	−1	884	99	83	92	12	p12.1
64	GAS8	336	NA	NA	NA	2.9	−1	999	NA	NA	NA	84	103	95	16	q24.3
65	RAB9A	382	NA	NA	NA	3.7	1	870	NA	NA	NA	98	97	97	23	p22.2
66	POLA3D	127	NA	NA	NA	2.7	−1	955	NA	NA	NA	91	109	98	8	p21.3
67	PSD3	116	7.3	−1	1000	NA	NA	NA	NA	NA	NA	97	104	100	8	p22
68	ZFPM2	213	4.2	1	991	6.3	1	996	NA	NA	NA	149	71	101	8	q23.1
69	ATP6V1C1	309	NA	NA	NA	2.4	1	858	NA	NA	NA	114	93	102	8	q22.3
70	MEF2C	36	NA	NA	NA	NA	NA	NA	2.2584	−1	839	109	98	103	5	q14.3
71	PKIA	185	3.3	1	999	NA	NA	NA	NA	NA	NA	115	99	104	8	q21.12
72	ADAMTS18	276	3.5	−1	902	NA	NA	NA	NA	NA	NA	100	114	105	16	q23.1
73	STYXL1	65	NA	NA	NA	NA	NA	NA	2.3049	1	883	104	110	106	7	q11.23
74	EPM2A	51	NA	NA	NA	NA	NA	NA	2.3972	−1	920	113	105	108	6	q24.3
75	LEPREL1	19	NA	NA	NA	2.6	1	755	NA	NA	NA	106	119	110	3	q28
76	GABRA2	22	NA	NA	NA	NA	NA	NA	2.2755	−1	876	119	107	111	4	p12
77	RCOR2	230	NA	NA	NA	NA	NA	NA	1.7131	−1	514	108	120	114	11	q13.1
78	MFHAS1	95	3.3	−1	958	NA	NA	NA	NA	NA	NA	121	108	115	8	p23.1

Table 14-2b

Final-RANK	gene	gene-start	gene-end	genesBtwn	contg	clump-index	dstprev	dstnext	min-disto-ROL	IndexO-Proxy1	NYU-Zadjust	MSKs1-Zadust	MSKS2-Zadjust
39	ANKRD11	87881536	88084470	11	1	61	246990	−72136	−72136	1	0.47	0.85	NA
40	NRXN1	49999148	51113178	155	0	NA	28619013	NA	28619013	1	NA	NA	0.59
41	ADCY8	131861736	132123654	0	1	45	861663	−378337	−378337	1	0.52	1.97	NA
42	TRDN	123579182	123999937	96	0	NA	20654529	−5440605	−5440605	1	NA	NA	0.48
43	STAU2	74495160	74821629	1	0	NA	199555	−119303	−119303	1	1.43	NA	NA
44	SF1	84288654	64302817	1	0	NA	24747	−560058	24747	1	NA	NA	0.23
45	CLIP2	73341739	73458196	15	1	9	1543149	−35065	−35055	1	NA	NA	0.52
46	CLDN3	72821283	72822536	5	0	NA	404089	−49338	−49338	1	NA	NA	0.29
47	ZSWIM4	13767274	13804044	1	0	NA	50124	NA	50124	1	NA	NA	0.38
48	GLRB	158216788	158312299	0	1	3	48887	−2584470	48887	1	NA	NA	0.31
49	DCHS2	155375138	155832318	14	0	NA	2584470	−60480408	2584470	1	NA	NA	0.37
50	TRPS1	116489900	116750429	20	1	43	7112653	−1971482	−1971482	1	0.42	0.33	NA
51	MDGA2	46379045	47213703	NA	NA	NA	NA	NA	NA	1	NA	NA	0.39
52	CNBD1	87947840	88435220	1	1	38	683350	−122823	−122823	1	0.91	0.91	NA
53	STAG3	99613474	99659778	2	0	NA	111895	−23787222	111895	1	NA	NA	0.21
54	GATA4	11599162	11854918	0	1	18	9709	−139646	9709	1	0.57	NA	NA
55	VPS13B	100094670	100958983	1	0	NA	83469	−187596	83469	1	0.98	NA	NA
56	DOCK5	25098204	25326636	2	0	NA	14747	−1478148	14747	1	1.97	NA	NA

TABLE 14-continued

57	ZHX2	123863082	124055936	9	0	NA	706230	−7112553	706280	1	NA	0.29	NA
58	ARHGEF5	143683366	143708657	NA	0	NA	NA	−13747479	−13747479	1	NA	NA	0.35
59	SDC2	97575058	97693213	1	1	39	1032370	−159108	−159108	1	0.68	NA	NA
60	MYLK	124811586	125065868	2	0	NA	210407	−8482769	210407	1	NA	0.38	NA
61	LPHN3	62045434	62620762	157	0	NA	30824069	NA	30824089	1	NA	NA	0.24
62	MOSPD3	100047651	100050932	0	1	12	5043	−3929	3929	1	NA	NA	0.17
63	GYS2	21580390	21849048	NA	NA	NA	NA	NA	NA	1	NA	NA	0.38
64	GAS8	88616509	88638880	NA	0	NA	NA	−21813	−21813	1	NA	0.42	NA
65	RAB9A	13617262	13637681	191	0	NA	35134932	NA	35134932	1	NA	0.85	NA
66	POLA3D	22158584	22184824	1	1	25	116113	−12768	−12768	1	NA	0.33	NA
67	PSD3	18429093	18915476	0	1	23	300007	−126090	−128090	1	3.23	NA	NA
68	ZFPM2	108400323	108885939	2	1	41	1444960	−729979	−729979	1	1.16	2.58	NA
69	ATP6V1C1	104102424	104154451	5	0	NA	427830	608753	427830	1	NA	0.21	NA
70	MEF2C	88051922	88214780	63	0	NA	26727467	−19278276	−19278276	1	NA	NA	0.15
71	PKIA	79590891	79678040	2	0	NA	1007876	−1648815	1007878	1	0.63	NA	NA
72	ADAMTS18	75873527	76026512	0	1	52	287400	−72291	287400	1	0.74	NA	NA
73	STYXL1	75463592	75615257	0	1	10	72	−1679	72	1	NA	NA	0.17
74	EPM2A	145988141	145088884	2	1	7	291927	−772282	291927	1	NA	NA	0.20
75	LEPREL1	191157213	191321407	NA	1	2	NA	−49278	−49278	1	NA	0.29	NA
76	GABRA2	45945341	46086561	NA	0	NA	NA	−1800760	−18007760	1	NA	NA	0.16
77	RCOR2	63435303	63440892	3	0	NA	81715	NA	81715	1	NA	NA	0.00
78	MFHAS1	8879409	888541	0	1	15	109315	−5420413	109315	1	0.63	NA	NA

Table 14-3a

Final-RANK	gene	index	NYU-2	NYU-dir	NYU-count	MSKs1-Z	MSKs1-dir	MSKs2-count	MSKs2-Z	MSKs2-dir	MSKs2 count	logrank-n52random	logank-n271random	logrank-composite	gene-Chr	gene-Cytoband
79	SCARA5	158	3.3	−1	925	NA	NA	NA	NA	NA	NA	130	101	116	8	p21.1
80	CCDC25	155	4.4	−1	995	NA	NA	NA	NA	NA	NA	132	100	117	8	p21.1
81	FAM3RA	323	NA	NA	NA	2.7	−1	885	NA	NA	NA	110	130	119	16	q24.3
82	CTSB	104	2.8	−1	941	NA	NA	NA	NA	NA	NA	111	135	122	8	p23.1
83	PTK2	235	NA	NA	NA	2.3	1	654	NA	NA	NA	107	144	123	8	q24.3
84	SPIRE2	331	NA	NA	NA	1.7	−1	508	NA	NA	NA	124	128	124	16	q24.3
85	C13or123	246	NA	NA	NA	NA	NA	NA	2.2139	−1	748	141	113	125	13	q13.3
86	BOD1L	20	NA	NA	NA	NA	NA	NA	2.3508	−1	884	129	127	126	4	p15.33
87	FAM16OB2	120	2.5	−1	899	1.8	−1	567	NA	NA	NA	127	133	129	8	p21.3
88	NUS1	46	NA	NA	NA	NA	NA	NA	2.2269	−1	859	123	139	130	6	q22.2
89	MTHFSD	309	NA	NA	NA	2.4	−1	824	NA	NA	NA	112	153	131	16	q24.1
90	UBA5	208	NA	NA	NA	2.2	1	733	NA	NA	NA	122	155	135.5	8	q22.3
91	GALNS	325	NA	NA	NA	2.3	−1	856	NA	NA	NA	131	147	137	16	q24.3
92	FSTL5	28	NA	NA	NA	NA	NA	NA	2.2407	−1	541	133	143	140	4	q32.2
93	SIM1	46	NA	NA	NA	NA	NA	NA	2.1943	1	833	120	165	141	6	q16.3
94	TG	231	3.8	1	997	NA	NA	NA	NA	NA	NA	136	149	144	8	q24.22
95	BFSP2	12	NA	NA	NA	2.4	1	678	NA	NA	NA	139	154	148	3	q22.1
96	MMP16	194	NA	NA	NA	3.5	1	931	NA	NA	NA	158	139	149	8	q21.3
97	RIMS2	210	2	1	692	4	1	939	NA	NA	NA	161	141	150	8	q22.3
98	PDS5B	245	NA	NA	NA	NA	NA	NA	2.0408	−1	661	145	159	151	13	q13.1
99	CDK7	31	NA	NA	NA	2.7	−1	988	NA	NA	NA	156	148	153	5	913.2
100	CNTNAP4	275	3.2	−1	825	NA	NA	NA	NA	NA	NA	196	126	156	16	q23.1
101	CFDP1	274	3	−1	925	NA	NA	NA	NA	NA	NA	137	187	157	16	q23.1
102	FBXL4	45	NA	NA	NA	NA	NA	NA	1.7473	−1	537	154	167	158	6	q16.2
103	RFX1	358	NA	NA	NA	NA	NA	NA	2.1724	1	861	134	201	163	19	p13.12

TABLE 14-continued

104	NALCN	256	NA	NA	NA	NA	NA	NA	2.1845	−1	731	182	152	165	13	q33.1
105	S1X1A	57	NA	NA	NA	NA	NA	NA	2.1787	1	835	177	161	167	7	q11.23
106	CYP7B1	162	NA	NA	NA	1.7	1	508	NA	NA	NA	147	204	168	8	q12.3
107	ARHGEF10	92	NA	NA	NA	2.9	−1	923	NA	NA	NA	215	145	171	8	p23.3
108	ENIPD4	141	2.7	−1	875	NA	NA	NA	NA	NA	NA	230	137	173	8	p21.3
109	ZNF704	188	NA	NA	NA	2.5	1	815	NA	NA	NA	211	151	174	8	q21.13
110	C8or179	105	2.9	−1	93	NA	NA	NA	NA	NA	NA	163	197	176	8	p22
111	SLC9A9	13	NA	NA	NA	2.7	1	746	NA	NA	NA	170	189	177	3	q24
112	CHMP7	139	NA	NA	NA	2.4	−1	925	NA	NA	NA	185	176	178	8	p21.3
113	GPC5	255	NA	NA	NA	NA	NA	NA	2.1374	−1	610	171	193	180	13	q31.3
114	MYC	222	4.2	1	972	NA	NA	NA	NA	NA	NA	218	157	184	8	q24.21
115	STIP1	239	NA	NA	NA	NA	NA	NA	1.7766	1	613	164	209	185	11	q13.1
116	ZBTB20	9	NA	NA	NA	1.8	1	513	NA	NA	NA	187	188	188	3	q13.31
117	MEN1	241	NA	NA	NA	NA	NA	NA	2.0513	1	730	176	203	188	11	q13.1
118	SLC26A7	195	NA	NA	NA	2.2	1	747	NA	NA	NA	213	188	189	8	q21.3

Table 14-3b

Final-RANK	gene	gene-start	gene-end	genesBtwn	contg	clump-index	dstprev	dstnext	min-disto-ROL	IndexO-Proxy1	NYU-Zadjust	MSKs1-Zadust	MSKS2-Zadjust
79	SCARA5	27783672	27906117	0	1	31	29490	−97583	29490	1	0.63	NA	NA
80	CCDC25	27646756	27686089	2	0	NA	97583	−188353	97583	1	1.29	NA	NA
81	FAM3RA	87302916	67330317	0	1	58	67370	−2604	−2604	1	NA	0.33	NA
82	CTSB	11737442	11763055	7	0	NA	1084499	−55179	−55179	1	0.38	NA	NA
83	PTK2	141737883	142080514	NA	0	NA	NA	−5943220	−5943220	1	NA	0.17	NA
84	SPIRE2	88422408	88485228	0	1	62	2292	−11842	2292	1	NA	0.00	NA
85	C13or123	38482003	38510252	21	0	NA	4175452	−6231846	4175452	1	NA	NA	0.14
86	BOD1L	13179484	13238426	76	0	NA	30632257	NA	30632257	1	NA	NA	0.19
87	FAM16OB2	22002660	22017835	0	1	24	2493	−82519	2493	1	0.25	0.02	NA
88	NUS1	118103310	118138577	15	0	NA	5440605	−16667349	5440605	1	NA	NA	0.14
89	MTHFSD	85121284	85157509	5	1	57	1036491	−15714	−15714	1	NA	0.21	NA
90	UBA5	103334748	103493671	3	0	NA	606753	−128437	−128437	1	NA	0.14	NA
91	GALNS	87407644	87450885	0	1	60	122	−4478	122	1	NA	0.17	NA
92	FSTL5	162524501	183304836	NA	0	NA	NA	4017824	−4017824	1	NA	NA	0.15
93	SIM1	100939606	101019494	0	1	6	43297	−1437036	43297	1	NA	NA	0.13
94	TG	133948387	134216325	0	1	48	−98170	−18153	−18153	1	0.91	NA	NA
95	BFSP2	134601480	134676746	58	0	NA	9790009	−8678754	−8678754	1	NA	0.21	NA
96	MMP16	89118580	89408833	9	0	NA	2921859	−683360	−683360	1	NA	0.74	NA
97	RIMS2	104582291	106333263	1	0	NA	127586	427830	127566	1	0.07	1.04	NA
98	PDS5B	32058564	32250157	21	0	NA	6231846	NA	6231846	1	NA	NA	0.08
99	CDK7	68566471	68609004	0	1	4	3274	11239	3274	1	NA	0.33	NA
100	CNTNAP4	74868677	75150636	1	0	NA	722891	−843789	722891	1	0.57	NA	NA
101	CFDP1	73885109	74024888	7	1	51	843789	−25857	−25657	1	0.47	NA	NA
102	FBXL4	99428055	99502570	7	0	NA	1437036	−5242052	1437036	1	NA	NA	0.01
103	RFX1	13933353	13978097	NA	0	NA	NA	−30862	−30682	1	NA	NA	0.13
104	NALCN	100504131	100866814	42	0	NA	12420243	−8187438	−8187438	1	NA	NA	0.13
105	S1X1A	72751472	72771925	1	0	NA	49338	NA	49338	1	NA	NA	0.13
108	CYP7B1	65671248	65873902	21	0	NA	2823061	−5476925	2623061	1	NA	0.00	NA
107	ARHGEF10	1759549	1894208	1	0	NA	86359	−115501	86359	1	NA	0.42	NA
108	ENIPD4	23299386	23371081	0	1	28	71227	18281	18281	1	0.33	NA	NA
109	ZNF704	81713324	81949571	0	1	37	93034	870671	98034	1	NA	0.25	NA
110	C8or179	12847554	12931653	0	1	19	53590	−1084499	53590	1	0.42	NA	NA

TABLE 14-continued

111	SLC9A9	144466755	145049979	50	0	NA	12271116	−9790009	−9790009	1	NA	0.33	NA
112	CHMP7	23157095	23175450	1	1	27	34647	−18511	−18511	1	NA	0.21	NA
113	GPC5	90848919	92316693	29	0	NA	8187438	−19509588	8187438	1	NA	NA	0.11
114	MYC	128816862	128822853	0	1	44	205193	318241	206193	1	1.16	NA	NA
115	STIP1	63709873	63726596	20	0	NA	560068	−19764	−19764	1	NA	NA	0.01
116	ZBTB20	115540230	116348817	51	0	NA	8462769	−8761797	8452769	1	NA	0.02	NA
117	MEN1	64327564	64335342	0	1	47	12898	−24747	12898	1	NA	NA	0.09
118	SLC26A7	92330692	92479654	5	0	NA	2729012	−2921859	2729012	1	NA	0.14	NA

Table 14-4a

Final-RANK	gene	index	NYU-2	NYU-dir	NYU-count	MSKs1-Z	MSKs1-dir	MSKs2-count	MSKs2-Z	MSKs2-dir	MSKs2 count	logrank-n52random	logank-n271random	logrank-composite	gene-Chr	gene-Cytoband
119	ALCAM	8	NA	NA	NA	NA	NA	NA	2.4802	1	586	194	188	191	3	q13.11
120	KIF13B	160	2.7	−1	854	NA	NA	NA	NA	NA	NA	188	194	192	8	p21.1
121	MBTPS1	291	2.7	−1	906	NA	NA	NA	NA	NA	NA	183	192	193	16	q24.1
122	PPP2R5B	243	NA	NA	NA	NA	NA	NA	1.8055	1	580	189	202	195	11	q13.1
123	VPS13C	260	NA	NA	NA	NA	NA	NA	1.7860	−1	550	201	180	197	15	q22.2
124	ASPSCR1	346	NA	NA	NA	NA	NA	NA	1.7635	1	549	219	178	198	17	q25.3
125	EPO	82	NA	NA	NA	NA	NA	NA	1.9843	1	735	169	235	201	7	q22.1
126	HEY1	187	3	1	988	NA	NA	NA	NA	NA	NA	206	195	203	8	q21.13
127	KALRN	11	NA	NA	NA	2.4	1	674	NA	NA	NA	197	205	204	3	q21.1
128	RGS22	203	2.7	1	956	NA	NA	NA	NA	NA	NA	191	215	205	8	q22.2
129	WDH7	353	NA	NA	NA	NA	NA	NA	1.9953	−1	653	200	217	210	18	q21.31
130	COL11A1	5	NA	NA	NA	NA	NA	NA	1.8924	−1	591	233	206	213	1	p21.1
131	CHDC	344	NA	NA	NA	NA	NA	NA	1.7523	1	523	221	218	215	17	q21.2
132	ATP2C2	296	3.6	−1	943	NA	NA	NA	NA	NA	NA	216	236	216	16	q24.1
133	CDH17	196	2.8	1	976	NA	NA	NA	NA	NA	NA	227	216	217	8	q22.1
134	CGKG	17	NA	NA	NA	1.9	1	568	NA	NA	NA	192	258	219	3	q27.3
135	GAK5	236	NA	NA	NA	2.4	−1	831	NA	NA	NA	210	237	220	10	q26.11
136	GAM1	52	NA	NA	NA	NA	NA	NA	1.8983	−1	58	179	283	223	6	q24.3
137	IMPA1	190	NA	NA	NA	1.9	1	647	NA	NA	NA	243	210	224	8	q21.13
138	RPL7	176	2.3	1	813	NA	NA	NA	NA	NA	NA	261	211	229	8	q21.11
139	COL21A1	38	NA	NA	NA	NA	NA	NA	1.8391	−1	595	235	245	232	6	p12.1
140	COL12A1	40	NA	NA	NA	NA	NA	NA	1.8241	−1	59	241	240	233	6	q14.1
141	MLYCD	289	2.4	−1	819	NA	NA	NA	NA	NA	NA	234	248	234	16	q23.3
142	AR	366	2.3	1	690	2.5	1	805	NA	NA	NA	256	221	235	23	q12
143	PLCB1	359	NA	NA	NA	NA	NA	NA	1.9352	−1	579	181	330	240	20	p12.3
144	ACTL8	3	NA	NA	NA	1.9	−1	582	NA	NA	NA	264	229	242	1	p36.13
145	IFDPI	257	NA	NA	NA	2.3	−1	729	NA	NA	NA	205	304	248	13	q34
146	IOCE	55	NA	NA	NA	NA	NA	NA	1.8487	1	580	250	260	255	7	p22.2
147	SMARCB1	380	NA	NA	NA	1.8	−1	523	NA	NA	NA	239	275	256	22	q11.23
148	MIDH	199	NA	NA	NA	1.9	1	584	NA	NA	NA	225	301	259	8	q22.1
149	NECAB2	290	NA	NA	NA	2	−1	688	NA	NA	NA	255	271	262	16	q23.3
150	DEF8	334	NA	NA	NA	1.9	−1	678	NA	NA	NA	214	335	266	16	q24.3
151	RNF40	262	NA	NA	NA	NA	NA	NA	2.0578	1	774	320	227	270	16	q11.2
152	TICAM2	37	NA	NA	NA	NA	NA	NA	1.8257	−1	589	303	241	271	5	q22.3
153	GLG1	271	2.1	−1	64	NA	NA	NA	NA	NA	NA	327	225	273	18	q22.3
154	MECOM	16	NA	NA	NA	2	1	587	NA	NA	NA	279	283	277	3	q26.2
155	TCEB1	178	1.8	1	590	NA	NA	NA	NA	NA	NA	275	277	278	8	q21.11

TABLE 14-continued

156	CTNNA2	7	NA	NA	NA	NA	NA	NA	1.8228	−1	533	331	231	280	2	p12
157	NIPAL2	200	1.9	1	654	NA	NA	NA	NA	NA	NA	289	265	282	8	q22.2
158	CDCA2	148	2	1	88	NA	NA	NA	NA	NA	NA	301	255	283	8	p21.2

Table 14-4b

Final-RANK	gene	gene-start	gene-end	genesBtwn	contg	clump-index	dstprev	dstnext	min-disto-ROL	IndexO-Proxy1	NYU-Zadjust	MSKs1-Zadust	MSKS2-Zadjust
119	ALCAM	106568403	106778433	49	0	NA	8761797	NA	8761797	1	NA	NA	0.23
120	KIF13B	28980715	29176629	NA	1	32	NA	−14009	−14009	1	0.33	NA	NA
121	MBTPS1	82644872	82708018	0	1	54	5371	−50994	5371	1	0.33	NA	NA
122	PPP2R5B	64448756	64458523	NA	0	NA	NA	−80139	−80139	1	NA	NA	0.02
123	VPS13C	59931884	60138939	NA	0	NA	NA	−24742144	−24742144	1	NA	NA	0.02
124	ASPSCR1	77528715	77568569	6	1	85	40474	−16362	−18382	1	NA	NA	0.01
125	EPO	100156359	100159257	146	0	NA	29534582	−31553	−31553	1	NA	NA	0.07
126	HEY1	80838801	80842653	3	1	38	87061	−97933	−97833	1	0.47	NA	NA
127	KALRN	125296275	125922726	76	0	NA	8678754	−210407	−210407	1	NA	0.21	NA
128	RGS22	101042452	101187520	7	0	NA	812460	−83469	−83469	1	0.33	NA	NA
129	WDH7	52489614	52848040	45	0	NA	12833135	−3157834	−3157834	1	NA	NA	0.07
130	COL11A1	103114611	103346640	NA	0	NA	NA	−4955408	−4955408	1	NA	NA	0.04
131	CHDC	37594632	37599722	482	0	NA	39903967	−7810	−7810	1	NA	NA	0.01
132	ATP2C2	82959534	83055293	0	1	55	13315	−38746	13315	1	0.80	NA	NA
133	CDH17	95206566	95289986	14	0	NA	2053354	−2729012	2053354	1	0.38	NA	NA
134	CGKG	18347686	18562717	23	0	NA	3269193	−17000632	3269193	1	NA	0.05	NA
135	GAK5	120957091	121205118	NA	NA	NA	NA	NA	NA	1	NA	0.21	NA
136	GAM1	148390611	148800427	83	0	NA	1881221	−291927	−291927	1	NA	NA	0.04
137	IMPA1	82732751	82751115	4	0	NA	2842997	−545893	−545893	1	NA	0.05	NA
138	RPL7	74365073	74375857	1	0	NA	119303	−352193	119303	1	0.17	NA	NA
139	COL21A1	56029347	56368851	NA	NA	NA	NA	NA	NA	1	NA	NA	0.03
140	COL12A1	75850762	75972343	18	0	NA	7686493	−4871884	−4871884	1	NA	NA	0.03
141	MLYCD	82490231	82507286	1	0	NA	52452	−102526	52452	1	0.21	NA	NA
142	AR	66680599	65860344	0	1	69	318585	904991	318585	1	0.17	0.29	NA
143	PLCB1	8061296	8813547	NA	NA	NA	NA	NA	NA	1	NA	NA	0.05
144	ACTL8	17954395	18026145	662	1	1	79289745	−57439	−57439	1	NA	0.05	NA
145	IFDPI	113287057	113343500	NA	0	NA	NA	−12420243	−12420243	1	NA	0.17	NA
146	IOCE	2565158	2820893	13	0	NA	2861082	NA	2881062	1	NA	NA	0.03
147	SMARCB1	22459150	22506703	290	0	NA	23030490	NA	23030490	1	NA	0.02	NA
148	MIDH	98725583	98807711	7	0	NA	465852	−1032370	465852	1	NA	0.05	NA
149	NECAB2	82559738	82593878	1	0	NA	50994	−52452	50994	1	NA	0.07	NA
150	DEF8	88542684	88561968	0	1	63	4521	−12678	4521	1	NA	0.05	NA
151	RNF40	30681100	30695129	NA	0	NA	NA	−392513	−392513	1	NA	NA	0.09
152	TICAM2	114942247	114989610	NA	0	NA	NA	−26727467	−26727467	1	NA	NA	0.03
153	GLG1	73043357	73198518	3	0	NA	288457	−1403582	286457	1	0.10	NA	NA
154	MECOM	170283981	170347054	89	0	NA	17000632	−8012470	−8012470	1	NA	0.07	NA
155	TCEB1	75021184	75046959	2	0	NA	262534	−199555	−199555	1	0.02	NA	NA
156	CTNNA2	79732191	80729415	NA	0	NA	NA	−28619013	−28619013	1	NA	NA	0.03
157	NIPAL2	99273563	99375797	1	0	NA	160240	465852	160240	1	0.05	NA	NA
158	CDCA2	25372428	25421353	0	1	29	336689	−591	−591	1	0.07	NA	NA

TABLE 14-continued

Table 14-5a

Final-RANK	gene	index	NYU-2	NYU-dir	NYU-count	MSKs1-Z	MSKs1-dir	MSKs2-count	MSKs2-Z	MSKs2-dir	MSKs2 count	logrank-n52random	logank-n271random	logrank-composite	gene-Chr	gene-Cytoband
159	WWP2	267	1.8	−1	527	NA	NA	NA	NA	NA	NA	251	315	284	16	q22.1
160	DDX19A	268	2.3	−1	755	NA	NA	NA	NA	NA	NA	220	383	285	16	q22.1
161	STK3	201	1.8	1	614	NA	NA	NA	NA	NA	NA	265	309	287	8	q22.2
162	DNAH2	337	1.8	−1	541	NA	NA	NA	NA	NA	NA	247	332	288	17	p13.1
163	NFAT5	266	2.3	−1	760	NA	NA	NA	NA	NA	NA	326	254	291	16	q22.1
164	CNGB1	283	1.8	−1	524	NA	NA	NA	NA	NA	NA	297	280	292	16	q13
165	UBE2CBP	41	2.8	−1	891	NA	NA	NA	NA	NA	NA	256	325	293	6	q14.1
186	C8or116	99	2.2	−1	725	NA	NA	NA	NA	NA	NA	285	293	294	8	p23.1
167	KIAA0196	270	2.6	1	819	NA	NA	NA	NA	NA	NA	253	334	295	8	q24.13
168	CLCNKB	1	NA	NA	NA	NA	NA	NA	2.0014	1	746	276	30	297	1	p36.13
169	C16or1180	264	2.2	−1	677	NA	NA	NA	NA	NA	NA	281	302	298	16	q21
170	ZFHX3	270	2.2	−1	656	NA	NA	NA	NA	NA	NA	313	273	299	16	q22.3
171	PPM1L	15	NA	NA	NA	2	1	628	NA	NA	NA	270	329	303	3	q26.1
172	NKIRAS2	338	NA	NA	NA	NA	NA	NA	1.9834	1	679	298	290	304	17	q21.2
173	RSPO2	215	1.8	1	550	NA	NA	NA	NA	NA	NA	306	292	305	8	q23.1
174	XPO7	119	2.3	−1	735	NA	NA	NA	NA	NA	NA	329	272	306	8	p21.3
175	ME1	42	2.5	−1	728	NA	NA	NA	NA	NA	NA	282	321	307	6	q14.2
176	NLGN4Y	363	NA	NA	NA	NA	NA	NA	2.4183	−1	734	339	275	312	24	q11.221
177	LZTS1	118	2	−1	645	NA	NA	NA	NA	NA	NA	300	316	316	8	p21.3
178	FBXL18	56	NA	NA	NA	NA	NA	NA	1.8646	1	652	323	294	317	7	p22.1
179	TBC1D108	251	NA	NA	NA	NA	NA	NA	1.8243	1	573	278	347	321	16	p11.2
180	WDR59	272	2.1	−1	653	NA	NA	NA	NA	NA	NA	304	320	322	16	q23.1
181	BLK	101	2.1	−1	671	NA	NA	NA	NA	NA	NA	315	314	325	8	p23.1
182	MEPCE	71	NA	NA	NA	NA	NA	NA	2.1134	1	782	350	285	327	7	q22.1
183	DLGAP2	91	NA	NA	NA	2.2	−1	882	NA	NA	NA	358	288	330	8	p23.3
184	ZFAT	234	2.5	1	796	NA	NA	NA	NA	NA	NA	325	317	331	8	q24.22
185	FASN	348	NA	NA	NA	NA	NA	NA	3.0027	1	963	296	350	332	17	q25.3
186	GIGYF1	81	NA	NA	NA	NA	NA	NA	2.7127	1	957	335	311	335	7	q22.1
187	ANXA13	219	2.1	1	692	NA	NA	NA	NA	NA	NA	310	345	336	8	q24.13
188	CDYL2	280	2.5	−1	899	NA	NA	NA	NA	NA	NA	316	351	339	16	q23.2
189	TOX	161	4.3	1	993	NA	NA	NA	NA	NA	NA	338	342	349	8	q12.1
190	NKX2-6	143	2.4	−1	870	NA	NA	NA	NA	NA	NA	340	366	357	8	p21.2
191	RALYL	191	2.8	1	985	NA	NA	NA	NA	NA	NA	345	362	359	2	q21.2
192	TBC1D22A	361	NA	NA	NA	4.6	−1	999	NA	NA	NA	367	346	363	22	q13.31
193	TFE3	383	NA	NA	NA	2.1	1	591	NA	NA	NA	362	350	364	23	p11.23
194	KCNAB1	14	NA	NA	NA	5.8	1	996	NA	NA	NA	363	367	367	3	q25.31
195	SULF1	166	5.2	1	1000	3.4	1	994	NA	NA	NA	3	4	3	8	q13.2
198	RAB6C	342	NA	NA	NA	NA	NA	NA	3.5399	1	998	6	3	5	17	q21.2
197	DHX58	339	NA	NA	NA	NA	NA	NA	8.9116	1	952	14	16	16	17	q21.2
198	ASAP1	224	NA	NA	NA	3.6	1	974	NA	NA	NA	21	23	20	8	q24.21

Table 14-5b

Final-RANK	gene	gene-start	gene-end	genesBtwn	contg	clump-index	dstprev	dstnext	min-disto-ROL	IndexO-Proxy1	NYU-Zadjust	MSKs1-Zadust	MSKS2-Zadjust
159	WWP2	88353710	68533145	5	0	NA	405177	−57856	−57658	1	0.02	NA	NA
160	DDX19A	68938322	68984780	0	1	50	6059	405177	6059	1	0.17	NA	NA

TABLE 14-continued

161	STK3	99536037	99907074	1	0	NA	187596	−160240	−160240	1	0.02	NA	NA
162	DNAH2	7562745	7577783	NA	NA	NA	NA	NA	NA	1	0.02	NA	NA
163	NFAT5	68156498	68296054	2	0	NA	57656	−7528258	57656	1	0.17	NA	NA
164	CNGB1	56475004	58582513	3	0	NA	142487	NA	142487	1	0.02	NA	NA
165	UBE2CBP	83658836	83832269	3	0	NA	144558	−7685493	144558	1	0.38	NA	NA
166	C8or116	11021390	11025155	0	1	17	154255	−697587	154255	1	0.14	NA	NA
167	KIAA0196	125105691	125173191	3	0	NA	2323848	−1286853	−1286863	1	0.29	NA	NA
168	CLCNKB	16242834	16256390	29	0	NA	1482527	NA	1482527	1	NA	NA	0.07
169	C16or1180	56706000	56720'97	10	0	NA	3524069	−142487	−142487	1	0.14	NA	NA
170	ZFHX3	71374285	7163975	2	0	NA	1403582	−2343793	1403582	1	0.14	NA	NA
171	PPM1L	161956791	162271511	13	0	NA	8012470	−4217170	−4217170	1	NA	0.07	NA
172	NKIRAS2	37422564	37431180	1	0	NA	75799	NA	75799	1	NA	NA	0.06
173	RSPO2	108980721	109165062	9	1	42	4139285	401262	−401262	1	0.02	NA	NA
174	XPO7	21833126	21920041	3	0	NA	82619	−1627372	82619	1	0.17	NA	NA
175	ME1	83976827	84197498	41	0	NA	7084576	−144558	−144558	1	0.25	NA	NA
176	NLGN4Y	15144026	15466924	NA	NA	NA	NA	NA	NA	1	NA	NA	0.21
177	LZTS1	20147956	20205754	2	0	NA	1627372	850362	−850362	1	0.07	NA	NA
178	FBXL18	5481955	5523646	NA	0	NA	NA	−2861062	−2861062	1	NA	NA	0.04
179	TBC1D108	30275925	30288587	14	0	NA	392513	NA	392513	1	NA	NA	0.00
180	WDR59	73464975	73576518	5	0	NA	243911	−266457	243911	1	0.10	NA	NA
181	BLK	11388930	11459518	1	0	NA	139848	−185868	139646	1	0.10	NA	NA
182	MEPCE	99865190	99869676	2	0	NA	32404	−29640	−29540	1	NA	NA	0.11
183	DLGAP2	1436939	1644048	1	0	NA	115501	NA	115501	1	NA	0.14	NA
184	ZFAT	135559215	135794453	8	0	NA	5943220	−1248464	−1248464	1	0.25	NA	NA
185	FASN	77629504	77649395	NA	1	66	NA	−262	−262	1	NA	NA	0.47
186	GIGYF1	100115066	100124806	1	0	NA	31553	−23059	−23069	1	NA	NA	0.33
187	ANXA13	124762216	124818828	11	0	NA	1286863	−706280	−706280	1	0.10	NA	NA
188	CDYL2	79195176	79395680	3	0	NA	248923	−1391844	248823	1	0.25	NA	NA
189	TOX	59880531	60194321	10	0	NA	5476925	NA	5476925	1	1.23	NA	NA
190	NICX2-6	23615909	23620056	6	0	NA	1478148	−129901	−129901	1	0.21	NA	NA
191	RALYL	85601112	85963979	12	0	NA	1691298	−2842997	1691298	1	0.38	NA	NA
192	TBC1D22A	45537193	45948399	NA	0	NA	NA	−28030490	−23030490	1	NA	1.43	NA
193	TFE3	48772813	48787722	NA	0	NA	NA	−35134932	−35134932	1	NA	0.10	NA
194	KCNAB1	157321095	157739821	22	0	NA	4217170	−12271116	4217170	1	NA	2.24	NA
195	SULF1	70541427	70735701	0	1	33	11428	647617	11428	0	1.83	0.68	NA
195	RAB6C	37530524	37560548	0	1	64	1891	−1627	−1627	0	NA	NA	0.76
197	DHX58	37506979	37518277	0	1	64	380	−75799	380	0	NA	NA	4.22
198	ASAP1	131133535	131483399	0	1	45	378337	−2104073	378337	0	NA	0.80	NA

Table 14-6a

Final-RANK	gene	index	NYU-2	NYU-dir	NYU-count	MSKs1-Z	MSKs1-dir	MSKs2-count	MSKs2-Z	MSKs2-dir	MSKs2 count	logrank-n52random	logank-n271random	logrank-composite	gene-Chr	gene-Cytoband
199	CA5A	313	2.6	1	832	3.8	−1	955	NA	NA	NA	23	28	26	16	q24.2
200	C6or1118	53	NA	NA	NA	NA	NA	NA	2.7921	−1	976	35	36	36	6	q27
201	NCOA2	169	3.2	1	997	2.4	1	806	NA	NA	NA	35	40	37	8	q13.3
202	PKD1L2	283	4.9	−1	999	2	−1	715	NA	NA	NA	41	45	42	15	q23.2
203	BANP	314	2.6	−1	901	3.3	−1	957	NA	NA	NA	43	49	46	16	q24.2
204	KIAA1967	133	2.8	−1	925	3.1	−1	989	NA	NA	NA	50	57	52	8	p21.3
205	COPG2	89	NA	NA	NA	NA	NA	NA	3.1195	1	935	56	52	53	7	q32.2
206	ZNF706	205	NA	NA	NA	2.8	1	889	NA	NA	NA	53	56	54	8	q22.3
207	GAN	285	2.7	−1	889	2.4	−1	902	NA	NA	NA	54	61	55	16	q23.2

TABLE 14-continued

208	PLCG2	286	2.9	−1	833	2.7	−1	913	NA	NA	NA	61	50	56	16	q23.2
209	C19or157	358	NA	NA	NA	NA	NA	NA	2.7945	1	992	59	58	59	19	p1312
210	PDGFRL	111	4.8	−1	998	NA	NA	NA	NA	NA	NA	60	55	60	8	p22
211	ESD	249	NA	NA	NA	NA	NA	NA	2.5793	−1	973	65	59	62	13	q14.2
212	CPA5	85	NA	NA	NA	NA	NA	NA	2.7623	1	924	70	63	67	7	q32.2
213	BIN3	131	1.7	−1	507	2.8	1	995	NA	NA	NA	71	73	70	8	p21.3
214	ZFHX4	181	4.3	1	1000	NA	NA	NA	NA	NA	NA	74	76	73	8	q21.11
215	CPA6	163	3.8	1	1000	NA	NA	NA	NA	NA	NA	77	81	75	8	q13.2
216	EYA1	172	3.4	1	997	NA	NA	NA	NA	NA	NA	73	89	77	8	q13.3
217	CHRNA2	153	3.5	−1	999	NA	NA	NA	NA	NA	NA	76	87	79	8	p21.2
218	TNKS	97	4	1	1000	NA	NA	NA	NA	NA	NA	77	84	84	8	p23.1
219	HNF4O	183	4.1	1	1000	NA	NA	NA	NA	NA	NA	103	72	87	8	q21.11
220	LHCH1	248	NA	NA	NA	NA	NA	NA	2.3847	−1	NA	79	94	88	13	q14.13
221	ADHA1A	149	3.9	−1	991	NA	NA	NA	NA	NA	NA	98	79	89	8	p21.2
222	EPHX2	154	3.3	−1	997	NA	NA	NA	NA	NA	NA	89	88	90	8	p21.1
223	SORBS3	130	NA	NA	NA	3	−1	957	NA	NA	NA	83	95	91	8	p21.3
224	GRIA2	27	NA	NA	NA	NA	NA	NA	2.2933	−1	843	94	95	93	4	q32.1
225	POLIM2	131	NA	NA	NA	2.9	−1	993	NA	NA	NA	91	91	94	8	p21.3
226	MTMR7	109	3.7	−1	971	NA	NA	NA	NA	NA	NA	86	108	96	8	p22
227	FBXO24	76	NA	NA	NA	NA	NA	NA	2.4831	1	817	118	85	99	7	q22.1
228	CRISPLD1	182	4.9	1	1000	NA	NA	NA	NA	NA	NA	95	124	107	8	q21.11
229	DPYS	211	3.2	1	975	NA	NA	NA	NA	NA	NA	92	129	109	8	q22.3
230	DTNA	351	NA	NA	NA	NA	NA	NA	2.2378	−1	734	102	125	112	18	q12.1
231	KLHDC4	311	NA	NA	NA	2.5	−1	987	NA	NA	NA	116	111	113	16	q24.2
232	CYBA	319	NA	NA	NA	2.9	−1	941	NA	NA	NA	117	121	118	16	q24.3
233	JPH3	310	2.4	−1	788	2.4	−1	908	NA	NA	NA	101	142	120	16	q24.2
234	TMEM120A	64	NA	NA	NA	NA	NA	NA	1.7093	1	511	128	115	121	7	q11.23
235	MTUS1	112	3.6	−1	976	NA	NA	NA	NA	NA	NA	143	116	127	8	p22
236	C8or134	165	6	1	1000	NA	NA	NA	NA	NA	NA	126	132	128	8	q13.2
237	GRHL2	206	NA	NA	NA	2.4	1	790	NA	NA	NA	125	140	132	8	q22.3
238	CPA2	83	NA	NA	NA	NA	NA	NA	2.1399	1	717	153	117	133	7	q32.2

Table 14-6b

Final-RANK	gene	gene-start	gene-end	genesBtwn	contg	clump-index	dstprev	dstnext	min-disto-ROL	IndexO-Proxy1	NYU-Zadjust	MSKs1-Zadust	MSKS2-Zadjust
199	CA5A	88479126	88527813	0	1	58	14926	−18511	14928	0	0.29	0.91	NA
200	C6or1118	165613148	165643101	0	1	8	17665	−18812721	17665	0	NA	NA	0.37
201	NCOA2	71178380	71478574	1	1	33	233471	−32264	−32264	C	0.57	0.21	NA
202	PKD1L2	79591985	79811477	0	1	53	18320	−4504	4504	0	1.63	0.07	NA
203	BANP	86542539	86666425	0	1	58	378801	−14926	−14926	0	0.29	0.63	NA
204	KIAA1967	22518202	22533920	0	1	28	−14	−597	−14	0	0.38	0.52	NA
205	COPG2	129933404	129935887	106	1	13	13747479	−41	−41	0	NA	NA	0.53
206	ZNF706	102278444	102287136	0	1	40	287028	−243699	−243699	0	NA	0.38	NA
207	GAN	79906076	79971441	0	1	53	398967	−23828	−23828	0	0.33	0.21	NA
208	PLCG2	80370408	80549399	0	1	53	76965	−398967	76965	0	0.42	0.33	NA
209	C19or157	13854168	13877909	0	1	68	105	−50124	105	0	NA	NA	0.37
210	PDGFRL	17478443	17545655	0	1	21	−71	−6086	−71	0	1.56	NA	NA
211	ESD	48243393	46269368	0	1	48	36148	20807	−20607	0	NA	NA	0.28
212	CPA5	129771892	129795807	0	1	13	11551	−20643	11651	0	NA	NA	0.36
213	BIN3	22533906	22582553	0	1	26	18566	14	14	0	0.00	0.38	NA
214	ZFHX4	77756078	77942076	1	1	35	1648815	−1114478	−1114478	0	1.23	NA	NA

TABLE 14-continued

215	CPA6	68496963	68821134	0	1	33	205773	−2623061	205773	0	0.91	NA	NA
216	EYA1	72272222	72437021	0	1	34	479311	463009	−463009	0	0.68	NA	NA
217	CHRNA2	27373195	27392730	0	1	30	11832	−376	−375	0	0.74	NA	NA
218	TNKS	9450855	9677266	0	1	16	271923	−522716	271923	0	1.04	NA	NA
219	HNF4O	76482732	76641600	0	1	35	1114478	373386	−373386	0	1.10	NA	NA
220	LHCH1	46025304	46222786	0	1	48	20607	−2766260	20607	0	NA	NA	0.20
221	ADHA1A	26661584	26778839	0	1	30	370899	−89977	−89977	0	0.98	NA	NA
222	EPHX2	27404552	27458403	2	1	30	188353	−11832	−11832	0	0.53	NA	NA
223	SORBS3	22465196	22488852	0	1	28	3247	−10816	324	0	NA	0.47	NA
224	GRIA2	158361186	158506577	9	1	3	4017824	−48887	−48887	0	NA	NA	0.17
225	POLIM2	22492199	22511483	0	1	26	1584	−3247	1584	0	NA	0.42	NA
226	MTMR7	17199923	17315207	0	1	21	83768	−1533557	83768	0	0.85	NA	NA
227	FBXO24	100021892	100006574	0	1	12	1144	−180	−180	0	NA	NA	0.24
228	CRISPLD1	76059531	76109346	0	1	35	373386	−129712	−129712	0	1.63	NA	NA
229	DPYS	106460029	105548453	0	1	41	22190	−127565	22190	0	0.57	NA	NA
230	DTNA	30327279	30725806	62	1	67	17395350	−269766	−269766	0	NA	NA	0.15
231	KLHDC4	86298920	86357056	0	1	58	64075	−9657	−9657	0	NA	0.25	NA
232	CYBA	87237199	67244958	0	1	58	891	−2814	891	0	NA	0.42	NA
233	JPH3	86194000	86289263	0	1	58	9657	−1036491	9657	0	0.21	0.21	NA
234	TMEM120A	75454238	75461913	0	1	10	1679	−248023	1679	0	NA	NA	0.00
235	MTUS1	17545584	17702666	1	1	21	121980	71	71	0	0.80	NA	NA
236	C8or134	69406511	69893810	0	1	33	647617	−99060	−99060	0	2.37	NA	NA
237	GRHL2	102574162	102750995	0	1	40	16952	−287026	16952	0	NA	0.21	NA
238	CPA2	129693939	129716870	0	1	13	3360	−29534682	3360	0	NA	NA	0.11

Table 14-7a

Final-RANK	gene	index	NYU-2	NYU-dir	NYU-count	MSKs1-Z	MSKs1-dir	MSKs2-count	MSKs2-Z	MSKs2-dir	MSKs2 count	logrank-n52random	logank-n271random	logrank-composite	gene-Chr	gene-Cytoband
239	NAT2	115	3.3	−1	993	NA	NA	NA	NA	NA	NA	140	134	134	8	p22
240	DPYSL2	148	3.3	−1	967	NA	NA	NA	NA	NA	NA	155	122	135.5	8	p21.2
241	ZDHHC7	300	NA	NA	NA	2.5	−1	839	NA	NA	NA	159	123	138	16	q24.1
242	ELP3	153	3.4	−1	939	NA	NA	NA	NA	NA	NA	165	118	139	8	p21.1
243	RHOBTB2	136	NA	NA	NA	1.7	−1	501	NA	NA	NA	133	150	142	8	p21.3
244	NEIL2	103	2.7	−1	921	NA	NA	NA	NA	NA	NA	150	135	143	8	p23.1
245	HR	122	NA	NA	NA	2.7	−1	895	NA	NA	NA	186	112	145	8	p21.3
246	EFA3A	226	3.1	1	985	NA	NA	NA	NA	NA	NA	144	148	146	8	q24.22
247	STMN4	150	3.3	−1	994	NA	NA	NA	NA	NA	NA	162	131	147	8	p21.2
248	PRDM14	168	4.7	1	996	NA	NA	NA	NA	NA	NA	135	171	152	8	q13.3
249	MARVELD2	35	NA	NA	NA	3	−1	988	NA	NA	NA	142	184	154	5	q13.2
250	SLC39A14	128	1.8	−1	560	2.2	−1	791	NA	NA	NA	152	160	155	8	p21.3
251	ACTL6B	80	NA	NA	NA	NA	NA	NA	1.7362	1	538	188	158	159	7	q22.1
252	TUSC3	108	3.1	−1	945	NA	NA	NA	NA	NA	NA	157	170	180	8	p22
253	COX4NB	305	NA	NA	NA	2.5	−1	938	NA	NA	NA	148	172	161	16	q24.1
254	XKR9	171	2.7	1	929	NA	NA	NA	NA	NA	NA	165	183	162	8	q13.3
255	C16or146	281	NA	NA	NA	2.2	−1	768	NA	NA	NA	151	183	164	16	q23.2
256	TAF9	33	NA	NA	NA	2.8	−1	983	NA	NA	NA	175	162	166	5	q13.2
257	KCNO3	228	5	1	1000	NA	NA	NA	NA	NA	NA	167	180	169	8	q24.22
258	UTRN	50	NA	NA	NA	NA	NA	NA	2.3296	−1	766	174	174	170	6	q24.2
259	RAD17	34	NA	NA	NA	2.6	−1	959	NA	NA	NA	172	182	172	5	q13.2
260	ZFPM1	315	NA	NA	NA	2.5	−1	924	NA	NA	NA	146	219	175	16	q24.2
261	PTDSS1	197	2.5	1	874	NA	NA	NA	NA	NA	NA	184	177	179	8	q22.1

TABLE 14-continued

262	IRF8	300	NA	NA	NA	2.5	−1	976	NA	NA	NA	199	169	181	16	q24.1
263	YWHAZ	204	NA	NA	NA	2.2	1	722	NA	NA	NA	204	168	182	8	q22.3
264	MRPS36	30	NA	NA	NA	2.6	−1	952	NA	NA	NA	195	175	183	5	q13.2
265	LACTB2	170	2.6	1	932	NA	NA	NA	NA	NA	NA	160	223	187	8	q13.3
268	SNAI3	321	NA	NA	NA	2.4	−1	914	NA	NA	NA	231	156	190	16	q24.3
267	TMEM71	229	2.9	1	983	NA	NA	NA	NA	NA	NA	180	207	194	8	q24.22
268	PREX2	184	7.5	1	1000	NA	NA	NA	NA	NA	NA	190	199	195	8	913.2
269	CPA1	86	NA	NA	NA	NA	NA	NA	2.0683	1	716	228	173	199	7	q32.2
270	PHF20L1	230	2.8	1	901	NA	NA	NA	NA	NA	NA	198	200	200	8	q24.22
271	KIAA0513	301	NA	NA	NA	2.1	−1	816	NA	NA	NA	212	188	202	16	q24.1
272	PI15	181	3	1	991	NA	NA	NA	NA	NA	NA	238	179	206	8	q21.11
273	PCM1	113	1.7	−1	529	NA	NA	NA	NA	NA	NA	183	234	207	8	p22
274	SH204A	117	2.9	−1	908	NA	NA	NA	NA	NA	NA	249	172	208	8	p21.3
275	C16or174	304	NA	NA	NA	2.3	−1	939	NA	NA	NA	202	214	209	16	q24.1
278	TP63	18	NA	NA	NA	3	1	822	NA	NA	NA	203	223	211	3	q28
277	DACH1	254	NA	NA	NA	NA	NA	NA	1.8675	−1	570	252	185	212	13	q21.33
278	TNFRSF10A	130	NA	NA	NA	2.2	−1	774	NA	NA	NA	245	196	214	8	p21.3

Table 14-7b

Final-RANK	gene	gene-start	gene-end	genesBtwn	contg	clump-index	dstprev	dstnext	min-disto-ROL	IndexO-Proxy1	NYU-Zadjust	MSKs1-Zadust	MSKS2-Zadjust
239	NAT2	18283035	18303003	0	1	23	126090	−306248	126090	0	0.63	NA	NA
240	DPYSL2	26491327	26571607	0	1	30	89977	−533035	89977	0	0.63	NA	NA
241	ZDHHC7	83565573	83602642	0	1	56	16269	−64959	16269	0	NA	0.25	NA
242	ELP3	27999759	28104584	6	1	31	899246	−2452	−2452	0	0.68	NA	NA
243	RHOBTB2	22913059	22933655	2	1	26	115396	−306299	115396	0	NA	0.00	NA
244	NEIL2	11664827	11882283	1	1	18	55179	−9709	−9709	0	0.33	NA	NA
245	HR	22027877	22045325	0	1	24	6152	−4474	4474	0	NA	0.33	NA
246	EFA3A	132985517	133095071	0	1	45	10596	−861863	10596	0	0.52	NA	NA
247	STMN4	27148738	27171843	0	1	30	26478	370899	25478	0	0.63	NA	NA
248	PRDM14	71126574	71146116	0	1	33	32264	−216812	32264	0	1.49	NA	NA
249	MARVELD2	68746699	88773646	82	1	4	19278276	−315	−315	0	NA	0.47	NA
250	SLC39A14	22280737	22347462	0	1	26	7079	−116113	7079	0	0.02	0.14	NA
251	ACTL6B	10007868	100092007	1	1	12	23059	−1569	−1569	0	NA	NA	0.01
252	TUSC3	15442101	15688368	6	1	20	1533557	301882	−301882	0	0.52	NA	NA
253	COX4NB	24369737	84390601	0	1	57	96	27547	96	0	NA	0.25	NA
254	XKR9	7175584a	71809213	0	1	34	483009	−11902	−11902	0	0.33	NA	NA
255	C16or146	79644603	79668373	0	1	53	5057	−248923	5057	0	NA	0.14	NA
256	TAF9	68696327	68701596	0	1	4	−716	−31935	−716	0	NA	0.29	NA
257	KCNO3	133210438	133551961	1	1	45	217672	−43354	−43354	0	2.37	NA	NA
258	UTRN	144654566	145215859	0	1	7	772282	−20654629	772282	0	NA	NA	0.18
259	RAD17	68700880	68746384	0	1	4	315	716	315	0	NA	0.29	NA
260	ZFPM1	87047226	87126890	0	1	58	18723	−378801	16723	0	NA	0.25	NA
261	PTDSS1	97343340	97415950	0	1	39	159108	−2053354	159108	0	0.25	NA	NA
262	IRF8	84490275	84513710	0	1	57	587924	−92165	−92166	0	NA	0.25	NA
263	YWHAZ	101999980	102034745	0	1	40	243699	−812460	243699	0	NA	0.14	NA
264	MRPS36	68548329	68577710	0	1	4	−11239	−7390	−7390	0	NA	0.29	NA
265	LACTB2	71712045	71743946	0	1	34	11902	−233471	11902	0	0.29	NA	NA
266	SNAI3	87271591	87280383	0	1	58	10028	−14572	10028	0	NA	0.21	NA
267	TMEM71	133779833	133842010	0	1	46	14776	−217672	14776	0	0.42	NA	NA
268	PREX2	69028907	69308451	0	1	33	99060	−205773	99060	0	3.36	NA	NA

TABLE 14-continued

269	CPA1	129807458	129815165	0	1	13	8445	−11661	8445	0	NA	NA	0.09	
270	PHF20L1	133856786	133930234	0	1	46	18153	−14776	−14776	0	0.38	NA	NA	
271	KIAA0513	83618911	83685327	2	1	56	517197	−16289	−18289	0	NA	0.10	NA	
272	PI15	75899327	75929819	0	1	35	129712	−457439	129712	0	0.47	NA	NA	
273	PCM1	17824646	17935562	0	1	22	22652	−121980	22852	0	0.00	NA	NA	
274	SH204A	19215483	19297594	5	1	23	850362	300007	−300007	0	0.42	NA	NA	
275	C16or174	84298624	84342190	0	1	57	27547	−16535	−18535	0	NA	0.17	NA	
276	TP63	190831910	191107935	0	1	2	49278	−3269193	49278	0	NA	0.47	NA	
277	DACH1	70910099	71339331	28	1	49	19509588	−1329507	−1329507	0	NA	NA	0.04	
278	TNFRSF10A	23104916	23138584	0	1	27	18511	−27431	18511	0	NA	0.14	NA	

Table 14-8a

Final-RANK	gene	index	NYU-2	NYU-dir	NYU-count	MSKs1-Z	MSKs1-dir	MSKs2-count	MSKs2-Z	MSKs2-dir	MSKs2 count	logrank-n52random	logank-n271random	logrank-composite	gene-Chr	gene-Cytoband
279	MDH2	66	NA	NA	NA	NA	NA	NA	1.9653	1	728	236	208	218	7	q11.23
280	PAG1	189	NA	NA	NA	2	1	776	NA	NA	NA	173	290	221	8	q21.13
281	SLC25A37	142	2.6	−1	845	NA	NA	NA	NA	NA	NA	226	222	222	8	p21.2
282	BCAR1	273	2.5	−1	846	NA	NA	NA	NA	NA	NA	240	213	225	16	q23.1
283	COX4I1	306	NA	NA	NA	2.6	−1	911	NA	NA	NA	178	269	226	16	q24.1
284	EIF4H	59	NA	NA	NA	NA	NA	NA	2.0065	1	775	224	236	227	7	q11.23
285	ZC3H18	317	NA	NA	NA	2.1	−1	878	NA	NA	NA	217	244	228	16	q24.2
286	STMN2	188	2.8	1	982	NA	NA	NA	NA	NA	NA	284	198	230	8	q21.13
287	AFG3L1	335	NA	NA	NA	2.3	−1	947	NA	NA	NA	254	224	231	16	q24.3
288	HSD17B2	287	2.6	−1	791	NA	NA	NA	NA	NA	NA	229	250	236	16	q23.3
289	MVD	320	NA	NA	NA	2.3	−1	901	NA	NA	NA	223	268	237	16	q24.3
290	DLC1	106	6.5	−1	1000	NA	NA	NA	NA	NA	NA	207	288	238	8	p22
291	EPHA7	44	NA	NA	NA	NA	NA	NA	1.7755	−1	529	237	252	239	6	q16.1
292	TRIM35	151	2.6	−1	936	NA	NA	NA	NA	NA	NA	209	287	241	8	p21.2
293	LHRC50	290	2.4	1	830	NA	NA	NA	NA	NA	NA	232	262	243	16	q24.1
294	CNOB3	192	1.8	1	534	NA	NA	NA	NA	NA	NA	319	191	244	8	q21.3
295	ASCC3	47	NA	NA	NA	NA	NA	NA	1.7954	−1	535	246	249	245	6	q16.3
296	AFC2	61	NA	NA	NA	NA	NA	NA	1.8399	1	625	208	296	246	7	q11.23
297	CLEC3A	278	2.3	−1	781	NA	NA	NA	NA	NA	NA	257	232	247	16	q23.1
298	IL17C	318	NA	NA	NA	1.8	−1	639	NA	NA	NA	244	256	249	16	q24.3
299	BMP1	125	NA	NA	NA	2.2	−1	819	NA	NA	NA	259	242	250	8	p21.3
300	CPA4	84	NA	NA	NA	NA	NA	NA	1.9432	1	632	242	261	251	7	q32.2
301	OC90	227	1.9	1	640	NA	NA	NA	NA	NA	NA	262	243	252	8	q24.22
302	HEPH	364	1.8	1	537	NA	NA	NA	NA	NA	NA	292	220	253	23	q12
303	LAP12	212	NA	NA	NA	2	1	635	NA	NA	NA	277	233	254	8	q22.3
304	AGFQ2	74	NA	NA	NA	NA	NA	NA	2.2839	1	749	317	212	257	7	q22.1
305	TAPA1	174	2.3	1	803	NA	NA	NA	NA	NA	NA	257	263	258	8	q13.3
306	GINS2	303	NA	NA	NA	2.1	−1	861	NA	NA	NA	268	253	260	16	q24.1
307	CENPH	29	NA	NA	NA	1.9	−1	693	NA	NA	NA	286	233	261	5	q13.2
308	KLHL36	297	NA	NA	NA	1.8	−1	606	NA	NA	NA	222	312	263	16	q24.1
309	ARHGEF1OL	2	NA	NA	NA	2.1	−1	730	NA	NA	NA	258	289	264	1	p36.13
310	TRAPPC2L	326	NA	NA	NA	1.9	−1	670	NA	NA	NA	302	230	265	16	q24.3
311	TCF25	332	NA	NA	NA	2.1	−1	821	NA	NA	NA	272	264	267	18	q24.3
312	TNFRSF10D	137	1.9	−1	603	NA	NA	NA	NA	NA	NA	288	250	268	8	p21.3
313	MYCM2	93	2.1	−1	705	NA	NA	NA	NA	NA	NA	295	245	269	8	p23.3
314	GCSH	282	NA	NA	NA	1.9	−1	673	NA	NA	NA	248	295	272	16	q23.2
315	KIAA1609	296	NA	NA	NA	1.9	−1	641	NA	NA	NA	260	284	274	16	q24.1

TABLE 14-continued

316	FANCA	330	NA	NA	NA	1.9	−1	612	NA	NA	NA	299	247	275	16	q24.3
317	ERI1	96	1.9	−1	600	NA	NA	NA	NA	NA	NA	312	239	276	8	q23.1
318	HSDL1	292	NA	NA	NA	2	−1	885	NA	NA	NA	273	278	278	16	q24.1

Table 14-8b

Final-RANK	gene	gene-start	gene-end	genesBtwn	contg	clump-index	dstprev	dstnext	min-disto-ROL	IndexO-Proxy1	NYU-Zadjust	MSKs1-Zadust	MSKS2-Zadjust
279	MDH2	75515329	75533864	2	1	10	260189	−72	−72	0	NA	NA	0.06
280	PAG1	82042605	82186858	8	1	37	545883	−93034	−930334	0	NA	0.07	NA
281	SLC25A37	23442308	23486008	1	1	28	129901	−71227	−71227	0	0.29	NA	NA
282	BCAR1	73820429	73859452	0	1	51	25657	−243911	25657	0	0.25	NA	NA
283	COX4I1	84390697	84396109	0	1	57	92166	−96	−96	0	NA	0.29	NA
284	EIF4H	73226625	73249358	0	1	9	12304	−404089	12304	0	NA	NA	0.07
285	ZC3H18	87164343	87225755	0	1	58	6745	−294	−294	0	NA	0.10	NA
286	STMN2	80685916	80740888	0	1	36	97933	−1007876	9933	0	0.38	NA	NA
287	AFG3L1	88566489	88594595	1	1	63	21813	−4521	4521	0	NA	0.17	NA
288	HSD17B2	80626364	80689638	1	1	53	750123	−76965	−76965	0	0.29	NA	NA
289	MVD	87245849	87257019	0	1	58	14572	−891	−891	0	NA	0.17	NA
290	DLC1	12985243	13416766	1	1	19	574978	−53590	−53590	0	2.71	NA	NA
291	EPHA7	94007864	94185993	9	1	5	5242062	−2654236	−2654238	0	NA	NA	0.01
292	TRIM35	27198321	27224751	0	1	30	155	26478	165	0	0.29	NA	NA
293	LHRC50	82736366	82769024	3	1	54	116798	−101	−101	0	0.21	NA	NA
294	CNOB3	87656277	87825017	0	1	38	122823	−1691298	122823	0	0.02	NA	NA
295	ASCC3	101062791	101435961	79	1	6	16667349	−43297	−43297	0	NA	NA	0.02
296	AFC2	73283770	73306674	0	1	9	35065	−1671	−1871	0	NA	NA	0.03
297	CLEC3A	76613944	76623495	0	1	52	67557	−280292	67557	0	0.17	NA	NA
298	IL17C	87232502	87234385	0	1	56	2814	−6746	2814	0	NA	0.02	NA
299	BMP1	22078645	22125782	0	1	25	7380	−8355	7380	0	NA	0.14	NA
300	CPA4	129720230	129751249	0	1	13	20643	−3360	−3360	0	NA	NA	0.06
301	OC90	133105687	133167084	0	1	45	43354	−10596	−10596	0	0.05	NA	NA
302	HEPH	65298388	65403955	0	1	69	328248	NA	328848	0	0.02	NA	NA
303	LAP12	105570643	105670344	0	1	41	72999	−22190	−22190	0	NA	0.07	NA
304	AGFQ2	99974770	100003778	0	1	12	5792	−44412	5792	0	NA	NA	0.16
305	TAPA1	73086040	73150373	0	1	34	492151	−176755	−176755	0	0.17	NA	NA
306	GINS2	84268782	84280089	0	1	57	18535	−1471	−1471	0	NA	0.10	NA
307	CENPH	68521131	68541939	0	1	4	7390	NA	7390	0	NA	0.05	NA
308	KLHL36	83239632	83253416	0	1	56	37634	−143838	37634	0	NA	0.02	NA
309	ARHGEF1OL	17738917	17898956	0	1	1	57439	−1482527	57439	0	NA	0.10	NA
310	TRAPPC2L	87451007	87455020	0	1	60	13748	−122	−122	0	NA	0.05	NA
311	TCF25	88467520	88505287	0	1	82	7881	−2292	−2292	0	NA	0.10	NA
312	TNFRSF10D	23049051	23077485	0	1	27	27431	−115396	27431	0	0.05	NA	NA
313	MYCM2	1980566	2080779	0	1	14	699503	−86359	−86369	0	0.10	NA	NA
314	GCSH	79673430	79587481	0	1	53	4504	−5057	4504	0	NA	0.05	NA
315	KIAA1609	83068608	83095794	1	1	55	143838	−13315	−13315	0	NA	0.05	NA
316	FANCA	88331460	88410565	0	1	62	11842	−246990	11842	0	NA	0.05	NA
317	ERI1	8897856	8928139	1	1	15	522716	−109315	−109315	0	0.05	NA	NA
318	HSDL1	82713389	82736285	0	1	54	101	−5371	101	0	NA	0.07	NA

TABLE 14-continued

Table 14-9a

Final-RANK	gene	index	NYU-2	NYU-dir	NYU-count	MSKs1-Z	MSKs1-dir	MSKs2-count	MSKs2-Z	MSKs2-dir	MSKs2 count	logrank-n52random	logank-n271random	logrank-composite	gene-Chr	gene-Cytoband
319	KIAA0182	302	NA	NA	NA	2	−1	781	NA	NA	NA	305	251	281	16	q24.1
320	CBFA2T3	327	NA	NA	NA	1.9	−1	698	NA	NA	NA	274	297	286	16	q24.3
321	EGR3	135	NA	NA	NA	2	−1	751	NA	NA	NA	308	267	289	8	p21.3
322	PCOLCE	77	NA	NA	NA	NA	NA	NA	1.8050	1	608	294	281	290	7	q22.1
323	C16or1B5	316	NA	NA	NA	2.1	−1	801	NA	NA	NA	290	291	295	16	q24.2
324	HMBOX1	159	1.8	−1	553	NA	NA	NA	NA	NA	NA	287	306	300	8	p21.1
325	MTMR9	100	1.9	−1	674	NA	NA	NA	NA	NA	NA	343	257	301	8	p23.1
326	MSC	173	2	1	675	NA	NA	NA	NA	NA	NA	291	305	302	8	q13.3
327	ST3GAL2	289	2.4	−1	774	NA	NA	NA	NA	NA	NA	259	340	308	16	q22.1
328	FOXF1	308	NA	NA	NA	2.2	−1	894	NA	NA	NA	344	270	309	16	q24.1
329	C8or158	132	NA	NA	NA	3	−1	999	NA	NA	NA	334	279	310	8	p21.3
330	KCTD9	145	2	−1	663	NA	NA	NA	NA	NA	NA	271	344	311	8	p21.2
331	ANGPT1	214	2.4	1	818	NA	NA	NA	NA	NA	NA	333	282	313	8	q23.1
332	GDAP1	180	2	1	683	NA	NA	NA	NA	NA	NA	283	333	314	8	q21.11
333	HNF166	322	NA	NA	NA	2.2		877	NA	NA	NA	263	360	315	16	q24.3
334	KLHL1	253	NA	NA	NA	NA	NA	NA	1.8630	−1	568	293	325	318	13	q21.33
335	LOXL2	140	NA	NA	NA	1.9	−1	675	NA	NA	NA	322	298	319	8	p21.3
336	WISP1	233	2.2	1	777	NA	NA	NA	NA	NA	NA	280	343	320	8	q24.22
337	C8or180	157	3.6	−1	957	NA	NA	NA	NA	NA	NA	357	274	323	8	p21.1
338	LA12	60	NA	NA	NA	NA	NA	NA	1.9646	1	697	328	300	324	7	q11.23
339	USP10	298	2.3	−1	691	NA	NA	NA	NA	NA	NA	321	310	326	16	q24.1
340	CDH15	328	NA	NA	NA	1.9	−1	673	NA	NA	NA	330	303	328	16	q24.3
341	WFCC1	294	2.3	−1	713	NA	NA	NA	NA	NA	NA	311	327	329	16	q24.1
342	C7or151	73	NA	NA	NA	NA	NA	NA	2.1914	1	773	307	339	333	7	q22.1
343	EBF2	14	5.1	−1	999	NA	NA	NA	NA	NA	NA	309	337	334	8	p21.2
344	CCCC125	32	NA	NA	NA	2	−1	721	NA	NA	NA	336	319	337	5	q13.2
345	LGI3	124	NA	NA	NA	2	−1	678	NA	NA	NA	332	323	338	8	p21.3
346	NUDT18	121	NA	NA	NA	2.3	−1	786	NA	NA	NA	314	354	340	8	p21.3
347	PHYHIP	125	NA	NA	NA	2.2	−1	860	NA	NA	NA	351	308	341	8	p21.3
348	PILRA	70	NA	NA	NA	NA	NA	NA	1.8998	1	701	353	318	342	7	q22.1
349	KATZA	340	NA	NA	NA	NA	NA	NA	3.1978	1	993	318	357	343	17	q921.2
350	CSMD3	216	4.9	1	998	4.2	1	809	NA	NA	NA	351	324	344	8	q23.3
351	REEP4	123	NA	NA	NA	2.5	−1	847	NA	NA	NA	324	352	345	8	p21.3
352	TUBB3	333	NA	NA	NA	2.6	−1	843	NA	NA	NA	348	328	346	16	q24.3
353	CDT1	324	NA	NA	NA	2	−1	745	NA	NA	NA	365	313	347	16	q24.3
354	EDA2R	365	2	1	629	NA	NA	NA	NA	NA	NA	349	331	348	23	q12
355	DUS1L	34	NA	NA	NA	NA	NA	NA	2.2705	1	904	364	322	350	17	q25.3
358	LACH4	75	NA	NA	NA	NA	NA	NA	2.2304	1	831	342	349	351	7	q22.1
357	TMEM75	223	3.5	1	992	NA	NA	NA	NA	NA	NA	337	356	352	8	q24.21
358	NUDT7	277	2.2	−1	730	NA	NA	NA	NA	NA	NA	355	338	353	16	q23.1

Table 14-9b

Final-RANK	gene	gene-start	gene-end	genesBtwn	contg	clump-index	dstprev	dstnext	min-disto-ROL	IndexO-Proxy1	NYU-Zadjust	MSKs1-Zadust	MSKS2-Zadjust
319	KIAA0182	84202524	84267311	0	1	57	1471	−517197	1471	0	NA	0.07	NA
320	CBFA2T3	87463768	87570902	2	1	60	194752	−13748	−13748	0	NA	0.05	NA

TABLE 14-continued

321	EGR3	22601119	22606760	0	1	26	306299	−18566	−18566	0	NA	0.07	NA	
322	PCOLCE	100037818	100043732	0	1	12	3929	−1144	−1144	0	NA	NA	0.02	
323	C16or1B5	87147613	87164049	0	1	58	294	−18723	294	0	NA	0.10	NA	
324	HMBOX1	28803830	28988706	0	1	32	14009	899246	14009	0	0.02	NA	NA	
325	MTMR9	11179410	11223062	6	1	17	165868	−154255	−154255	0	0.05	NA	NA	
326	MSC	72916332	72919285	0	1	34	176755	−479311	176755	0	0.07	NA	NA	
327	ST3GAL2	68970839	69000492	28	1	50	2343793	−6059	6059	0	0.21	NA	NA	
328	FOXF1	85101634	85105570	0	1	57	15714	−587924	15714	0	NA	0.14	NA	
329	C8or158	22513067	22517605	0	1	26	597	−1584	597	0	NA	0.47	NA	
330	KCTD9	25341283	25371837	0	1	29	591	−14747	591	0	0.07	NA	NA	
331	ANGPT1	108330899	108579459	0	1	42	401282	−1444960	401262	0	0.21	NA	NA	
332	GDAP1	75425173	75441888	0	1	35	457439	−23056	−22066	0	0.07	NA	NA	
333	HNF166	87290411	87300312	1	1	58	2604	−10028	2601	0	NA	0.14	NA	
334	KLHL1	69172727	69580592	0	1	49	1329507	−2470149	1329507	0	NA	NA	0.04	
335	LOXL2	23210097	23317667	0	1	28	−18281	−34647	−18281	0	NA	0.05	NA	
336	WISP1	134272494	134310751	2	1	46	1248464	−88015	−88015	0	0.14	NA	NA	
337	C8or180	27936607	27997307	0	1	31	2452	−29490	2452	0	0.80	NA	NA	
338	LA12	73261662	73282099	0	1	9	1671	−12304	1671	0	NA	NA	0.06	
339	USP10	83291050	83371026	0	1	56	40087	−37634	−37634	0	0.17	NA	NA	
340	COH15	87765664	87789400	0	1	61	72136	−194762	72136	0	NA	0.05	NA	
341	WFCC1	82885822	82920888	0	1	55	38748	−116798	38746	0	0.17	NA	NA	
342	C7or151	99919485	99900358	0	1	12	44412	−4648	4648	0	NA	NA	0.13	
343	EBF2	25758042	25958292	2	1	29	533035	−336689	−336689	0	1.78	NA	NA	
344	CCCC125	68612278	68664392	0	1	4	31935	−3274	3274	0	NA	0.07	NA	
345	LGI3	22060290	22070290	1	1	24	8355	−4897	−4897	0	NA	0.07	NA	
346	NUDT18	22020328	22023403	0	1	24	4474	−2493	−2493	0	NA	0.17	NA	
347	PHYHIP	22133162	22145796	0	1	25	12768	−7380	−7380	0	NA	0.14	NA	
348	PILRA	99808004	99835850	1	1	11	29540	−5616	−5616	0	NA	NA	0.05	
349	KATZA	37518657	37526872	0	1	64	1489	−380	−380	0	NA	NA	0.57	
350	CSMD3	113304337	114518418	0	1	43	1971482	−4139285	1971482	0	1.63	1.16	NA	
351	REEP4	22051478	22055393	0	1	24	4897	−8152	489	0	NA	0.25	NA	
352	TUBB3	88513168	88530006	1	1	62	12678	−7881	−7881	0	NA	0.29	NA	
353	CDT1	87397687	87403186	1	1	59	4478	−67370	4478	0	NA	0.07	NA	
354	EDA2R	65732204	65775508	0	1	69	904991	328248	−328248	0	0.07	NA	NA	
355	DUS1L	77609043	77629242	0	1	66	262	−40474	262	0	NA	NA	0.16	
355	LACH4	100009570	100021712	0	1	12	180	−5792	180	0	NA	NA	0.14	
357	TMEM75	129029046	129029462	2	1	44	2104073	−206193	−206193	0	0.74	NA	NA	
358	NUDT7	76313912	76333852	0	1	52	280292	−287400	280292	0	0.14	NA	NA	

Table 14-10a

Final-RANK	gene	index	NYU-2	NYU-dir	NYU-count	MSKs1-Z	MSKs1-dir	MSKs2-count	MSKs2-Z	MSKs2-dir	MSKs2 count	logrank-n52random	logank-n271random	logrank-composite	gene-Chr	gene-Cytoband
359	TSGA14	87	NA	NA	NA	NA	NA	NA	9.3754	1	968	354	341	354	7	q32.2
360	CDC428PG	242	NA	NA	NA	NA	NA	NA	2.3279	1	813	360	335	355	11	q13.1
361	TSC22D4	72	NA	NA	NA	NA	NA	NA	2.1304	1	867	341	359	356	7	q22.1
362	NOTUM	345	NA	NA	NA	NA	NA	NA	2.6756	1	983	358	348	358	17	q25.3
363	HSPB9	341	NA	NA	NA	NA	NA	NA	2.9366	1	987	346	361	360	17	q21.2
364	TFA2	79	NA	NA	NA	NA	NA	NA	2.6230	1	950	352	355	361	7	q22.1
365	SLA	232	2.2	1	786	NA	NA	NA	NA	NA	NA	347	365	362	8	q24.22
366	WWOX	279	9.3	−1	1000	NA	NA	NA	NA	NA	NA	359	364	365	16	q23.1

TABLE 14-continued

367	POUSF1B	221	2.9	1	989	NA	NA	NA	NA	NA	NA	366	358	366	8	q24.21
368	CPHN1	367	5.8	1	999	NA	NA	NA	NA	NA	NA	368	368	368	23	q12

Table 14-10b

Final-RANK	gene	gene-start	gene-end	genesBtwn	contg	clump-index	dstprev	dstnext	min-disto-ROL	IndexO-Proxy1	NYU-Zadjust	MSKs1-Zadust	MSKS2-Zadjust
359	TSGA14	129823611	129868133	0	1	13	45149	−8446	−8446	0	NA	NA	4.49
360	CDC42BPG	64348240	64368517	2	1	47	80139	−12898	−12888	0	NA	NA	0.18
361	TSC22D4	99902080	99914838	0	1	12	4648	−32404	4648	0	NA	NA	0.11
362	NOTUM	77503689	77512353	0	1	65	16362	−39903857	16352	0	NA	NA	0.32
363	HSPB9	37528361	37526897	0	1	64	1627	−1489	−1489	0	NA	NA	0.44
364	TFA2	100055975	100077109	0	1	12	1589	−5043	1589	0	NA	NA	0.29
365	SLA	134118155	134184479	0	1	46	88015	98170	88015	0	0.14	NA	NA
366	WWOX	76891052	77803532	2	1	52	1391644	−67557	−67557	0	4.45	NA	NA
367	POUSF1B	128497039	128498621	0	1	44	318241	−23233848	318241	0	0.42	NA	NA
368	OPHN1	67179440	67570372	NA	1	69	NA	−318596	−318596	0	2.24	NA	NA

What is claimed is:

1. A method of diagnosing and treating a human subject who has or had breast or lung cancer, the method comprising

(a) obtaining a tissue or DNA sample from the subject,

(b) determining in the sample the number of copies per cell of at least 12 genes and/or genomic regions of a metastatic gene signature set, wherein the metastatic gene signature set consists of the PPP3CC genomic region, the SLCO5A1 genomic region, the SLC7A5 genomic region, the SLC7A2 genomic region, the CRISPLD2 genomic region, the CDH13 gene, the CDH8 gene, the CDH2 gene, the ASAH1 genomic region, the KCNB2 genomic region, the KCNH4 genomic region, the CTD8 gene, the JPH1 genomic region, the MEST genomic region, the NCALD genomic region, the COL19A1 gene, the MAP3K7 genomic region, the YWHAG gene, the NOLA genomic region, and the ENOX1 gene, wherein said detecting comprises performing nucleic acid hybridization, and wherein

the PPP3CC genomic region consists of the genes PPP3CC, KIAA1967, BIN3, SORBS3, PDLIM2, RHOBTB2, SLC39A14, EGR3, and C8orf58,

the SLCO5A1 genomic region consists of the genes SLCOSA1, SULF1, NCOA2, CPA6, C8orf34, PRDM14, and PREX2,

the SLC7A5 genomic region consists of the genes SLC7A5, CASA, BANP, KLHDC4, CYBA, JPH3, ZFPM1, SNAI3, ZC3H18, MVD, IL17C, C16orf85, and RNF166,

the SLC7A2 genomic region consists of the genes SLC7A2, MTMR7 and MTUS1,

the CRISPLD2 genomic region consists of the genes CRISPLD2, ZDHHC7, KIAA0513, KLHL36, and USP10,

the ASAH1 genomic region consists of the genes ASAH1 and PCM1,

the KCNB2 genomic region consists of the genes KCNB2, EYA1, XKR9, and TRPA1,

the KCNH4 genomic region consists of the genes KCNH4, RAB5C, DHX58, KAT2A, and HSPB9,

the JPH1 genomic region consists of the genes JPH1, HNF4G, CRISPLD1, PI15, and GDAP1,

the MEST genomic region consists of the genes MEST, COPG2, CPA5, CPA2, CPA1, CPA4, and TSGA14,

the NCALD genomic region consists of the genes NCALD, ZNF706, GRHL2, and YWHAZ,

the MAP3K7 genomic region consists of the genes MAP3K7 and EPHA7, and

the NOL4 genomic region consists of the genes NOLA and DTNA,

(c) determining an aggregate score for the at least 12 members as compared to the number of copies per cell in non-cancer cells,

(d) based on the determination in step (c), diagnosing that the subject has risk of metastasis,

(e) developing a pan-cancer metastatic potential score (panMPS) based on CNA (copy number alternation) genes,

(f) predicting a metastasis-free survival for breast or lung cancer based on the panMPS in step (e), and

(g) treating the subject with at least one therapy selected from the group consisting of surgery, radiation therapy, chemotherapy or biologically targeted therapy.

2. The method of claim 1, wherein the at least 12 genes and/or genomic regions include the PPP3CC genomic region, the SLCOSA1 genomic region, the SLC7A5 genomic region, the SLC7A2 genomic region, the CRISPLD2 genomic region, the CDH13 gene, the CDH8 gene, the CDH2 gene, the ASAH1 genomic region, the KCNB2 genomic region, the KCNH4 genomic region, and the CTD8 gene.

3. The method of claim 1, wherein the at least 12 genes and/or genomic regions include all of the genes and genomic regions in said metastatic gene signature set.

4. The method of claim 3, further comprising determining the number of copies per cell of at least one additional gene or genomic region selected from the group consisting of PPP3CC, SLCO5A1, SLC7A5, SLC7A2, CRISPLD2, CDH13, CDH8, CDH2, ASAH1, KCNB2, KCNH4, KCTD8, JPH1, MEST, NCALD, COL19A1, MAP3K7, YWAHG, NOLA, ENOX1, CSMD1, SGCZ, PDE10A, PCDH9, HTR2A, HIP1, CD226, DCC, CC2D1A, PTK2B, BCMO1, MACRDO1, GRID2, DIAPH3, PILRB, MEIS2, MSRA, DPYD, ANKRD11, NRXN1, ADCY8, TRDN, STAU2, SF1, CLIP2, CLDN3, ZSWIM4, GLRB, DCHS2, TRPS1, MDGA2, CNBD1, STAG3, GATA4, VPS13B, DOCK5, ZHX2, ARHGEF5, SDC2, MYLK, LPHN3, MOSPD3, GYS2, GAS8, RAB9A, POLR3D, PSD3, ZFPM2, ATP6V1C1, MEF2C, PKIA, ADAMTS18, STYXL1, EPM2A, LEPREL1, GABRA2, RCOR2, MFHAS1, SCARA5, CCDC25, FAM38A, CTSB, PTK2, SPIRE2, C13orf23, BOD1L, FAM160B2, NUS1, MTHFSD, UBR5, GALNS, FSTL5, SIM1, TG, BFSP2, MMP16, RIMS2, PDS5B, CDK7, CNTNAP4, CFDP1, FBXL4, RFX1, NALCN, STX1A, CYP7B1, ARHGEF10, ENTPD4, ZNF704, C8orf79, SLC9A9, CHMP7, GPC5, MYC, STIP1, ZBTB20, MEN1, SLC26A7, ALCAM, KIF13B, MBTPS1, PPP2R5B, VPS13C, ASPRSCR1, EPO, HEY1, KALRN, RGS22, WDR7, COL11A1, GHDC, ATP2C2, CDH17, DGKG, GRK5, GRM1, IMPA1, RPL7, COL21A1, COL12A1, MLYCD, AR, PLCB1, ACTL8, TFDP1, IQCE, SMARCB1, MTDH, NECAB2, DEF8, RNF40, TICAM2, GLG1, MECOM, TCEB1, CTNNA2, NIPAL2, CDCA2, WWP2, DDX19A, STK3, DNAH2, NFAT5, CNGB1, UBE2CBP, C8orf16, KIAA0196, CLCNKB, C16orf80, ZFHX3, PPM1L, NKIRAS2, RSPO2, XPO7, ME1, NLGN4Y, LZTS1, FBXL18, TBC1D10B, WDR59, BLK, MEPCE, DLGAP2, ZFAT, FASN, GIGYF1, ANXA13, CDYL2, TOX, NKX2-6, RALYL, TBC1D22A, TFE3, KCNAB1, SULF1, RAB5C, DHX58, ASAP1, CASA, C6orf118, NCOA2, PKD1L2, BANP, KIAA1967, COPG2, ZNF706, GAN, PLCG2, C19orf57, PDGFRL, ESD, CPA5, BIN3, ZFHX4, CPA6, EYA1, CHRNA2, TNKS, HNF4G, LRCH1, ADRA1A, EPHX2, SORBS3, GRIA2, PDLIM2, MTMR7, FBXO24, CRISPLD1, DPYS, DTNA, KLHDC4, CYBA, JPH3, TMEM120A, MTUS1, C8orf34, GRHL2, CPA2, NAT2, DPYSL2, ZDHHC7, ELP3, RHOBTB2, NEIL2, HR, EFR3A, STMN4, PRDM14, MARVELD2, SLC39A14, ACTL6B, TUSC3, COX4NB, XKR9, C16orf46, TAF9, KCNQ3, UTRN, RAD17, ZFPM1, PTDSS1, IRF8, YWHAZ, MRPS36, LACTB2, SNAI3, TMEM71, PREX2, CPA1, PHF20L1, KIAA0513, PI15, PCM1, SH2D4A, C16orf74, TP63, DACH1, TNFRSF10A, MDH2, PAG1, SLC25A37, BCAR1, COX411, EIF4H, ZC3H18, STMN2, AFG3L1, HSD17B2, MVD, DLC1, EPHA7, TRIM35, LRRC50, CNGB3, ASCC3, RFC2, CLEC3A, IL17C, BMP1, CPA4, OC90, HEPH, LRP12, AGFG2, TRPA1, GINS2, CENPH, KLHL36, ARHGEF10L, TRAPPC2L, TCF25, TNFRSF10D, MYOM2, GCSH, KIAA1609, FANCA, ERI1, HSDL1, KIAA0182, CBFA2T3, EGR3, PCOLCE, C16orf85, HMBOX1, MTMR9, MSC, ST3GAL2, FOXF1, C8orf58, KCTD9, ANGPT1, GDAP1, RNF166, KLHL1,

LOXL2, WISP1, C8orf80, LAT2, USP10, CDH15, WFDC1, C7orf51, EBF2, CCDC125, LGI3, NUDT18, PHYHIP, PILRA, KAT2A, CSMD3, REEP4, TUBB3, CDT1, EDA2R, DUS1L, LRCH4, TMEM75, NUDT7, TSGA14, CDC42BPG, TSC22D4, NOTUM, HSPB9, TFR2, SLA, WWOX, POU5F1B, and OPHN1.

5. The method of claim **4**, wherein said at least one additional gene or genomic region comprises 20 genes and/or genomic regions selected from the group consisting of PPP3CC, SLCOSA1, SLC7A5, SLC7A2, CRISPLD2, CDH13, CDH8, CDH2, ASAH1, KCNB2, KCNH4, KCTD8, JPH1, MEST, NCALD, COL19A1, MAP3K7, YWAHG, NOL4, ENOX1, CSMD1, SGCZ, PDE10A, PCDH9, HTR2A, HIP1, CD226, DCC, CC2D1A, PTK2B, BCMO1, MACRDO1, GRID2, DIAPH3, PILRB, MEIS2, MSRA, DPYD, ANKRD11, NRXN1, ADCY8, TRDN, STAU2, SF1, CLIP2, CLDN3, ZSWIM4, GLRB, DCHS2, TRPS1, MDGA2, CNBD1, STAG3, GATA4, VPS13B, DOCK5, ZHX2, ARHGEF5, SDC2, MYLK, LPHN3, MOSPD3, GYS2, GAS8, RAB9A, POLR3D, PSD3, ZFPM2, ATP6V1C1, MEF2C, PKIA, ADAMTS18, STYXL1, EPM2A, LEPREL1, GABRA2, RCOR2, MFHAS1, SCARA5, CCDC25, FAM38A, CTSB, PTK2, SPIRE2, C13orf23, BOD1L, FAM160B2, NUS1, MTHFSD, UBR5, GALNS, FSTL5, SIM1, TG, BFSP2, MMP16, RIMS2, PDS5B, CDK7, CNTNAP4, CFDP1, FBXL4, RFX1, NALCN, STX1A, CYP7B1, ARHGEF10, ENTPD4, ZNF704, C8orf79, SLC9A9, CHMP7, GPC5, MYC, STIP1, ZBTB20, MEN1, SLC26A7, ALCAM, KIF13B, MBTPS1, PPP2R5B, VPS13C, ASPRSCR1, EPO, HEY1, KALRN, RGS22, WDR7, COL11A1, GHDC, ATP2C2, CDH17, DGKG, GRK5, GRM1, IMPA1, RPL7, COL21A1, COL12A1, MLYCD, AR, PLCB1, ACTL8, TFDP1, IQCE, SMARCB1, MTDH, NECAB2, DEF8, RNF40, TICAM2, GLG1, MECOM, TCEB1, CTNNA2, NIPAL2, CDCA2, WWP2, DDX19A, STK3, DNAH2, NFAT5, CNGB1, UBE2CBP, C8orf16, KIAA0196, CLCNKB, C16orf80, ZFHX3, PPM1L, NKIRAS2, RSPO2, XPO7, ME1, NLGN4Y, LZTS1, FBXL18, TBC1D10B, WDR59, BLK, MEPCE, DLGAP2, ZFAT, FASN, GIGYF1, ANXA13, CDYL2, TOX, NKX2-6, RALYL, TBC1D22A, TFE3, KCNAB1, SULF1, RAB5C, DHX58, ASAP1, CA5A, C6orf118, NCOA2, PKD1L2, BANP, KIAA1967, COPG2, ZNF706, GAN, PLCG2, C19orf57, PDGFRL, ESD, CPA5, BIN3, ZFHX4, CPA6, EYA1, CHRNA2, TNKS, HNF4G, LRCH1, ADRA1A, EPHX2, SORBS3, GRIA2, PDLIM2, MTMR7, FBXO24, CRISPLD1, DPYS, DTNA, KLHDC4, CYBA, JPH3, TMEM120A, MTUS1, C8orf34, GRHL2, CPA2, NAT2, DPYSL2, ZDHHC7, ELP3, RHOBTB2, NEIL2, HR, EFR3A, STMN4, PRDM14, MARVELD2, SLC39A14, ACTL6B, TUSC3, COX4NB, XKR9, C16orf46, TAF9, KCNQ3, UTRN, RAD17, ZFPM1, PTDSS1, IRF8, YWHAZ, MRPS36, LACTB2, SNAI3, TMEM71, PREX2, CPA1, PHF20L1, KIAA0513, PI15, PCM1, SH2D4A, C16orf74, TP63, DACH1, TNFRSF10A, MDH2, PAG1, SLC25A37, BCAR1, COX411, EIF4H, ZC3H18, STMN2, AFG3L1, HSD17B2, MVD, DLC1, EPHA7, TRIM35, LRRC50, CNGB3, ASCC3, RFC2, CLEC3A, IL17C, BMP1, CPA4, OC90, HEPH, LRP12, AGFG2, TRPA1, GINS2, CENPH, KLHL36, ARHGEF10L, TRAPPC2L, TCF25, TNFRSF10D, MYOM2, GCSH, KIAA1609, FANCA, ERI1, HSDL1, KIAA0182, CBFA2T3, EGR3, PCOLCE, C16orf85, HMBOX1, MTMR9, MSC, ST3GAL2, FOXF1, C8orf58, KCTD9, ANGPT1, GDAP1, RNF166, KLHL1, LOXL2, WISP1, C8orf80, LAT2, USP10, CDH15, WFDC1, C7orf51, EBF2, CCDC125, LGI3, NUDT18, PHYHIP, PILRA, KAT2A, CSMD3, REEP4, TUBB3, CDT1, EDA2R, DUS1L, LRCH4, TMEM75, NUDT7, TSGA14, CDC42BPG, TSC22D4, NOTUM, HSPB9, TFR2, SLA, WWOX, POU5F1B, and OPHN1.

6. The method of claim **5**, wherein said 20 genes and/or genomic regions consist of CSMD1, SGCZ, PDE10A, PCDH9, HTR2A, HIP1, CD226, DCC, CC2D1A, PTK2B, BCMO1, MACRDO1, GRID2, DIAPH3, PILRB, MEIS2, MSRA, DPYD, ANKRD11, and NRXN1.

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