



(12) **DEMANDE DE BREVET CANADIEN**
CANADIAN PATENT APPLICATION
(13) **A1**

(86) Date de dépôt PCT/PCT Filing Date: 2018/03/09 (87) Date publication PCT/PCT Publication Date: 2018/09/13 (85) Entrée phase nationale/National Entry: 2019/09/09 (86) N° demande PCT/PCT Application No.: US 2018/021826 (87) N° publication PCT/PCT Publication No.: 2018/165600 (30) Priorité/Priority: 2017/03/09 (US62/469,174)	(51) Cl.Int./Int.Cl. <i>G01N 33/574</i> (2006.01), <i>C12Q 1/68</i> (2018.01) (71) Demandeurs/Applicants: DECIPHER BIOSCIENCES, INC., US; THE REGENTS OF THE UNIVERSITY OF MICHIGAN, US (72) Inventeurs/Inventors: DAVICIONI, ELAI, US; ERHO, NICHOLAS, CA; ZHAO, SHUANG G., US; CHANG, S. LAURA, US; FENG, FELIX Y., US (74) Agent: MBM INTELLECTUAL PROPERTY LAW LLP
---	--

(54) Titre : SOUS-TYPAGE DU CANCER DE LA PROSTATE POUR PREDIRE LA REPONSE A UNE THERAPIE HORMONALE

(54) Title: SUBTYPING PROSTATE CANCER TO PREDICT RESPONSE TO HORMONE THERAPY

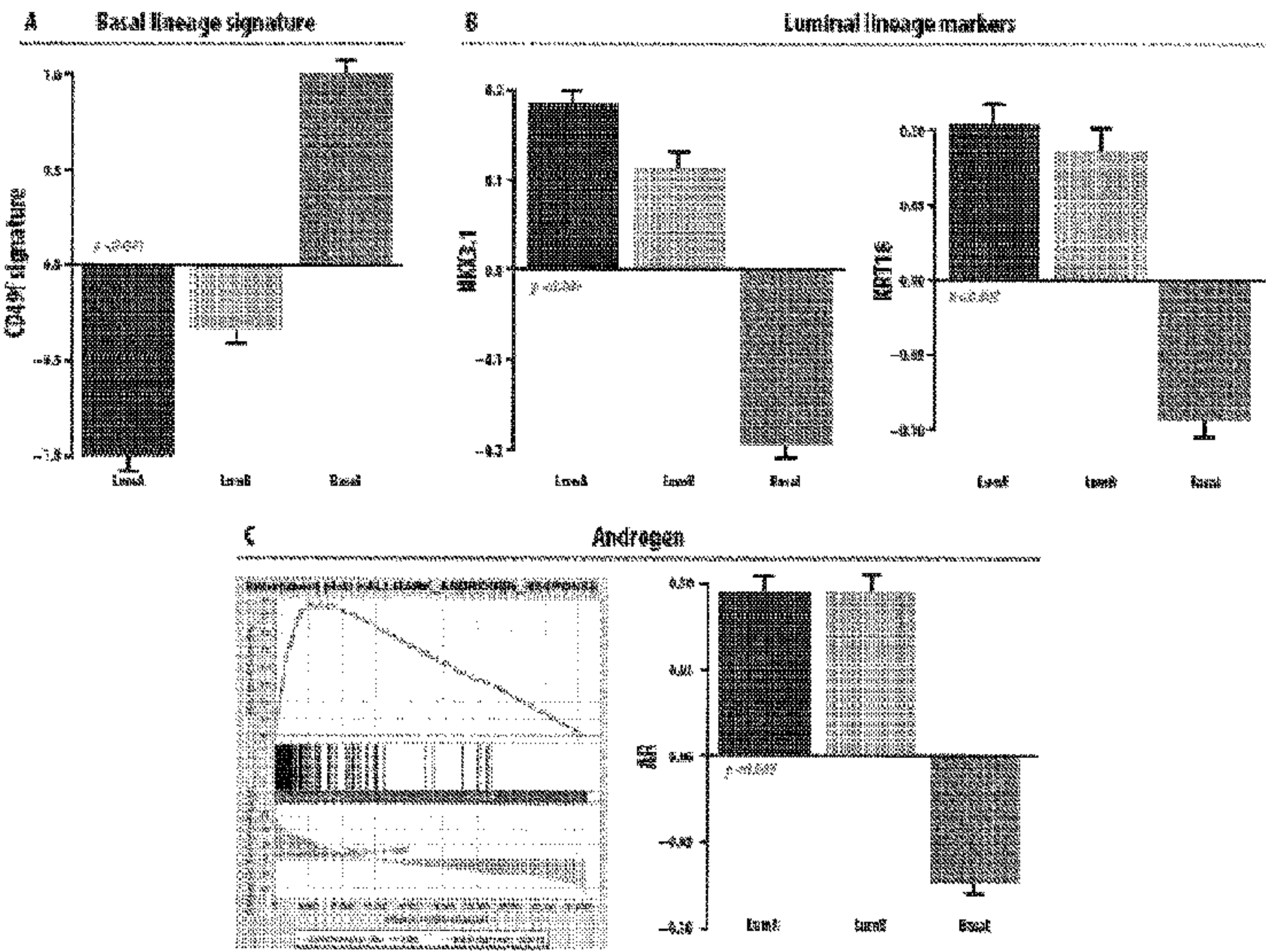


FIGURE 2

(57) **Abrégé/Abstract:**

The present invention relates to methods, systems and kits for the diagnosis, prognosis and the determination of progression of cancer in a subject. The invention also provides biomarkers that define subgroups of prostate cancer, clinically useful classifiers for distinguishing prostate cancer subtypes, bioinformatic methods for determining clinically useful classifiers, and methods of use of each of the foregoing. The methods, systems and kits can provide expression-based analysis of biomarkers for purposes of subtyping prostate cancer in a subject. Further disclosed herein, in certain instances, are probe sets for use in subtyping prostate cancer in a subject. Classifiers for subtyping a prostate cancer are provided. Methods of treating cancer based on molecular subtyping are also provided.

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property
Organization
International Bureau(43) International Publication Date
13 September 2018 (13.09.2018)(10) International Publication Number
WO 2018/165600 A1

(51) International Patent Classification:

G01N 33/574 (2006.01) *G06F 19/20* (2011.01)
C12Q 1/68 (2018.01)

(21) International Application Number:

PCT/US2018/021826

(22) International Filing Date:

09 March 2018 (09.03.2018)

(25) Filing Language:

English

(26) Publication Language:

English

(30) Priority Data:

62/469,174 09 March 2017 (09.03.2017) US

(71) Applicants: GENOMEDX BIOSCIENCES, INC.
[US/US]; 1038 Homer Street, Vancouver, BC V6B2W9
(CA). THE REGENTS OF THE UNIVERSITY OFMICHIGAN [US/US]; 1600 Huron Parkway, 2nd Floor,
Ann Arbor, MI 48109-2590 (US).(72) Inventors: DAVICIONI, Elai; 6172 Calle Vera Cruz,
La Jolla, CA 92037 (US). ERHO, Nicholas; 1401 438
Seymour Street, Vancouver, BC V6B 6H4 (CA). ZHAO,
Shuang, G.; 2261 Placid Way, Ann Arbor, MI 48105 (US).
CHANG, S., Laura; 2261 Placid Way, Ann Arbor, CA
48105 (US). FENG, Felix, Y.; 332 Darrell Road, Hillsbor-
ough, CA 94010 (US).(74) Agent: MALLON, Joseph J. et al.; Knobbe Martens Olson
& Bear LLP, 2040 Main Street, Fourteenth Floor, Irvine,
CA 92614 (US).(81) Designated States (*unless otherwise indicated, for every
kind of national protection available*): AE, AG, AL, AM,
AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ,
CA, CH, CL, CN, CO, CR, CU, CZ, DE, DJ, DK, DM, DO,
DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN,

(54) Title: SUBTYPING PROSTATE CANCER TO PREDICT RESPONSE TO HORMONE THERAPY

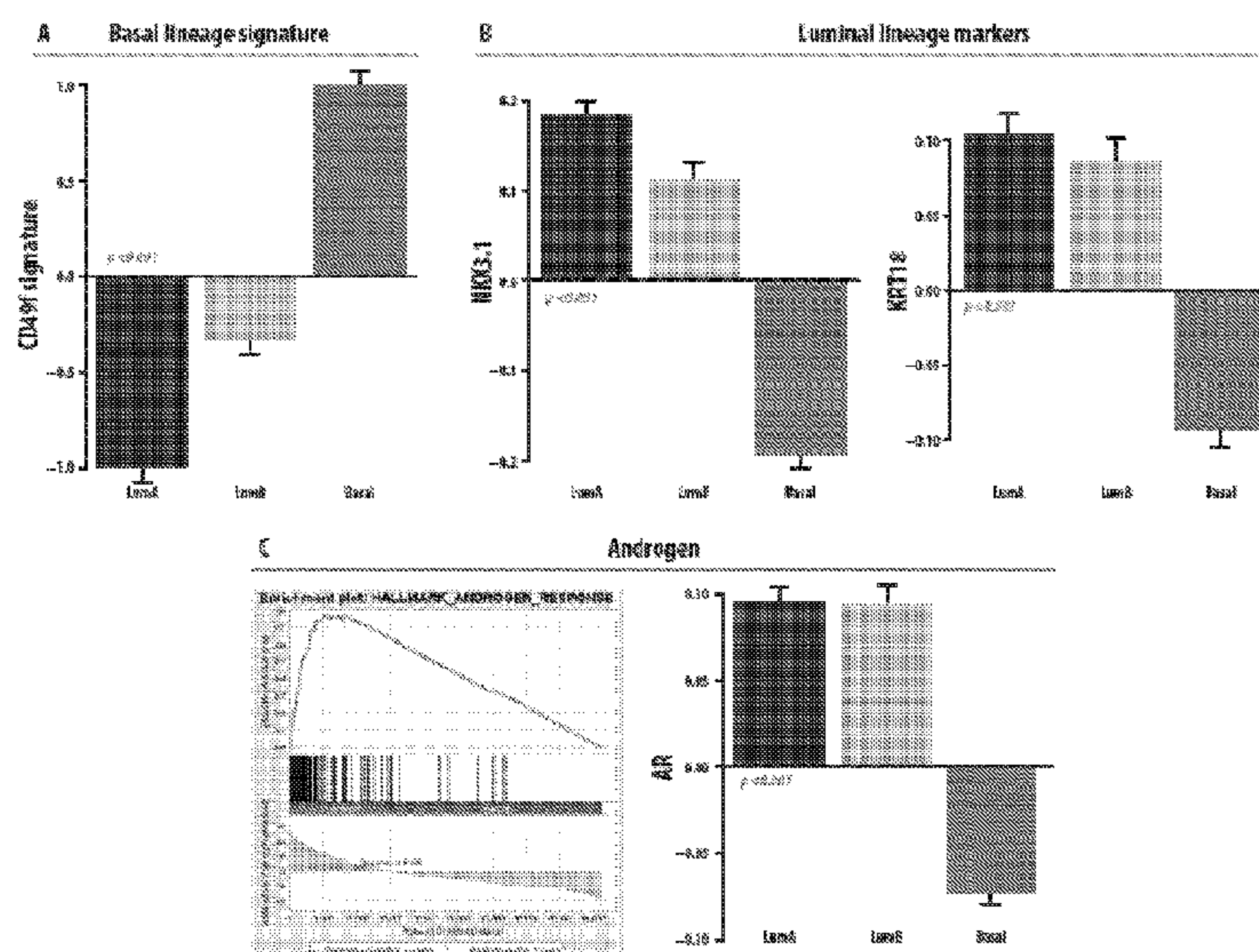


FIGURE 2

(57) **Abstract:** The present invention relates to methods, systems and kits for the diagnosis, prognosis and the determination of progression of cancer in a subject. The invention also provides biomarkers that define subgroups of prostate cancer, clinically useful classifiers for distinguishing prostate cancer subtypes, bioinformatic methods for determining clinically useful classifiers, and methods of use of each of the foregoing. The methods, systems and kits can provide expression-based analysis of biomarkers for purposes of subtyping prostate cancer in a subject. Further disclosed herein, in certain instances, are probe sets for use in subtyping prostate cancer in a subject. Classifiers for subtyping a prostate cancer are provided. Methods of treating cancer based on molecular subtyping are also provided.

[Continued on next page]



WO 2018/165600 A1

WO 2018/165600 A1

HR, HU, ID, IL, IN, IR, IS, JO, JP, KE, KG, KH, KN, KP, KR, KW, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) Designated States (*unless otherwise indicated, for every kind of regional protection available*): ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

Published:

- *with international search report (Art. 21(3))*
- *before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments (Rule 48.2(h))*
- *with sequence listing part of description (Rule 5.2(a))*

SUBTYPING PROSTATE CANCER TO PREDICT RESPONSE TO HORMONE THERAPY

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims benefit of priority under 35 U.S.C. §119(e) of U.S. Serial No. 62/469,174, filed March 9, 2017, the entire contents of which is incorporated herein by reference in its entirety.

INCORPORATION OF SEQUENCE LISTING

[0002] The material in the accompanying sequence listing is hereby incorporated by reference into this application. The accompanying sequence listing text file, name GBX1280_1WO_Sequence_Listing.txt, was created on March 9, 2018, and is **289** kb. The file can be assessed using Microsoft Word on a computer that uses Windows OS.

FIELD OF THE INVENTION

[0003] The present invention relates to methods, systems and kits for the diagnosis, prognosis and the determination of cancer progression of prostate cancer in a subject. The invention also provides biomarkers that define subgroups of prostate cancer, clinically useful classifiers for distinguishing prostate cancer subtypes, bioinformatic methods for determining clinically useful classifiers, and methods of use of each of the foregoing. The methods, systems and kits can provide expression-based analysis of biomarkers for purposes of subtyping prostate cancer in a subject. Further disclosed herein, in certain instances, are probe sets for use in subtyping prostate cancer in a subject. Classifiers for subtyping a prostate cancer are provided. Methods of treating cancer based on molecular subtyping are also provided. The methods and classifiers of the present invention are also useful for predicting response to hormonal therapy (e.g., androgen deprivation therapy).

BACKGROUND OF THE INVENTION

[0004] Cancer is the uncontrolled growth of abnormal cells anywhere in a body. The abnormal cells are termed cancer cells, malignant cells, or tumor cells. Many cancers and the abnormal cells that compose the cancer tissue are further identified by the name of the tissue that the abnormal cells originated from (for example, prostate cancer). Cancer cells can proliferate uncontrollably and form a mass of cancer cells. Cancer cells can break away from this original mass of cells, travel through the blood and lymph systems, and lodge in other organs where they can again repeat the uncontrolled growth cycle. This process of cancer cells leaving an area and growing in another body area is often termed metastatic spread or metastatic disease. For example, if prostate cancer cells spread to a bone (or anywhere else), it can mean that the individual has metastatic prostate cancer.

[0005] Standard clinical parameters such as tumor size, grade, lymph node involvement and tumor–node–metastasis (TNM) staging (American Joint Committee on Cancer <http://www.cancerstaging.org>) may correlate with outcome and serve to stratify patients with respect to (neo)adjuvant chemotherapy, immunotherapy, antibody therapy and/or radiotherapy regimens. Incorporation of molecular markers in clinical practice may define tumor subtypes that are more likely to respond to targeted therapy. However, stage-matched tumors grouped by histological or molecular subtypes may respond differently to the same treatment regimen. Additional key genetic and epigenetic alterations may exist with important etiological contributions. A more detailed understanding of the molecular mechanisms and regulatory pathways at work in cancer cells and the tumor microenvironment (TME) could dramatically improve the design of novel anti-tumor drugs and inform the selection of optimal therapeutic strategies. The development and implementation of diagnostic, prognostic and therapeutic biomarkers to characterize the biology of each tumor may assist clinicians in making important decisions with regard to individual patient care and treatment. Thus, provided herein are methods, systems and kits for the diagnosis, prognosis and the determination of cancer progression of cancer in a subject. The invention also provides biomarkers that define subgroups of prostate cancer, clinically useful classifiers for distinguishing prostate cancer subtypes, bioinformatic methods for determining clinically useful classifiers, and methods of use of each of the foregoing. The methods, systems and kits can provide expression-based analysis of biomarkers for purposes of subtyping prostate cancer in a subject. Further disclosed herein, in certain instances, are probe sets for use in subtyping prostate cancer in a subject. Classifiers for subtyping a prostate cancer are provided. Methods of treating cancer based on molecular subtyping are also provided. The classifiers of the present invention are useful for identifying prostate cancer patients that will respond to hormone therapy (e.g., androgen deprivation therapy).

[0006] This background information is provided for the purpose of making known information believed by the applicant to be of possible relevance to the present invention. No admission is necessarily intended, nor should be construed, that any of the preceding information constitutes prior art against the present invention.

SUMMARY OF THE INVENTION

[0007] The present invention relates to methods, systems and kits for the diagnosis, prognosis and the determination of cancer progression of cancer in a subject. The invention also provides biomarkers that define subgroups of prostate cancer, clinically useful classifiers for distinguishing prostate cancer subtypes, bioinformatic methods for determining clinically useful classifiers, and methods of use of each of the foregoing. The methods, systems and kits

can provide expression-based analysis of biomarkers for purposes of subtyping prostate cancer in a subject. Further disclosed herein, in certain instances, are probe sets for use in subtyping prostate cancer in a subject. Classifiers for subtyping a prostate cancer are provided. Methods of treating cancer based on molecular subtyping are also provided.

[0008] In one embodiment, the present invention provides a method comprising: providing a biological sample from a prostate cancer subject; detecting the presence or expression level of at least one or more targets selected from Table 8, Table 9 or SEQ ID NOs: 1-1029; and subtyping the prostate cancer in the subject according to a genomic subtyping classifier based on the presence or expression levels of the plurality of targets wherein said subtyping comprises assigning the prostate cancer to one of three subtypes selected from the group consisting of a luminal A subtype, a luminal B subtype, and a basal subtype. In some embodiments, the method further comprises administering androgen deprivation therapy to the subject if the subtyping indicates that the subject has the luminal B subtype and administering an anti-cancer treatment other than the androgen deprivation therapy to the subject if the subtyping indicates that the subject has the luminal A subtype or the basal subtype, wherein the anti-cancer treatment other than androgen deprivation therapy is selected from the group consisting of surgery, chemotherapy, radiation therapy, immunotherapy, biological therapy, neoadjuvant chemotherapy, and photodynamic therapy.

[0009] In one embodiment, the present invention provides a method comprising: a) providing a biological sample from a subject having prostate cancer; b) detecting the presence or expression level in the biological sample for a plurality of targets selected from Table 8, Table 9 or SEQ ID NOs: 1-1029 and c) subtyping the prostate cancer in the subject according to a genomic subtyping classifier based on the presence or expression levels of the plurality of targets, wherein said subtyping comprises assigning the prostate cancer to one of three subtypes selected from the group consisting of a luminal A subtype, a luminal B subtype, and a basal subtype.

[0010] In one embodiment, the present invention provides a method comprising: a) providing a biological sample from a subject having prostate cancer; b) detecting the presence or expression level in the biological sample for a plurality of targets selected from the group consisting of CDC20; KIF2C; PHGDH; NUF2; CENPF; EXO1; UBE2T; RRM2; MLPH; GPR160; CCNB1; CXXC5; PTTG1; FGFR4; FOXC1; ESR1; ANLN; BLVRA; EGFR; ACTR3B; NAT1; MYC; SFRP1; MELK; BAG1; CEP55; MKI67; TMEM45B; PGR; MDM2; KRT5; FOXA1; ORC6; CDH3; ERBB2; GRB7; CDC6; MAPT; BIRC5; KRT14; KRT17; TYMS; NDC80; SLC39A6; BCL2; CCNE1; MIA; MYBL2; UBE2C; MMP11; TDRD1; CACNA1D; NCALD; HLA-DMB; KCNH8; PDE3B; PLA2G7; CSGALNACT1; PART1; HES1; F3; GPR110; SH3RF; PDE8B; SEPT9; CRISP3;

AMD1; KCNG3; PLA1A; MYO6; FRK; SH3YL1; ACER3; C8orf4; GHR; ITPR1; KHDRBS3; NPY; GUCY1A3; ARHGDIB; LAMC2; VWA2; ZNF432; MORN1; CYorf15B; AMPD3; QDPR; HDAC1; KIF16B; GJB1; ITPR3; ZNF615; ANKRD6; APOD; STEAP4; RGS17; MAP7; C22orf36; NKAIN1; CHN2; LRRFIP1; SERGEF; ATP8A2; NDRG1; CDC42SE1; LUZP2; HNF1B; TFAP2A; ANKRD34B; SLC12A2; PRAC; SLC5A4; ACSL3; CD24P4; DNASE2B; SLC22A3; ODC1; SMOC2; UGDH; DSC2; WNK2; RAB3B; FAM198B; KCNC2; SNAP91; FAM65B; AMACR; ZNF385B; CDK19; ARHGAP18; IL5RA; SLC16A1; CNTLN; FKBP10; SLC45A2; CLIP1; HEXB; NEFH; ODZ1; SS18L2; HPGD; FAM3B; MIPEP; NCAPD3; INPP4B; ANPEP; TFF3; IL31RA; EHHADH; RP11-45B20.2; CCDC141; RLN1; ABHD2; SCIN; ALOX15B; MON1B; MME; BANK1; LEPREL1; VGLL3; NPR3; OR4K7P; OR4K6P; POTE2; RP11; TTN; FAP5; GPR116; RP11.403; and FABP5P7; and c) subtyping the prostate cancer in the subject according to a genomic subtyping classifier based on the presence or expression levels of the plurality of targets, wherein said subtyping comprises assigning the prostate cancer to one of three subtypes selected from the group consisting of a luminal A subtype, a luminal B subtype, and a basal subtype.

[0011] In one embodiment, the present invention provides a method comprising: a) providing a biological sample from a subject having prostate cancer and b) detecting the presence or expression level in the biological sample for a plurality of targets selected from Table 8, Table 9 or SEQ ID NOs: 1-1029. In some embodiments, the method further comprises subtyping the prostate cancer in the subject according to a genomic subtyping classifier based on the presence or expression levels of the plurality of targets, wherein said subtyping comprises assigning the prostate cancer to one of three subtypes selected from the group consisting of a luminal A subtype, a luminal B subtype, and a basal subtype.

[0012] In some embodiments, the method further comprises administering androgen deprivation therapy to the subject if the subtyping indicates that the subject has the luminal B subtype and administering an anti-cancer treatment other than the androgen deprivation therapy to the subject if the subtyping indicates that the subject has the luminal A subtype or the basal subtype, wherein the anti-cancer treatment other than androgen deprivation therapy is selected from the group consisting of surgery, chemotherapy, radiation therapy, immunotherapy, biological therapy, neoadjuvant chemotherapy, and photodynamic therapy.

[0013] In some embodiments, the present invention provides a method comprising: providing a biological sample from a prostate cancer subject; detecting the presence or expression level of at least one or more targets selected from Table 8, Table 9 or SEQ ID NOs: 1-1029; and administering a treatment to the subject, wherein the treatment is selected from the group consisting of surgery, chemotherapy, radiation therapy, immunotherapy/biological therapy, hormonal therapy, and photodynamic therapy. In some embodiments, the treatment is

androgen deprivation therapy. In some embodiments, the present invention provides a method of subtyping prostate cancer in a subject, comprising: providing a biological sample comprising prostate cancer cells from the subject, and determining the level of expression or amplification of at least one or more targets selected from Table 8, Table 9 or SEQ ID NOs: 1-1029 using at least one reagent that specifically binds to said targets; wherein the alteration of said expression level provides an indication of the prostate cancer subtype. In some embodiments, the alteration in the expression level of said target is reduced expression of said target. In other embodiments, the alteration in the expression level of said target is increased expression of said target. In yet other embodiments, the level of expression of said target is determined by using a method selected from the group consisting of in situ hybridization, a PCR-based method, an array-based method, an immunohistochemical method, an RNA assay method and an immunoassay method. In other embodiments, the reagent is selected from the group consisting of a nucleic acid probe, one or more nucleic acid primers, and an antibody. In still other embodiments, the target comprises a nucleic acid sequence.

[0014] In some embodiments, the present invention also provides a method of diagnosing, prognosing, assessing the risk of recurrence or predicting benefit from therapy in a subject with prostate cancer, comprising: providing a biological sample comprising prostate cancer cells from the subject; assaying an expression level in the biological sample from the subject for a plurality of targets using at least one reagent that specifically binds to said targets, wherein the plurality of targets comprises one or more targets selected from Table 8, Table 9 or SEQ ID NOs: 1-1029; and diagnosing, prognosing, assessing the risk of recurrence or predicting benefit from therapy in the subject based on the expression levels of the plurality of targets. In some embodiments, the expression level of the target is reduced expression of the target. In other embodiments, the expression level of said target is increased expression of said target. In yet other embodiments, the level of expression of said target is determined by using a method selected from the group consisting of in situ hybridization, a PCR-based method, an array-based method, an immunohistochemical method, an RNA assay method and an immunoassay method. In other embodiments, the reagent is selected from the group consisting of a nucleic acid probe, one or more nucleic acid primers, and an antibody. In other embodiments, the target comprises a nucleic acid sequence.

[0015] In some embodiments, the present invention provides a system for analyzing a cancer, comprising, a probe set comprising a plurality of target sequences, wherein the plurality of target sequences hybridizes to one or more targets selected from Table 8, Table 9 or SEQ ID NOs: 1-1029; or the plurality of target sequences comprises one or more targets selected from

Table 8, Table 9 or SEQ ID NOs: 1-1029; and a computer model or algorithm for analyzing an expression level and/or expression profile of the target hybridized to the probe in a sample from a subject suffering from prostate cancer. In some embodiments, the method further comprises a label that specifically binds to the target, the probe, or a combination thereof.

[0016] In some embodiments, the present invention provides a method comprising: (a) providing a biological sample from a subject with prostate cancer; (b) detecting the presence or expression level in the biological sample for a plurality of targets, wherein the plurality of targets comprises one or more targets selected from Table 8, Table 9 or SEQ ID NOs: 1-1029; (c) subtyping the prostate cancer in the subject based on the presence or expression levels of the plurality of targets; and (d) administering a treatment to the subject, wherein the treatment is selected from the group consisting of surgery, chemotherapy, radiation therapy, immunotherapy/biological therapy, hormonal therapy, and photodynamic therapy. In some embodiments, the present invention provides a method of treating a subject with prostate cancer, comprising: providing a biological sample comprising prostate cancer cells from the subject; determining the level of expression or amplification of at least one or more targets selected from Table 8, Table 9 or SEQ ID NOs: 1-1029 using at least one reagent that specifically binds to said targets; subtyping the prostate cancer based on the level of expression or amplification of the at least one or more targets; and prescribing a treatment regimen based on the prostate cancer subtype. In some embodiments, the prostate cancer subtype is selected from the group consisting of luminal A, luminal B, and basal.

[0017] In some embodiments, the present invention provides a kit for analyzing a prostate cancer, comprising, a probe set comprising a plurality of target sequences, wherein the plurality of target sequences comprises at least one target sequence listed in Table 8, Table 9 or SEQ ID NOs: 1-1029; and a computer model or algorithm for analyzing an expression level and/or expression profile of the target sequences in a sample. In some embodiments, the method further comprises a computer model or algorithm for correlating the expression level or expression profile with disease state or outcome. In other embodiments, the method further comprises a computer model or algorithm for designating a treatment modality for the individual. In yet other embodiments, the method further comprises a computer model or algorithm for normalizing expression level or expression profile of the target sequences. In some embodiments, the method further comprises sequencing the plurality of targets. In some embodiments, the method further comprises hybridizing the plurality of targets to a solid support. In some embodiments, the solid support is a bead or array. In some embodiments, assaying the expression level of a plurality of targets may comprise the use of a probe set. In some embodiments, assaying the expression level may comprise the use of a classifier. The

classifier may comprise a probe selection region (PSR). In some embodiments, the classifier may comprise the use of an algorithm. The algorithm may comprise a machine learning algorithm. In some embodiments, assaying the expression level may also comprise sequencing the plurality of targets.

[0018] Further disclosed herein methods for molecular subtyping of prostate cancer, wherein the subtypes have an AUC value of at least about 0.40 to predict patient outcomes. In some embodiments, patient outcomes are selected from the group consisting of biochemical recurrence (BCR), metastasis (MET) and prostate cancer death (PCSM) after radical prostatectomy. The AUC of the subtype may be at least about 0.40, 0.45, 0.50, 0.55, 0.60, 0.61, 0.62, 0.63, 0.64, 0.65, 0.66, 0.67, 0.68, 0.69, 0.70 or more.

[0019] Further disclosed herein is a method for subtyping a prostate cancer, comprising determining the level of expression or amplification of at least one or more targets of the present invention, wherein the significance of the expression level of the one or more targets is based on one or more metrics selected from the group comprising T-test, P-value, KS (Kolmogorov Smirnov) P-value, accuracy, accuracy P-value, positive predictive value (PPV), negative predictive value (NPV), sensitivity, specificity, AUC, AUC P-value (Auc.pvalue), Wilcoxon Test P-value, Median Fold Difference (MFD), Kaplan Meier (KM) curves, survival AUC (survAUC), Kaplan Meier P-value (KM P-value), Univariable Analysis Odds Ratio P-value (uvaORPval), multivariable analysis Odds Ratio P-value (mvaORPval), Univariable Analysis Hazard Ratio P-value (uvaHRPval) and Multivariable Analysis Hazard Ratio P-value (mvaHRPval). The significance of the expression level of the one or more targets may be based on two or more metrics selected from the group comprising AUC, AUC P-value (Auc.pvalue), Wilcoxon Test P-value, Median Fold Difference (MFD), Kaplan Meier (KM) curves, survival AUC (survAUC), Univariable Analysis Odds Ratio P-value (uvaORPval), multivariable analysis Odds Ratio P-value (mvaORPval), Kaplan Meier P-value (KM P-value), Univariable Analysis Hazard Ratio P-value (uvaHRPval) and Multivariable Analysis Hazard Ratio P-value (mvaHRPval). The molecular subtypes of the present invention are useful for predicting clinical characteristics of subjects with prostate cancer. In some embodiments, the clinical characteristics are selected from the group consisting of seminal vesical invasion (SVI), lymph node invasion (LNI), prostate-specific antigen (PSA), and gleason score (GS).

INCORPORATION BY REFERENCE

[0020] All publications, patents, and patent applications mentioned in this specification are herein incorporated by reference in their entireties to the same extent as if each individual

publication, patent, or patent application was specifically and individually indicated to be incorporated by reference.

BRIEF DESCRIPTION OF THE DRAWINGS

[0021] Figures 1A-1B set forth data showing PAM50 clustering and clinical outcomes in prostate cancer. (A) The PAM50 genes cluster prostate cancer samples into three subtypes, luminal A (dark blue), luminal B (light blue) and basal (red), in the pooled prostate cancer cohorts (MCI, II, CC, TJU, JHU, DVA) using hierarchical clustering of the genes. Each column represents a patient sample and each row represents a gene. (B) Kaplan-Meier curves showing that the PAM50 clusters risk stratify bRFS (biochemical recurrence-free survival), DMFS (distant metastasis-free survival), PCSS (prostate cancer specific survival), and OS (overall survival).

[0022] Figures 2A-2C set forth data showing basal and luminal subtypes are associated with basal and luminal lineage markers.

[0023] Figures 3A-3D set forth data showing Prospective validation in GRID. PAM50 clusters in a prospective validation cohort of 2215 prostate cancer samples run on a commercial clinical platform (A). AR expression increases in luminal samples (B), the basal lineage CD49f signature in the basal subtype (C), and NKX3-1 and KRT18 expression in the luminal subtypes (D). Bar-plots show the mean with standard error of median centered gene expression, and P-values are from ANOVA.

[0024] Figures 4A-4C set forth data showing predicted response in ADT. A matched cohort was obtained from the MCI and MCII cohorts which matched 1:2 ADT treated and untreated patients based on Gleason, PSA, LNI, ECE, SVI, and SMS resulting in 315 total patients (A). Kaplan-Meier curves are shown for the luminal B and non-luminal B patients, which group the luminal A and basal patients (B). A bar plot (C) is shown comparing the 10-year metastasis rates for treated and untreated patients in the luminal B and non-luminal B patients, with the interaction term Wald $p=0.006$.

[0025] Figure 5 sets forth data showing Heatmaps depicting the PAM50 subtypes (each column represents a sample, each row represents a gene, dark blue = Luminal A, light blue = Luminal B, red = Basal) with genes in the same order as shown in Figure 1A.

[0026] Figure 6 sets forth data showing differences in genetic signatures for breast and prostate cancer for the markers of a genomic classifier of the present invention. A heatmap of the PAM50 clusters in the breast cohort from Parker et al. are shown for basal, luminal A, and luminal B. Boxplots demonstrate that in breast cancer, ER is higher in luminal versus basal, and that PR is highest in luminal A. A heatmap of the PAM50 clusters in prostate cancer is shown (MCI, II, CC, TJU, JHU, DVA) with the same order of genes as displayed

for the breast cancer data. Boxplots show that ER does not demonstrate the same differences between luminal and basal as in breast, but PR does show lower expression in luminal B compared to luminal A as in breast cancer.

[0027] Figure 7 sets forth data showing luminal subtypes are associated with MYC and KRAS.

[0028] Figure 8 sets forth data showing PAM50 proliferation score across subtypes. Box plots of the PAM50 proliferation score across the basal, luminal A and luminal B subtypes within the retrospective and prospective cohorts. ANOVA p-value < 0.001 for both cohorts.

[0029] Figure 9 sets forth data showing survival outcomes for the matched cohort, separating patients receiving adjuvant and salvage ADT. Kaplan-Meier curves are shown to visualize effect of adjuvant and salvage ADT separately within the Luminal B and non-Luminal B patients. Patients receiving adjuvant ADT and their matched no ADT samples. Patients receiving salvage ADT and their matched no ADT samples.

[0030] Figure 10 sets forth data showing Decipher and mCCP are not predictive for response to post-operative ADT in a matched cohort.

DETAILED DESCRIPTION OF THE INVENTION

[0031] The present invention discloses systems and methods for diagnosing, predicting, and/or monitoring the status or outcome of a prostate cancer in a subject using expression-based analysis of a plurality of targets. Generally, the method comprises (a) optionally providing a sample from a subject; (b) assaying the expression level for a plurality of targets in the sample; and (c) diagnosing, predicting and/or monitoring the status or outcome of a prostate cancer based on the expression level of the plurality of targets.

[0032] Assaying the expression level for a plurality of targets in the sample may comprise applying the sample to a microarray. In some instances, assaying the expression level may comprise the use of an algorithm. The algorithm may be used to produce a classifier. Alternatively, the classifier may comprise a probe selection region. In some instances, assaying the expression level for a plurality of targets comprises detecting and/or quantifying the plurality of targets. In some embodiments, assaying the expression level for a plurality of targets comprises sequencing the plurality of targets. In some embodiments, assaying the expression level for a plurality of targets comprises amplifying the plurality of targets. In some embodiments, assaying the expression level for a plurality of targets comprises quantifying the plurality of targets. In some embodiments, assaying the expression level for a plurality of targets comprises conducting a multiplexed reaction on the plurality of targets.

[0033] In some instances, the plurality of targets comprises one or more targets selected from Table 8, Table 9 or SEQ ID NOs: 1-1029. In some instances, the plurality of targets

comprises at least about 2, at least about 3, at least about 4, at least about 5, at least about 6, at least about 7, at least about 8, at least about 9, at least about 10, at least about 20, at least about 30, at least about 40, or at least about 50 targets selected from Table 8, Table 9 or SEQ ID NOs: 1-1029.

[0034] Further disclosed herein are methods for subtyping prostate cancer. Generally, the method comprises: (a) providing a sample comprising prostate cancer cells from a subject; (b) assaying the expression level for a plurality of targets in the sample; and (c) subtyping the cancer based on the expression level of the plurality of targets. In some instances, the plurality of targets comprises one or more targets selected from Table 8, Table 9 or SEQ ID NOs: 1-1029. In some instances, the plurality of targets comprises at least about 2, at least about 3, at least about 4, at least about 5, at least about 6, at least about 7, at least about 8, at least about 9, at least about 10, at least about 20, at least about 30, at least about 40, or at least about 50 targets selected from Table 8, Table 9 or SEQ ID NOs: 1-1029.

[0035] In some instances, subtyping the prostate cancer comprises determining whether the cancer would respond to an anti-cancer therapy. Alternatively, subtyping the prostate cancer comprises identifying the cancer as non-responsive to an anti-cancer therapy. Optionally, subtyping the prostate cancer comprises identifying the cancer as responsive to an anti-cancer therapy.

[0036] Before the present invention is described in further detail, it is to be understood that this invention is not limited to the particular methodology, compositions, articles or machines described, as such methods, compositions, articles or machines can, of course, vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the present invention.

Targets

[0037] The methods disclosed herein often comprise assaying the expression level of a plurality of targets. The plurality of targets may comprise coding targets and/or non-coding targets of a protein-coding gene or a non protein-coding gene. A protein-coding gene structure may comprise an exon and an intron. The exon may further comprise a coding sequence (CDS) and an untranslated region (UTR). The protein-coding gene may be transcribed to produce a pre-mRNA and the pre-mRNA may be processed to produce a mature mRNA. The mature mRNA may be translated to produce a protein.

[0038] A non protein-coding gene structure may comprise an exon and intron. Usually, the exon region of a non protein-coding gene primarily contains a UTR. The non protein-coding gene may be transcribed to produce a pre-mRNA and the pre-mRNA may be processed to produce a non-coding RNA (ncRNA).

[0039] A coding target may comprise a coding sequence of an exon. A non-coding target may comprise a UTR sequence of an exon, intron sequence, intergenic sequence, promoter sequence, non-coding transcript, CDS antisense, intronic antisense, UTR antisense, or non-coding transcript antisense. A non-coding transcript may comprise a non-coding RNA (ncRNA).

[0040] In some instances, the plurality of targets may be differentially expressed. In some instances, a plurality of probe selection regions (PSRs) is differentially expressed.

[0041] In some instances, the plurality of targets comprises one or more targets selected from at least about 10, at least about 20, at least about 30, at least about 40, or at least about 50 targets selected from Table 8, Table 9 or SEQ ID NOs: 1-1029. In some instances, the plurality of targets comprises at least about 2, at least about 3, at least about 4, at least about 5, at least about 6, at least about 7, at least about 8, at least about 9, at least about 10, at least about 20, at least about 30, at least about 40, or at least about 50 targets selected from Table 8, Table 9 or SEQ ID NOs: 1-1029.

[0042] In some instances, the plurality of targets comprises a coding target, non-coding target, or any combination thereof. In some instances, the coding target comprises an exonic sequence. In other instances, the non-coding target comprises a non-exonic or exonic sequence. Alternatively, a non-coding target comprises a UTR sequence, an intronic sequence, antisense, or a non-coding RNA transcript. In some instances, a non-coding target comprises sequences which partially overlap with a UTR sequence or an intronic sequence. A non-coding target also includes non-exonic and/or exonic transcripts. Exonic sequences may comprise regions on a protein-coding gene, such as an exon, UTR, or a portion thereof. Non-exonic sequences may comprise regions on a protein-coding, non protein-coding gene, or a portion thereof. For example, non-exonic sequences may comprise intronic regions, promoter regions, intergenic regions, a non-coding transcript, an exon anti-sense region, an intronic anti-sense region, UTR anti-sense region, non-coding transcript anti-sense region, or a portion thereof. In other instances, the plurality of targets comprises a non-coding RNA transcript.

[0043] The plurality of targets may comprise one or more targets selected from a classifier disclosed herein. The classifier may be generated from one or more models or algorithms. The one or more models or algorithms may be Naïve Bayes (NB), recursive Partitioning (Rpart), random forest (RF), support vector machine (SVM), k-nearest neighbor (KNN), high dimensional discriminate analysis (HDDA), or a combination thereof. The classifier may have an AUC of equal to or greater than 0.60. The classifier may have an AUC of equal to or greater than 0.61. The classifier may have an AUC of equal to or greater than 0.62. The

classifier may have an AUC of equal to or greater than 0.63. The classifier may have an AUC of equal to or greater than 0.64. The classifier may have an AUC of equal to or greater than 0.65. The classifier may have an AUC of equal to or greater than 0.66. The classifier may have an AUC of equal to or greater than 0.67. The classifier may have an AUC of equal to or greater than 0.68. The classifier may have an AUC of equal to or greater than 0.69. The classifier may have an AUC of equal to or greater than 0.70. The classifier may have an AUC of equal to or greater than 0.75. The classifier may have an AUC of equal to or greater than 0.77. The classifier may have an AUC of equal to or greater than 0.78. The classifier may have an AUC of equal to or greater than 0.79. The classifier may have an AUC of equal to or greater than 0.80. The AUC may be clinically significant based on its 95% confidence interval (CI). The accuracy of the classifier may be at least about 70%. The accuracy of the classifier may be at least about 73%. The accuracy of the classifier may be at least about 75%. The accuracy of the classifier may be at least about 77%. The accuracy of the classifier may be at least about 80%. The accuracy of the classifier may be at least about 83%. The accuracy of the classifier may be at least about 84%. The accuracy of the classifier may be at least about 86%. The accuracy of the classifier may be at least about 88%. The accuracy of the classifier may be at least about 90%. The p-value of the classifier may be less than or equal to 0.05. The p-value of the classifier may be less than or equal to 0.04. The p-value of the classifier may be less than or equal to 0.03. The p-value of the classifier may be less than or equal to 0.02. The p-value of the classifier may be less than or equal to 0.01. The p-value of the classifier may be less than or equal to 0.008. The p-value of the classifier may be less than or equal to 0.006. The p-value of the classifier may be less than or equal to 0.004. The p-value of the classifier may be less than or equal to 0.002. The p-value of the classifier may be less than or equal to 0.001.

[0044] The plurality of targets may comprise one or more targets selected from a Random Forest (RF) classifier. The plurality of targets may comprise two or more targets selected from a Random Forest (RF) classifier. The plurality of targets may comprise three or more targets selected from a Random Forest (RF) classifier. The plurality of targets may comprise 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 25, 30, 40, 50 or more targets selected from a Random Forest (RF) classifier. The RF classifier may be an RF2, and RF3, or an RF4 classifier. The RF classifier may be an RF50 classifier (e.g., a Random Forest classifier with 50 targets).

[0045] A RF classifier of the present invention may comprise two or more targets comprising two or more targets selected from Table 8, Table 9 or SEQ ID NOs: 1-1029.

[0046] The plurality of targets may comprise one or more targets selected from an SVM classifier. The plurality of targets may comprise 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 25, 30, 40, 50 or more targets selected from an SVM classifier. The plurality of targets may comprise 12, 13, 14, 15, 17, 20, 22, 25, 27, 30, 40, 50 or more targets selected from an SVM classifier. The plurality of targets may comprise 32, 35, 37, 40, 43, 45, 47, 50 or more targets selected from an SVM classifier. The SVM classifier may be an SVM2 classifier.

[0047] A SVM classifier of the present invention may comprise two or more targets comprising two or more targets selected from Table 8, Table 9 or SEQ ID NOs: 1-1029.

[0048] The plurality of targets may comprise one or more targets selected from a KNN classifier. The plurality of targets may comprise 2, 3, 4, 5, 6, 7, 8, 9, 10 or more targets selected from a KNN classifier. The plurality of targets may comprise 12, 13, 14, 15, 17, 20, 22, 25, 27, 30 or more targets selected from a KNN classifier. The plurality of targets may comprise 32, 35, 37, 40, 43, 45, 47, 50 or more targets selected from a KNN classifier.

[0049] The KNN classifier may be a KNN50 classifier. A KNN classifier of the present invention may comprise fifty or more targets comprising fifty or more targets selected from Table 8, Table 9 or SEQ ID NOs: 1-1029.

[0050] The plurality of targets may comprise one or more targets selected from a Naïve Bayes (NB) classifier. The plurality of targets may comprise 2, 3, 4, 5, 6, 7, 8, 9, 10 or more targets selected from an NB classifier. The plurality of targets may comprise 12, 13, 14, 15, 17, 20, 22, 25, 27, 30 or more targets selected from an NB classifier. The plurality of targets may comprise 32, 35, 37, 40, 43, 45, 47, 50 or more targets selected from a NB classifier.

[0051] The NB classifier may be a NB2 classifier. An NB classifier of the present invention may comprise two or more targets comprising two or more targets selected from Table 8, Table 9 or SEQ ID NOs: 1-1029.

[0052] The plurality of targets may comprise one or more targets selected from a recursive Partitioning (Rpart) classifier. The plurality of targets may comprise 2, 3, 4, 5, 6, 7, 8, 9, 10 or more targets selected from an Rpart classifier. The plurality of targets may comprise 12, 13, 14, 15, 17, 20, 22, 25, 27, 30 or more targets selected from an Rpart classifier. The plurality of targets may comprise 32, 35, 37, 40, 43, 45, 47, 50 or more targets selected from an Rpart classifier.

[0053] The Rpart classifier may be an Rpart2 classifier. An Rpart classifier of the present invention may comprise two or more targets comprising two or more targets selected from Table 8, Table 9 or SEQ ID NOs: 1-1029.

[0054] The plurality of targets may comprise one or more targets selected from a high dimensional discriminate analysis (HDDA) classifier. The plurality of targets may comprise

two or more targets selected from a high dimensional discriminate analysis (HDDA) classifier. The plurality of targets may comprise three or more targets selected from a high dimensional discriminate analysis (HDDA) classifier. The plurality of targets may comprise 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 30, 40, 50 or more targets selected from a high dimensional discriminate analysis (HDDA) classifier.

[0055] The plurality of targets may comprise one or more targets selected from CDC20, KIF2C, PHGDH, NUF2, CENPF, EXO1, UBE2T, RRM2, MLPH, GPR160, CCNB1, CXXC5, PTTG1, FGFR4, FOXC1, ESR1, ANLN, BLVRA, EGFR, ACTR3B, NAT1, MYC, SFRP1, MELK, BAG1, CEP55, MKI67, TMEM45B, PGR, MDM2, KRT5, FOXA1, ORC6, CDH3, ERBB2, GRB7, CDC6, MAPT, BIRC5, KRT14, KRT17, TYMS, NDC80, SLC39A6, BCL2, CCNE1, MIA, MYBL2, UBE2C, and MMP11; CDC20; CDC20 and KIF2C; CDC20 and PHGDH; CDC20 and NUF2; CDC20 and CENPF; CDC20 and EXO1; CDC20 and UBE2T; CDC20 and RRM2; CDC20 and MLPH; CDC20 and GPR160; CDC20 and CCNB1; CDC20 and CXXC5; CDC20 and PTTG1; CDC20 and FGFR4; CDC20 and FOXC1; CDC20 and ESR1; CDC20 and ANLN; CDC20 and BLVRA; CDC20 and EGFR; CDC20 and ACTR3B; CDC20 and NAT1; CDC20 and MYC; CDC20 and SFRP1; CDC20 and MELK; CDC20 and BAG1; CDC20 and CEP55; CDC20 and MKI67; CDC20 and TMEM45B; CDC20 and PGR; CDC20 and MDM2; CDC20 and KRT5; CDC20 and FOXA1; CDC20 and ORC6; CDC20 and CDH3; CDC20 and ERBB2; CDC20 and GRB7; CDC20 and CDC6; CDC20 and MAPT; CDC20 and BIRC5; CDC20 and KRT14; CDC20 and KRT17; CDC20 and TYMS; CDC20 and NDC80; CDC20 and SLC39A6; CDC20 and BCL2; CDC20 and CCNE1; CDC20 and MIA; CDC20 and MYBL2; CDC20 and UBE2C; CDC20 and MMP11; CDC20, KIF2C and PHGDH; CDC20, KIF2C and NUF2; CDC20, KIF2C and CENPF; CDC20, KIF2C and EXO1; CDC20, KIF2C and UBE2T; CDC20, KIF2C and RRM2; CDC20, KIF2C and MLPH; CDC20, KIF2C and GPR160; CDC20, KIF2C and CCNB1; CDC20, KIF2C and CXXC5; CDC20, KIF2C and PTTG1; CDC20, KIF2C and FGFR4; CDC20, KIF2C and FOXC1; CDC20, KIF2C and ESR1; CDC20, KIF2C and ANLN; CDC20, KIF2C and BLVRA; CDC20, KIF2C and EGFR; CDC20, KIF2C and ACTR3B; CDC20, KIF2C and NAT1; CDC20, KIF2C and MYC; CDC20, KIF2C and SFRP1; CDC20, KIF2C and MELK; CDC20, KIF2C and BAG1; CDC20, KIF2C and CEP55; CDC20, KIF2C and MKI67; CDC20, KIF2C and TMEM45B; CDC20, KIF2C and PGR; CDC20, KIF2C and MDM2; CDC20, KIF2C and KRT5; CDC20, KIF2C and FOXA1; CDC20, KIF2C and ORC6; CDC20, KIF2C and CDH3; CDC20, KIF2C and ERBB2; CDC20, KIF2C and GRB7; CDC20, KIF2C and CDC6; CDC20, KIF2C and MAPT; CDC20, KIF2C and BIRC5; CDC20, KIF2C and KRT14; CDC20, KIF2C and KRT17; CDC20, KIF2C and TYMS; CDC20, KIF2C and NDC80; CDC20, KIF2C and SLC39A6; CDC20, KIF2C and BCL2; CDC20, KIF2C and CCNE1; CDC20, KIF2C and MIA; CDC20, KIF2C and MYBL2; CDC20, KIF2C and UBE2C; CDC20, KIF2C and MMP11; CDC20, KIF2C, PHGDH and NUF2; CDC20, KIF2C, PHGDH and CENPF; CDC20, KIF2C, PHGDH and EXO1; CDC20, KIF2C, PHGDH and UBE2T; CDC20, KIF2C, PHGDH and

RRM2; CDC20, KIF2C, PHGDH and MLPH; CDC20, KIF2C, PHGDH and GPR160; CDC20, KIF2C, PHGDH and CCNB1; CDC20, KIF2C, PHGDH and CXXC5; CDC20, KIF2C, PHGDH and PTTG1; CDC20, KIF2C, PHGDH and FGFR4; CDC20, KIF2C, PHGDH and FOXC1; CDC20, KIF2C, PHGDH and ESR1; CDC20, KIF2C, PHGDH and ANLN; CDC20, KIF2C, PHGDH and BLVRA; CDC20, KIF2C, PHGDH and EGFR; CDC20, KIF2C, PHGDH and ACTR3B; CDC20, KIF2C, PHGDH and NAT1; CDC20, KIF2C, PHGDH and MYC; CDC20, KIF2C, PHGDH and SFRP1; CDC20, KIF2C, PHGDH and MELK; CDC20, KIF2C, PHGDH and BAG1; CDC20, KIF2C, PHGDH and CEP55; CDC20, KIF2C, PHGDH and MKI67; CDC20, KIF2C, PHGDH and TMEM45B; CDC20, KIF2C, PHGDH and PGR; CDC20, KIF2C, PHGDH and MDM2; CDC20, KIF2C, PHGDH and KRT5; CDC20, KIF2C, PHGDH and FOXA1; CDC20, KIF2C, PHGDH and ORC6; CDC20, KIF2C, PHGDH and CDH3; CDC20, KIF2C, PHGDH and ERBB2; CDC20, KIF2C, PHGDH and GRB7; CDC20, KIF2C, PHGDH and CDC6; CDC20, KIF2C, PHGDH and MAPT; CDC20, KIF2C, PHGDH and BIRC5; CDC20, KIF2C, PHGDH and KRT14; CDC20, KIF2C, PHGDH and KRT17; CDC20, KIF2C, PHGDH and TYMS; CDC20, KIF2C, PHGDH and NDC80; CDC20, KIF2C, PHGDH and SLC39A6; CDC20, KIF2C, PHGDH and BCL2; CDC20, KIF2C, PHGDH and CCNE1; CDC20, KIF2C, PHGDH and MIA; CDC20, KIF2C, PHGDH and MYBL2; CDC20, KIF2C, PHGDH and UBE2C; CDC20, KIF2C, PHGDH and MMP11; KIF2C; KIF2C and PHGDH; KIF2C and NUF2; KIF2C and CENPF; KIF2C and EXO1; KIF2C and UBE2T; KIF2C and RRM2; KIF2C and MLPH; KIF2C and GPR160; KIF2C and CCNB1; KIF2C and CXXC5; KIF2C and PTTG1; KIF2C and FGFR4; KIF2C and FOXC1; KIF2C and ESR1; KIF2C and ANLN; KIF2C and BLVRA; KIF2C and EGFR; KIF2C and ACTR3B; KIF2C and NAT1; KIF2C and MYC; KIF2C and SFRP1; KIF2C and MELK; KIF2C and BAG1; KIF2C and CEP55; KIF2C and MKI67; KIF2C and TMEM45B; KIF2C and PGR; KIF2C and MDM2; KIF2C and KRT5; KIF2C and FOXA1; KIF2C and ORC6; KIF2C and CDH3; KIF2C and ERBB2; KIF2C and GRB7; KIF2C and CDC6; KIF2C and MAPT; KIF2C and BIRC5; KIF2C and KRT14; KIF2C and KRT17; KIF2C and TYMS; KIF2C and NDC80; KIF2C and SLC39A6; KIF2C and BCL2; KIF2C and CCNE1; KIF2C and MIA; KIF2C and MYBL2; KIF2C and UBE2C; KIF2C and MMP11; KIF2C, PHGDH and NUF2; KIF2C, PHGDH and CENPF; KIF2C, PHGDH and EXO1; KIF2C, PHGDH and UBE2T; KIF2C, PHGDH and RRM2; KIF2C, PHGDH and MLPH; KIF2C, PHGDH and GPR160; KIF2C, PHGDH and CCNB1; KIF2C, PHGDH and CXXC5; KIF2C, PHGDH and PTTG1; KIF2C, PHGDH and FGFR4; KIF2C, PHGDH and FOXC1; KIF2C, PHGDH and ESR1; KIF2C, PHGDH and ANLN; KIF2C, PHGDH and BLVRA; KIF2C, PHGDH and EGFR; KIF2C, PHGDH and ACTR3B; KIF2C, PHGDH and NAT1; KIF2C, PHGDH and MYC; KIF2C, PHGDH and SFRP1; KIF2C, PHGDH and MELK; KIF2C, PHGDH and BAG1; KIF2C, PHGDH and CEP55; KIF2C, PHGDH and MKI67; KIF2C, PHGDH and TMEM45B; KIF2C, PHGDH and PGR; KIF2C, PHGDH and MDM2; KIF2C, PHGDH and KRT5; KIF2C, PHGDH and FOXA1; KIF2C, PHGDH and ORC6; KIF2C, PHGDH and CDH3; KIF2C, PHGDH and ERBB2; KIF2C, PHGDH and GRB7; KIF2C, PHGDH and CDC6; KIF2C, PHGDH and MAPT; KIF2C, PHGDH and BIRC5; KIF2C, PHGDH and KRT14; KIF2C, PHGDH

and KRT17; KIF2C, PHGDH and TYMS; KIF2C, PHGDH and NDC80; KIF2C, PHGDH and SLC39A6; KIF2C, PHGDH and BCL2; KIF2C, PHGDH and CCNE1; KIF2C, PHGDH and MIA; KIF2C, PHGDH and MYBL2; KIF2C, PHGDH and UBE2C; KIF2C, PHGDH and MMP11; KIF2C, PHGDH, NUF2 and CENPF; KIF2C, PHGDH, NUF2 and EXO1; KIF2C, PHGDH, NUF2 and UBE2T; KIF2C, PHGDH, NUF2 and RRM2; KIF2C, PHGDH, NUF2 and MLPH; KIF2C, PHGDH, NUF2 and GPR160; KIF2C, PHGDH, NUF2 and CCNB1; KIF2C, PHGDH, NUF2 and CXXC5; KIF2C, PHGDH, NUF2 and PTTG1; KIF2C, PHGDH, NUF2 and FGFR4; KIF2C, PHGDH, NUF2 and FOXC1; KIF2C, PHGDH, NUF2 and ESR1; KIF2C, PHGDH, NUF2 and ANLN; KIF2C, PHGDH, NUF2 and BLVRA; KIF2C, PHGDH, NUF2 and EGFR; KIF2C, PHGDH, NUF2 and ACTR3B; KIF2C, PHGDH, NUF2 and NAT1; KIF2C, PHGDH, NUF2 and MYC; KIF2C, PHGDH, NUF2 and SFRP1; KIF2C, PHGDH, NUF2 and MELK; KIF2C, PHGDH, NUF2 and BAG1; KIF2C, PHGDH, NUF2 and CEP55; KIF2C, PHGDH, NUF2 and MKI67; KIF2C, PHGDH, NUF2 and TMEM45B; KIF2C, PHGDH, NUF2 and PGR; KIF2C, PHGDH, NUF2 and MDM2; KIF2C, PHGDH, NUF2 and KRT5; KIF2C, PHGDH, NUF2 and FOXA1; KIF2C, PHGDH, NUF2 and ORC6; KIF2C, PHGDH, NUF2 and CDH3; KIF2C, PHGDH, NUF2 and ERBB2; KIF2C, PHGDH, NUF2 and GRB7; KIF2C, PHGDH, NUF2 and CDC6; KIF2C, PHGDH, NUF2 and MAPT; KIF2C, PHGDH, NUF2 and BIRC5; KIF2C, PHGDH, NUF2 and KRT14; KIF2C, PHGDH, NUF2 and KRT17; KIF2C, PHGDH, NUF2 and TYMS; KIF2C, PHGDH, NUF2 and NDC80; KIF2C, PHGDH, NUF2 and SLC39A6; KIF2C, PHGDH, NUF2 and BCL2; KIF2C, PHGDH, NUF2 and CCNE1; KIF2C, PHGDH, NUF2 and MIA; KIF2C, PHGDH, NUF2 and MYBL2; KIF2C, PHGDH, NUF2 and UBE2C; KIF2C, PHGDH, NUF2 and MMP11; PHGDH; PHGDH and NUF2; PHGDH and CENPF; PHGDH and EXO1; PHGDH and UBE2T; PHGDH and RRM2; PHGDH and MLPH; PHGDH and GPR160; PHGDH and CCNB1; PHGDH and CXXC5; PHGDH and PTTG1; PHGDH and FGFR4; PHGDH and FOXC1; PHGDH and ESR1; PHGDH and ANLN; PHGDH and BLVRA; PHGDH and EGFR; PHGDH and ACTR3B; PHGDH and NAT1; PHGDH and MYC; PHGDH and SFRP1; PHGDH and MELK; PHGDH and BAG1; PHGDH and CEP55; PHGDH and MKI67; PHGDH and TMEM45B; PHGDH and PGR; PHGDH and MDM2; PHGDH and KRT5; PHGDH and FOXA1; PHGDH and ORC6; PHGDH and CDH3; PHGDH and ERBB2; PHGDH and GRB7; PHGDH and CDC6; PHGDH and MAPT; PHGDH and BIRC5; PHGDH and KRT14; PHGDH and KRT17; PHGDH and TYMS; PHGDH and NDC80; PHGDH and SLC39A6; PHGDH and BCL2; PHGDH and CCNE1; PHGDH and MIA; PHGDH and MYBL2; PHGDH and UBE2C; PHGDH and MMP11; PHGDH, NUF2 and CENPF; PHGDH, NUF2 and EXO1; PHGDH, NUF2 and UBE2T; PHGDH, NUF2 and RRM2; PHGDH, NUF2 and MLPH; PHGDH, NUF2 and GPR160; PHGDH, NUF2 and CCNB1; PHGDH, NUF2 and CXXC5; PHGDH, NUF2 and PTTG1; PHGDH, NUF2 and FGFR4; PHGDH, NUF2 and FOXC1; PHGDH, NUF2 and ESR1; PHGDH, NUF2 and ANLN; PHGDH, NUF2 and BLVRA; PHGDH, NUF2 and EGFR; PHGDH, NUF2 and ACTR3B; PHGDH, NUF2 and NAT1; PHGDH, NUF2 and MYC; PHGDH, NUF2 and SFRP1; PHGDH, NUF2 and MELK; PHGDH, NUF2 and BAG1; PHGDH, NUF2 and CEP55; PHGDH, NUF2 and MKI67;

PHGDH, NUF2 and TMEM45B; PHGDH, NUF2 and PGR; PHGDH, NUF2 and MDM2; PHGDH, NUF2 and KRT5; PHGDH, NUF2 and FOXA1; PHGDH, NUF2 and ORC6; PHGDH, NUF2 and CDH3; PHGDH, NUF2 and ERBB2; PHGDH, NUF2 and GRB7; PHGDH, NUF2 and CDC6; PHGDH, NUF2 and MAPT; PHGDH, NUF2 and BIRC5; PHGDH, NUF2 and KRT14; PHGDH, NUF2 and KRT17; PHGDH, NUF2 and TYMS; PHGDH, NUF2 and NDC80; PHGDH, NUF2 and SLC39A6; PHGDH, NUF2 and BCL2; PHGDH, NUF2 and CCNE1; PHGDH, NUF2 and MIA; PHGDH, NUF2 and MYBL2; PHGDH, NUF2 and UBE2C; PHGDH, NUF2 and MMP11; PHGDH, NUF2, CENPF and EXO1; PHGDH, NUF2, CENPF and UBE2T; PHGDH, NUF2, CENPF and RRM2; PHGDH, NUF2, CENPF and MLPH; PHGDH, NUF2, CENPF and GPR160; PHGDH, NUF2, CENPF and CCNB1; PHGDH, NUF2, CENPF and CXXC5; PHGDH, NUF2, CENPF and PTTG1; PHGDH, NUF2, CENPF and FGFR4; PHGDH, NUF2, CENPF and FOXC1; PHGDH, NUF2, CENPF and ESR1; PHGDH, NUF2, CENPF and ANLN; PHGDH, NUF2, CENPF and BLVRA; PHGDH, NUF2, CENPF and EGFR; PHGDH, NUF2, CENPF and ACTR3B; PHGDH, NUF2, CENPF and NAT1; PHGDH, NUF2, CENPF and MYC; PHGDH, NUF2, CENPF and SFRP1; PHGDH, NUF2, CENPF and MELK; PHGDH, NUF2, CENPF and BAG1; PHGDH, NUF2, CENPF and CEP55; PHGDH, NUF2, CENPF and MKI67; PHGDH, NUF2, CENPF and TMEM45B; PHGDH, NUF2, CENPF and PGR; PHGDH, NUF2, CENPF and MDM2; PHGDH, NUF2, CENPF and KRT5; PHGDH, NUF2, CENPF and FOXA1; PHGDH, NUF2, CENPF and ORC6; PHGDH, NUF2, CENPF and CDH3; PHGDH, NUF2, CENPF and ERBB2; PHGDH, NUF2, CENPF and GRB7; PHGDH, NUF2, CENPF and CDC6; PHGDH, NUF2, CENPF and MAPT; PHGDH, NUF2, CENPF and BIRC5; PHGDH, NUF2, CENPF and KRT14; PHGDH, NUF2, CENPF and KRT17; PHGDH, NUF2, CENPF and TYMS; PHGDH, NUF2, CENPF and NDC80; PHGDH, NUF2, CENPF and SLC39A6; PHGDH, NUF2, CENPF and BCL2; PHGDH, NUF2, CENPF and CCNE1; PHGDH, NUF2, CENPF and MIA; PHGDH, NUF2, CENPF and MYBL2; PHGDH, NUF2, CENPF and UBE2C; PHGDH, NUF2, CENPF and MMP11; NUF2; NUF2 and CENPF; NUF2 and EXO1; NUF2 and UBE2T; NUF2 and RRM2; NUF2 and MLPH; NUF2 and GPR160; NUF2 and CCNB1; NUF2 and CXXC5; NUF2 and PTTG1; NUF2 and FGFR4; NUF2 and FOXC1; NUF2 and ESR1; NUF2 and ANLN; NUF2 and BLVRA; NUF2 and EGFR; NUF2 and ACTR3B; NUF2 and NAT1; NUF2 and MYC; NUF2 and SFRP1; NUF2 and MELK; NUF2 and BAG1; NUF2 and CEP55; NUF2 and MKI67; NUF2 and TMEM45B; NUF2 and PGR; NUF2 and MDM2; NUF2 and KRT5; NUF2 and FOXA1; NUF2 and ORC6; NUF2 and CDH3; NUF2 and ERBB2; NUF2 and GRB7; NUF2 and CDC6; NUF2 and MAPT; NUF2 and BIRC5; NUF2 and KRT14; NUF2 and KRT17; NUF2 and TYMS; NUF2 and NDC80; NUF2 and SLC39A6; NUF2 and BCL2; NUF2 and CCNE1; NUF2 and MIA; NUF2 and MYBL2; NUF2 and UBE2C; NUF2 and MMP11; NUF2, CENPF and EXO1; NUF2, CENPF and UBE2T; NUF2, CENPF and RRM2; NUF2, CENPF and MLPH; NUF2, CENPF and GPR160; NUF2, CENPF and CCNB1; NUF2, CENPF and CXXC5; NUF2, CENPF and PTTG1; NUF2, CENPF and FGFR4; NUF2, CENPF and FOXC1; NUF2, CENPF and ESR1; NUF2, CENPF and ANLN; NUF2, CENPF and BLVRA; NUF2, CENPF and EGFR; NUF2, CENPF and ACTR3B;

NUF2, CENPF and NAT1; NUF2, CENPF and MYC; NUF2, CENPF and SFRP1; NUF2, CENPF and MELK; NUF2, CENPF and BAG1; NUF2, CENPF and CEP55; NUF2, CENPF and MKI67; NUF2, CENPF and TMEM45B; NUF2, CENPF and PGR; NUF2, CENPF and MDM2; NUF2, CENPF and KRT5; NUF2, CENPF and FOXA1; NUF2, CENPF and ORC6; NUF2, CENPF and CDH3; NUF2, CENPF and ERBB2; NUF2, CENPF and GRB7; NUF2, CENPF and CDC6; NUF2, CENPF and MAPT; NUF2, CENPF and BIRC5; NUF2, CENPF and KRT14; NUF2, CENPF and KRT17; NUF2, CENPF and TYMS; NUF2, CENPF and NDC80; NUF2, CENPF and SLC39A6; NUF2, CENPF and BCL2; NUF2, CENPF and CCNE1; NUF2, CENPF and MIA; NUF2, CENPF and MYBL2; NUF2, CENPF and UBE2C; NUF2, CENPF and MMP11; NUF2, CENPF, EXO1 and UBE2T; NUF2, CENPF, EXO1 and RRM2; NUF2, CENPF, EXO1 and MLPH; NUF2, CENPF, EXO1 and GPR160; NUF2, CENPF, EXO1 and CCNB1; NUF2, CENPF, EXO1 and CXXC5; NUF2, CENPF, EXO1 and PTTG1; NUF2, CENPF, EXO1 and FGFR4; NUF2, CENPF, EXO1 and FOXC1; NUF2, CENPF, EXO1 and ESR1; NUF2, CENPF, EXO1 and ANLN; NUF2, CENPF, EXO1 and BLVRA; NUF2, CENPF, EXO1 and EGFR; NUF2, CENPF, EXO1 and ACTR3B; NUF2, CENPF, EXO1 and NAT1; NUF2, CENPF, EXO1 and MYC; NUF2, CENPF, EXO1 and SFRP1; NUF2, CENPF, EXO1 and MELK; NUF2, CENPF, EXO1 and BAG1; NUF2, CENPF, EXO1 and CEP55; NUF2, CENPF, EXO1 and MKI67; NUF2, CENPF, EXO1 and TMEM45B; NUF2, CENPF, EXO1 and PGR; NUF2, CENPF, EXO1 and MDM2; NUF2, CENPF, EXO1 and KRT5; NUF2, CENPF, EXO1 and FOXA1; NUF2, CENPF, EXO1 and ORC6; NUF2, CENPF, EXO1 and CDH3; NUF2, CENPF, EXO1 and ERBB2; NUF2, CENPF, EXO1 and GRB7; NUF2, CENPF, EXO1 and CDC6; NUF2, CENPF, EXO1 and MAPT; NUF2, CENPF, EXO1 and BIRC5; NUF2, CENPF, EXO1 and KRT14; NUF2, CENPF, EXO1 and KRT17; NUF2, CENPF, EXO1 and TYMS; NUF2, CENPF, EXO1 and NDC80; NUF2, CENPF, EXO1 and SLC39A6; NUF2, CENPF, EXO1 and BCL2; NUF2, CENPF, EXO1 and CCNE1; NUF2, CENPF, EXO1 and MIA; NUF2, CENPF, EXO1 and MYBL2; NUF2, CENPF, EXO1 and UBE2C; NUF2, CENPF, EXO1 and MMP11; CENPF; CENPF and EXO1; CENPF and UBE2T; CENPF and RRM2; CENPF and MLPH; CENPF and GPR160; CENPF and CCNB1; CENPF and CXXC5; CENPF and PTTG1; CENPF and FGFR4; CENPF and FOXC1; CENPF and ESR1; CENPF and ANLN; CENPF and BLVRA; CENPF and EGFR; CENPF and ACTR3B; CENPF and NAT1; CENPF and MYC; CENPF and SFRP1; CENPF and MELK; CENPF and BAG1; CENPF and CEP55; CENPF and MKI67; CENPF and TMEM45B; CENPF and PGR; CENPF and MDM2; CENPF and KRT5; CENPF and FOXA1; CENPF and ORC6; CENPF and CDH3; CENPF and ERBB2; CENPF and GRB7; CENPF and CDC6; CENPF and MAPT; CENPF and BIRC5; CENPF and KRT14; CENPF and KRT17; CENPF and TYMS; CENPF and NDC80; CENPF and SLC39A6; CENPF and BCL2; CENPF and CCNE1; CENPF and MIA; CENPF and MYBL2; CENPF and UBE2C; CENPF and MMP11; CENPF, EXO1 and UBE2T; CENPF, EXO1 and RRM2; CENPF, EXO1 and MLPH; CENPF, EXO1 and GPR160; CENPF, EXO1 and CCNB1; CENPF, EXO1 and CXXC5; CENPF, EXO1 and PTTG1; CENPF, EXO1 and FGFR4; CENPF, EXO1 and FOXC1; CENPF, EXO1 and ESR1; CENPF, EXO1 and ANLN; CENPF, EXO1 and

BLVRA; CENPF, EXO1 and EGFR; CENPF, EXO1 and ACTR3B; CENPF, EXO1 and NAT1; CENPF, EXO1 and MYC; CENPF, EXO1 and SFRP1; CENPF, EXO1 and MELK; CENPF, EXO1 and BAG1; CENPF, EXO1 and CEP55; CENPF, EXO1 and MKI67; CENPF, EXO1 and TMEM45B; CENPF, EXO1 and PGR; CENPF, EXO1 and MDM2; CENPF, EXO1 and KRT5; CENPF, EXO1 and FOXA1; CENPF, EXO1 and ORC6; CENPF, EXO1 and CDH3; CENPF, EXO1 and ERBB2; CENPF, EXO1 and GRB7; CENPF, EXO1 and CDC6; CENPF, EXO1 and MAPT; CENPF, EXO1 and BIRC5; CENPF, EXO1 and KRT14; CENPF, EXO1 and KRT17; CENPF, EXO1 and TYMS; CENPF, EXO1 and NDC80; CENPF, EXO1 and SLC39A6; CENPF, EXO1 and BCL2; CENPF, EXO1 and CCNE1; CENPF, EXO1 and MIA; CENPF, EXO1 and MYBL2; CENPF, EXO1 and UBE2C; CENPF, EXO1 and MMP11; CENPF, EXO1, UBE2T and RRM2; CENPF, EXO1, UBE2T and MLPH; CENPF, EXO1, UBE2T and GPR160; CENPF, EXO1, UBE2T and CCNB1; CENPF, EXO1, UBE2T and CXXC5; CENPF, EXO1, UBE2T and PTTG1; CENPF, EXO1, UBE2T and FGFR4; CENPF, EXO1, UBE2T and FOXC1; CENPF, EXO1, UBE2T and ESR1; CENPF, EXO1, UBE2T and ANLN; CENPF, EXO1, UBE2T and BLVRA; CENPF, EXO1, UBE2T and EGFR; CENPF, EXO1, UBE2T and ACTR3B; CENPF, EXO1, UBE2T and NAT1; CENPF, EXO1, UBE2T and MYC; CENPF, EXO1, UBE2T and SFRP1; CENPF, EXO1, UBE2T and MELK; CENPF, EXO1, UBE2T and BAG1; CENPF, EXO1, UBE2T and CEP55; CENPF, EXO1, UBE2T and MKI67; CENPF, EXO1, UBE2T and TMEM45B; CENPF, EXO1, UBE2T and PGR; CENPF, EXO1, UBE2T and MDM2; CENPF, EXO1, UBE2T and KRT5; CENPF, EXO1, UBE2T and FOXA1; CENPF, EXO1, UBE2T and ORC6; CENPF, EXO1, UBE2T and CDH3; CENPF, EXO1, UBE2T and ERBB2; CENPF, EXO1, UBE2T and GRB7; CENPF, EXO1, UBE2T and CDC6; CENPF, EXO1, UBE2T and MAPT; CENPF, EXO1, UBE2T and BIRC5; CENPF, EXO1, UBE2T and KRT14; CENPF, EXO1, UBE2T and KRT17; CENPF, EXO1, UBE2T and TYMS; CENPF, EXO1, UBE2T and NDC80; CENPF, EXO1, UBE2T and SLC39A6; CENPF, EXO1, UBE2T and BCL2; CENPF, EXO1, UBE2T and CCNE1; CENPF, EXO1, UBE2T and MIA; CENPF, EXO1, UBE2T and MYBL2; CENPF, EXO1, UBE2T and UBE2C; CENPF, EXO1, UBE2T and MMP11; EXO1; EXO1 and UBE2T; EXO1 and RRM2; EXO1 and MLPH; EXO1 and GPR160; EXO1 and CCNB1; EXO1 and CXXC5; EXO1 and PTTG1; EXO1 and FGFR4; EXO1 and FOXC1; EXO1 and ESR1; EXO1 and ANLN; EXO1 and BLVRA; EXO1 and EGFR; EXO1 and ACTR3B; EXO1 and NAT1; EXO1 and MYC; EXO1 and SFRP1; EXO1 and MELK; EXO1 and BAG1; EXO1 and CEP55; EXO1 and MKI67; EXO1 and TMEM45B; EXO1 and PGR; EXO1 and MDM2; EXO1 and KRT5; EXO1 and FOXA1; EXO1 and ORC6; EXO1 and CDH3; EXO1 and ERBB2; EXO1 and GRB7; EXO1 and CDC6; EXO1 and MAPT; EXO1 and BIRC5; EXO1 and KRT14; EXO1 and KRT17; EXO1 and TYMS; EXO1 and NDC80; EXO1 and SLC39A6; EXO1 and BCL2; EXO1 and CCNE1; EXO1 and MIA; EXO1 and MYBL2; EXO1 and UBE2C; EXO1 and MMP11; EXO1, UBE2T and RRM2; EXO1, UBE2T and MLPH; EXO1, UBE2T and GPR160; EXO1, UBE2T and CCNB1; EXO1, UBE2T and CXXC5; EXO1, UBE2T and PTTG1; EXO1, UBE2T and FGFR4; EXO1, UBE2T and FOXC1; EXO1, UBE2T and ESR1; EXO1, UBE2T and ANLN; EXO1, UBE2T and

BLVRA; EXO1, UBE2T and EGFR; EXO1, UBE2T and ACTR3B; EXO1, UBE2T and NAT1; EXO1, UBE2T and MYC; EXO1, UBE2T and SFRP1; EXO1, UBE2T and MELK; EXO1, UBE2T and BAG1; EXO1, UBE2T and CEP55; EXO1, UBE2T and MKI67; EXO1, UBE2T and TMEM45B; EXO1, UBE2T and PGR; EXO1, UBE2T and MDM2; EXO1, UBE2T and KRT5; EXO1, UBE2T and FOXA1; EXO1, UBE2T and ORC6; EXO1, UBE2T and CDH3; EXO1, UBE2T and ERBB2; EXO1, UBE2T and GRB7; EXO1, UBE2T and CDC6; EXO1, UBE2T and MAPT; EXO1, UBE2T and BIRC5; EXO1, UBE2T and KRT14; EXO1, UBE2T and KRT17; EXO1, UBE2T and TYMS; EXO1, UBE2T and NDC80; EXO1, UBE2T and SLC39A6; EXO1, UBE2T and BCL2; EXO1, UBE2T and CCNE1; EXO1, UBE2T and MIA; EXO1, UBE2T and MYBL2; EXO1, UBE2T and UBE2C; EXO1, UBE2T and MMP11; EXO1, UBE2T, RRM2 and MLPH; EXO1, UBE2T, RRM2 and GPR160; EXO1, UBE2T, RRM2 and CCNB1; EXO1, UBE2T, RRM2 and CXXC5; EXO1, UBE2T, RRM2 and PTTG1; EXO1, UBE2T, RRM2 and FGFR4; EXO1, UBE2T, RRM2 and FOXC1; EXO1, UBE2T, RRM2 and ESR1; EXO1, UBE2T, RRM2 and ANLN; EXO1, UBE2T, RRM2 and BLVRA; EXO1, UBE2T, RRM2 and EGFR; EXO1, UBE2T, RRM2 and ACTR3B; EXO1, UBE2T, RRM2 and NAT1; EXO1, UBE2T, RRM2 and MYC; EXO1, UBE2T, RRM2 and SFRP1; EXO1, UBE2T, RRM2 and MELK; EXO1, UBE2T, RRM2 and BAG1; EXO1, UBE2T, RRM2 and CEP55; EXO1, UBE2T, RRM2 and MKI67; EXO1, UBE2T, RRM2 and TMEM45B; EXO1, UBE2T, RRM2 and PGR; EXO1, UBE2T, RRM2 and MDM2; EXO1, UBE2T, RRM2 and KRT5; EXO1, UBE2T, RRM2 and FOXA1; EXO1, UBE2T, RRM2 and ORC6; EXO1, UBE2T, RRM2 and CDH3; EXO1, UBE2T, RRM2 and ERBB2; EXO1, UBE2T, RRM2 and GRB7; EXO1, UBE2T, RRM2 and CDC6; EXO1, UBE2T, RRM2 and MAPT; EXO1, UBE2T, RRM2 and BIRC5; EXO1, UBE2T, RRM2 and KRT14; EXO1, UBE2T, RRM2 and KRT17; EXO1, UBE2T, RRM2 and TYMS; EXO1, UBE2T, RRM2 and NDC80; EXO1, UBE2T, RRM2 and SLC39A6; EXO1, UBE2T, RRM2 and BCL2; EXO1, UBE2T, RRM2 and CCNE1; EXO1, UBE2T, RRM2 and MIA; EXO1, UBE2T, RRM2 and MYBL2; EXO1, UBE2T, RRM2 and UBE2C; EXO1, UBE2T, RRM2 and MMP11; UBE2T; UBE2T and RRM2; UBE2T and MLPH; UBE2T and GPR160; UBE2T and CCNB1; UBE2T and CXXC5; UBE2T and PTTG1; UBE2T and FGFR4; UBE2T and FOXC1; UBE2T and ESR1; UBE2T and ANLN; UBE2T and BLVRA; UBE2T and EGFR; UBE2T and ACTR3B; UBE2T and NAT1; UBE2T and MYC; UBE2T and SFRP1; UBE2T and MELK; UBE2T and BAG1; UBE2T and CEP55; UBE2T and MKI67; UBE2T and TMEM45B; UBE2T and PGR; UBE2T and MDM2; UBE2T and KRT5; UBE2T and FOXA1; UBE2T and ORC6; UBE2T and CDH3; UBE2T and ERBB2; UBE2T and GRB7; UBE2T and CDC6; UBE2T and MAPT; UBE2T and BIRC5; UBE2T and KRT14; UBE2T and KRT17; UBE2T and TYMS; UBE2T and NDC80; UBE2T and SLC39A6; UBE2T and BCL2; UBE2T and CCNE1; UBE2T and MIA; UBE2T and MYBL2; UBE2T and UBE2C; UBE2T and MMP11; RRM2; RRM2 and MLPH; RRM2 and GPR160; RRM2 and CCNB1; RRM2 and CXXC5; RRM2 and PTTG1; RRM2 and FGFR4; RRM2 and FOXC1; RRM2 and ESR1; RRM2 and ANLN; RRM2 and BLVRA; RRM2 and EGFR; RRM2 and ACTR3B; RRM2 and NAT1; RRM2 and MYC; RRM2 and SFRP1; RRM2 and MELK; RRM2

and BAG1; RRM2 and CEP55; RRM2 and MKI67; RRM2 and TMEM45B; RRM2 and PGR; RRM2 and MDM2; RRM2 and KRT5; RRM2 and FOXA1; RRM2 and ORC6; RRM2 and CDH3; RRM2 and ERBB2; RRM2 and GRB7; RRM2 and CDC6; RRM2 and MAPT; RRM2 and BIRC5; RRM2 and KRT14; RRM2 and KRT17; RRM2 and TYMS; RRM2 and NDC80; RRM2 and SLC39A6; RRM2 and BCL2; RRM2 and CCNE1; RRM2 and MIA; RRM2 and MYBL2; RRM2 and UBE2C; RRM2 and MMP11; MLPH; MLPH and GPR160; MLPH and CCNB1; MLPH and CXXC5; MLPH and PTTG1; MLPH and FGFR4; MLPH and FOXC1; MLPH and ESR1; MLPH and ANLN; MLPH and BLVRA; MLPH and EGFR; MLPH and ACTR3B; MLPH and NAT1; MLPH and MYC; MLPH and SFRP1; MLPH and MELK; MLPH and BAG1; MLPH and CEP55; MLPH and MKI67; MLPH and TMEM45B; MLPH and PGR; MLPH and MDM2; MLPH and KRT5; MLPH and FOXA1; MLPH and ORC6; MLPH and CDH3; MLPH and ERBB2; MLPH and GRB7; MLPH and CDC6; MLPH and MAPT; MLPH and BIRC5; MLPH and KRT14; MLPH and KRT17; MLPH and TYMS; MLPH and NDC80; MLPH and SLC39A6; MLPH and BCL2; MLPH and CCNE1; MLPH and MIA; MLPH and MYBL2; MLPH and UBE2C; MLPH and MMP11; GPR160; GPR160 and CCNB1; GPR160 and CXXC5; GPR160 and PTTG1; GPR160 and FGFR4; GPR160 and FOXC1; GPR160 and ESR1; GPR160 and ANLN; GPR160 and BLVRA; GPR160 and EGFR; GPR160 and ACTR3B; GPR160 and NAT1; GPR160 and MYC; GPR160 and SFRP1; GPR160 and MELK; GPR160 and BAG1; GPR160 and CEP55; GPR160 and MKI67; GPR160 and TMEM45B; GPR160 and PGR; GPR160 and MDM2; GPR160 and KRT5; GPR160 and FOXA1; GPR160 and ORC6; GPR160 and CDH3; GPR160 and ERBB2; GPR160 and GRB7; GPR160 and CDC6; GPR160 and MAPT; GPR160 and BIRC5; GPR160 and KRT14; GPR160 and KRT17; GPR160 and TYMS; GPR160 and NDC80; GPR160 and SLC39A6; GPR160 and BCL2; GPR160 and CCNE1; GPR160 and MIA; GPR160 and MYBL2; GPR160 and UBE2C; GPR160 and MMP11; CCNB1; CCNB1 and CXXC5; CCNB1 and PTTG1; CCNB1 and FGFR4; CCNB1 and FOXC1; CCNB1 and ESR1; CCNB1 and ANLN; CCNB1 and BLVRA; CCNB1 and EGFR; CCNB1 and ACTR3B; CCNB1 and NAT1; CCNB1 and MYC; CCNB1 and SFRP1; CCNB1 and MELK; CCNB1 and BAG1; CCNB1 and CEP55; CCNB1 and MKI67; CCNB1 and TMEM45B; CCNB1 and PGR; CCNB1 and MDM2; CCNB1 and KRT5; CCNB1 and FOXA1; CCNB1 and ORC6; CCNB1 and CDH3; CCNB1 and ERBB2; CCNB1 and GRB7; CCNB1 and CDC6; CCNB1 and MAPT; CCNB1 and BIRC5; CCNB1 and KRT14; CCNB1 and KRT17; CCNB1 and TYMS; CCNB1 and NDC80; CCNB1 and SLC39A6; CCNB1 and BCL2; CCNB1 and CCNE1; CCNB1 and MIA; CCNB1 and MYBL2; CCNB1 and UBE2C; CCNB1 and MMP11; CXXC5; CXXC5 and PTTG1; CXXC5 and FGFR4; CXXC5 and FOXC1; CXXC5 and ESR1; CXXC5 and ANLN; CXXC5 and BLVRA; CXXC5 and EGFR; CXXC5 and ACTR3B; CXXC5 and NAT1; CXXC5 and MYC; CXXC5 and SFRP1; CXXC5 and MELK; CXXC5 and BAG1; CXXC5 and CEP55; CXXC5 and MKI67; CXXC5 and TMEM45B; CXXC5 and PGR; CXXC5 and MDM2; CXXC5 and KRT5; CXXC5 and FOXA1; CXXC5 and ORC6; CXXC5 and CDH3; CXXC5 and ERBB2; CXXC5 and GRB7; CXXC5 and CDC6; CXXC5 and MAPT; CXXC5 and BIRC5; CXXC5 and KRT14; CXXC5 and KRT17; CXXC5 and TYMS; CXXC5 and

NDC80; CXXC5 and SLC39A6; CXXC5 and BCL2; CXXC5 and CCNE1; CXXC5 and MIA; CXXC5 and MYBL2; CXXC5 and UBE2C; CXXC5 and MMP11; PTTG1; PTTG1 and FGFR4; PTTG1 and FOXC1; PTTG1 and ESR1; PTTG1 and ANLN; PTTG1 and BLVRA; PTTG1 and EGFR; PTTG1 and ACTR3B; PTTG1 and NAT1; PTTG1 and MYC; PTTG1 and SFRP1; PTTG1 and MELK; PTTG1 and BAG1; PTTG1 and CEP55; PTTG1 and MKI67; PTTG1 and TMEM45B; PTTG1 and PGR; PTTG1 and MDM2; PTTG1 and KRT5; PTTG1 and FOXA1; PTTG1 and ORC6; PTTG1 and CDH3; PTTG1 and ERBB2; PTTG1 and GRB7; PTTG1 and CDC6; PTTG1 and MAPT; PTTG1 and BIRC5; PTTG1 and KRT14; PTTG1 and KRT17; PTTG1 and TYMS; PTTG1 and NDC80; PTTG1 and SLC39A6; PTTG1 and BCL2; PTTG1 and CCNE1; PTTG1 and MIA; PTTG1 and MYBL2; PTTG1 and UBE2C; PTTG1 and MMP11; FGFR4; FGFR4 and FOXC1; FGFR4 and ESR1; FGFR4 and ANLN; FGFR4 and BLVRA; FGFR4 and EGFR; FGFR4 and ACTR3B; FGFR4 and NAT1; FGFR4 and MYC; FGFR4 and SFRP1; FGFR4 and MELK; FGFR4 and BAG1; FGFR4 and CEP55; FGFR4 and MKI67; FGFR4 and TMEM45B; FGFR4 and PGR; FGFR4 and MDM2; FGFR4 and KRT5; FGFR4 and FOXA1; FGFR4 and ORC6; FGFR4 and CDH3; FGFR4 and ERBB2; FGFR4 and GRB7; FGFR4 and CDC6; FGFR4 and MAPT; FGFR4 and BIRC5; FGFR4 and KRT14; FGFR4 and KRT17; FGFR4 and TYMS; FGFR4 and NDC80; FGFR4 and SLC39A6; FGFR4 and BCL2; FGFR4 and CCNE1; FGFR4 and MIA; FGFR4 and MYBL2; FGFR4 and UBE2C; FGFR4 and MMP11; FOXC1; FOXC1 and ESR1; FOXC1 and ANLN; FOXC1 and BLVRA; FOXC1 and EGFR; FOXC1 and ACTR3B; FOXC1 and NAT1; FOXC1 and MYC; FOXC1 and SFRP1; FOXC1 and MELK; FOXC1 and BAG1; FOXC1 and CEP55; FOXC1 and MKI67; FOXC1 and TMEM45B; FOXC1 and PGR; FOXC1 and MDM2; FOXC1 and KRT5; FOXC1 and FOXA1; FOXC1 and ORC6; FOXC1 and CDH3; FOXC1 and ERBB2; FOXC1 and GRB7; FOXC1 and CDC6; FOXC1 and MAPT; FOXC1 and BIRC5; FOXC1 and KRT14; FOXC1 and KRT17; FOXC1 and TYMS; FOXC1 and NDC80; FOXC1 and SLC39A6; FOXC1 and BCL2; FOXC1 and CCNE1; FOXC1 and MIA; FOXC1 and MYBL2; FOXC1 and UBE2C; FOXC1 and MMP11; ESR1; ESR1 and ANLN; ESR1 and BLVRA; ESR1 and EGFR; ESR1 and ACTR3B; ESR1 and NAT1; ESR1 and MYC; ESR1 and SFRP1; ESR1 and MELK; ESR1 and BAG1; ESR1 and CEP55; ESR1 and MKI67; ESR1 and TMEM45B; ESR1 and PGR; ESR1 and MDM2; ESR1 and KRT5; ESR1 and FOXA1; ESR1 and ORC6; ESR1 and CDH3; ESR1 and ERBB2; ESR1 and GRB7; ESR1 and CDC6; ESR1 and MAPT; ESR1 and BIRC5; ESR1 and KRT14; ESR1 and KRT17; ESR1 and TYMS; ESR1 and NDC80; ESR1 and SLC39A6; ESR1 and BCL2; ESR1 and CCNE1; ESR1 and MIA; ESR1 and MYBL2; ESR1 and UBE2C; ESR1 and MMP11; ANLN; ANLN and BLVRA; ANLN and EGFR; ANLN and ACTR3B; ANLN and NAT1; ANLN and MYC; ANLN and SFRP1; ANLN and MELK; ANLN and BAG1; ANLN and CEP55; ANLN and MKI67; ANLN and TMEM45B; ANLN and PGR; ANLN and MDM2; ANLN and KRT5; ANLN and FOXA1; ANLN and ORC6; ANLN and CDH3; ANLN and ERBB2; ANLN and GRB7; ANLN and CDC6; ANLN and MAPT; ANLN and BIRC5; ANLN and KRT14; ANLN and KRT17; ANLN and TYMS; ANLN and NDC80; ANLN and SLC39A6; ANLN and BCL2; ANLN and CCNE1; ANLN and MIA; ANLN and MYBL2; ANLN and

UBE2C; ANLN and MMP11; BLVRA; BLVRA and EGFR; BLVRA and ACTR3B; BLVRA and NAT1; BLVRA and MYC; BLVRA and SFRP1; BLVRA and MELK; BLVRA and BAG1; BLVRA and CEP55; BLVRA and MKI67; BLVRA and TMEM45B; BLVRA and PGR; BLVRA and MDM2; BLVRA and KRT5; BLVRA and FOXA1; BLVRA and ORC6; BLVRA and CDH3; BLVRA and ERBB2; BLVRA and GRB7; BLVRA and CDC6; BLVRA and MAPT; BLVRA and BIRC5; BLVRA and KRT14; BLVRA and KRT17; BLVRA and TYMS; BLVRA and NDC80; BLVRA and SLC39A6; BLVRA and BCL2; BLVRA and CCNE1; BLVRA and MIA; BLVRA and MYBL2; BLVRA and UBE2C; BLVRA and MMP11; EGFR; EGFR and ACTR3B; EGFR and NAT1; EGFR and MYC; EGFR and SFRP1; EGFR and MELK; EGFR and BAG1; EGFR and CEP55; EGFR and MKI67; EGFR and TMEM45B; EGFR and PGR; EGFR and MDM2; EGFR and KRT5; EGFR and FOXA1; EGFR and ORC6; EGFR and CDH3; EGFR and ERBB2; EGFR and GRB7; EGFR and CDC6; EGFR and MAPT; EGFR and BIRC5; EGFR and KRT14; EGFR and KRT17; EGFR and TYMS; EGFR and NDC80; EGFR and SLC39A6; EGFR and BCL2; EGFR and CCNE1; EGFR and MIA; EGFR and MYBL2; EGFR and UBE2C; EGFR and MMP11; ACTR3B; ACTR3B and NAT1; ACTR3B and MYC; ACTR3B and SFRP1; ACTR3B and MELK; ACTR3B and BAG1; ACTR3B and CEP55; ACTR3B and MKI67; ACTR3B and TMEM45B; ACTR3B and PGR; ACTR3B and MDM2; ACTR3B and KRT5; ACTR3B and FOXA1; ACTR3B and ORC6; ACTR3B and CDH3; ACTR3B and ERBB2; ACTR3B and GRB7; ACTR3B and CDC6; ACTR3B and MAPT; ACTR3B and BIRC5; ACTR3B and KRT14; ACTR3B and KRT17; ACTR3B and TYMS; ACTR3B and NDC80; ACTR3B and SLC39A6; ACTR3B and BCL2; ACTR3B and CCNE1; ACTR3B and MIA; ACTR3B and MYBL2; ACTR3B and UBE2C; ACTR3B and MMP11; NAT1; NAT1 and MYC; NAT1 and SFRP1; NAT1 and MELK; NAT1 and BAG1; NAT1 and CEP55; NAT1 and MKI67; NAT1 and TMEM45B; NAT1 and PGR; NAT1 and MDM2; NAT1 and KRT5; NAT1 and FOXA1; NAT1 and ORC6; NAT1 and CDH3; NAT1 and ERBB2; NAT1 and GRB7; NAT1 and CDC6; NAT1 and MAPT; NAT1 and BIRC5; NAT1 and KRT14; NAT1 and KRT17; NAT1 and TYMS; NAT1 and NDC80; NAT1 and SLC39A6; NAT1 and BCL2; NAT1 and CCNE1; NAT1 and MIA; NAT1 and MYBL2; NAT1 and UBE2C; NAT1 and MMP11; MYC; MYC and SFRP1; MYC and MELK; MYC and BAG1; MYC and CEP55; MYC and MKI67; MYC and TMEM45B; MYC and PGR; MYC and MDM2; MYC and KRT5; MYC and FOXA1; MYC and ORC6; MYC and CDH3; MYC and ERBB2; MYC and GRB7; MYC and CDC6; MYC and MAPT; MYC and BIRC5; MYC and KRT14; MYC and KRT17; MYC and TYMS; MYC and NDC80; MYC and SLC39A6; MYC and BCL2; MYC and CCNE1; MYC and MIA; MYC and MYBL2; MYC and UBE2C; MYC and MMP11; SFRP1; SFRP1 and MELK; SFRP1 and BAG1; SFRP1 and CEP55; SFRP1 and MKI67; SFRP1 and TMEM45B; SFRP1 and PGR; SFRP1 and MDM2; SFRP1 and KRT5; SFRP1 and FOXA1; SFRP1 and ORC6; SFRP1 and CDH3; SFRP1 and ERBB2; SFRP1 and GRB7; SFRP1 and CDC6; SFRP1 and MAPT; SFRP1 and BIRC5; SFRP1 and KRT14; SFRP1 and KRT17; SFRP1 and TYMS; SFRP1 and NDC80; SFRP1 and SLC39A6; SFRP1 and BCL2; SFRP1 and CCNE1; SFRP1 and MIA; SFRP1 and MYBL2; SFRP1 and UBE2C; SFRP1 and MMP11; MELK; MELK and BAG1;

MELK and CEP55; MELK and MKI67; MELK and TMEM45B; MELK and PGR; MELK and MDM2; MELK and KRT5; MELK and FOXA1; MELK and ORC6; MELK and CDH3; MELK and ERBB2; MELK and GRB7; MELK and CDC6; MELK and MAPT; MELK and BIRC5; MELK and KRT14; MELK and KRT17; MELK and TYMS; MELK and NDC80; MELK and SLC39A6; MELK and BCL2; MELK and CCNE1; MELK and MIA; MELK and MYBL2; MELK and UBE2C; MELK and MMP11; BAG1; BAG1 and CEP55; BAG1 and MKI67; BAG1 and TMEM45B; BAG1 and PGR; BAG1 and MDM2; BAG1 and KRT5; BAG1 and FOXA1; BAG1 and ORC6; BAG1 and CDH3; BAG1 and ERBB2; BAG1 and GRB7; BAG1 and CDC6; BAG1 and MAPT; BAG1 and BIRC5; BAG1 and KRT14; BAG1 and KRT17; BAG1 and TYMS; BAG1 and NDC80; BAG1 and SLC39A6; BAG1 and BCL2; BAG1 and CCNE1; BAG1 and MIA; BAG1 and MYBL2; BAG1 and UBE2C; BAG1 and MMP11; CEP55; CEP55 and MKI67; CEP55 and TMEM45B; CEP55 and PGR; CEP55 and MDM2; CEP55 and KRT5; CEP55 and FOXA1; CEP55 and ORC6; CEP55 and CDH3; CEP55 and ERBB2; CEP55 and GRB7; CEP55 and CDC6; CEP55 and MAPT; CEP55 and BIRC5; CEP55 and KRT14; CEP55 and KRT17; CEP55 and TYMS; CEP55 and NDC80; CEP55 and SLC39A6; CEP55 and BCL2; CEP55 and CCNE1; CEP55 and MIA; CEP55 and MYBL2; CEP55 and UBE2C; CEP55 and MMP11; MKI67; MKI67 and TMEM45B; MKI67 and PGR; MKI67 and MDM2; MKI67 and KRT5; MKI67 and FOXA1; MKI67 and ORC6; MKI67 and CDH3; MKI67 and ERBB2; MKI67 and GRB7; MKI67 and CDC6; MKI67 and MAPT; MKI67 and BIRC5; MKI67 and KRT14; MKI67 and KRT17; MKI67 and TYMS; MKI67 and NDC80; MKI67 and SLC39A6; MKI67 and BCL2; MKI67 and CCNE1; MKI67 and MIA; MKI67 and MYBL2; MKI67 and UBE2C; MKI67 and MMP11; TMEM45B; TMEM45B and PGR; TMEM45B and MDM2; TMEM45B and KRT5; TMEM45B and FOXA1; TMEM45B and ORC6; TMEM45B and CDH3; TMEM45B and ERBB2; TMEM45B and GRB7; TMEM45B and CDC6; TMEM45B and MAPT; TMEM45B and BIRC5; TMEM45B and KRT14; TMEM45B and KRT17; TMEM45B and TYMS; TMEM45B and NDC80; TMEM45B and SLC39A6; TMEM45B and BCL2; TMEM45B and CCNE1; TMEM45B and MIA; TMEM45B and MYBL2; TMEM45B and UBE2C; TMEM45B and MMP11; PGR; PGR and MDM2; PGR and KRT5; PGR and FOXA1; PGR and ORC6; PGR and CDH3; PGR and ERBB2; PGR and GRB7; PGR and CDC6; PGR and MAPT; PGR and BIRC5; PGR and KRT14; PGR and KRT17; PGR and TYMS; PGR and NDC80; PGR and SLC39A6; PGR and BCL2; PGR and CCNE1; PGR and MIA; PGR and MYBL2; PGR and UBE2C; PGR and MMP11; MDM2; MDM2 and KRT5; MDM2 and FOXA1; MDM2 and ORC6; MDM2 and CDH3; MDM2 and ERBB2; MDM2 and GRB7; MDM2 and CDC6; MDM2 and MAPT; MDM2 and BIRC5; MDM2 and KRT14; MDM2 and KRT17; MDM2 and TYMS; MDM2 and NDC80; MDM2 and SLC39A6; MDM2 and BCL2; MDM2 and CCNE1; MDM2 and MIA; MDM2 and MYBL2; MDM2 and UBE2C; MDM2 and MMP11; KRT5; KRT5 and FOXA1; KRT5 and ORC6; KRT5 and CDH3; KRT5 and ERBB2; KRT5 and GRB7; KRT5 and CDC6; KRT5 and MAPT; KRT5 and BIRC5; KRT5 and KRT14; KRT5 and KRT17; KRT5 and TYMS; KRT5 and NDC80; KRT5 and SLC39A6; KRT5 and BCL2; KRT5 and CCNE1; KRT5 and MIA; KRT5 and MYBL2; KRT5 and UBE2C;

KRT5 and MMP11; FOXA1; FOXA1 and ORC6; FOXA1 and CDH3; FOXA1 and ERBB2; FOXA1 and GRB7; FOXA1 and CDC6; FOXA1 and MAPT; FOXA1 and BIRC5; FOXA1 and KRT14; FOXA1 and KRT17; FOXA1 and TYMS; FOXA1 and NDC80; FOXA1 and SLC39A6; FOXA1 and BCL2; FOXA1 and CCNE1; FOXA1 and MIA; FOXA1 and MYBL2; FOXA1 and UBE2C; FOXA1 and MMP11; ORC6; ORC6 and CDH3; ORC6 and ERBB2; ORC6 and GRB7; ORC6 and CDC6; ORC6 and MAPT; ORC6 and BIRC5; ORC6 and KRT14; ORC6 and KRT17; ORC6 and TYMS; ORC6 and NDC80; ORC6 and SLC39A6; ORC6 and BCL2; ORC6 and CCNE1; ORC6 and MIA; ORC6 and MYBL2; ORC6 and UBE2C; ORC6 and MMP11; CDH3; CDH3 and ERBB2; CDH3 and GRB7; CDH3 and CDC6; CDH3 and MAPT; CDH3 and BIRC5; CDH3 and KRT14; CDH3 and KRT17; CDH3 and TYMS; CDH3 and NDC80; CDH3 and SLC39A6; CDH3 and BCL2; CDH3 and CCNE1; CDH3 and MIA; CDH3 and MYBL2; CDH3 and UBE2C; CDH3 and MMP11; ERBB2; ERBB2 and GRB7; ERBB2 and CDC6; ERBB2 and MAPT; ERBB2 and BIRC5; ERBB2 and KRT14; ERBB2 and KRT17; ERBB2 and TYMS; ERBB2 and NDC80; ERBB2 and SLC39A6; ERBB2 and BCL2; ERBB2 and CCNE1; ERBB2 and MIA; ERBB2 and MYBL2; ERBB2 and UBE2C; ERBB2 and MMP11; GRB7; GRB7 and CDC6; GRB7 and MAPT; GRB7 and BIRC5; GRB7 and KRT14; GRB7 and KRT17; GRB7 and TYMS; GRB7 and NDC80; GRB7 and SLC39A6; GRB7 and BCL2; GRB7 and CCNE1; GRB7 and MIA; GRB7 and MYBL2; GRB7 and UBE2C; GRB7 and MMP11; CDC6; CDC6 and MAPT; CDC6 and BIRC5; CDC6 and KRT14; CDC6 and KRT17; CDC6 and TYMS; CDC6 and NDC80; CDC6 and SLC39A6; CDC6 and BCL2; CDC6 and CCNE1; CDC6 and MIA; CDC6 and MYBL2; CDC6 and UBE2C; CDC6 and MMP11; MAPT; MAPT and BIRC5; MAPT and KRT14; MAPT and KRT17; MAPT and TYMS; MAPT and NDC80; MAPT and SLC39A6; MAPT and BCL2; MAPT and CCNE1; MAPT and MIA; MAPT and MYBL2; MAPT and UBE2C; MAPT and MMP11; BIRC5; BIRC5 and KRT14; BIRC5 and KRT17; BIRC5 and TYMS; BIRC5 and NDC80; BIRC5 and SLC39A6; BIRC5 and BCL2; BIRC5 and CCNE1; BIRC5 and MIA; BIRC5 and MYBL2; BIRC5 and UBE2C; BIRC5 and MMP11; KRT14; KRT14 and KRT17; KRT14 and TYMS; KRT14 and NDC80; KRT14 and SLC39A6; KRT14 and BCL2; KRT14 and CCNE1; KRT14 and MIA; KRT14 and MYBL2; KRT14 and UBE2C; KRT14 and MMP11; KRT17; KRT17 and TYMS; KRT17 and NDC80; KRT17 and SLC39A6; KRT17 and BCL2; KRT17 and CCNE1; KRT17 and MIA; KRT17 and MYBL2; KRT17 and UBE2C; KRT17 and MMP11; TYMS; TYMS and NDC80; TYMS and SLC39A6; TYMS and BCL2; TYMS and CCNE1; TYMS and MIA; TYMS and MYBL2; TYMS and UBE2C; TYMS and MMP11; NDC80; NDC80 and SLC39A6; NDC80 and BCL2; NDC80 and CCNE1; NDC80 and MIA; NDC80 and MYBL2; NDC80 and UBE2C; NDC80 and MMP11; SLC39A6; SLC39A6 and BCL2; SLC39A6 and CCNE1; SLC39A6 and MIA; SLC39A6 and MYBL2; SLC39A6 and UBE2C; SLC39A6 and MMP11; BCL2; BCL2 and CCNE1; BCL2 and MIA; BCL2 and MYBL2; BCL2 and UBE2C; BCL2 and MMP11; CCNE1; CCNE1 and MIA; CCNE1 and MYBL2; CCNE1 and UBE2C; CCNE1 and MMP11; MIA; MIA and MYBL2; MIA and UBE2C; MIA and MMP11; MYBL2; MYBL2 and UBE2C; MYBL2 and MMP11; UBE2C; UBE2C and MMP11; MMP11; TDRD1, CACNA1D,

NCALD, HLA-DMB, KCNH8, PDE3B, PLA2G7, CSGALNACT1, PART1, HES1, F3, GPR110, SH3RF, PDE8B, and SEPT9; TDRD1; TDRD1 and CACNA1D; TDRD1 and NCALD; TDRD1 and HLA-DMB; TDRD1 and KCNH8; TDRD1 and PDE3B; TDRD1 and PLA2G7; TDRD1 and CSGALNACT1; TDRD1 and PART1; TDRD1 and HES1; TDRD1 and F3; TDRD1 and GPR110; TDRD1 and SH3RF; TDRD1 and PDE8B; TDRD1 and SEPT9; CACNA1D; CACNA1D and NCALD; CACNA1D and HLA-DMB; CACNA1D and KCNH8; CACNA1D and PDE3B; CACNA1D and PLA2G7; CACNA1D and CSGALNACT1; CACNA1D and PART1; CACNA1D and HES1; CACNA1D and F3; CACNA1D and GPR110; CACNA1D and SH3RF; CACNA1D and PDE8B; CACNA1D and SEPT9; NCALD; NCALD and HLA-DMB; NCALD and KCNH8; NCALD and PDE3B; NCALD and PLA2G7; NCALD and CSGALNACT1; NCALD and PART1; NCALD and HES1; NCALD and F3; NCALD and GPR110; NCALD and SH3RF; NCALD and PDE8B; NCALD and SEPT9; HLA-DMB; HLA-DMB and KCNH8; HLA-DMB and PDE3B; HLA-DMB and PLA2G7; HLA-DMB and CSGALNACT1; HLA-DMB and PART1; HLA-DMB and HES1; HLA-DMB and F3; HLA-DMB and GPR110; HLA-DMB and SH3RF; HLA-DMB and PDE8B; HLA-DMB and SEPT9; KCNH8; KCNH8 and PDE3B; KCNH8 and PLA2G7; KCNH8 and CSGALNACT1; KCNH8 and PART1; KCNH8 and HES1; KCNH8 and F3; KCNH8 and GPR110; KCNH8 and SH3RF; KCNH8 and PDE8B; KCNH8 and SEPT9; PDE3B; PDE3B and PLA2G7; PDE3B and CSGALNACT1; PDE3B and PART1; PDE3B and HES1; PDE3B and F3; PDE3B and GPR110; PDE3B and SH3RF; PDE3B and PDE8B; PDE3B and SEPT9; PLA2G7; PLA2G7 and CSGALNACT1; PLA2G7 and PART1; PLA2G7 and HES1; PLA2G7 and F3; PLA2G7 and GPR110; PLA2G7 and SH3RF; PLA2G7 and PDE8B; PLA2G7 and SEPT9; CSGALNACT1; CSGALNACT1 and PART1; CSGALNACT1 and HES1; CSGALNACT1 and F3; CSGALNACT1 and GPR110; CSGALNACT1 and SH3RF; CSGALNACT1 and PDE8B; CSGALNACT1 and SEPT9; PART1; PART1 and HES1; PART1 and F3; PART1 and GPR110; PART1 and SH3RF; PART1 and PDE8B; PART1 and SEPT9; HES1; HES1 and F3; HES1 and GPR110; HES1 and SH3RF; HES1 and PDE8B; HES1 and SEPT9; F3; F3 and GPR110; F3 and SH3RF; F3 and PDE8B; F3 and SEPT9; GPR110; GPR110 and SH3RF; GPR110 and PDE8B; GPR110 and SEPT9; SH3RF; SH3RF and PDE8B; SH3RF and SEPT9; PDE8B; PDE8B and SEPT9; SEPT9; CRISP3, AMD1, KCNG3, PLA1A, MYO6, FRK, GPR110, SH3YL1, ACER3, C8orf4, GHR, ITPR1, KHDRBS3, NPY, and GUCY1A3; CRISP3; CRISP3 and AMD1; CRISP3 and KCNG3; CRISP3 and PLA1A; CRISP3 and MYO6; CRISP3 and FRK; CRISP3 and GPR110; CRISP3 and SH3YL1; CRISP3 and ACER3; CRISP3 and C8orf4; CRISP3 and GHR; CRISP3 and ITPR1; CRISP3 and KHDRBS3; CRISP3 and NPY; CRISP3 and GUCY1A3; AMD1; AMD1 and KCNG3; AMD1 and PLA1A; AMD1 and MYO6; AMD1 and FRK; AMD1 and GPR110; AMD1 and SH3YL1; AMD1 and ACER3; AMD1 and C8orf4; AMD1 and GHR; AMD1 and ITPR1; AMD1 and KHDRBS3; AMD1 and NPY; AMD1 and GUCY1A3; KCNG3; KCNG3 and PLA1A; KCNG3 and MYO6; KCNG3 and FRK; KCNG3 and GPR110; KCNG3 and SH3YL1; KCNG3 and ACER3; KCNG3 and C8orf4; KCNG3 and GHR; KCNG3 and ITPR1; KCNG3 and KHDRBS3; KCNG3 and NPY; KCNG3 and

GUCY1A3; PLA1A; PLA1A and MYO6; PLA1A and FRK; PLA1A and GPR110; PLA1A and SH3YL1; PLA1A and ACER3; PLA1A and C8orf4; PLA1A and GHR; PLA1A and ITPR1; PLA1A and KHDRBS3; PLA1A and NPY; PLA1A and GUCY1A3; MYO6; MYO6 and FRK; MYO6 and GPR110; MYO6 and SH3YL1; MYO6 and ACER3; MYO6 and C8orf4; MYO6 and GHR; MYO6 and ITPR1; MYO6 and KHDRBS3; MYO6 and NPY; MYO6 and GUCY1A3; FRK; FRK and GPR110; FRK and SH3YL1; FRK and ACER3; FRK and C8orf4; FRK and GHR; FRK and ITPR1; FRK and KHDRBS3; FRK and NPY; FRK and GUCY1A3; GPR110 and SH3YL1; GPR110 and ACER3; GPR110 and C8orf4; GPR110 and GHR; GPR110 and ITPR1; GPR110 and KHDRBS3; GPR110 and NPY; GPR110 and GUCY1A3; SH3YL1; SH3YL1 and ACER3; SH3YL1 and C8orf4; SH3YL1 and GHR; SH3YL1 and ITPR1; SH3YL1 and KHDRBS3; SH3YL1 and NPY; SH3YL1 and GUCY1A3; ACER3; ACER3 and C8orf4; ACER3 and GHR; ACER3 and ITPR1; ACER3 and KHDRBS3; ACER3 and NPY; ACER3 and GUCY1A3; C8orf4; C8orf4 and GHR; C8orf4 and ITPR1; C8orf4 and KHDRBS3; C8orf4 and NPY; C8orf4 and GUCY1A3; GHR; GHR and ITPR1; GHR and KHDRBS3; GHR and NPY; GHR and GUCY1A3; ITPR1; ITPR1 and KHDRBS3; ITPR1 and NPY; ITPR1 and GUCY1A3; KHDRBS3; KHDRBS3 and NPY; KHDRBS3 and GUCY1A3; NPY; NPY and GUCY1A3; GUCY1A3; ARHGDIB, LAMC2, VWA2, ZNF432, MORN1, CYorf15B, AMPD3, QDPR, HDAC1, KIF16B, GJB1, ITPR3, ZNF615, ANKRD6, and APOD; ARHGDIB; ARHGDIB and LAMC2; ARHGDIB and VWA2; ARHGDIB and ZNF432; ARHGDIB and MORN1; ARHGDIB and CYorf15B; ARHGDIB and AMPD3; ARHGDIB and QDPR; ARHGDIB and HDAC1; ARHGDIB and KIF16B; ARHGDIB and GJB1; ARHGDIB and ITPR3; ARHGDIB and ZNF615; ARHGDIB and ANKRD6; ARHGDIB and APOD; LAMC2; LAMC2 and VWA2; LAMC2 and ZNF432; LAMC2 and MORN1; LAMC2 and CYorf15B; LAMC2 and AMPD3; LAMC2 and QDPR; LAMC2 and HDAC1; LAMC2 and KIF16B; LAMC2 and GJB1; LAMC2 and ITPR3; LAMC2 and ZNF615; LAMC2 and ANKRD6; LAMC2 and APOD; VWA2; VWA2 and ZNF432; VWA2 and MORN1; VWA2 and CYorf15B; VWA2 and AMPD3; VWA2 and QDPR; VWA2 and HDAC1; VWA2 and KIF16B; VWA2 and GJB1; VWA2 and ITPR3; VWA2 and ZNF615; VWA2 and ANKRD6; VWA2 and APOD; ZNF432; ZNF432 and MORN1; ZNF432 and CYorf15B; ZNF432 and AMPD3; ZNF432 and QDPR; ZNF432 and HDAC1; ZNF432 and KIF16B; ZNF432 and GJB1; ZNF432 and ITPR3; ZNF432 and ZNF615; ZNF432 and ANKRD6; ZNF432 and APOD; MORN1; MORN1 and CYorf15B; MORN1 and AMPD3; MORN1 and QDPR; MORN1 and HDAC1; MORN1 and KIF16B; MORN1 and GJB1; MORN1 and ITPR3; MORN1 and ZNF615; MORN1 and ANKRD6; MORN1 and APOD; CYorf15B; CYorf15B and AMPD3; CYorf15B and QDPR; CYorf15B and HDAC1; CYorf15B and KIF16B; CYorf15B and GJB1; CYorf15B and ITPR3; CYorf15B and ZNF615; CYorf15B and ANKRD6; CYorf15B and APOD; AMPD3; AMPD3 and QDPR; AMPD3 and HDAC1; AMPD3 and KIF16B; AMPD3 and GJB1; AMPD3 and ITPR3; AMPD3 and ZNF615; AMPD3 and ANKRD6; AMPD3 and APOD; QDPR; QDPR and HDAC1; QDPR and KIF16B; QDPR and GJB1; QDPR and ITPR3; QDPR and ZNF615; QDPR and ANKRD6; QDPR and APOD; HDAC1; HDAC1 and KIF16B; HDAC1 and GJB1; HDAC1 and

ITPR3; HDAC1 and ZNF615; HDAC1 and ANKRD6; HDAC1 and APOD; KIF16B; KIF16B and GJB1; KIF16B and ITPR3; KIF16B and ZNF615; KIF16B and ANKRD6; KIF16B and APOD; GJB1; GJB1 and ITPR3; GJB1 and ZNF615; GJB1 and ANKRD6; GJB1 and APOD; ITPR3; ITPR3 and ZNF615; ITPR3 and ANKRD6; ITPR3 and APOD; ZNF615; ZNF615 and ANKRD6; ZNF615 and APOD; ANKRD6; ANKRD6 and APOD; APOD; STEAP4, RGS17, MAP7, C22orf36, NKAIN1, CHN2, LRRFIP1, SERGEF, ATP8A2, NDRG1, CDC42SE1, LUZP2, HNF1B, TFAP2A and ANKRD34B STEAP4; STEAP4 and RGS17; STEAP4 and MAP7; STEAP4 and C22orf36; STEAP4 and NKAIN1; STEAP4 and CHN2; STEAP4 and LRRFIP1; STEAP4 and SERGEF; STEAP4 and ATP8A2; STEAP4 and NDRG1; STEAP4 and CDC42SE1; STEAP4 and LUZP2; STEAP4 and HNF1B; STEAP4 and TFAP2A; STEAP4 and ANKRD34B; RGS17; RGS17 and MAP7; RGS17 and C22orf36; RGS17 and NKAIN1; RGS17 and CHN2; RGS17 and LRRFIP1; RGS17 and SERGEF; RGS17 and ATP8A2; RGS17 and NDRG1; RGS17 and CDC42SE1; RGS17 and LUZP2; RGS17 and HNF1B; RGS17 and TFAP2A; RGS17 and ANKRD34B; MAP7; MAP7 and C22orf36; MAP7 and NKAIN1; MAP7 and CHN2; MAP7 and LRRFIP1; MAP7 and SERGEF; MAP7 and ATP8A2; MAP7 and NDRG1; MAP7 and CDC42SE1; MAP7 and LUZP2; MAP7 and HNF1B; MAP7 and TFAP2A; MAP7 and ANKRD34B; C22orf36; C22orf36 and NKAIN1; C22orf36 and CHN2; C22orf36 and LRRFIP1; C22orf36 and SERGEF; C22orf36 and ATP8A2; C22orf36 and NDRG1; C22orf36 and CDC42SE1; C22orf36 and LUZP2; C22orf36 and HNF1B; C22orf36 and TFAP2A; C22orf36 and ANKRD34B; NKAIN1; NKAIN1 and CHN2; NKAIN1 and LRRFIP1; NKAIN1 and SERGEF; NKAIN1 and ATP8A2; NKAIN1 and NDRG1; NKAIN1 and CDC42SE1; NKAIN1 and LUZP2; NKAIN1 and HNF1B; NKAIN1 and TFAP2A; NKAIN1 and ANKRD34B; CHN2; CHN2 and LRRFIP1; CHN2 and SERGEF; CHN2 and ATP8A2; CHN2 and NDRG1; CHN2 and CDC42SE1; CHN2 and LUZP2; CHN2 and HNF1B; CHN2 and TFAP2A; CHN2 and ANKRD34B; LRRFIP1; LRRFIP1 and SERGEF; LRRFIP1 and ATP8A2; LRRFIP1 and NDRG1; LRRFIP1 and CDC42SE1; LRRFIP1 and LUZP2; LRRFIP1 and HNF1B; LRRFIP1 and TFAP2A; LRRFIP1 and ANKRD34B; SERGEF; SERGEF and ATP8A2; SERGEF and NDRG1; SERGEF and CDC42SE1; SERGEF and LUZP2; SERGEF and HNF1B; SERGEF and TFAP2A; SERGEF and ANKRD34B; ATP8A2; ATP8A2 and NDRG1; ATP8A2 and CDC42SE1; ATP8A2 and LUZP2; ATP8A2 and HNF1B; ATP8A2 and TFAP2A; ATP8A2 and ANKRD34B; NDRG1; NDRG1 and CDC42SE1; NDRG1 and LUZP2; NDRG1 and HNF1B; NDRG1 and TFAP2A; NDRG1 and ANKRD34B; CDC42SE1; CDC42SE1 and LUZP2; CDC42SE1 and HNF1B; CDC42SE1 and TFAP2A; CDC42SE1 and ANKRD34B; LUZP2; LUZP2 and HNF1B; LUZP2 and TFAP2A; LUZP2 and ANKRD34B; HNF1B; HNF1B and TFAP2A; HNF1B and ANKRD34B; TFAP2A; TFAP2A and ANKRD34B; ANKRD34B; SLC12A2, PRAC, SLC5A4, ACSL3, CD24P4, DNASE2B, SLC22A3, ODC1, SMOC2, UGDH, DSC2, WNK2, RAB3B, FAM198B, KCNC2 and SNAP91; SLC12A2; SLC12A2 and PRAC; SLC12A2 and SLC5A4; SLC12A2 and ACSL3; SLC12A2 and CD24P4; SLC12A2 and DNASE2B; SLC12A2 and SLC22A3; SLC12A2 and ODC1; SLC12A2 and SMOC2; SLC12A2 and UGDH; SLC12A2 and DSC2; SLC12A2 and WNK2; SLC12A2 and RAB3B;

SLC12A2 and FAM198B; SLC12A2 and KCNC2; SLC12A2 and SNAP91; PRAC; PRAC and SLC5A4; PRAC and ACSL3; PRAC and CD24P4; PRAC and DNASE2B; PRAC and SLC22A3; PRAC and ODC1; PRAC and SMOC2; PRAC and UGDH; PRAC and DSC2; PRAC and WNK2; PRAC and RAB3B; PRAC and FAM198B; PRAC and KCNC2; PRAC and SNAP91; SLC5A4; SLC5A4 and ACSL3; SLC5A4 and CD24P4; SLC5A4 and DNASE2B; SLC5A4 and SLC22A3; SLC5A4 and ODC1; SLC5A4 and SMOC2; SLC5A4 and UGDH; SLC5A4 and DSC2; SLC5A4 and WNK2; SLC5A4 and RAB3B; SLC5A4 and FAM198B; SLC5A4 and KCNC2; SLC5A4 and SNAP91; ACSL3; ACSL3 and CD24P4; ACSL3 and DNASE2B; ACSL3 and SLC22A3; ACSL3 and ODC1; ACSL3 and SMOC2; ACSL3 and UGDH; ACSL3 and DSC2; ACSL3 and WNK2; ACSL3 and RAB3B; ACSL3 and FAM198B; ACSL3 and KCNC2; ACSL3 and SNAP91; CD24P4; CD24P4 and DNASE2B; CD24P4 and SLC22A3; CD24P4 and ODC1; CD24P4 and SMOC2; CD24P4 and UGDH; CD24P4 and DSC2; CD24P4 and WNK2; CD24P4 and RAB3B; CD24P4 and FAM198B; CD24P4 and KCNC2; CD24P4 and SNAP91; DNASE2B; DNASE2B and SLC22A3; DNASE2B and ODC1; DNASE2B and SMOC2; DNASE2B and UGDH; DNASE2B and DSC2; DNASE2B and WNK2; DNASE2B and RAB3B; DNASE2B and FAM198B; DNASE2B and KCNC2; DNASE2B and SNAP91; SLC22A3; SLC22A3 and ODC1; SLC22A3 and SMOC2; SLC22A3 and UGDH; SLC22A3 and DSC2; SLC22A3 and WNK2; SLC22A3 and RAB3B; SLC22A3 and FAM198B; SLC22A3 and KCNC2; SLC22A3 and SNAP91; ODC1; ODC1 and SMOC2; ODC1 and UGDH; ODC1 and DSC2; ODC1 and WNK2; ODC1 and RAB3B; ODC1 and FAM198B; ODC1 and KCNC2; ODC1 and SNAP91; SMOC2; SMOC2 and UGDH; SMOC2 and DSC2; SMOC2 and WNK2; SMOC2 and RAB3B; SMOC2 and FAM198B; SMOC2 and KCNC2; SMOC2 and SNAP91; UGDH; UGDH and DSC2; UGDH and WNK2; UGDH and RAB3B; UGDH and FAM198B; UGDH and KCNC2; UGDH and SNAP91; DSC2; DSC2 and WNK2; DSC2 and RAB3B; DSC2 and FAM198B; DSC2 and KCNC2; DSC2 and SNAP91; WNK2; WNK2 and RAB3B; WNK2 and FAM198B; WNK2 and KCNC2; WNK2 and SNAP91; RAB3B; RAB3B and FAM198B; RAB3B and KCNC2; RAB3B and SNAP91; FAM198B; FAM198B and KCNC2; FAM198B and SNAP91; KCNC2; KCNC2 and SNAP91; SNAP91; FAM65B, AMACR, ZNF385B, CDK19, ARHGAP18, IL5RA, SLC16A1, CNTLN, FKBP10, SLC45A2, CLIP1, HEXB, NEFH, ODZ1 and SS18L2; FAM65B; FAM65B and AMACR; FAM65B and ZNF385B; FAM65B and CDK19; FAM65B and ARHGAP18; FAM65B and IL5RA; FAM65B and SLC16A1; FAM65B and CNTLN; FAM65B and FKBP10; FAM65B and SLC45A2; FAM65B and CLIP1; FAM65B and HEXB; FAM65B and NEFH; FAM65B and ODZ1; FAM65B and SS18L2; AMACR; AMACR and ZNF385B; AMACR and CDK19; AMACR and ARHGAP18; AMACR and IL5RA; AMACR and SLC16A1; AMACR and CNTLN; AMACR and FKBP10; AMACR and SLC45A2; AMACR and CLIP1; AMACR and HEXB; AMACR and NEFH; AMACR and ODZ1; AMACR and SS18L2; ZNF385B; ZNF385B and CDK19; ZNF385B and ARHGAP18; ZNF385B and IL5RA; ZNF385B and SLC16A1; ZNF385B and CNTLN; ZNF385B and FKBP10; ZNF385B and SLC45A2; ZNF385B and CLIP1; ZNF385B and HEXB; ZNF385B and NEFH; ZNF385B and ODZ1; ZNF385B and SS18L2; CDK19; CDK19 and

ARHGAP18; CDK19 and IL5RA; CDK19 and SLC16A1; CDK19 and CNTLN; CDK19 and FKBP10; CDK19 and SLC45A2; CDK19 and CLIP1; CDK19 and HEXB; CDK19 and NEFH; CDK19 and ODZ1; CDK19 and SS18L2; ARHGAP18; ARHGAP18 and IL5RA; ARHGAP18 and SLC16A1; ARHGAP18 and CNTLN; ARHGAP18 and FKBP10; ARHGAP18 and SLC45A2; ARHGAP18 and CLIP1; ARHGAP18 and HEXB; ARHGAP18 and NEFH; ARHGAP18 and ODZ1; ARHGAP18 and SS18L2; IL5RA; IL5RA and SLC16A1; IL5RA and CNTLN; IL5RA and FKBP10; IL5RA and SLC45A2; IL5RA and CLIP1; IL5RA and HEXB; IL5RA and NEFH; IL5RA and ODZ1; IL5RA and SS18L2; SLC16A1; SLC16A1 and CNTLN; SLC16A1 and FKBP10; SLC16A1 and SLC45A2; SLC16A1 and CLIP1; SLC16A1 and HEXB; SLC16A1 and NEFH; SLC16A1 and ODZ1; SLC16A1 and SS18L2; CNTLN; CNTLN and FKBP10; CNTLN and SLC45A2; CNTLN and CLIP1; CNTLN and HEXB; CNTLN and NEFH; CNTLN and ODZ1; CNTLN and SS18L2; FKBP10; FKBP10 and SLC45A2; FKBP10 and CLIP1; FKBP10 and HEXB; FKBP10 and NEFH; FKBP10 and ODZ1; FKBP10 and SS18L2; SLC45A2; SLC45A2 and CLIP1; SLC45A2 and HEXB; SLC45A2 and NEFH; SLC45A2 and ODZ1; SLC45A2 and SS18L2; CLIP1; CLIP1 and HEXB; CLIP1 and NEFH; CLIP1 and ODZ1; CLIP1 and SS18L2; HEXB; HEXB and NEFH; HEXB and ODZ1; HEXB and SS18L2; NEFH; NEFH and ODZ1; NEFH and SS18L2; ODZ1; ODZ1 and SS18L2; SS18L2; HPGD, FAM3B, MIPEP, NCAPD3, INPP4B, ANPEP, TFF3, IL31RA, EHHADH, RP11-45B20.2, CCDC141, RLN1, ABHD2 and SCIN; HPGD; HPGD and FAM3B; HPGD and MIPEP; HPGD and NCAPD3; HPGD and INPP4B; HPGD and ANPEP; HPGD and TFF3; HPGD and IL31RA; HPGD and EHHADH; HPGD and RP11-45B20.2; HPGD and CCDC141; HPGD and RLN1; HPGD and ABHD2; HPGD and SCIN; FAM3B; FAM3B and MIPEP; FAM3B and NCAPD3; FAM3B and INPP4B; FAM3B and ANPEP; FAM3B and TFF3; FAM3B and IL31RA; FAM3B and EHHADH; FAM3B and RP11-45B20.2; FAM3B and CCDC141; FAM3B and RLN1; FAM3B and ABHD2; FAM3B and SCIN; MIPEP; MIPEP and NCAPD3; MIPEP and INPP4B; MIPEP and ANPEP; MIPEP and TFF3; MIPEP and IL31RA; MIPEP and EHHADH; MIPEP and RP11-45B20.2; MIPEP and CCDC141; MIPEP and RLN1; MIPEP and ABHD2; MIPEP and SCIN; NCAPD3; NCAPD3 and INPP4B; NCAPD3 and ANPEP; NCAPD3 and TFF3; NCAPD3 and IL31RA; NCAPD3 and EHHADH; NCAPD3 and RP11-45B20.2; NCAPD3 and CCDC141; NCAPD3 and RLN1; NCAPD3 and ABHD2; NCAPD3 and SCIN; INPP4B; INPP4B and ANPEP; INPP4B and TFF3; INPP4B and IL31RA; INPP4B and EHHADH; INPP4B and RP11-45B20.2; INPP4B and CCDC141; INPP4B and RLN1; INPP4B and ABHD2; INPP4B and SCIN; ANPEP; ANPEP and TFF3; ANPEP and IL31RA; ANPEP and EHHADH; ANPEP and RP11-45B20.2; ANPEP and CCDC141; ANPEP and RLN1; ANPEP and ABHD2; ANPEP and SCIN; TFF3; TFF3 and IL31RA; TFF3 and EHHADH; TFF3 and RP11-45B20.2; TFF3 and CCDC141; TFF3 and RLN1; TFF3 and ABHD2; TFF3 and SCIN; IL31RA; IL31RA and EHHADH; IL31RA and RP11-45B20.2; IL31RA and CCDC141; IL31RA and RLN1; IL31RA and ABHD2; IL31RA and SCIN; EHHADH; EHHADH and RP11-45B20.2; EHHADH and CCDC141; EHHADH and RLN1; EHHADH and ABHD2; EHHADH and SCIN; RP11-45B20.2; RP11-45B20.2 and CCDC141; RP11-45B20.2 and

RLN1; RP11-45B20.2 and ABHD2; RP11-45B20.2 and SCIN; CCDC141; CCDC141 and RLN1; CCDC141 and ABHD2; CCDC141 and SCIN; RLN1; RLN1 and ABHD2; RLN1 and SCIN; ABHD2; ABHD2 and SCIN; SCIN; TFF3, ALOX15B, and MON1B; TFF3 and ALOX15B; TFF3 and MON1B; ALOX15B; ALOX15B, and MON1B; MON1B; MME, BANK1, LEPREL1, VGLL3, NPR3, OR4K7P, OR4K6P, POTE2, RP11, TTN, FAP5 and GPR116; MME; MME and BANK1; MME and LEPREL1; MME and VGLL3; MME and NPR3; MME and OR4K7P; MME and OR4K6P; MME and POTE2; MME and RP11; MME and TTN; MME and FAP5; MME and GPR116; BANK1; BANK1 and LEPREL1; BANK1 and VGLL3; BANK1 and NPR3; BANK1 and OR4K7P; BANK1 and OR4K6P; BANK1 and POTE2; BANK1 and RP11; BANK1 and TTN; BANK1 and FAP5; BANK1 and GPR116; LEPREL1; LEPREL1 and VGLL3; LEPREL1 and NPR3; LEPREL1 and OR4K7P; LEPREL1 and OR4K6P; LEPREL1 and POTE2; LEPREL1 and RP11; LEPREL1 and TTN; LEPREL1 and FAP5; LEPREL1 and GPR116; VGLL3; VGLL3 and NPR3; VGLL3 and OR4K7P; VGLL3 and OR4K6P; VGLL3 and POTE2; VGLL3 and RP11; VGLL3 and TTN; VGLL3 and FAP5; VGLL3 and GPR116; NPR3; NPR3 and OR4K7P; NPR3 and OR4K6P; NPR3 and POTE2; NPR3 and RP11; NPR3 and TTN; NPR3 and FAP5; NPR3 and GPR116; OR4K7P; OR4K7P and OR4K6P; OR4K7P and POTE2; OR4K7P and RP11; OR4K7P and TTN; OR4K7P and FAP5; OR4K7P and GPR116; OR4K6P; OR4K6P and POTE2; OR4K6P and RP11; OR4K6P and TTN; OR4K6P and FAP5; OR4K6P and GPR116; POTE2; POTE2 and RP11; POTE2 and TTN; POTE2 and FAP5; POTE2 and GPR116; RP11; RP11 and TTN; RP11 and FAP5; RP11 and GPR116; TTN; TTN and FAP5; TTN and GPR116; FAP5; FAP5 and GPR116; GPR116; MME, BANK1, LEPREL1, VGLL3, NPR3, OR4K6P, OR4K7P, POTE2, RP11.403, TTN and FABP5P7; RP11.403; RP11.403 and TTN; RP11.403 and FABP5P7; TTN; TTN and FABP5P7; and FABP5P7. The plurality of targets may comprise 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 30, 40, 50 or more targets.

[0056] The plurality of targets may comprise CDC20; KIF2C; PHGDH; NUF2; CENPF; EXO1; UBE2T; RRM2; MLPH; GPR160; CCNB1; CXXC5; PTTG1; FGFR4; FOXC1; ESR1; ANLN; BLVRA; EGFR; ACTR3B; NAT1; MYC; SFRP1; MELK; BAG1; CEP55; MKI67; TMEM45B; PGR; MDM2; KRT5; FOXA1; ORC6; CDH3; ERBB2; GRB7; CDC6; MAPT; BIRC5; KRT14; KRT17; TYMS; NDC80; SLC39A6; BCL2; CCNE1; MIA; MYBL2; UBE2C; MMP11; TDRD1; CACNA1D; NCALD; HLA-DMB; KCNH8; PDE3B; PLA2G7; CSGALNACT1; PART1; HES1; F3; GPR110; SH3RF; PDE8B; SEPT9; CRISP3; AMD1; KCNG3; PLA1A; MYO6; FRK; SH3YL1; ACER3; C8orf4; GHR; ITPR1; KHDRBS3; NPY; GUCY1A3; ARHGDIB; LAMC2; VWA2; ZNF432; MORN1; CYorf15B; AMPD3; QDPR; HDAC1; KIF16B; GJB1; ITPR3; ZNF615; ANKRD6; APOD; STEAP4; RGS17; MAP7; C22orf36; NKAIN1; CHN2; LRRFIP1; SERGEF; ATP8A2; NDRG1; CDC42SE1; LUZP2; HNF1B; TFAP2A; ANKRD34B; SLC12A2; PRAC; SLC5A4; ACSL3; CD24P4; DNASE2B; SLC22A3; ODC1; SMOC2; UGDH; DSC2; WNK2; RAB3B; FAM198B; KCNC2; SNAP91; FAM65B; AMACR; ZNF385B; CDK19; ARHGAP18; IL5RA; SLC16A1; CNTLN; FKBP10; SLC45A2; CLIP1; HEXB; NEFH; ODZ1; SS18L2; HPGD;

FAM3B; MIPEP; NCAPD3; INPP4B; ANPEP; TFF3; IL31RA; EHHADH; RP11-45B20.2; CCDC141; RLN1; ABHD2; SCIN; ALOX15B; MON1B; MME; BANK1; LEPREL1; VGLL3; NPR3; OR4K7P; OR4K6P; POTE2; RP11; TTN; FAP5; GPR116; RP11.403; and FABP5P7.

Probes/Primers

[0057] The present invention provides for a probe set for diagnosing, monitoring and/or predicting a status or outcome of a prostate cancer in a subject comprising a plurality of probes, wherein (i) the probes in the set are capable of detecting an expression level of at least one target selected from ; and (ii) the expression level determines the cancer status of the subject with at least about 40% specificity.

[0058] The probe set may comprise one or more polynucleotide probes. Individual polynucleotide probes comprise a nucleotide sequence derived from the nucleotide sequence of the target sequences or complementary sequences thereof. The nucleotide sequence of the polynucleotide probe is designed such that it corresponds to, or is complementary to the target sequences. The polynucleotide probe can specifically hybridize under either stringent or lowered stringency hybridization conditions to a region of the target sequences, to the complement thereof, or to a nucleic acid sequence (such as a cDNA) derived therefrom.

[0059] The selection of the polynucleotide probe sequences and determination of their uniqueness may be carried out *in silico* using techniques known in the art, for example, based on a BLASTN search of the polynucleotide sequence in question against gene sequence databases, such as the Human Genome Sequence, UniGene, dbEST or the non-redundant database at NCBI. In one embodiment of the invention, the polynucleotide probe is complementary to a region of a target mRNA derived from a target sequence in the probe set. Computer programs can also be employed to select probe sequences that may not cross hybridize or may not hybridize non-specifically.

[0060] In some instances, microarray hybridization of RNA, extracted from prostate cancer tissue samples and amplified, may yield a dataset that is then summarized and normalized by the fRMA technique. After removal (or filtration) of cross-hybridizing PSRs, and PSRs containing less than 4 probes, the remaining PSRs can be used in further analysis. Following fRMA and filtration, the data can be decomposed into its principal components and an analysis of variance model is used to determine the extent to which a batch effect remains present in the first 10 principal components.

[0061] These remaining PSRs can then be subjected to filtration by a T-test between CR (clinical recurrence) and non-CR samples. Using a p-value cut-off of 0.01, the remaining features (e.g., PSRs) can be further refined. Feature selection can be performed by regularized logistic regression using the elastic-net penalty. The regularized regression may

be bootstrapped over 1000 times using all training data; with each iteration of bootstrapping, features that have non-zero co-efficient following 3-fold cross validation can be tabulated. In some instances, features that were selected in at least 25% of the total runs were used for model building.

[0062] The polynucleotide probes of the present invention may range in length from about 15 nucleotides to the full length of the coding target or non-coding target. In one embodiment of the invention, the polynucleotide probes are at least about 15 nucleotides in length. In another embodiment, the polynucleotide probes are at least about 20 nucleotides in length. In a further embodiment, the polynucleotide probes are at least about 25 nucleotides in length. In another embodiment, the polynucleotide probes are between about 15 nucleotides and about 500 nucleotides in length. In other embodiments, the polynucleotide probes are between about 15 nucleotides and about 450 nucleotides, about 15 nucleotides and about 400 nucleotides, about 15 nucleotides and about 350 nucleotides, about 15 nucleotides and about 300 nucleotides, about 15 nucleotides and about 250 nucleotides, about 15 nucleotides and about 200 nucleotides in length. In some embodiments, the probes are at least 15 nucleotides in length. In some embodiments, the probes are at least 15 nucleotides in length. In some embodiments, the probes are at least 20 nucleotides, at least 25 nucleotides, at least 50 nucleotides, at least 75 nucleotides, at least 100 nucleotides, at least 125 nucleotides, at least 150 nucleotides, at least 200 nucleotides, at least 225 nucleotides, at least 250 nucleotides, at least 275 nucleotides, at least 300 nucleotides, at least 325 nucleotides, at least 350 nucleotides, at least 375 nucleotides in length.

[0063] The polynucleotide probes of a probe set can comprise RNA, DNA, RNA or DNA mimetics, or combinations thereof, and can be single-stranded or double-stranded. Thus the polynucleotide probes can be composed of naturally-occurring nucleobases, sugars and covalent internucleoside (backbone) linkages as well as polynucleotide probes having non-naturally-occurring portions which function similarly. Such modified or substituted polynucleotide probes may provide desirable properties such as, for example, enhanced affinity for a target gene and increased stability. The probe set may comprise a coding target and/or a non-coding target. Preferably, the probe set comprises a combination of a coding target and non-coding target.

[0064] In some embodiments, the probe set comprise a plurality of target sequences that hybridize to at least about 5 coding targets and/or non-coding targets selected from Table 8, Table 9 or SEQ ID NOs: 1-1029. Alternatively, the probe set comprise a plurality of target sequences that hybridize to at least about 10 coding targets and/or non-coding targets selected from Table 8, Table 9 or SEQ ID NOs: 1-1029. In some embodiments, the probe set comprise

a plurality of target sequences that hybridize to at least about 15 coding targets and/or non-coding targets selected from Table 8, Table 9 or SEQ ID NOs: 1-1029. In some embodiments, the probe set comprise a plurality of target sequences that hybridize to at least about 20 coding targets and/or non-coding targets selected from Table 8, Table 9 or SEQ ID NOs: 1-1029. In some embodiments, the probe set comprise a plurality of target sequences that hybridize to at least about 30 coding targets and/or non-coding targets selected from Table 8, Table 9 or SEQ ID NOs: 1-1029. In some embodiments, the probe set comprise a plurality of target sequences that hybridize to at least about 40 coding targets and/or non-coding targets selected from Table 8, Table 9 or SEQ ID NOs: 1-1029. In some embodiments, the probe set comprise a plurality of target sequences that hybridize to at least about 50 coding targets and/or non-coding targets selected from Table 8, Table 9 or SEQ ID NOs: 1-1029.

[0065] The system of the present invention further provides for primers and primer pairs capable of amplifying target sequences defined by the probe set, or fragments or subsequences or complements thereof. The nucleotide sequences of the probe set may be provided in computer-readable media for *in silico* applications and as a basis for the design of appropriate primers for amplification of one or more target sequences of the probe set.

[0066] Primers based on the nucleotide sequences of target sequences can be designed for use in amplification of the target sequences. For use in amplification reactions such as PCR, a pair of primers can be used. The exact composition of the primer sequences is not critical to the invention, but for most applications the primers may hybridize to specific sequences of the probe set under stringent conditions, particularly under conditions of high stringency, as known in the art. The pairs of primers are usually chosen so as to generate an amplification product of at least about 50 nucleotides, more usually at least about 100 nucleotides. Algorithms for the selection of primer sequences are generally known, and are available in commercial software packages. These primers may be used in standard quantitative or qualitative PCR-based assays to assess transcript expression levels of RNAs defined by the probe set. Alternatively, these primers may be used in combination with probes, such as molecular beacons in amplifications using real-time PCR.

[0067] In one embodiment, the primers or primer pairs, when used in an amplification reaction, specifically amplify at least a portion of a nucleic acid sequence of a target selected from Table 8, Table 9 or SEQ ID NOs: 1-1029 (or subgroups thereof as set forth herein), an RNA form thereof, or a complement to either thereof.

[0068] A label can optionally be attached to or incorporated into a probe or primer polynucleotide to allow detection and/or quantitation of a target polynucleotide representing

the target sequence of interest. The target polynucleotide may be the expressed target sequence RNA itself, a cDNA copy thereof, or an amplification product derived therefrom, and may be the positive or negative strand, so long as it can be specifically detected in the assay being used. Similarly, an antibody may be labeled.

[0069] In certain multiplex formats, labels used for detecting different targets may be distinguishable. The label can be attached directly (e.g., via covalent linkage) or indirectly, e.g., via a bridging molecule or series of molecules (e.g., a molecule or complex that can bind to an assay component, or via members of a binding pair that can be incorporated into assay components, e.g. biotin-avidin or streptavidin). Many labels are commercially available in activated forms which can readily be used for such conjugation (for example through amine acylation), or labels may be attached through known or determinable conjugation schemes, many of which are known in the art.

[0070] Labels useful in the invention described herein include any substance which can be detected when bound to or incorporated into the biomolecule of interest. Any effective detection method can be used, including optical, spectroscopic, electrical, piezoelectrical, magnetic, Raman scattering, surface plasmon resonance, colorimetric, calorimetric, etc. A label is typically selected from a chromophore, a lumiphore, a fluorophore, one member of a quenching system, a chromogen, a hapten, an antigen, a magnetic particle, a material exhibiting nonlinear optics, a semiconductor nanocrystal, a metal nanoparticle, an enzyme, an antibody or binding portion or equivalent thereof, an aptamer, and one member of a binding pair, and combinations thereof. Quenching schemes may be used, wherein a quencher and a fluorophore as members of a quenching pair may be used on a probe, such that a change in optical parameters occurs upon binding to the target introduce or quench the signal from the fluorophore. One example of such a system is a molecular beacon. Suitable quencher/fluorophore systems are known in the art. The label may be bound through a variety of intermediate linkages. For example, a polynucleotide may comprise a biotin-binding species, and an optically detectable label may be conjugated to biotin and then bound to the labeled polynucleotide. Similarly, a polynucleotide sensor may comprise an immunological species such as an antibody or fragment, and a secondary antibody containing an optically detectable label may be added.

[0071] Chromophores useful in the methods described herein include any substance which can absorb energy and emit light. For multiplexed assays, a plurality of different signaling chromophores can be used with detectably different emission spectra. The chromophore can be a lumophore or a fluorophore. Typical fluorophores include fluorescent dyes,

semiconductor nanocrystals, lanthanide chelates, polynucleotide-specific dyes and green fluorescent protein.

[0072] In some embodiments, polynucleotides of the invention comprise at least 20 consecutive bases of the nucleic acid sequence of a target selected from Table 8, Table 9 or SEQ ID NOs: 1-1029 or a complement thereto. The polynucleotides may comprise at least 21, 22, 23, 24, 25, 27, 30, 32, 35 or more consecutive bases of the nucleic acids sequence of a target selected from Table 8, Table 9 or SEQ ID NOs: 1-1029, as applicable.

[0073] The polynucleotides may be provided in a variety of formats, including as solids, in solution, or in an array. The polynucleotides may optionally comprise one or more labels, which may be chemically and/or enzymatically incorporated into the polynucleotide.

[0074] In some embodiments, one or more polynucleotides provided herein can be provided on a substrate. The substrate can comprise a wide range of material, either biological, nonbiological, organic, inorganic, or a combination of any of these. For example, the substrate may be a polymerized Langmuir Blodgett film, functionalized glass, Si, Ge, GaAs, GaP, SiO₂, SiN₄, modified silicon, or any one of a wide variety of gels or polymers such as (poly)tetrafluoroethylene, (poly)vinylidenedifluoride, polystyrene, cross-linked polystyrene, polyacrylic, polylactic acid, polyglycolic acid, poly(lactide coglycolide), polyanhydrides, poly(methyl methacrylate), poly(ethylene-co-vinyl acetate), polysiloxanes, polymeric silica, latexes, dextran polymers, epoxies, polycarbonates, or combinations thereof. Conducting polymers and photoconductive materials can be used.

[0075] The substrate can take the form of an array, a photodiode, an optoelectronic sensor such as an optoelectronic semiconductor chip or optoelectronic thin-film semiconductor, or a biochip. The location(s) of probe(s) on the substrate can be addressable; this can be done in highly dense formats, and the location(s) can be microaddressable or nanoaddressable.

Diagnostic Samples

[0076] Diagnostic samples for use with the systems and in the methods of the present invention comprise nucleic acids suitable for providing RNAs expression information. In principle, the biological sample from which the expressed RNA is obtained and analyzed for target sequence expression can be any material suspected of comprising prostate cancer tissue or cells. The diagnostic sample can be a biological sample used directly in a method of the invention. Alternatively, the diagnostic sample can be a sample prepared from a biological sample.

[0077] In one embodiment, the sample or portion of the sample comprising or suspected of comprising cancer tissue or cells can be any source of biological material, including cells, tissue or fluid, including bodily fluids. Non-limiting examples of the source of the sample

include an aspirate, a needle biopsy, a cytology pellet, a bulk tissue preparation or a section thereof obtained for example by surgery or autopsy, lymph fluid, blood, plasma, serum, tumors, and organs. In some embodiments, the sample is from urine. Alternatively, the sample is from blood, plasma or serum. In some embodiments, the sample is from saliva.

[0078] The samples may be archival samples, having a known and documented medical outcome, or may be samples from current patients whose ultimate medical outcome is not yet known.

[0079] In some embodiments, the sample may be dissected prior to molecular analysis. The sample may be prepared via macrodissection of a bulk tumor specimen or portion thereof, or may be treated via microdissection, for example via Laser Capture Microdissection (LCM).

[0080] The sample may initially be provided in a variety of states, as fresh tissue, fresh frozen tissue, fine needle aspirates, and may be fixed or unfixed. Frequently, medical laboratories routinely prepare medical samples in a fixed state, which facilitates tissue storage. A variety of fixatives can be used to fix tissue to stabilize the morphology of cells, and may be used alone or in combination with other agents. Exemplary fixatives include crosslinking agents, alcohols, acetone, Bouin's solution, Zenker solution, Hely solution, osmic acid solution and Carnoy solution.

[0081] Crosslinking fixatives can comprise any agent suitable for forming two or more covalent bonds, for example an aldehyde. Sources of aldehydes typically used for fixation include formaldehyde, paraformaldehyde, glutaraldehyde or formalin. Preferably, the crosslinking agent comprises formaldehyde, which may be included in its native form or in the form of paraformaldehyde or formalin. One of skill in the art would appreciate that for samples in which crosslinking fixatives have been used special preparatory steps may be necessary including for example heating steps and proteinase-k digestion; see methods.

[0082] One or more alcohols may be used to fix tissue, alone or in combination with other fixatives. Exemplary alcohols used for fixation include methanol, ethanol and isopropanol.

[0083] Formalin fixation is frequently used in medical laboratories. Formalin comprises both an alcohol, typically methanol, and formaldehyde, both of which can act to fix a biological sample.

[0084] Whether fixed or unfixed, the biological sample may optionally be embedded in an embedding medium. Exemplary embedding media used in histology including paraffin, Tissue-Tek® V.I.P.TM, Paramat, Paramat Extra, Paraplast, Paraplast X-tra, Paraplast Plus, Peel Away Paraffin Embedding Wax, Polyester Wax, Carbowax Polyethylene Glycol, PolyfinTM, Tissue Freezing Medium TFMFM, Cryo-GefTM, and OCT Compound (Electron Microscopy Sciences, Hatfield, PA). Prior to molecular analysis, the embedding material may

be removed via any suitable techniques, as known in the art. For example, where the sample is embedded in wax, the embedding material may be removed by extraction with organic solvent(s), for example xylenes. Kits are commercially available for removing embedding media from tissues. Samples or sections thereof may be subjected to further processing steps as needed, for example serial hydration or dehydration steps.

[0085] In some embodiments, the sample is a fixed, wax-embedded biological sample. Frequently, samples from medical laboratories are provided as fixed, wax-embedded samples, most commonly as formalin-fixed, paraffin embedded (FFPE) tissues.

[0086] Whatever the source of the biological sample, the target polynucleotide that is ultimately assayed can be prepared synthetically (in the case of control sequences), but typically is purified from the biological source and subjected to one or more preparative steps. The RNA may be purified to remove or diminish one or more undesired components from the biological sample or to concentrate it. Conversely, where the RNA is too concentrated for the particular assay, it may be diluted.

RNA Extraction

[0087] RNA can be extracted and purified from biological samples using any suitable technique. A number of techniques are known in the art, and several are commercially available (e.g., FormaPure nucleic acid extraction kit, Agencourt Biosciences, Beverly MA, High Pure FFPE RNA Micro Kit, Roche Applied Science, Indianapolis, IN). RNA can be extracted from frozen tissue sections using TRIzol (Invitrogen, Carlsbad, CA) and purified using RNeasy Protect kit (Qiagen, Valencia, CA). RNA can be further purified using DNase I treatment (Ambion, Austin, TX) to eliminate any contaminating DNA. RNA concentrations can be made using a Nanodrop ND-1000 spectrophotometer (Nanodrop Technologies, Rockland, DE). RNA can be further purified to eliminate contaminants that interfere with cDNA synthesis by cold sodium acetate precipitation. RNA integrity can be evaluated by running electropherograms, and RNA integrity number (RIN, a correlative measure that indicates intactness of mRNA) can be determined using the RNA 6000 PicoAssay for the Bioanalyzer 2100 (Agilent Technologies, Santa Clara, CA).

Kits

[0088] Kits for performing the desired method(s) are also provided, and comprise a container or housing for holding the components of the kit, one or more vessels containing one or more nucleic acid(s), and optionally one or more vessels containing one or more reagents. The reagents include those described in the composition of matter section above, and those reagents useful for performing the methods described, including amplification reagents, and may include one or more probes, primers or primer pairs, enzymes (including polymerases

and ligases), intercalating dyes, labeled probes, and labels that can be incorporated into amplification products.

[0089] In some embodiments, the kit comprises primers or primer pairs specific for those subsets and combinations of target sequences described herein. The primers or pairs of primers suitable for selectively amplifying the target sequences. The kit may comprise at least two, three, four or five primers or pairs of primers suitable for selectively amplifying one or more targets. The kit may comprise at least 5, 10, 15, 20, 30, 40, 50, 60, 70, 80, 90, 100 or more primers or pairs of primers suitable for selectively amplifying one or more targets.

[0090] In some embodiments, the primers or primer pairs of the kit, when used in an amplification reaction, specifically amplify a non-coding target, coding target, exonic, or non-exonic target described herein, a nucleic acid sequence corresponding to a target selected from Table 8, Table 9 or SEQ ID NOs: 1-1029, an RNA form thereof, or a complement to either thereof. The kit may include a plurality of such primers or primer pairs which can specifically amplify a corresponding plurality of different amplify a non-coding target, coding target, exonic, or non-exonic transcript described herein, a nucleic acid sequence corresponding to a target selected from Table 8, Table 9 or SEQ ID NOs: 1-1029, RNA forms thereof, or complements thereto. At least two, three, four or five primers or pairs of primers suitable for selectively amplifying the one or more targets can be provided in kit form. In some embodiments, the kit comprises from five to fifty primers or pairs of primers suitable for amplifying the one or more targets.

[0091] The reagents may independently be in liquid or solid form. The reagents may be provided in mixtures. Control samples and/or nucleic acids may optionally be provided in the kit. Control samples may include tissue and/or nucleic acids obtained from or representative of tumor samples from patients showing no evidence of disease, as well as tissue and/or nucleic acids obtained from or representative of tumor samples from patients that develop systemic cancer.

[0092] The nucleic acids may be provided in an array format, and thus an array or microarray may be included in the kit. The kit optionally may be certified by a government agency for use in prognosing the disease outcome of cancer patients and/or for designating a treatment modality.

[0093] Instructions for using the kit to perform one or more methods of the invention can be provided with the container, and can be provided in any fixed medium. The instructions may be located inside or outside the container or housing, and/or may be printed on the interior or exterior of any surface thereof. A kit may be in multiplex form for concurrently detecting

and/or quantitating one or more different target polynucleotides representing the expressed target sequences.

Amplification and Hybridization

[0094] Following sample collection and nucleic acid extraction, the nucleic acid portion of the sample comprising RNA that is or can be used to prepare the target polynucleotide(s) of interest can be subjected to one or more preparative reactions. These preparative reactions can include *in vitro* transcription (IVT), labeling, fragmentation, amplification and other reactions. mRNA can first be treated with reverse transcriptase and a primer to create cDNA prior to detection, quantitation and/or amplification; this can be done *in vitro* with purified mRNA or *in situ*, e.g., in cells or tissues affixed to a slide.

[0095] By "amplification" is meant any process of producing at least one copy of a nucleic acid, in this case an expressed RNA, and in many cases produces multiple copies. An amplification product can be RNA or DNA, and may include a complementary strand to the expressed target sequence. DNA amplification products can be produced initially through reverse translation and then optionally from further amplification reactions. The amplification product may include all or a portion of a target sequence, and may optionally be labeled. A variety of amplification methods are suitable for use, including polymerase-based methods and ligation-based methods. Exemplary amplification techniques include the polymerase chain reaction method (PCR), the ligase chain reaction (LCR), ribozyme-based methods, self-sustained sequence replication (3SR), nucleic acid sequence-based amplification (NASBA), the use of Q Beta replicase, reverse transcription, nick translation, and the like.

[0096] Asymmetric amplification reactions may be used to preferentially amplify one strand representing the target sequence that is used for detection as the target polynucleotide. In some cases, the presence and/or amount of the amplification product itself may be used to determine the expression level of a given target sequence. In other instances, the amplification product may be used to hybridize to an array or other substrate comprising sensor polynucleotides which are used to detect and/or quantitate target sequence expression.

[0097] The first cycle of amplification in polymerase-based methods typically forms a primer extension product complementary to the template strand. If the template is single-stranded RNA, a polymerase with reverse transcriptase activity is used in the first amplification to reverse transcribe the RNA to DNA, and additional amplification cycles can be performed to copy the primer extension products. The primers for a PCR must, of course, be designed to hybridize to regions in their corresponding template that can produce an amplifiable segment; thus, each primer must hybridize so that its 3' nucleotide is paired to a nucleotide in its

complementary template strand that is located 3' from the 3' nucleotide of the primer used to replicate that complementary template strand in the PCR.

[0098] The target polynucleotide can be amplified by contacting one or more strands of the target polynucleotide with a primer and a polymerase having suitable activity to extend the primer and copy the target polynucleotide to produce a full-length complementary polynucleotide or a smaller portion thereof. Any enzyme having a polymerase activity that can copy the target polynucleotide can be used, including DNA polymerases, RNA polymerases, reverse transcriptases, enzymes having more than one type of polymerase or enzyme activity. The enzyme can be thermolabile or thermostable. Mixtures of enzymes can also be used. Exemplary enzymes include: DNA polymerases such as DNA Polymerase I ("Pol I"), the Klenow fragment of Pol I, T4, T7, Sequenase® T7, Sequenase® Version 2.0 T7, *Tub*, *Taq*, *Tth*, *Pfic*, *Pfu*, *Tsp*, *Tfl*, *Tli* and *Pyrococcus sp* GB-D DNA polymerases; RNA polymerases such as *E. coil*, SP6, T3 and T7 RNA polymerases; and reverse transcriptases such as AMV, M-MuLV, MMLV, RNase H MMLV (SuperScript®), SuperScript® II, ThermoScript®, HIV-1, and RAV2 reverse transcriptases. All of these enzymes are commercially available. Exemplary polymerases with multiple specificities include RAV2 and *Tli* (exo-) polymerases. Exemplary thermostable polymerases include *Tub*, *Taq*, *Tth*, *Pfic*, *Pfu*, *Tsp*, *Tfl*, *Tli* and *Pyrococcus sp*. GB-D DNA polymerases.

[0099] Suitable reaction conditions are chosen to permit amplification of the target polynucleotide, including pH, buffer, ionic strength, presence and concentration of one or more salts, presence and concentration of reactants and cofactors such as nucleotides and magnesium and/or other metal ions (e.g., manganese), optional cosolvents, temperature, thermal cycling profile for amplification schemes comprising a polymerase chain reaction, and may depend in part on the polymerase being used as well as the nature of the sample. Cosolvents include formamide (typically at from about 2 to about 10 %), glycerol (typically at from about 5 to about 10 %), and DMSO (typically at from about 0.9 to about 10 %). Techniques may be used in the amplification scheme in order to minimize the production of false positives or artifacts produced during amplification. These include "touchdown" PCR, hot-start techniques, use of nested primers, or designing PCR primers so that they form stem-loop structures in the event of primer-dimer formation and thus are not amplified. Techniques to accelerate PCR can be used, for example centrifugal PCR, which allows for greater convection within the sample, and comprising infrared heating steps for rapid heating and cooling of the sample. One or more cycles of amplification can be performed. An excess of one primer can be used to produce an excess of one primer extension product during PCR; preferably, the primer extension product produced in excess is the amplification product to be

detected. A plurality of different primers may be used to amplify different target polynucleotides or different regions of a particular target polynucleotide within the sample.

[00100] An amplification reaction can be performed under conditions which allow an optionally labeled sensor polynucleotide to hybridize to the amplification product during at least part of an amplification cycle. When the assay is performed in this manner, real-time detection of this hybridization event can take place by monitoring for light emission or fluorescence during amplification, as known in the art.

[00101] Where the amplification product is to be used for hybridization to an array or microarray, a number of suitable commercially available amplification products are available. These include amplification kits available from NuGEN, Inc. (San Carlos, CA), including the WT-Ovation™ System, WT-Ovation™ System v2, WT-Ovation™ Pico System, WT-Ovation™ FFPE Exon Module, WT-Ovation™ FFPE Exon Module RiboAmp and RiboAmp^{Plus} RNA Amplification Kits (MDS Analytical Technologies (formerly Arcturus) (Mountain View, CA), Genisphere, Inc. (Hatfield, PA), including the RampUp Plus™ and SenseAmp™ RNA Amplification kits, alone or in combination. Amplified nucleic acids may be subjected to one or more purification reactions after amplification and labeling, for example using magnetic beads (e.g., RNAClean magnetic beads, Agencourt Biosciences).

[00102] Multiple RNA biomarkers can be analyzed using real-time quantitative multiplex RT-PCR platforms and other multiplexing technologies such as GenomeLab GeXP Genetic Analysis System (Beckman Coulter, Foster City, CA), SmartCycler® 9600 or GeneXpert® Systems (Cepheid, Sunnyvale, CA), ABI 7900 HT Fast Real Time PCR system (Applied Biosystems, Foster City, CA), LightCycler® 480 System (Roche Molecular Systems, Pleasanton, CA), xMAP 100 System (Luminex, Austin, TX) Solexa Genome Analysis System (Illumina, Hayward, CA), OpenArray Real Time qPCR (BioTrove, Woburn, MA) and BeadXpress System (Illumina, Hayward, CA).

Detection and/or Quantification of Target Sequences

[00103] Any method of detecting and/or quantitating the expression of the encoded target sequences can in principle be used in the invention. The expressed target sequences can be directly detected and/or quantitated, or may be copied and/or amplified to allow detection of amplified copies of the expressed target sequences or its complement.

[00104] Methods for detecting and/or quantifying a target can include Northern blotting, sequencing, array or microarray hybridization, by enzymatic cleavage of specific structures (e.g., an Invader® assay, Third Wave Technologies, e.g. as described in U.S. Pat. Nos. 5,846,717, 6,090,543; 6,001,567; 5,985,557; and 5,994,069) and amplification methods, e.g. RT-PCR, including in a TaqMan® assay (PE Biosystems, Foster City, Calif., e.g. as

described in U.S. Pat. Nos. 5,962,233 and 5,538,848), and may be quantitative or semi-quantitative, and may vary depending on the origin, amount and condition of the available biological sample. Combinations of these methods may also be used. For example, nucleic acids may be amplified, labeled and subjected to microarray analysis.

[00105] In some instances, target sequences may be detected by sequencing. Sequencing methods may comprise whole genome sequencing or exome sequencing. Sequencing methods such as Maxim-Gilbert, chain-termination, or high-throughput systems may also be used. Additional, suitable sequencing techniques include classic dideoxy sequencing reactions (Sanger method) using labeled terminators or primers and gel separation in slab or capillary, sequencing by synthesis using reversibly terminated labeled nucleotides, pyrosequencing, 454 sequencing, allele specific hybridization to a library of labeled oligonucleotide probes, sequencing by synthesis using allele specific hybridization to a library of labeled clones that is followed by ligation, real time monitoring of the incorporation of labeled nucleotides during a polymerization step, and SOLiD sequencing.

[00106] Additional methods for detecting and/or quantifying a target include single-molecule sequencing (e.g., Helicos, PacBio), sequencing by synthesis (e.g., Illumina, Ion Torrent), sequencing by ligation (e.g., ABI SOLiD), sequencing by hybridization (e.g., Complete Genomics), in situ hybridization, bead-array technologies (e.g., Luminex xMAP, Illumina BeadChips), branched DNA technology (e.g., Panomics, Genisphere). Sequencing methods may use fluorescent (e.g., Illumina) or electronic (e.g., Ion Torrent, Oxford Nanopore) methods of detecting nucleotides.

Reverse Transcription for QRT-PCR Analysis

[00107] Reverse transcription can be performed by any method known in the art. For example, reverse transcription may be performed using the Omniscript kit (Qiagen, Valencia, CA), Superscript III kit (Invitrogen, Carlsbad, CA), for RT-PCR. Target-specific priming can be performed in order to increase the sensitivity of detection of target sequences and generate target-specific cDNA.

TaqMan[®] Gene Expression Analysis

[00108] TaqMan[®] RT-PCR can be performed using Applied Biosystems Prism (ABI) 7900 HT instruments in a 5 1.11 volume with target sequence-specific cDNA equivalent to 1 ng total RNA.

[00109] Primers and probes concentrations for TaqMan analysis are added to amplify fluorescent amplicons using PCR cycling conditions such as 95°C for 10 minutes for one cycle, 95°C for 20 seconds, and 60°C for 45 seconds for 40 cycles. A reference sample can

be assayed to ensure reagent and process stability. Negative controls (e.g., no template) should be assayed to monitor any exogenous nucleic acid contamination.

Classification Arrays

[00110] The present invention contemplates that a probe set or probes derived therefrom may be provided in an array format. In the context of the present invention, an "array" is a spatially or logically organized collection of polynucleotide probes. An array comprising probes specific for a coding target, non-coding target, or a combination thereof may be used. Alternatively, an array comprising probes specific for two or more of transcripts of a target selected from Table 8, Table 9 or SEQ ID NOs: 1-1029 or a product derived thereof can be used. Desirably, an array may be specific for 5, 10, 15, 20, 25, 30, 40, 50 or more of transcripts of a target selected from Table 8, Table 9 or SEQ ID NOs: 1-1029. Expression of these sequences may be detected alone or in combination with other transcripts. In some embodiments, an array is used which comprises a wide range of sensor probes for prostate-specific expression products, along with appropriate control sequences. In some instances, the array may comprise the Human Exon 1.0 ST Array (HuEx 1.0 ST, Affymetrix, Inc., Santa Clara, CA.).

[00111] Typically the polynucleotide probes are attached to a solid substrate and are ordered so that the location (on the substrate) and the identity of each are known. The polynucleotide probes can be attached to one of a variety of solid substrates capable of withstanding the reagents and conditions necessary for use of the array. Examples include, but are not limited to, polymers, such as (poly)tetrafluoroethylene, (poly)vinylidenedifluoride, polystyrene, polycarbonate, polypropylene and polystyrene; ceramic; silicon; silicon dioxide; modified silicon; (fused) silica, quartz or glass; functionalized glass; paper, such as filter paper; diazotized cellulose; nitrocellulose filter; nylon membrane; and polyacrylamide gel pad. Substrates that are transparent to light are useful for arrays that may be used in an assay that involves optical detection.

[00112] Examples of array formats include membrane or filter arrays (for example, nitrocellulose, nylon arrays), plate arrays (for example, multiwell, such as a 24-, 96-, 256-, 384-, 864- or 1536-well, microtitre plate arrays), pin arrays, and bead arrays (for example, in a liquid "slurry"). Arrays on substrates such as glass or ceramic slides are often referred to as chip arrays or "chips." Such arrays are well known in the art. In one embodiment of the present invention, the Cancer Prognosticarray is a chip.

Data Analysis

[00113] In some embodiments, one or more pattern recognition methods can be used in analyzing the expression level of target sequences. The pattern recognition method can

comprise a linear combination of expression levels, or a nonlinear combination of expression levels. In some embodiments, expression measurements for RNA transcripts or combinations of RNA transcript levels are formulated into linear or non-linear models or algorithms (e.g., an 'expression signature') and converted into a likelihood score. This likelihood score indicates the probability that a biological sample is from a patient who may exhibit no evidence of disease, who may exhibit systemic cancer, or who may exhibit biochemical recurrence. The likelihood score can be used to distinguish these disease states. The models and/or algorithms can be provided in machine readable format, and may be used to correlate expression levels or an expression profile with a disease state, and/or to designate a treatment modality for a patient or class of patients.

[00114] Assaying the expression level for a plurality of targets may comprise the use of an algorithm or classifier. Array data can be managed, classified, and analyzed using techniques known in the art. Assaying the expression level for a plurality of targets may comprise probe set modeling and data pre-processing. Probe set modeling and data pre-processing can be derived using the Robust Multi-Array (RMA) algorithm or variants GC-RMA, *f*RMA, Probe Logarithmic Intensity Error (PLIER) algorithm or variant iterPLIER. Variance or intensity filters can be applied to pre-process data using the RMA algorithm, for example by removing target sequences with a standard deviation of < 10 or a mean intensity of < 100 intensity units of a normalized data range, respectively.

[00115] Alternatively, assaying the expression level for a plurality of targets may comprise the use of a machine learning algorithm. The machine learning algorithm may comprise a supervised learning algorithm. Examples of supervised learning algorithms may include Average One-Dependence Estimators (AODE), Artificial neural network (e.g., Backpropagation), Bayesian statistics (e.g., Naive Bayes classifier, Bayesian network, Bayesian knowledge base), Case-based reasoning, Decision trees, Inductive logic programming, Gaussian process regression, Group method of data handling (GMDH), Learning Automata, Learning Vector Quantization, Minimum message length (decision trees, decision graphs, etc.), Lazy learning, Instance-based learning Nearest Neighbor Algorithm, Analogical modeling, Probably approximately correct learning (PAC) learning, Ripple down rules, a knowledge acquisition methodology, Symbolic machine learning algorithms, Subsymbolic machine learning algorithms, Support vector machines, Random Forests, Ensembles of classifiers, Bootstrap aggregating (bagging), and Boosting. Supervised learning may comprise ordinal classification such as regression analysis and Information fuzzy networks (IFN). Alternatively, supervised learning methods may comprise statistical classification, such as AODE, Linear classifiers (e.g., Fisher's linear discriminant, Logistic

regression, Naive Bayes classifier, Perceptron, and Support vector machine), quadratic classifiers, k-nearest neighbor, Boosting, Decision trees (e.g., C4.5, Random forests), Bayesian networks, and Hidden Markov models.

[00116] The machine learning algorithms may also comprise an unsupervised learning algorithm. Examples of unsupervised learning algorithms may include artificial neural network, Data clustering, Expectation-maximization algorithm, Self-organizing map, Radial basis function network, Vector Quantization, Generative topographic map, Information bottleneck method, and IBSEAD. Unsupervised learning may also comprise association rule learning algorithms such as Apriori algorithm, Eclat algorithm and FP-growth algorithm. Hierarchical clustering, such as Single-linkage clustering and Conceptual clustering, may also be used. Alternatively, unsupervised learning may comprise partitional clustering such as K-means algorithm and Fuzzy clustering.

[00117] In some instances, the machine learning algorithms comprise a reinforcement learning algorithm. Examples of reinforcement learning algorithms include, but are not limited to, temporal difference learning, Q-learning and Learning Automata. Alternatively, the machine learning algorithm may comprise Data Pre-processing.

[00118] Preferably, the machine learning algorithms may include, but are not limited to, Average One-Dependence Estimators (AODE), Fisher's linear discriminant, Logistic regression, Perceptron, Multilayer Perceptron, Artificial Neural Networks, Support vector machines, Quadratic classifiers, Boosting, Decision trees, C4.5, Bayesian networks, Hidden Markov models, High-Dimensional Discriminant Analysis, and Gaussian Mixture Models. The machine learning algorithm may comprise support vector machines, Naïve Bayes classifier, k-nearest neighbor, high-dimensional discriminant analysis, or Gaussian mixture models. In some instances, the machine learning algorithm comprises Random Forests.

Cancer

[00119] The systems, compositions and methods disclosed herein may be used to diagnosis, monitor and/or predict the status or outcome of a cancer. Generally, a cancer is characterized by the uncontrolled growth of abnormal cells anywhere in a body. The abnormal cells may be termed cancer cells, malignant cells, or tumor cells. Cancer is not confined to humans; animals and other living organisms can get cancer.

[00120] In some instances, the cancer may be malignant. Alternatively, the cancer may be benign. The cancer may be a recurrent and/or refractory cancer. Most cancers can be classified as a carcinoma, sarcoma, leukemia, lymphoma, myeloma, or a central nervous system cancer.

[00121] The cancer may be a sarcoma. Sarcomas are cancers of the bone, cartilage, fat, muscle, blood vessels, or other connective or supportive tissue. Sarcomas include, but are not limited to, bone cancer, fibrosarcoma, chondrosarcoma, Ewing's sarcoma, malignant hemangioendothelioma, malignant schwannoma, bilateral vestibular schwannoma, osteosarcoma, soft tissue sarcomas (e.g. alveolar soft part sarcoma, angiosarcoma, cystosarcoma phylloides, dermatofibrosarcoma, desmoid tumor, epithelioid sarcoma, extraskeletal osteosarcoma, fibrosarcoma, hemangiopericytoma, hemangiosarcoma, Kaposi's sarcoma, leiomyosarcoma, liposarcoma, lymphangiosarcoma, lymphosarcoma, malignant fibrous histiocyoma, neurofibrosarcoma, rhabdomyosarcoma, and synovial sarcoma).

[00122] Alternatively, the cancer may be a carcinoma. Carcinomas are cancers that begin in the epithelial cells, which are cells that cover the surface of the body, produce hormones, and make up glands. By way of non-limiting example, carcinomas include breast cancer, pancreatic cancer, lung cancer, colon cancer, colorectal cancer, rectal cancer, kidney cancer, bladder cancer, stomach cancer, prostate cancer, liver cancer, ovarian cancer, brain cancer, vaginal cancer, vulvar cancer, uterine cancer, oral cancer, penic cancer, testicular cancer, esophageal cancer, skin cancer, cancer of the fallopian tubes, head and neck cancer, gastrointestinal stromal cancer, adenocarcinoma, cutaneous or intraocular melanoma, cancer of the anal region, cancer of the small intestine, cancer of the endocrine system, cancer of the thyroid gland, cancer of the parathyroid gland, cancer of the adrenal gland, cancer of the urethra, cancer of the renal pelvis, cancer of the ureter, cancer of the endometrium, cancer of the cervix, cancer of the pituitary gland, neoplasms of the central nervous system (CNS), primary CNS lymphoma, brain stem glioma, and spinal axis tumors. In some instances, the cancer is a skin cancer, such as a basal cell carcinoma, squamous, melanoma, nonmelanoma, or actinic (solar) keratosis. Preferably, the cancer is a prostate cancer. Alternatively, the cancer may be a thyroid cancer, bladder cancer, or pancreatic cancer.

[00123] In some instances, the cancer is a lung cancer. Lung cancer can start in the airways that branch off the trachea to supply the lungs (bronchi) or the small air sacs of the lung (the alveoli). Lung cancers include non-small cell lung carcinoma (NSCLC), small cell lung carcinoma, and mesothelioma. Examples of NSCLC include squamous cell carcinoma, adenocarcinoma, and large cell carcinoma. The mesothelioma may be a cancerous tumor of the lining of the lung and chest cavity (pleura) or lining of the abdomen (peritoneum). The mesothelioma may be due to asbestos exposure. The cancer may be a brain cancer, such as a glioblastoma.

[00124] Alternatively, the cancer may be a central nervous system (CNS) tumor. CNS tumors may be classified as gliomas or nongliomas. The glioma may be malignant glioma,

high grade glioma, diffuse intrinsic pontine glioma. Examples of gliomas include astrocytomas, oligodendrogliomas (or mixtures of oligodendroglioma and astrocytoma elements), and ependymomas. Astrocytomas include, but are not limited to, low-grade astrocytomas, anaplastic astrocytomas, glioblastoma multiforme, pilocytic astrocytoma, pleomorphic xanthoastrocytoma, and subependymal giant cell astrocytoma. Oligodendrogliomas include low-grade oligodendrogliomas (or oligoastrocytomas) and anaplastic oligodendrogliomas. Nongliomas include meningiomas, pituitary adenomas, primary CNS lymphomas, and medulloblastomas. In some instances, the cancer is a meningioma.

[00125] The cancer may be a leukemia. The leukemia may be an acute lymphocytic leukemia, acute myelocytic leukemia, chronic lymphocytic leukemia, or chronic myelocytic leukemia. Additional types of leukemias include hairy cell leukemia, chronic myelomonocytic leukemia, and juvenile myelomonocytic-leukemia.

[00126] In some instances, the cancer is a lymphoma. Lymphomas are cancers of the lymphocytes and may develop from either B or T lymphocytes. The two major types of lymphoma are Hodgkin's lymphoma, previously known as Hodgkin's disease, and non-Hodgkin's lymphoma. Hodgkin's lymphoma is marked by the presence of the Reed-Sternberg cell. Non-Hodgkin's lymphomas are all lymphomas which are not Hodgkin's lymphoma. Non-Hodgkin lymphomas may be indolent lymphomas and aggressive lymphomas. Non-Hodgkin's lymphomas include, but are not limited to, diffuse large B cell lymphoma, follicular lymphoma, mucosa-associated lymphatic tissue lymphoma (MALT), small cell lymphocytic lymphoma, mantle cell lymphoma, Burkitt's lymphoma, mediastinal large B cell lymphoma, Waldenström macroglobulinemia, nodal marginal zone B cell lymphoma (NMZL), splenic marginal zone lymphoma (SMZL), extranodal marginal zone B cell lymphoma, intravascular large B cell lymphoma, primary effusion lymphoma, and lymphomatoid granulomatosis.

Cancer Staging

[00127] Diagnosing, predicting, or monitoring a status or outcome of a cancer may comprise determining the stage of the cancer. Generally, the stage of a cancer is a description (usually numbers I to IV with IV having more progression) of the extent the cancer has spread. The stage often takes into account the size of a tumor, how deeply it has penetrated, whether it has invaded adjacent organs, how many lymph nodes it has metastasized to (if any), and whether it has spread to distant organs. Staging of cancer can be used as a predictor of survival, and cancer treatment may be determined by staging. Determining the stage of the cancer may

occur before, during, or after treatment. The stage of the cancer may also be determined at the time of diagnosis.

[00128] Cancer staging can be divided into a clinical stage and a pathologic stage. Cancer staging may comprise the TNM classification. Generally, the TNM Classification of Malignant Tumours (TNM) is a cancer staging system that describes the extent of cancer in a patient's body. T may describe the size of the tumor and whether it has invaded nearby tissue, N may describe regional lymph nodes that are involved, and M may describe distant metastasis (spread of cancer from one body part to another). In the TNM (Tumor, Node, Metastasis) system, clinical stage and pathologic stage are denoted by a small "c" or "p" before the stage (e.g., cT3N1M0 or pT2N0).

[00129] Often, clinical stage and pathologic stage may differ. Clinical stage may be based on all of the available information obtained before a surgery to remove the tumor. Thus, it may include information about the tumor obtained by physical examination, radiologic examination, and endoscopy. Pathologic stage can add additional information gained by examination of the tumor microscopically by a pathologist. Pathologic staging can allow direct examination of the tumor and its spread, contrasted with clinical staging which may be limited by the fact that the information is obtained by making indirect observations at a tumor which is still in the body. The TNM staging system can be used for most forms of cancer.

[00130] Alternatively, staging may comprise Ann Arbor staging. Generally, Ann Arbor staging is the staging system for lymphomas, both in Hodgkin's lymphoma (previously called Hodgkin's disease) and Non-Hodgkin lymphoma (abbreviated NHL). The stage may depend on both the place where the malignant tissue is located (as located with biopsy, CT scanning and increasingly positron emission tomography) and on systemic symptoms due to the lymphoma ("B symptoms": night sweats, weight loss of >10% or fevers). The principal stage may be determined by location of the tumor. Stage I may indicate that the cancer is located in a single region, usually one lymph node and the surrounding area. Stage I often may not have outward symptoms. Stage II can indicate that the cancer is located in two separate regions, an affected lymph node or organ and a second affected area, and that both affected areas are confined to one side of the diaphragm - that is, both are above the diaphragm, or both are below the diaphragm. Stage III often indicates that the cancer has spread to both sides of the diaphragm, including one organ or area near the lymph nodes or the spleen. Stage IV may indicate diffuse or disseminated involvement of one or more extralymphatic organs, including any involvement of the liver, bone marrow, or nodular involvement of the lungs.

[00131] Modifiers may also be appended to some stages. For example, the letters A, B, E, X, or S can be appended to some stages. Generally, A or B may indicate the absence of

constitutional (B-type) symptoms is denoted by adding an "A" to the stage; the presence is denoted by adding a "B" to the stage. E can be used if the disease is "extranodal" (not in the lymph nodes) or has spread from lymph nodes to adjacent tissue. X is often used if the largest deposit is >10 cm large ("bulky disease"), or whether the mediastinum is wider than 1/3 of the chest on a chest X-ray. S may be used if the disease has spread to the spleen.

[00132] The nature of the staging may be expressed with CS or PS. CS may denote that the clinical stage as obtained by doctor's examinations and tests. PS may denote that the pathological stage as obtained by exploratory laparotomy (surgery performed through an abdominal incision) with splenectomy (surgical removal of the spleen).

Therapeutic regimens

[00133] Diagnosing, predicting, or monitoring a status or outcome of a cancer may comprise treating a cancer or preventing a cancer progression. In addition, diagnosing, predicting, or monitoring a status or outcome of a cancer may comprise identifying or predicting responders to an anti-cancer therapy. In some instances, diagnosing, predicting, or monitoring may comprise determining a therapeutic regimen. Determining a therapeutic regimen may comprise administering an anti-cancer therapy. Alternatively, determining a therapeutic regimen may comprise modifying, recommending, continuing or discontinuing an anti-cancer regimen. In some instances, if the sample expression patterns are consistent with the expression pattern for a known disease or disease outcome, the expression patterns can be used to designate one or more treatment modalities (e.g., therapeutic regimens, anti-cancer regimen). An anti-cancer regimen may comprise one or more anti-cancer therapies. Examples of anti-cancer therapies include surgery, chemotherapy, radiation therapy, immunotherapy/biological therapy, photodynamic therapy.

[00134] Surgical oncology uses surgical methods to diagnose, stage, and treat cancer, and to relieve certain cancer-related symptoms. Surgery may be used to remove the tumor (e.g., excisions, resections, debulking surgery), reconstruct a part of the body (e.g., restorative surgery), and/or to relieve symptoms such as pain (e.g., palliative surgery). Surgery may also include cryosurgery. Cryosurgery (also called cryotherapy) may use extreme cold produced by liquid nitrogen (or argon gas) to destroy abnormal tissue. Cryosurgery can be used to treat external tumors, such as those on the skin. For external tumors, liquid nitrogen can be applied directly to the cancer cells with a cotton swab or spraying device. Cryosurgery may also be used to treat tumors inside the body (internal tumors and tumors in the bone). For internal tumors, liquid nitrogen or argon gas may be circulated through a hollow instrument called a cryoprobe, which is placed in contact with the tumor. An ultrasound or MRI may be used to guide the cryoprobe and monitor the freezing of the cells, thus limiting damage to nearby

healthy tissue. A ball of ice crystals may form around the probe, freezing nearby cells. Sometimes more than one probe is used to deliver the liquid nitrogen to various parts of the tumor. The probes may be put into the tumor during surgery or through the skin (percutaneously). After cryosurgery, the frozen tissue thaws and may be naturally absorbed by the body (for internal tumors), or may dissolve and form a scab (for external tumors).

[00135] Chemotherapeutic agents may also be used for the treatment of cancer. Examples of chemotherapeutic agents include alkylating agents, anti-metabolites, plant alkaloids and terpenoids, vinca alkaloids, podophyllotoxin, taxanes, topoisomerase inhibitors, and cytotoxic antibiotics. Cisplatin, carboplatin, and oxaliplatin are examples of alkylating agents. Other alkylating agents include mechlorethamine, cyclophosphamide, chlorambucil, ifosfamide. Alkylating agents may impair cell function by forming covalent bonds with the amino, carboxyl, sulfhydryl, and phosphate groups in biologically important molecules. Alternatively, alkylating agents may chemically modify a cell's DNA.

[00136] Anti-metabolites are another example of chemotherapeutic agents. Anti-metabolites may masquerade as purines or pyrimidines and may prevent purines and pyrimidines from becoming incorporated in to DNA during the "S" phase (of the cell cycle), thereby stopping normal development and division. Antimetabolites may also affect RNA synthesis. Examples of metabolites include azathioprine and mercaptopurine.

[00137] Alkaloids may be derived from plants and block cell division may also be used for the treatment of cancer. Alkylolds may prevent microtubule function. Examples of alkaloids are vinca alkaloids and taxanes. Vinca alkaloids may bind to specific sites on tubulin and inhibit the assembly of tubulin into microtubules (M phase of the cell cycle). The vinca alkaloids may be derived from the Madagascar periwinkle, *Catharanthus roseus* (formerly known as *Vinca rosea*). Examples of vinca alkaloids include, but are not limited to, vincristine, vinblastine, vinorelbine, or vindesine. Taxanes are diterpenes produced by the plants of the genus *Taxus* (yews). Taxanes may be derived from natural sources or synthesized artificially. Taxanes include paclitaxel (Taxol) and docetaxel (Taxotere). Taxanes may disrupt microtubule function. Microtubules are essential to cell division, and taxanes may stabilize GDP-bound tubulin in the microtubule, thereby inhibiting the process of cell division. Thus, in essence, taxanes may be mitotic inhibitors. Taxanes may also be radiosensitizing and often contain numerous chiral centers.

[00138] Alternative chemotherapeutic agents include podophyllotoxin. Podophyllotoxin is a plant-derived compound that may help with digestion and may be used to produce cytostatic drugs such as etoposide and teniposide. They may prevent the cell from entering the G1 phase (the start of DNA replication) and the replication of DNA (the S phase).

[00139] Topoisomerases are essential enzymes that maintain the topology of DNA. Inhibition of type I or type II topoisomerases may interfere with both transcription and replication of DNA by upsetting proper DNA supercoiling. Some chemotherapeutic agents may inhibit topoisomerases. For example, some type I topoisomerase inhibitors include *camptothecins*: irinotecan and topotecan. Examples of type II inhibitors include amsacrine, etoposide, etoposide phosphate, and teniposide.

[00140] Another example of chemotherapeutic agents is cytotoxic antibiotics. Cytotoxic antibiotics are a group of antibiotics that are used for the treatment of cancer because they may interfere with DNA replication and/or protein synthesis. Cytotoxic antibiotics include, but are not limited to, actinomycin, anthracyclines, doxorubicin, daunorubicin, valrubicin, idarubicin, epirubicin, bleomycin, plicamycin, and mitomycin.

[00141] In some instances, the anti-cancer treatment may comprise radiation therapy. Radiation can come from a machine outside the body (external-beam radiation therapy) or from radioactive material placed in the body near cancer cells (internal radiation therapy, more commonly called brachytherapy). Systemic radiation therapy uses a radioactive substance, given by mouth or into a vein that travels in the blood to tissues throughout the body.

[00142] External-beam radiation therapy may be delivered in the form of photon beams (either x-rays or gamma rays). A photon is the basic unit of light and other forms of electromagnetic radiation. An example of external-beam radiation therapy is called 3-dimensional conformal radiation therapy (3D-CRT). 3D-CRT may use computer software and advanced treatment machines to deliver radiation to very precisely shaped target areas. Many other methods of external-beam radiation therapy are currently being tested and used in cancer treatment. These methods include, but are not limited to, intensity-modulated radiation therapy (IMRT), image-guided radiation therapy (IGRT), Stereotactic radiosurgery (SRS), Stereotactic body radiation therapy (SBRT), and proton therapy.

[00143] Intensity-modulated radiation therapy (IMRT) is an example of external-beam radiation and may use hundreds of tiny radiation beam-shaping devices, called collimators, to deliver a single dose of radiation. The collimators can be stationary or can move during treatment, allowing the intensity of the radiation beams to change during treatment sessions. This kind of dose modulation allows different areas of a tumor or nearby tissues to receive different doses of radiation. IMRT is planned in reverse (called inverse treatment planning). In inverse treatment planning, the radiation doses to different areas of the tumor and surrounding tissue are planned in advance, and then a high-powered computer program calculates the required number of beams and angles of the radiation treatment. In contrast,

during traditional (forward) treatment planning, the number and angles of the radiation beams are chosen in advance and computers calculate how much dose may be delivered from each of the planned beams. The goal of IMRT is to increase the radiation dose to the areas that need it and reduce radiation exposure to specific sensitive areas of surrounding normal tissue.

[00144] Another example of external-beam radiation is image-guided radiation therapy (IGRT). In IGRT, repeated imaging scans (CT, MRI, or PET) may be performed during treatment. These imaging scans may be processed by computers to identify changes in a tumor's size and location due to treatment and to allow the position of the patient or the planned radiation dose to be adjusted during treatment as needed. Repeated imaging can increase the accuracy of radiation treatment and may allow reductions in the planned volume of tissue to be treated, thereby decreasing the total radiation dose to normal tissue.

[00145] Tomotherapy is a type of image-guided IMRT. A tomotherapy machine is a hybrid between a CT imaging scanner and an external-beam radiation therapy machine. The part of the tomotherapy machine that delivers radiation for both imaging and treatment can rotate completely around the patient in the same manner as a normal CT scanner. Tomotherapy machines can capture CT images of the patient's tumor immediately before treatment sessions, to allow for very precise tumor targeting and sparing of normal tissue.

[00146] Stereotactic radiosurgery (SRS) can deliver one or more high doses of radiation to a small tumor. SRS uses extremely accurate image-guided tumor targeting and patient positioning. Therefore, a high dose of radiation can be given without excess damage to normal tissue. SRS can be used to treat small tumors with well-defined edges. It is most commonly used in the treatment of brain or spinal tumors and brain metastases from other cancer types. For the treatment of some brain metastases, patients may receive radiation therapy to the entire brain (called whole-brain radiation therapy) in addition to SRS. SRS requires the use of a head frame or other device to immobilize the patient during treatment to ensure that the high dose of radiation is delivered accurately.

[00147] Stereotactic body radiation therapy (SBRT) delivers radiation therapy in fewer sessions, using smaller radiation fields and higher doses than 3D-CRT in most cases. SBRT may treat tumors that lie outside the brain and spinal cord. Because these tumors are more likely to move with the normal motion of the body, and therefore cannot be targeted as accurately as tumors within the brain or spine, SBRT is usually given in more than one dose. SBRT can be used to treat small, isolated tumors, including cancers in the lung and liver. SBRT systems may be known by their brand names, such as the CyberKnife®.

[00148] In proton therapy, external-beam radiation therapy may be delivered by proton. Protons are a type of charged particle. Proton beams differ from photon beams mainly in the

way they deposit energy in living tissue. Whereas photons deposit energy in small packets all along their path through tissue, protons deposit much of their energy at the end of their path (called the Bragg peak) and deposit less energy along the way. Use of protons may reduce the exposure of normal tissue to radiation, possibly allowing the delivery of higher doses of radiation to a tumor.

[00149] Other charged particle beams such as electron beams may be used to irradiate superficial tumors, such as skin cancer or tumors near the surface of the body, but they cannot travel very far through tissue.

[00150] Internal radiation therapy (brachytherapy) is radiation delivered from radiation sources (radioactive materials) placed inside or on the body. Several brachytherapy techniques are used in cancer treatment. Interstitial brachytherapy may use a radiation source placed within tumor tissue, such as within a prostate tumor. Intracavitary brachytherapy may use a source placed within a surgical cavity or a body cavity, such as the chest cavity, near a tumor. Episcleral brachytherapy, which may be used to treat melanoma inside the eye, may use a source that is attached to the eye. In brachytherapy, radioactive isotopes can be sealed in tiny pellets or “seeds.” These seeds may be placed in patients using delivery devices, such as needles, catheters, or some other type of carrier. As the isotopes decay naturally, they give off radiation that may damage nearby cancer cells. Brachytherapy may be able to deliver higher doses of radiation to some cancers than external-beam radiation therapy while causing less damage to normal tissue.

[00151] Brachytherapy can be given as a low-dose-rate or a high-dose-rate treatment. In low-dose-rate treatment, cancer cells receive continuous low-dose radiation from the source over a period of several days. In high-dose-rate treatment, a robotic machine attached to delivery tubes placed inside the body may guide one or more radioactive sources into or near a tumor, and then removes the sources at the end of each treatment session. High-dose-rate treatment can be given in one or more treatment sessions. An example of a high-dose-rate treatment is the MammoSite® system. Brachytherapy may be used to treat patients with breast cancer who have undergone breast-conserving surgery.

[00152] The placement of brachytherapy sources can be temporary or permanent. For permanent brachytherapy, the sources may be surgically sealed within the body and left there, even after all of the radiation has been given off. In some instances, the remaining material (in which the radioactive isotopes were sealed) does not cause any discomfort or harm to the patient. Permanent brachytherapy is a type of low-dose-rate brachytherapy. For temporary brachytherapy, tubes (catheters) or other carriers are used to deliver the radiation sources, and both the carriers and the radiation sources are removed after treatment. Temporary

brachytherapy can be either low-dose-rate or high-dose-rate treatment. Brachytherapy may be used alone or in addition to external-beam radiation therapy to provide a “boost” of radiation to a tumor while sparing surrounding normal tissue.

[00153] In systemic radiation therapy, a patient may swallow or receive an injection of a radioactive substance, such as radioactive iodine or a radioactive substance bound to a monoclonal antibody. Radioactive iodine (^{131}I) is a type of systemic radiation therapy commonly used to help treat cancer, such as thyroid cancer. Thyroid cells naturally take up radioactive iodine. For systemic radiation therapy for some other types of cancer, a monoclonal antibody may help target the radioactive substance to the right place. The antibody joined to the radioactive substance travels through the blood, locating and killing tumor cells. For example, the drug ibritumomab tiuxetan (Zevalin®) may be used for the treatment of certain types of B-cell non-Hodgkin lymphoma (NHL). The antibody part of this drug recognizes and binds to a protein found on the surface of B lymphocytes. The combination drug regimen of tositumomab and iodine I 131 tositumomab (Bexxar®) may be used for the treatment of certain types of cancer, such as NHL. In this regimen, nonradioactive tositumomab antibodies may be given to patients first, followed by treatment with tositumomab antibodies that have ^{131}I attached. Tositumomab may recognize and bind to the same protein on B lymphocytes as ibritumomab. The nonradioactive form of the antibody may help protect normal B lymphocytes from being damaged by radiation from ^{131}I .

[00154] Some systemic radiation therapy drugs relieve pain from cancer that has spread to the bone (bone metastases). This is a type of palliative radiation therapy. The radioactive drugs samarium-153-lexidronam (Quadramet®) and strontium-89 chloride (Metastron®) are examples of radiopharmaceuticals may be used to treat pain from bone metastases.

[00155] Biological therapy (sometimes called immunotherapy, biotherapy, or biological response modifier (BRM) therapy) uses the body's immune system, either directly or indirectly, to fight cancer or to lessen the side effects that may be caused by some cancer treatments. Biological therapies include interferons, interleukins, colony-stimulating factors, monoclonal antibodies, vaccines, gene therapy, and nonspecific immunomodulating agents.

[00156] Interferons (IFNs) are types of cytokines that occur naturally in the body. Interferon alpha, interferon beta, and interferon gamma are examples of interferons that may be used in cancer treatment.

[00157] Like interferons, interleukins (ILs) are cytokines that occur naturally in the body and can be made in the laboratory. Many interleukins have been identified for the treatment of cancer. For example, interleukin-2 (IL-2 or aldesleukin), interleukin 7, and interleukin 12

have may be used as an anti-cancer treatment. IL-2 may stimulate the growth and activity of many immune cells, such as lymphocytes, that can destroy cancer cells. Interleukins may be used to treat a number of cancers, including leukemia, lymphoma, and brain, colorectal, ovarian, breast, kidney and prostate cancers.

[00158] Colony-stimulating factors (CSFs) (sometimes called hematopoietic growth factors) may also be used for the treatment of cancer. Some examples of CSFs include, but are not limited to, G-CSF (filgrastim) and GM-CSF (sargramostim). CSFs may promote the division of bone marrow stem cells and their development into white blood cells, platelets, and red blood cells. Bone marrow is critical to the body's immune system because it is the source of all blood cells. Because anticancer drugs can damage the body's ability to make white blood cells, red blood cells, and platelets, stimulation of the immune system by CSFs may benefit patients undergoing other anti-cancer treatment, thus CSFs may be combined with other anti-cancer therapies, such as chemotherapy. CSFs may be used to treat a large variety of cancers, including lymphoma, leukemia, multiple myeloma, melanoma, and cancers of the brain, lung, esophagus, breast, uterus, ovary, prostate, kidney, colon, and rectum.

[00159] Another type of biological therapy includes monoclonal antibodies (MOABs or MoABs). These antibodies may be produced by a single type of cell and may be specific for a particular antigen. To create MOABs, a human cancer cells may be injected into mice. In response, the mouse immune system can make antibodies against these cancer cells. The mouse plasma cells that produce antibodies may be isolated and fused with laboratory-grown cells to create "hybrid" cells called hybridomas. Hybridomas can indefinitely produce large quantities of these pure antibodies, or MOABs. MOABs may be used in cancer treatment in a number of ways. For instance, MOABs that react with specific types of cancer may enhance a patient's immune response to the cancer. MOABs can be programmed to act against cell growth factors, thus interfering with the growth of cancer cells.

[00160] MOABs may be linked to other anti-cancer therapies such as chemotherapeutics, radioisotopes (radioactive substances), other biological therapies, or other toxins. When the antibodies latch onto cancer cells, they deliver these anti-cancer therapies directly to the tumor, helping to destroy it. MOABs carrying radioisotopes may also prove useful in diagnosing certain cancers, such as colorectal, ovarian, and prostate.

[00161] Rituxan® (rituximab) and Herceptin® (trastuzumab) are examples of MOABs that may be used as a biological therapy. Rituxan may be used for the treatment of non-Hodgkin lymphoma. Herceptin can be used to treat metastatic breast cancer in patients with tumors that produce excess amounts of a protein called HER2. Alternatively, MOABs may be used

to treat lymphoma, leukemia, melanoma, and cancers of the brain, breast, lung, kidney, colon, rectum, ovary, prostate, and other areas.

[00162] Cancer vaccines are another form of biological therapy. Cancer vaccines may be designed to encourage the patient's immune system to recognize cancer cells. Cancer vaccines may be designed to treat existing cancers (therapeutic vaccines) or to prevent the development of cancer (prophylactic vaccines). Therapeutic vaccines may be injected in a person after cancer is diagnosed. These vaccines may stop the growth of existing tumors, prevent cancer from recurring, or eliminate cancer cells not killed by prior treatments. Cancer vaccines given when the tumor is small may be able to eradicate the cancer. On the other hand, prophylactic vaccines are given to healthy individuals before cancer develops. These vaccines are designed to stimulate the immune system to attack viruses that can cause cancer. By targeting these cancer-causing viruses, development of certain cancers may be prevented. For example, cervarix and gardasil are vaccines to treat human papilloma virus and may prevent cervical cancer. Therapeutic vaccines may be used to treat melanoma, lymphoma, leukemia, and cancers of the brain, breast, lung, kidney, ovary, prostate, pancreas, colon, and rectum. Cancer vaccines can be used in combination with other anti-cancer therapies.

[00163] Gene therapy is another example of a biological therapy. Gene therapy may involve introducing genetic material into a person's cells to fight disease. Gene therapy methods may improve a patient's immune response to cancer. For example, a gene may be inserted into an immune cell to enhance its ability to recognize and attack cancer cells. In another approach, cancer cells may be injected with genes that cause the cancer cells to produce cytokines and stimulate the immune system.

[00164] In some instances, biological therapy includes nonspecific immunomodulating agents. Nonspecific immunomodulating agents are substances that stimulate or indirectly augment the immune system. Often, these agents target key immune system cells and may cause secondary responses such as increased production of cytokines and immunoglobulins. Two nonspecific immunomodulating agents used in cancer treatment are bacillus Calmette-Guerin (BCG) and levamisole. BCG may be used in the treatment of superficial bladder cancer following surgery. BCG may work by stimulating an inflammatory, and possibly an immune, response. A solution of BCG may be instilled in the bladder. Levamisole is sometimes used along with fluorouracil (5-FU) chemotherapy in the treatment of stage III (Dukes' C) colon cancer following surgery. Levamisole may act to restore depressed immune function.

[00165] Photodynamic therapy (PDT) is an anti-cancer treatment that may use a drug, called a photosensitizer or photosensitizing agent, and a particular type of light. When

photosensitizers are exposed to a specific wavelength of light, they may produce a form of oxygen that kills nearby cells. A photosensitizer may be activated by light of a specific wavelength. This wavelength determines how far the light can travel into the body. Thus, photosensitizers and wavelengths of light may be used to treat different areas of the body with PDT.

[00166] In the first step of PDT for cancer treatment, a photosensitizing agent may be injected into the bloodstream. The agent may be absorbed by cells all over the body but may stay in cancer cells longer than it does in normal cells. Approximately 24 to 72 hours after injection, when most of the agent has left normal cells but remains in cancer cells, the tumor can be exposed to light. The photosensitizer in the tumor can absorb the light and produces an active form of oxygen that destroys nearby cancer cells. In addition to directly killing cancer cells, PDT may shrink or destroy tumors in two other ways. The photosensitizer can damage blood vessels in the tumor, thereby preventing the cancer from receiving necessary nutrients. PDT may also activate the immune system to attack the tumor cells.

[00167] The light used for PDT can come from a laser or other sources. Laser light can be directed through fiber optic cables (thin fibers that transmit light) to deliver light to areas inside the body. For example, a fiber optic cable can be inserted through an endoscope (a thin, lighted tube used to look at tissues inside the body) into the lungs or esophagus to treat cancer in these organs. Other light sources include light-emitting diodes (LEDs), which may be used for surface tumors, such as skin cancer. PDT is usually performed as an outpatient procedure. PDT may also be repeated and may be used with other therapies, such as surgery, radiation, or chemotherapy.

[00168] Extracorporeal photopheresis (ECP) is a type of PDT in which a machine may be used to collect the patient's blood cells. The patient's blood cells may be treated outside the body with a photosensitizing agent, exposed to light, and then returned to the patient. ECP may be used to help lessen the severity of skin symptoms of cutaneous T-cell lymphoma that has not responded to other therapies. ECP may be used to treat other blood cancers, and may also help reduce rejection after transplants.

[00169] Additionally, photosensitizing agent, such as porfimer sodium or Photofrin®, may be used in PDT to treat or relieve the symptoms of esophageal cancer and non-small cell lung cancer. Porfimer sodium may relieve symptoms of esophageal cancer when the cancer obstructs the esophagus or when the cancer cannot be satisfactorily treated with laser therapy alone. Porfimer sodium may be used to treat non-small cell lung cancer in patients for whom the usual treatments are not appropriate, and to relieve symptoms in patients with non-small cell lung cancer that obstructs the airways. Porfimer sodium may also be used for the

treatment of precancerous lesions in patients with Barrett esophagus, a condition that can lead to esophageal cancer.

[00170] Laser therapy may use high-intensity light to treat cancer and other illnesses. Lasers can be used to shrink or destroy tumors or precancerous growths. Lasers are most commonly used to treat superficial cancers (cancers on the surface of the body or the lining of internal organs) such as basal cell skin cancer and the very early stages of some cancers, such as cervical, penile, vaginal, vulvar, and non-small cell lung cancer.

[00171] Lasers may also be used to relieve certain symptoms of cancer, such as bleeding or obstruction. For example, lasers can be used to shrink or destroy a tumor that is blocking a patient's trachea (windpipe) or esophagus. Lasers also can be used to remove colon polyps or tumors that are blocking the colon or stomach.

[00172] Laser therapy is often given through a flexible endoscope (a thin, lighted tube used to look at tissues inside the body). The endoscope is fitted with optical fibers (thin fibers that transmit light). It is inserted through an opening in the body, such as the mouth, nose, anus, or vagina. Laser light is then precisely aimed to cut or destroy a tumor.

[00173] Laser-induced interstitial thermotherapy (LITT), or interstitial laser photocoagulation, also uses lasers to treat some cancers. LITT is similar to a cancer treatment called hyperthermia, which uses heat to shrink tumors by damaging or killing cancer cells. During LITT, an optical fiber is inserted into a tumor. Laser light at the tip of the fiber raises the temperature of the tumor cells and damages or destroys them. LITT is sometimes used to shrink tumors in the liver.

[00174] Laser therapy can be used alone, but most often it is combined with other treatments, such as surgery, chemotherapy, or radiation therapy. In addition, lasers can seal nerve endings to reduce pain after surgery and seal lymph vessels to reduce swelling and limit the spread of tumor cells.

[00175] Lasers used to treat cancer may include carbon dioxide (CO₂) lasers, argon lasers, and neodymium:yttrium-aluminum-garnet (Nd:YAG) lasers. Each of these can shrink or destroy tumors and can be used with endoscopes. CO₂ and argon lasers can cut the skin's surface without going into deeper layers. Thus, they can be used to remove superficial cancers, such as skin cancer. In contrast, the Nd:YAG laser is more commonly applied through an endoscope to treat internal organs, such as the uterus, esophagus, and colon. Nd:YAG laser light can also travel through optical fibers into specific areas of the body during LITT. Argon lasers are often used to activate the drugs used in PDT.

[00176] For patients with high test scores consistent with systemic disease outcome after prostatectomy, additional treatment modalities such as adjuvant chemotherapy (e.g.,

docetaxel, mitoxantrone and prednisone), systemic radiation therapy (e.g., samarium or strontium) and/or anti-androgen therapy (e.g., surgical castration, finasteride, dutasteride) can be designated. Such patients would likely be treated immediately with anti-androgen therapy alone or in combination with radiation therapy in order to eliminate presumed micro-metastatic disease, which cannot be detected clinically but can be revealed by the target sequence expression signature.

[00177] Such patients can also be more closely monitored for signs of disease progression. For patients with intermediate test scores consistent with biochemical recurrence only (BCR-only or elevated PSA that does not rapidly become manifested as systemic disease only localized adjuvant therapy (e.g., radiation therapy of the prostate bed) or short course of anti-androgen therapy would likely be administered. For patients with low scores or scores consistent with no evidence of disease (NED) adjuvant therapy would not likely be recommended by their physicians in order to avoid treatment-related side effects such as metabolic syndrome (e.g., hypertension, diabetes and/or weight gain), osteoporosis, proctitis, incontinence or impotence. Patients with samples consistent with NED could be designated for watchful waiting, or for no treatment. Patients with test scores that do not correlate with systemic disease but who have successive PSA increases could be designated for watchful waiting, increased monitoring, or lower dose or shorter duration anti-androgen therapy.

[00178] Target sequences can be grouped so that information obtained about the set of target sequences in the group can be used to make or assist in making a clinically relevant judgment such as a diagnosis, prognosis, or treatment choice.

[00179] A patient report is also provided comprising a representation of measured expression levels of a plurality of target sequences in a biological sample from the patient, wherein the representation comprises expression levels of target sequences corresponding to any one, two, three, four, five, six, eight, ten, twenty, thirty, forty, fifty or more of the target sequences corresponding to a target selected from Table 8, Table 9 or SEQ ID NOs: 1-1029, the subsets described herein, or a combination thereof. In some embodiments, the representation of the measured expression level(s) may take the form of a linear or nonlinear combination of expression levels of the target sequences of interest. The patient report may be provided in a machine (e.g., a computer) readable format and/or in a hard (paper) copy. The report can also include standard measurements of expression levels of said plurality of target sequences from one or more sets of patients with known disease status and/or outcome. The report can be used to inform the patient and/or treating physician of the expression levels of the expressed target sequences, the likely medical diagnosis and/or implications, and optionally may recommend a treatment modality for the patient.

[00180] Also provided are representations of the gene expression profiles useful for treating, diagnosing, prognosticating, and otherwise assessing disease. In some embodiments, these profile representations are reduced to a medium that can be automatically read by a machine such as computer readable media (magnetic, optical, and the like). The articles can also include instructions for assessing the gene expression profiles in such media. For example, the articles may comprise a readable storage form having computer instructions for comparing gene expression profiles of the portfolios of genes described above. The articles may also have gene expression profiles digitally recorded therein so that they may be compared with gene expression data from patient samples. Alternatively, the profiles can be recorded in different representational format. A graphical recordation is one such format. Clustering algorithms can assist in the visualization of such data.

Subtyping

[00181] The inventors of the present invention discovered that luminal and basal subtyping of prostate cancer is prognostic and predicts response to androgen deprivation therapy. Prostate cancer subtypes useful in the methods of the present invention include, for example, luminal A, luminal B, and basal subtypes. Molecular subtyping is a method of classifying prostate cancers into one of multiple genetically-distinct categories, or subtypes. Each subtype responds differently to different kinds of treatments, and some subtypes indicate a higher risk of recurrence. Subtypes of the present invention may be used to predict outcomes such as distant metastasis-free survival (DMFS), biochemical recurrence-free survival (bRFS), prostate cancer specific survival (PCSS), and overall survival (OS). As described herein, each subtype has a unique molecular and clinical fingerprint. The subtyping methods described herein may be used to predict prostate cancer response to androgen deprivation therapy.

[00182] Differential expression analysis one or more of the targets listed in Table 8, Table 9 or SEQ ID NOs: 1-1029 allow for the identification of the molecular subtype of a prostate cancer.

[00183] In some instances, the molecular subtyping methods of the present invention are used in combination with other biomarkers, like tumor grade and hormone levels, for analyzing the prostate cancer.

Clinical Associations and Patient Outcomes

[00184] Molecular subtypes of the present invention have distinct clinical associations. Clinical associations that correlate to molecular subtypes include, for example, preoperative serum PSA, Gleason score (GS), extraprostatic extension (EPE), surgical margin status (SM), lymph node involvement (LNI), and seminal vesicle invasion (SVI).

[00185] In some embodiments, molecular subtypes of the present invention are used to predict patient outcomes such as biochemical recurrence (BCR), metastasis (MET) and prostate cancer death (PCSM) after radical prostatectomy. In other embodiments, molecular subtypes of the present invention are used to predict patient outcomes such as distant metastasis-free survival (DMFS), biochemical recurrence-free survival (bRFS), prostate cancer specific survival (PCSS), and overall survival (OS).

Treatment Response Prediction

[00186] In some embodiments, the molecular subtypes of the present invention are useful for predicting response to Androgen Deprivation Therapy (ADT) following radical prostatectomy. Androgen deprivation therapy (ADT), also called androgen suppression therapy, is an antihormone therapy whose main use is in treating prostate cancer. Prostate cancer cells usually require androgen hormones, such as testosterone, to grow. ADT reduces the levels of androgen hormones, with drugs or surgery, to prevent the prostate cancer cells from growing. The pharmaceutical approaches include antiandrogens and chemical castration.

[00187] In other embodiments, the molecular subtypes of the present invention are useful for predicting response to Radiation Therapy (RT) following radical prostatectomy.

EXAMPLES

Example 1: A Genetic Classifier (PAM50) to Identify Subtypes in Prostate Cancer and Predict Response to Therapy.

[00188] A genetic signature (PAM50) to identify subtypes in prostate cancer tissue and predict response to therapy was developed as follows. Affymetrix Human Exon 1.0 ST microarray (Affymetrix, Santa Clara, CA) data from formalin-fixed paraffin-embedded radical prostatectomy samples were obtained from six published retrospective patient cohorts (n=1,567) and one prospective cohort (n=2,215) for a total of 3,782 samples. Retrospective cohorts were from the Mayo Clinic (MC I and II), Cleveland Clinic (CC), Johns Hopkins University (JHU), Thomas Jefferson University (TJU), and Durham VA (DVA). Data collection was approved and supervised by local institutional review boards (IRB). 2,215 de-identified, anonymized, and prospectively-collected patients from clinical use of the Decipher test were obtained from Decipher GRID™ (ClinicalTrials.gov ID: NCT02609269). Clinical outcomes were not available for Decipher GRID. Informed consent and IRB approval for Decipher GRID were obtained. Microarray processing was performed in a CLIA-certified clinical operations laboratory (GenomeDx Biosciences, Inc, San Diego, CA). Microarrays were normalized using Single Channel Array Normalization. (Piccolo et al. *Genomics*. 2012;100(6):337-344.)

PAM50 clustering

[00189] PAM50 clustering was performed based on the original algorithm from Parker et al. *J Clin Oncol.* 2009;27(8):1160-1167. Source code was downloaded from [https://genome.unc.edu/pubsup/breastGEO/] and used without modification. Gene expression data were median-centered in each cohort individually as required by the PAM50 algorithm. The normal-like subtype was excluded as the prostate cancer samples were macro-dissected limiting the amount of normal tissue present in our data. The HER2 subtype was also excluded given the lack of HER2 amplification in prostate cancer (Ullen et al. *Acta Oncol.* 2005;44(5):490-495). Assignment of subtype in the prostate cancer samples was thus assigned by the greatest correlation with luminal A, luminal B, or basal.

Clinical endpoints

[00190] All primary and secondary endpoints were preplanned. The primary clinical endpoint was distant metastasis-free survival (DMFS), with secondary clinical endpoints of biochemical recurrence-free survival (BRFS), prostate cancer specific survival (PCSS), and overall survival (OS). All endpoints were defined from time of surgery until time of the event, death, or last follow-up.

Gene set enrichment analysis

[00191] Functional and biological analyses of the PAM50 subtypes in prostate cancer were investigated using Gene Set Enrichment Analysis (GSEA). First, a T-test was performed on every gene comparing expression in the specified subtype vs. not in that subtype. The T-statistic was used to generate a pre-ranked list which was input into GSEA.

Matched cohort design and predicting response to ADT

[00192] To investigate if subtype could predict ADT response, a matched cohort with 2:1 matching for ADT untreated and treated patients was created from the MCI and MCII cohorts in order to select patients from a single institution with a mix of post-operatively treated and untreated patients. This resulted in a cohort of 315 patients, 210 of which did not receive any ADT, and 105 which received ADT treatment. The decision to perform 2:1 matching was to maximize sample size using patients only from the MC cohorts. We chose to only include patients from the MC cohorts for this analysis because patients in these cohorts received a mix of adjuvant and salvage ADT and RT, allowing us to account for the effects of both in our models. JHMI patients did not receive any post-operative treatment. CCF patients did not receive adjuvant treatment, and information about salvage ADT treatment was unavailable in the dataset. All TJU and DVA patients were treated with radiation. We defined androgen deprivation therapy (ADT) as treatment (with LHRH agonist alone or in combination with androgen receptor antagonists) after radical prostatectomy but before the primary endpoint of

metastasis. Matching was performed based on Gleason, prostate specific antigen (PSA, ng/mL), positive surgical margins (SM), extracapsular extension (ECE), seminal vesicle invasion (SVI), lymph node invasion (LNI), as well as post-operative radiation therapy (RT). Data on the duration and dose of ADT were not available. Table 7 provides details of which patients in this matched cohort received adjuvant, salvage, or both ADT and/or RT. Nearly all lymph node positive patients from the MC cohorts received ADT, as well as some who received ADT for other reasons at the treating physicians' discretion.

Table 7: Number of patients receiving ADT and RT in the matched cohort (n=315)

	Adjuvant ADT Only	Salvage ADT Only	Both Adjuvant and Salvage ADT	No ADT
Adjuvant RT Only	4	6	2	23
Salvage RT Only	3	14	2	41
Both Adjuvant and Salvage RT	1	0	0	0
No RT	18	53	2	146

Abbreviations: ADT: Androgen deprivation therapy; RT: Radiation therapy

Statistical analysis

[00193] In the demographics tables, ANOVA and Chi-squared test were used to evaluate differences between continuous and categorical variables, respectively, between patient groups. Kaplan-Meier curves were generated by pooling clinical data from all available microarray cohorts. Gleason score was stratified into low (<7), intermediate (7), and high risk (8-10). PSA was stratified into low (<10 ng/mL), intermediate (10-20 ng/mL), and high risk (>20 ng/mL) in a similar manner. SM, ECE, SVI, and LNI were considered binary variables and defined by the respective institutions. Cox regression was used for both univariable and multivariable analysis (UVA/MVA). Stratification by cohort was used when performing UVA/MVA analyses to account for baseline differences between cohorts. The interaction term for treatment and subtype in a Cox model was used to evaluate prediction of treatment response, and a significant interaction Wald test p-value indicated that a subtype could predict response to ADT. Statistical significance was set as a two-tailed p-value <0.05. All statistical analyses were performed in R 3.1.2.

Microarray data accession

[00194] Microarray data is available on Gene Expression Omnibus with accession numbers GSE46691, GSE62116, GSE72291, GSE62667, GSE79956, GSE79957, and GSE79915. Subtyping target sequences (SEQ ID NOs 1-1029) are shown in Table 8.

Results

[00195] To subtype prostate cancers into luminal-like vs. basal-like subtypes, we applied the PAM50 classifier on 1,567 prostate cancer samples with a median clinical follow-up time of 10 years. 34.3% of samples are classified as luminal A, 28.5% as luminal B, and 37.1% as basal, with visually similar patterns of expression across all six independent cohorts (Figure 1A, Figure 5, Table 2). PAM50 expression patterns are also similar between breast and prostate cancer samples (Figure 6). Notably, ER and PR, which are highest in luminal and luminal A breast cancer, respectively⁸, do not demonstrate the same patterns in prostate cancer (Figure 6).

[00196] We next examined associations of luminal A, luminal B, and basal subtypes with clinical outcomes. Luminal B patients consistently have significantly worse outcomes for all endpoints compared to luminal A and basal subtypes (Figure 1B). The 10-year actuarial rates for bRFS are 29% for luminal B compared to 41% and 39% for luminal A and basal, respectively; for DMFS, 53% for luminal B compared to 73% for both other subtypes; for PCSS, 78% for luminal B compared to 89% and 86% for luminal A and basal; and for OS, 69% for luminal B versus 82% and 80% for luminal A and basal.

[00197] On univariable Cox analysis (Table 1, Table 3), basal and luminal A have improved bRFS, DMFS, PCSS, and OS compared to luminal B (bRFS: basal (vs. luminal B) $p<0.0001$, HR=0.69 [0.59-0.81], luminal A $p<0.0001$, HR=0.66 [0.57-0.78]; DMFS: basal $p<0.0001$, HR=0.5 [0.4-0.61], luminal A $p<0.0001$, HR=0.42 [0.34-0.53]; PCSS: basal $p=0.0003$, HR=0.59 [0.44-0.79], luminal A $p<0.0001$, HR=0.38 [0.27-0.53]; OS basal $p=0.0005$, HR=0.69 [0.56-0.85], luminal A $p<0.0001$, HR=0.56 [0.45-0.7]). However, luminal A does not exhibit significantly different bRFS ($p=0.61$, HR=1.04 [0.89-1.22]) and DMFS ($p=0.18$, HR=1.17 [0.93-1.49]) versus basal. Luminal A does demonstrate worse PCSS ($p=0.01$, HR=1.54 [1.09-2.16]) and OS ($p=0.05$, HR=1.25 [1-1.55]) compared to basal, though this is difficult to interpret in the setting of non-significant differences in metastasis and biochemical recurrence. Consistent with our data demonstrating that luminal B patients have the worst clinical outcomes, luminal B patients also have the highest pre-operative PSA levels, Gleason score, and rates of ECE and LNI, followed by basal and then luminal A (Table 2). On multivariable analysis (Table 1, Table 3), adjusting for clinicopathologic variables (age, PSA, Gleason score, SM, ECE, SVI, and LNI), basal and luminal A have significantly better independent prognosis than luminal B for bRFS (basal vs. luminal B: $p=0.01$, HR=0.81 [0.69-0.96]; luminal A vs. luminal B: $p=0.005$, HR=0.79 [0.66-0.93]) and DMFS (basal vs. luminal B: $p=0.0002$, HR=0.66 [0.53-0.82]; luminal A vs. luminal B: $p<0.0001$, HR=0.55 [0.43-0.69]). Luminal A also has significantly improved outcomes compared to luminal B for PCSS ($p<0.0001$, HR=0.50 [0.35-0.71]) and OS ($p=0.002$, HR=0.69 [0.55-0.87]). To provide comparison to a composite clinical classifier, we similarly show that basal and luminal A have significantly better prognosis than luminal B for all endpoints on multivariable analysis adjusting for age, LNI, and the assessment by risk using the D'Amico classifier (D'Amico et al. *JAMA*. 1998;280(11):969-974) (See Table 4).

Table 1: Univariable and Multivariable Analysis

		UVA		MVA	
		P-value	HR [95% CI]	P-value	HR [95% CI]
DMFS	Age (yrs)	0.88	1 [0.99-1.02]	0.15	0.99 [0.98-1]
	PSA 10-20 vs. <10	0.64	1.05 [0.85-1.31]	0.29	0.89 [0.71-1.11]
	PSA >20 vs. <10	3.8E-03	1.42 [1.12-1.79]	0.16	0.83 [0.64-1.08]
	Gleason 7 vs. <7	8.4E-05	4.57 [2.14-9.73]	1.3E-03	3.49 [1.63-7.47]
	Gleason 8-10 vs. <7	4.0E-12	14.32 [6.75-30.37]	2.4E-08	8.8 [4.1-18.88]
	SMS	0.08	1.18 [0.98-1.42]	0.74	1.03 [0.85-1.25]
	SVI	0.0E+00	2.57 [2.14-3.08]	3.5E-07	1.72 [1.39-2.11]
	ECE	3.7E-12	2.04 [1.67-2.5]	0.07	1.23 [0.99-1.54]
	LNI	0.0E+00	2.56 [2.06-3.19]	0.01	1.39 [1.09-1.78]
	Basal vs. LumB	9.0E-11	0.5 [0.4-0.61]	2.0E-04	0.66 [0.53-0.82]
	LumA vs. LumB	9.1E-14	0.42 [0.34-0.53]	5.4E-07	0.55 [0.43-0.69]
PCSS	Age (yrs)	0.86	1 [0.98-1.02]	0.24	0.99 [0.97-1.01]
	PSA 10-20 vs. <10	0.79	1.04 [0.76-1.42]	0.16	0.8 [0.58-1.09]
	PSA >20 vs. <10	0.07	1.35 [0.97-1.86]	0.01	0.62 [0.43-0.89]
	Gleason 7 vs. <7	0.02	3.35 [1.22-9.19]	0.06	2.7 [0.98-7.46]
	Gleason 8-10 vs. <7	2.4E-07	13.76 [5.08-37.23]	3.1E-05	8.6 [3.12-23.68]
	SMS	9.3E-04	1.56 [1.2-2.02]	0.11	1.25 [0.95-1.64]
	SVI	0.0E+00	3.15 [2.43-4.08]	2.0E-06	2.06 [1.53-2.78]
	ECE	5.1E-08	2.22 [1.67-2.96]	0.29	1.19 [0.87-1.63]
	LNI	2.2E-15	3.19 [2.4-4.25]	4.7E-03	1.6 [1.15-2.21]
	Basal vs. LumB	3.4E-04	0.59 [0.44-0.79]	0.21	0.83 [0.61-1.12]
	LumA vs. LumB	1.8E-08	0.38 [0.27-0.53]	8.1E-05	0.5 [0.35-0.71]

Abbreviations: PSA: prostate specific antigen, SMS: positive surgical margin status, ECE: extracapsular extension, SVI: seminal vesicle invasion, LNI: lymph node invasion, DMFS: distant metastasis-free survival, PCSS: prostate cancer-specific survival.

Table 2: Demographics for pooled retrospective cohort (n=1,567)

		Basal (n=582)	Luminal A (n=538)	Luminal B (n=447)	Total (n=1567)	P- value
Age (years)		62.4 +/- 6.98	62.5 +/- 6.71	62.4 +/- 6.92	62.4 +/- 6.87	0.975
PSA (ng/dL)	NA	1 (0.002)	1 (0.002)	1 (0.002)	3 (0.002)	
	< 10	351 (0.603)	318 (0.591)	238 (0.532)	907 (0.579)	
	10 to 20	131 (0.225)	145 (0.27)	113 (0.253)	389 (0.248)	0.002
	> 20	87 (0.149)	64 (0.119)	92 (0.206)	243 (0.155)	
Gleason	NA	13 (0.022)	11 (0.02)	4 (0.009)	28 (0.018)	
	<6	68 (0.117)	53 (0.099)	23 (0.051)	144 (0.092)	
	7	328 (0.564)	335 (0.623)	218 (0.488)	881 (0.562)	<0.00 01
	8 to 10	184 (0.316)	149 (0.277)	205 (0.459)	538 (0.343)	
SM	NA	2 (0.003)	1 (0.002)	1 (0.002)	4 (0.003)	
	No	297 (0.51)	261 (0.485)	214 (0.479)	772 (0.493)	
	Yes	284 (0.488)	276 (0.513)	232 (0.519)	792 (0.505)	0.554
SVI	NA	1 (0.002)	1 (0.002)	1 (0.002)	3 (0.002)	
	No	427 (0.734)	388 (0.721)	300 (0.671)	1115 (0.712)	0.077
	Yes	153 (0.263)	148 (0.275)	145 (0.324)	446 (0.285)	
ECE	NA	2 (0.003)	2 (0.004)	2 (0.004)	6 (0.004)	
	No	272 (0.467)	259 (0.481)	147 (0.329)	678 (0.433)	<0.00 01
	Yes	306 (0.526)	278 (0.517)	298 (0.667)	882 (0.563)	
LNI	NA	4 (0.007)	1 (0.002)	2 (0.004)	7 (0.004)	
	No	524 (0.9)	486 (0.903)	383 (0.857)	1393 (0.889)	0.032
	Yes	57 (0.098)	50 (0.093)	63 (0.141)	170 (0.108)	
	NA	1 (0.002)	2 (0.004)	1 (0.002)	4 (0.003)	

Abbreviations: PSA: prostate specific antigen, SM: positive surgical margins, SVI: seminal vesicle invasion, ECE: extracapsular extension, LNI: lymph node invasion.

Table 3: Univariable and multivariable analysis in pooled retrospective cohort (n=1,567)

		UVA		MVA	
		P-value	HR [95% CI]	P-value	HR [95% CI]
bRFS	Age (yrs)	0.36	1 [0.99-1.01]	0.97	1 [0.99-1.01]
	PSA 10-20 vs. <10	0.13	1.13 [0.97-1.32]	0.59	1.04 [0.89-1.22]
	PSA >20 vs. <10	8.7E-06	1.49 [1.25-1.77]	0.13	1.16 [0.96-1.4]
	Gleason 7 vs. <7	0.12	1.23 [0.95-1.61]	0.89	1.02 [0.77-1.34]
	Gleason 8-10 vs. <7	3.0E-11	2.49 [1.9-3.27]	3.9E-05	1.83 [1.37-2.43]
	SM	1.2E-04	1.31 [1.14-1.5]	0.03	1.17 [1.01-1.35]
	SVI	0.0E+00	2.01 [1.75-2.31]	4.5E-10	1.65 [1.41-1.93]
	ECE	1.6E-09	1.51 [1.32-1.73]	0.10	1.13 [0.98-1.31]
	LNI	4.3E-05	1.49 [1.23-1.8]	0.21	0.87 [0.71-1.08]
	Basal vs. LumB	3.2E-06	0.69 [0.59-0.81]	0.01	0.81 [0.69-0.96]
	LumA vs. LumB	5.4E-07	0.66 [0.57-0.78]	4.8E-03	0.79 [0.66-0.93]
OS	Age (yrs)	7.6E-05	1.03 [1.01-1.04]	0.01	1.02 [1-1.03]
	PSA 10-20 vs. <10	0.62	1.06 [0.85-1.31]	0.20	0.87 [0.7-1.08]
	PSA >20 vs. <10	0.01	1.35 [1.08-1.69]	0.15	0.83 [0.65-1.07]
	Gleason 7 vs. <7	1.1E-03	1.98 [1.32-2.98]	0.02	1.69 [1.11-2.59]
	Gleason 8-10 vs. <7	1.1E-14	5.01 [3.33-7.53]	5.2E-09	3.65 [2.36-5.63]
	SM	2.4E-03	1.32 [1.1-1.59]	0.06	1.2 [1-1.45]
	SVI	1.2E-13	1.96 [1.64-2.33]	1.7E-04	1.49 [1.21-1.83]
	ECE	1.2E-07	1.66 [1.38-2.01]	0.34	1.11 [0.9-1.37]
	LNI	6.0E-10	2.1 [1.66-2.65]	0.03	1.33 [1.02-1.72]
	Basal vs. LumB	5.1E-04	0.69 [0.56-0.85]	0.24	0.88 [0.71-1.09]
	LumA vs. LumB	2.8E-07	0.56 [0.45-0.7]	1.9E-03	0.69 [0.55-0.87]

Abbreviations: PSA: prostate specific antigen, SM: positive surgical margins, SVI: seminal vesicle invasion, ECE: extracapsular extension, LNI: lymph node invasion, bRFS: biochemical recurrence-free survival, OS: overall survival.

Table 4: Univariable and multivariable analysis in pooled retrospective cohort (n=1,567) to examine independence of subtypes from D'Amico Risk Classification

		UVA		MVA	
		P-value	HR [95% CI]	P-value	HR [95% CI]
bRFS	Age	0.36	1 [0.99-1.01]	0.30	1.01 [0.99-1.02]
	D'Amico	3.49E-10	1.87 [1.54-2.27]	5.71E-08	1.73 [1.42-2.1]
	LNI	4.32E-05	1.49 [1.23-1.8]	2.66E-15	3.46 [2.55-4.71]
	Basal vs. LumB	3.23E-06	0.69 [0.59-0.81]	0.01	0.78 [0.65-0.93]
	LumA vs. LumB	5.44E-07	0.66 [0.57-0.78]	1.40E-03	0.74 [0.61-0.89]
DMFS	Age	0.88	1 [0.99-1.02]	0.30	1.01 [0.99-1.03]
	D'Amico	3.71E-10	2.86 [2.06-3.97]	7.89E-08	2.48 [1.78-3.46]
	LNI	0.00	2.56 [2.06-3.19]	6.78E-10	3.21 [2.22-4.65]
	Basal vs. LumB	8.95E-11	0.5 [0.4-0.61]	2.19E-06	0.54 [0.42-0.7]
	LumA vs. LumB	9.14E-14	0.42 [0.34-0.53]	8.53E-08	0.49 [0.38-0.64]
PCSS	Age	0.86	1 [0.98-1.02]	0.31	1.01 [0.99-1.04]
	D'Amico	7.47E-06	3 [1.86-4.86]	6.06E-05	2.7 [1.66-4.4]
	LNI	2.22E-15	3.19 [2.4-4.25]	5.72E-04	2.71 [1.54-4.78]
	Basal vs. LumB	3.40E-04	0.59 [0.44-0.79]	0.06	0.71 [0.5-1.01]
	LumA vs. LumB	1.84E-08	0.38 [0.27-0.53]	7.95E-05	0.45 [0.3-0.67]
OS	Age	7.62E-05	1.03 [1.01-1.04]	1.09E-05	1.04 [1.02-1.06]
	D'Amico	2.63E-06	1.98 [1.49-2.63]	3.12E-05	1.85 [1.38-2.46]
	LNI	6.02E-10	2.1 [1.66-2.65]	2.28E-03	2.22 [1.33-3.71]
	Basal vs. LumB	5.09E-04	0.69 [0.56-0.85]	0.17	0.84 [0.66-1.08]
	LumA vs. LumB	2.77E-07	0.56 [0.45-0.7]	4.23E-05	0.57 [0.43-0.74]

Abbreviations: LNI: lymph node invasion.

Note: D'Amico high-risk was compared to intermediate and low risk combined, as there were only 19 low risk patients.

[00198] We then investigated the relationship between these subtypes and luminal and basal prostate cancer lineage markers. The basal lineage CD49f signature (Smith et al. *Proc Natl Acad Sci U S A.* 2015;112(47):E6544-6552) is increased in basal-like samples (ANOVA $p < 0.001$, Figure 2A). Concordantly, the luminal markers NKX3.1, KRT18, and AR are increased in luminal-like samples (ANOVA $p < 0.001$, Figure 2B-C). Consistent with our findings for AR, the androgen activity pathway is enriched in luminal compared to basal (ANOVA $p < 0.001$, Figure 2C). Examining the top GSEA hallmark concepts comparing luminal to basal (Supplementary Methods) reveals that the MYC pathway is the top enriched pathway in luminal-like samples, and genes down-regulated by KRAS are the top positive pathway in basal-like samples (negatively enriched in luminal samples). These results are concordant with MYC and KRAS expression, which are both increased in luminal-like samples (ANOVA $p < 0.001$, Figure 7). Upon observing that proliferation genes such as MKI67 are low in luminal A (Figure 1A), we formally examined the subtypes using the PAM50 proliferation score (Parker et al. *J Clin Oncol.* 2009;27(8):1160-1167). Luminal A

has a lower proliferation score than luminal B and basal ($p < 0.001$, Figure 8), which may explain the divergent clinical outcomes despite the biological similarities between luminal A and B.

[00199] We next independently validated the associations of these subtypes with biologic and clinicopathologic factors in Decipher GRID™, a prospectively-collected cohort of 2,215 prostatectomy patient expression profiles. PAM50 gene expression patterns are similar to the pooled retrospective cohorts, and trends of AR/AR-signaling (higher in luminal), CD49f signature (higher in basal), and NKX3.1 and KRT19 (both higher in luminal) gene expression are conserved (Figures 3A-D). 33.3% of samples are classified as luminal A, 32.6% as luminal B, and 34.1% as basal. We also confirmed MYC and KRAS expression patterns, which are both increased in luminal samples (Figure 7). Finally, while Decipher GRID does not have associated clinical outcomes, luminal B demonstrates the highest Gleason scores, as well as rates of SVI, ECE, and LNI, consistent with clinical outcomes and clinicopathologic data in our retrospective cohorts (Table 5).

Table 5: Demographics for GRID (n=2,215)

		Basal (n=755)	Luminal A (n=737)	Luminal B (723)	Total (n=2215)	P- value
Age (years)		64.1 +/- 7.09	64.4 +/- 6.64	64.9 +/- 6.61	64.4 +/- 6.79	0.109
PSA (ng/dL)	NA	67 (0.089)	63 (0.085)	59 (0.082)	189 (0.085)	
	< 10	382 (0.506)	373 (0.506)	360 (0.498)	1115 (0.503)	
	10 to 20	72 (0.095)	85 (0.115)	90 (0.124)	247 (0.112)	0.439
	> 20	33 (0.044)	28 (0.038)	36 (0.05)	97 (0.044)	
Gleason	NA	268 (0.355)	251 (0.341)	237 (0.328)	756 (0.341)	
	<6	61 (0.081)	53 (0.072)	29 (0.04)	143 (0.065)	
	7	453 (0.6)	489 (0.664)	431 (0.596)	1373 (0.62)	<0.00 01
	8 to 10	174 (0.23)	132 (0.179)	204 (0.282)	510 (0.23)	
	NA	67 (0.089)	63 (0.085)	59 (0.082)	189 (0.085)	
SM	No	310 (0.411)	295 (0.4)	299 (0.414)	904 (0.408)	
	Yes	375 (0.497)	376 (0.51)	365 (0.505)	1116 (0.504)	0.878
	NA	70 (0.093)	66 (0.09)	59 (0.082)	195 (0.088)	
SVI	No	530 (0.702)	554 (0.752)	499 (0.69)	1583 (0.715)	0.003
	Yes	152 (0.201)	116 (0.157)	165 (0.228)	433 (0.195)	
	NA	73 (0.097)	67 (0.091)	59 (0.082)	199 (0.09)	
ECE	No	336 (0.445)	325 (0.441)	260 (0.36)	921 (0.416)	
	Yes	348 (0.461)	345 (0.468)	403 (0.557)	1096 (0.495)	<0.00 01
	NA	71 (0.094)	67 (0.091)	60 (0.083)	198 (0.089)	
LNI	No	646 (0.856)	628 (0.852)	624 (0.863)	1898 (0.857)	0.015
	Yes	8 (0.011)	9 (0.012)	21 (0.029)	38 (0.017)	
	NA	101 (0.134)	100 (0.136)	78 (0.108)	279 (0.126)	

Abbreviations: PSA: prostate specific antigen, SM: positive surgical margins, SVI: seminal vesicle invasion, ECE: extracapsular extension, LNI: lymph node invasion.

[00200] The relationship between androgen signaling and luminal-like prostate cancer is of particular interest given the importance of ADT in treating prostate cancer. We investigated whether these subtypes could predict response to hormonal therapy in an exploratory subgroup analysis by first designing a post-prostatectomy ADT treated/untreated sub-cohort (n=315; ADT untreated n=210; ADT treated n=105) matched by clinicopathologic factors (Gleason, PSA, LNI, ECE, SVI, and SM), and post-operative RT (Figure 4A and Tables 6 and 7). Matching was performed with a 2:1 ratio of patients (ADT untreated:ADT treated). The matched cohort had a median follow-up time of 13 years. In this analysis, we pool the luminal A and basal subtypes to compare to luminal B, as the luminal A and basal subtypes have similar outcomes for ADT and no ADT in the matched cohorts. In the luminal B

subtype, which has the worst prognosis of the three subtypes and contains patients with increased expression of AR signaling genes, patients treated with ADT have improved DMFS compared to those that did not receive ADT (10-year metastasis rates of 33% vs. 55%, Figures 4B, 4C). However, in the non-luminal B patients, patients treated with ADT have worse DMFS compared to untreated patients (10-year metastasis rates of 37% vs. 21%, Figures 4B, 4C), with a similar trend in both luminal A and basal patients. Separating patients receiving adjuvant or salvage therapy in the matched cohort results in similar trends, although the p-values are insignificant due to the reduced numbers (Figure 9). Finally, we used interaction analysis in a Cox model of these matched patients to demonstrate a statistically significant interaction term between ADT and the luminal B subtype (p=0.006). Luminal B represents a subgroup of prostate cancers with poor prognosis combined with biological differences in AR signaling that result in improved response to post-operative ADT.

Table 6: Demographics for matched cohort (n=315)

		Basal (n=118)	Luminal A (n=124)	Luminal B (n=73)	Total (n=315)	P- value
Age (years)		64.4 +/- 6.64	64.2 +/- 7.04	64.8 +/- 6.65	64.4 +/- 6.79	0.860
PSA (ng/dL)	< 10	75 (0.636)	80 (0.645)	37 (0.507)	192 (0.61)	0.273
	10 to 20	19 (0.161)	24 (0.194)	17 (0.233)	60 (0.19)	
	> 20	24 (0.203)	20 (0.161)	19 (0.26)	63 (0.2)	
Gleason	<6	13 (0.11)	7 (0.056)	1 (0.014)	21 (0.067)	0.002
	7	72 (0.61)	91 (0.734)	41 (0.562)	204 (0.648)	
	8 to 10	33 (0.28)	26 (0.21)	31 (0.425)	90 (0.286)	
SM	No	57 (0.483)	49 (0.395)	32 (0.438)	138 (0.438)	0.387
	Yes	61 (0.517)	75 (0.605)	41 (0.562)	177 (0.562)	
SVI	No	105 (0.89)	100 (0.806)	62 (0.849)	267 (0.848)	0.196
	Yes	13 (0.11)	24 (0.194)	11 (0.151)	48 (0.152)	
ECE	No	70 (0.593)	79 (0.637)	34 (0.466)	183 (0.581)	0.059
	Yes	48 (0.407)	45 (0.363)	39 (0.534)	132 (0.419)	
LNI	No	118 (1)	124 (1)	73 (1)	315 (1)	NA

Abbreviations: PSA: prostate specific antigen, SM: positive surgical margins, SVI: seminal vesicle invasion, ECE: extracapsular extension, LNI: lymph node invasion.

Table 7: Number of patients receiving ADT and RT in the matched cohort (n=315)

	Adjuvant ADT Only	Salvage ADT Only	Both Adjuvant and Salvage ADT	No ADT
Adjuvant RT Only	4	6	2	23
Salvage RT Only	3	14	2	41
Both Adjuvant and Salvage RT	1	0	0	0
No RT	18	53	2	146

Abbreviations: ADT: Androgen deprivation therapy; RT: Radiation therapy

[00201] These results showed that a genomic classifier of the present invention could be utilized to identify three subtypes in prostate cancer subjects. These results suggested that the methods and markers of the present invention would be useful for diagnosing, prognosing, determining the progression of cancer, or predicting benefit from therapy in a subject having prostate cancer. These results further showed that the subtyping methods and genomic classifiers of the present invention are useful for predicting benefit from androgen deprivation therapy (ADT) and treating a subject with prostate cancer. The results showed that the subtyping methods of the present invention may be used to determine a treatment for a subject with prostate cancer.

Table 8: Subtyping Target Sequences

SEQ ID NO.	Gene	Affy Probeset ID	Sequence
1	CDC20	2333138	GGGTGCTAGGCCGGAAGGGGCTGCAGCCGAGGGTGGC CCTGATTTTGTGGCCGGCCAGGAGCGAAGGGGTCCCTT TCTGTCCCCTGAGCACCGTCGCCTCCT
2	CDC20	2333139	GCACCAACTGCAAGGACCCCTCCCCCTGCGGGC
3	CDC20	2333140	TTCGCGTTCGAGAGTGACCTGCACTCGCTGCTTCAGCTG GATGCACCCATCCCCAATGCACCCCCTGCGCGCTGGCA GCGCAAAGCCAAGGAAGCCGCAGGCCCGGCCCCCTCAC CCATGCGGGCCGCAACCGATCCCACAGCGC
4	CDC20	2333142	GCAAATCCAGTTCCAAGGTTTCAGACCACTCCTAGCAAA CCTGGCGGTGACCGCTATATCCCCCATCGCAGTGCTGCC CAGATGGAGGTGGCCAGCTTCCTCCTGAGCAAGGAGAA CCAGCCTGAAAACAGCCAGACGCCACCA
5	CDC20	2333144	GTAGAGGAAGCCAAGATCCTTCGGCTCAGTGGAAAACC ACAAAATGCGCCAGAGG
6	CDC20	2333145	CGAAGTTCCTGGTTCCTGGAGGGAG
7	CDC20	2333146	CCTCTTCCTATCTAAGATTGAGGGCAAG
8	CDC20	2333147	CAGAACAGACTGAAAGTACTCTACAGCCAA
9	CDC20	2333148	CCTGCCAGACCGTATCCTGGATGCGCCTGAAATCC
10	CDC20	2333149	ACCTGAACCTTGTGGATTGGAGTTCTGGGAATGTACTG GCCGTGGCACTGGACAACAGTGTGTACCTGTGGAGTGC AAGCTCTGGTGACATCCTGCAGCTTTTGCAAATGGAGC AGCCTGGGGAATATATATCCTCTGTGGCCTG

11	CDC20	2333150	CAGCAGCAGAAACGGCTTCGAAATATGACCAGTCACTC TGCCCCGAGTGGGCTCCCTAAGCTGGAACAGCTATAT
12	CDC20	2333151	CATCCACCACCATGATGTTTCGGGTAGCAGAACACCATG TGGCCACACTGAGTGGCCACAGCCAGGAAGTGTGTGGG CTGCGCTGGGCCCCAGATGGACGACATTTGGCCAGTGG T
13	CDC20	2333152	GTAATGATAACTTGGTCAATGTGTGGCCTAGTGCTCCTG GAGAGGGTGGCTGGGTTCCTCTGCAGACATTCACCCAG CATCAAGGGGCTGTCAA
14	CDC20	2333155	GTGTCCCTGGCAGTCCAATGTCCTGGCAACA
15	CDC20	2333156	GCCTGTCTGAGTGCCGTGGATGCCC
16	CDC20	2333158	TTATTTGGAAGTACCCAACCATGGC
17	CDC20	2333159	CACACATCCCGGGTCCTGAGTCTGACCATGAGCCCAGA TGGGGCCACAGTGGCATCCGCAGCAGCAGATGAGACCC TGAGGCTATGGCGCTGTTTTGAGTTGGACCC
18	CDC20	2333160	AGACCAACCCATCACCTCAGTTGTTTTTTAT
19	KIF2C	2334099	TGCGGCGGTTTACGCGGCGTTAAGACTTCGTAGGGTTA GCGAAATTGAGGTTTCTTGGTATTGCGCGTTTCTCTT
20	KIF2C	2334101	GTCCCTAGGTCAAGGGGACTCGTGA
21	KIF2C	2334103	GTTTAATTCACAGTGCCAATGTAAGGACTGT
22	KIF2C	2334105	TCTTAGGGTTAGGTAGCAGCTGTCAGGAACCTTGCCCCCT GCCCATAGATCCTAAAGGGCCCCCATTTGACTCTCAC CAGACAGTTAGAACTTGTTTCCTCCTCCGTGTCAGCCAT CAAGAGGTGCTTGGGGGGCTGTGCCCAGCAGGACCTCA CTGCCCAGCAGATCAGCAGGGGAGCCAAGTGGCCTAGA TCTGCTGTGGAGTACCCGACTGTTTGCCTGCCTGTCTGC CCTCCTCTTCACCTCATTCTCATCACTGACGTCTACCATT GGCTT
23	KIF2C	2334106	ATGATGTGGCTGCAATAAACCAGAACTCTTACAGCTT CTTCCCTTACATCCGAAGGACAATCTGCCCTTGC
24	KIF2C	2334107	CAAAAACGGAGATCCGTCAACTCCAAAATTCC
25	KIF2C	2334109	GGACCTATTTACCTTGTACAGAACTTGGAGGTTTGCC CCTGACCACCCTCGAGATCGTGCAGCACTGACTGGCTA CTGCTCTCGGTTCTCCA
26	KIF2C	2334111	CTGCCCCCACTAGGCCTTCCTGCCCTGCAG
27	KIF2C	2334112	GGCTGAAATACCATTGAGGATGGTCAGCGAGGAGATGG AAGAGCAAGTCCATTCCATCCGAGGC
28	KIF2C	2334113	AGGCCCAGAACTCTGAAATGAGAATGAA
29	KIF2C	2334114	TATGACAGTAGTTTTCCAAACTGGGAATTTGCCCGAAT GATTAAAGAATTTGCGGGCTACTTTGGAATGTCATCCACT TACTATGACTGATCC
30	KIF2C	2334117	GAGCACCCCTGAAATACTCTCCTTC
31	KIF2C	2334118	ACATGAACCCAAGTTGAAAGTGGACTTAACAAAGTATC TGGAGAACCAAGCATTCTGCTTTGACTTTGCATTTGATG AAACAGCTTCG
32	KIF2C	2334119	AGGCCACTGGTACAGACAATCTTTGAAGGTGGA
33	KIF2C	2334122	CGGGACGTCTTCCTCCTGAAGAATCAACCCTGCTACCG GAAGTTGGGCCTGGAAGTCTATGTGACATTCTTCGAGA TCTACAATGGGA
34	KIF2C	2334125	AGGACGGCAAGCAACAGGTGCAAGTGGTGGGGCTGCA GGAGCATCTGGTTAACTCTGCTGATGATGTCATCAAGA

			TGATCGACATGGGCAGC
35	KIF2C	2334126	GCTCCACGCGTGCTTCCAAATTATTCTTCGAGCTAAAG GGAGAATGCATGGCAAGTTCTCTTTGGTAGATCTGGCA GGGAATGAGCGAGGCGCGGACACTTCCAGTGCTGACCG GCAGACCCGCATGGAGGGGCGCAGAAATCAACAAGAGT CTC
36	KIF2C	2334130	GCTGGGTGAGGGGCTTTTCCAGTCCA
37	KIF2C	2334131	GCAAGGTTGCCATTCCATCCCCTTGGAGCCTCAAGCCTC GAAGCCTGGGCGGTGCCACATTCCTC
38	KIF2C	2334132	AGTACCAAGGGGGTGCTGTGGGATCTGAGACCTCCTTG TTTCCT
39	KIF2C	2334133	GAAGAGATGGAAGCCTGCTCTAACGGGGGCGCTGATTCC AG
40	KIF2C	2334134	CCAGATGTCCAGCTTTAACGAAGCCATGACTCAGA
41	KIF2C	2334135	AAGGACCAGACTGGCTTGAGCTCTCTGAGATGACCGAG CAGCCAGACTATGACCTGGAGACCTTTGTGAACAAAGC GGAATCTGCTCTGGCCCAGC
42	KIF2C	2334136	GTCATCAAGGCCTTGCGCCTGGCCATG
43	KIF2C	2334137	CGACTGCAAATAAAAATCTGTTTGGTTTG
44	KIF2C	2334138	GGGACAGGTTCTGGTAAATGCCAAGTATG
45	KIF2C	2334139	TTCTCAGTTGTCGCCCTCACGAGAGGAAGGAGCTCTT AGTTACCCTTTTGTGTTGCCCTTCTTTCCATCAAGGGGA ATGTTCTCAGCATAGAGCTTTCTCCGCAGCATCCTGCCT GCGTGGACTGGCTGCTAATGGAGAGCTCCCTGGGGTTG TCCTGGCTCTGGGGAGAGAGACGGAGCCTTTAGTACAG CTATCTGCTGGCTCTAAACCTTCTACGCCTTTGGGCCGA GCACTGAATGTCTT
46	KIF2C	2334140	GTCTCCCTAGAGATCCTAGAGGATCCCTACTGTTTTTC
47	PHGDH	2354635	AGGAGCCACATGCTCTCATCAAGCAGAAA
48	PHGDH	2354639	GTGCCCAACCAGTGAGGCCACGTTTCGAAAAGAAGAAA GAAACGACAACTAAAATACATGACTGTGTAGATGAGG
49	PHGDH	2354641	GCTGGAGAATACTGCCCAGTTACTCTAGCGCGCCAGGC CGAACCGCAGCTTCTTGGCTTAGGTACTTCTACTCACAG CGGCCGA
50	PHGDH	2354642	ATGGCTTTTGCAAATCTGCGGAAAGTGCTCATCAGTGA CAGCCTGGACCCTTGCTGCCGGAAGATCT
51	PHGDH	2354644	GCAGCCTAAGCATCATTCCTCTTCTCTTCTTAGTGGAGA TAAAATTACCCACTGCTCTCCTTACATT

52	PHGDH	2354645	GTGTGGGCCCTTACCCTAGAAGCCAACCTTCTCATGACCT TTCTCTATCTCCAGAATCCATGCAGTGGGAATGAAGGT AAAAGAAGGTTTTTCATGGGATCCAGCTGAGAGCTCTAC GGGGAAAATGGATCTGAGGAGCCATGTGCTCCATCTCT TTTATTTTACAGGTAGAGACTAGGGGTATAGAGTGAGG TGAATTACCGCAGTGACCCACACATTGTTGGCAGACCT AGGATTAGAACTCTGTCTTCCTGGTTCCTCAGCTTGGTGC TTTTGAAAGCATACTTGCTGCTTTCTTACCGGCCTGGTG TCTGCCACTTTGGGACAGAGTGTGGACTTGCTCACCTGC CCCATTTCTTAGGGATTCTCATTCTGTGTTTGAGCAAGA ATATTCTTATTCTGGAAAGAACCACATACCACAGGATT CTGGGTGAGCATAAGGAAGATTGTCTTGGGGATCTGAC TTAGCTCACGTATAGTGGCTATGATGAATTCAGTGTCTT ATTTTTTGCATATGTATATTTTTAGTCTAATATTGCCTGG GTGTCTGAGCAAGTCTAGATGAATTTAATTGCTCTCATT TTTCCCCTGCCCTCTTCCTTTGGTCTCTCTTTTAGGAAA TGTTTTTCTTTCAACATTCGTTTCATTCAATTATTTACTCA TTCGGCCAACCAACATTTATTGAGTGCCTTCCCTGTATC AGGGACAGGGGCTTACAAAGTAGAATTTGATCCCACCT CTGCCCTCAGTAGCTCAGTGTCTAATGGAGGTAGTGAT GTTCATTAAGCGTCGCCAGATACTGTGCTAGGTGCTGTG CCTGTTCTCTCTCGCTTGTTCCCTCACACACTTGAGAAGG CCGAAGCTGATTCATAGCTTGGAAGGCAGGGGCCTTGG ATTTGAACCCAGGCCTGACCAATGGCAGAACCTATCAG ATGTGTGGACAGATGACATTGCCTTTCTTTCTTTGGATA TATCAAAATCAGCCAGCAGGCAGGAACTCCCATTTT
53	PHGDH	2354646	TGTGTCTGATGGACATCCAGGCTGCAGG
54	PHGDH	2354647	ATGGTGCTGTCTAGAGAGATGAGCCAGGTGCCCAGAGC CCATGGGCCAATGCTGCCCTTTCTTGAGCATGCCAAAC AAAGCGGTTG
55	PHGDH	2354648	CAGTCTCCTCCACTCTAAGTAAAAATCAGCATGAGTCCT AGCCCACATTT
56	PHGDH	2354649	TGAGTATACCAAAGATATCTATGAACTGGCAGTCATCA GTGACTTCCTAAGGTTCCGGAAATGCATCTCTT
57	PHGDH	2354650	ATGTGCCTGCGGCTTTACGAGTTCTCACAGAATGACTTT C
58	PHGDH	2354651	ACTGTGAAGGCCTTATTGTTTCGCTCTGCCACCAAGGTGA CCGCTGATGTCATCAACGCAGCTGAGAAACTCC
59	PHGDH	2354652	ATCTGGAGGCCGCAACAAGGAAGGGCATCTT
60	PHGDH	2354653	TGAGTGCGGAGACTGACCACACCTAGGGAGAAAAAAC TCACTTGAGAGAAAGCTGAGTCCATTGGAAGGGCTTCC AGGAGGATGCCTGGTCTAGGGCCTGCATGGTCAACACA
61	PHGDH	2354657	ATTACTTTTCCCATGGCGAGACCTGCTTTCCCTCCTGCT GGAGGAGGATCTGGGGGAATTTACCTCTGCTCTAACTC CTCCCTGCAGTTTCCATCTGAGCTCTCTGGTATTCACTG ATATTC
62	PHGDH	2354660	GCAGATTCCCCAGGCGACGGCTTCGATGAAGGACGGCA AATGGGA
63	PHGDH	2354662	GAGAGGTAGCTACCCGGATGCAGTCCTTTGGGA
64	PHGDH	2354666	TTCCTTCTCCGTGGCACCCTACACATCAATATTCCTGG CAATATTCTTCATCATGGAGACTTCGGCAGCGACTTCAA

			CCAGATGAAA
65	PHGDH	2354667	GAAACATGGCTTGGATCATTCCGTCTCCCACCTCAGCCC CTCCGGAGCTGCCTGGACCTCATCATTCCGGAGAGTCT AAGTGGC
66	PHGDH	2354674	CAGTCCCAGCATCATTGTGTGGTCATGAGAATTAATTA AGCTGATCATGGTACTTAGTATATGGTAAATAGTACTTA GTATGTGGAACATGGTACTTAGTGTATGGTAAATTAAC TGGAGAATTA
67	PHGDH	2354675	GGTATGACCCCATCATTTCCTCCAGAGGTCTCGGCCTCCT TTGGTGTTCAGCA
68	PHGDH	2354677	CCTTTGCCCAGTGCAAGAAGGGGGGTGCGTGTGGTGAAC TGTGCCCGTGGAGGGATCGTGGACGAAGGCGCCCTGCT CC
69	PHGDH	2354682	GCCTTGGTGGACCATGAGAATGTCATCAGCTGTCCCCA CCTGGGTGCCAGCACCAAGGAGGCTCAGAGCCGCTGTG GG
70	PHGDH	2354687	ATGGTTGACTTTACAAGTTATCTCAATAAAAGTGGCCA GATGCCTAACTCAGAA
71	PHGDH	2354688	TGGACTTCGCATGCGTTGATATTTGAAGCACGATCATCA AACTTTGTGATAATTGATCGTAGTGTTTAGTAACAATG TAAACACTTAAAAAAATTCAAGATAGAAAATAAAAATG AAGGCAAGTTGGGACTGCCAGAGAAGACCCGTCCTCC TCATCCAAGTTATCTGCGACTCCCATATGTTTTGTGTCA AAGACTCACCTTTATTGTGCTGTCCAATCCCTTCCCCAG TGCAGAAACAAGTCTCCCATGGAGGGGGGCTGGGGCAG ACACAGTTTGCTGAAAGGAGCAATTTTGAGTGGTTGTG GCATTCTGTGTCCATTTCTGGCTCCACAGCTTTCTTCATT TGTAGGAACAAGTCCTTGTCCTGTTGTTAGTGGCTGATG GAAGTTGTCACCCACCAGGCACCAAGGCAGGAGTGACC CTATACTGTCTTTC
72	PHGDH	2354689	CCAAGCCTTGGATTGGTCTGGCAGAAGCTCTGGGGACA CTGATGCGAGCCTGGGCTGGGT
73	PHGDH	2354690	AATGCTGGGAAGTGCCTAAGCCCCGCAGTCATTGTCGG CCTCCTGAAAGAGGCTTCCAAGCAGGCGGATGTGAACT TGGTGAACGCTAAGCTGCTG
74	PHGDH	2354695	TGGGCTTGGTCCAAGGCACTACGCCTGTACTGCAGGGG CTCAATGGA
75	PHGDH	2354698	CAGGCGTGCGGCTGCTGTCCTACCAGACTTCACTGGTGT CAGATGGGGAGACCTGGCACGTCATGGGCATCTCCT
76	PHGDH	2354699	CCACTGTGATCAATAGGGAGAGAAAATCCACATTCTTG GGCTGAACGCGGGCCTCTGACACTGCTTACACT
77	NUF2	2364439	TCCAGTAGGAGGCGGCAAGTTTGAAAAGTGATGACGGT TGACGTTTGCTGATTTTTGACTTTGCTTGTAGCTGCTCCC CGAACTCGCCGTCTTCCTGTCGGCGGCCGGCACTGT
78	NUF2	2364440	TGAGCGCGAGAGGACGGAGGAAGGAAGCCTGCAGACA GACGCCTTCTCCATCCCAAGGCGCGGGCAGGTGCCGGG ACGCTGGGCCTGGCGGTGTTTTCGTCGTGCTCAGCGGTG GGAG

79	NUF2	2364441	TCAAACCTATGTAGTTGGAAAGTGTCTTCATCTCTCGTTA ATGAATAAATTGTAACCTGAAATTGTACTTCGAAAGAAT GATAGAATTTGGATATTGGAGGAGGTTCCAAAAGGAAA TACTGGAAGTTTGGGAAAGTTAGGAGACTAACTTGGAG CAGAAATTTCAATTCAATTATTAAAGGGTTTAGAAGCCT AGCAGAAAAATTTG
80	NUF2	2364442	AATGTAGCTGAGATTGTGATTCATATTCGCAATAAGAT CTTAACAGGAGCTGATGGTAAAAACCTCACCAAGAATG ATCTTTATCCAAATC
81	NUF2	2364444	CATGATCTACATGAGAGCCTTACAAATAGTATATGGAA TTCGACTGGAACATTTT
82	NUF2	2364445	TGAACTCTGAAGTCATGTATCCACATTTAATGGAAGGC TTCTTACCATTTCAGCAATTTAGTTACTCATCT
83	NUF2	2364449	TTTAAGTGGCATTATCAACTTTATTCACTTC
84	NUF2	2364451	TCCTCTGCGGACAAAATGCAACAGTTAAACGCCGCACA CCAGGAGGCATTAATGAAACTGG
85	NUF2	2364452	TGAGGACAGGTATTTTCATTTTAGCCTT
86	NUF2	2364453	ATTCAGGAGCTACAACAATCACTAAA
87	NUF2	2364457	AAAATGAAAGATACGGTCCAGAAGCTTAAA
88	NUF2	2364459	ATCTATGGAGACTCAGTTGACTGCCTGCCTTCATGTCAG TTGGAAGTGCAGTTATATCAAAAGAAAATACAGGACCT TTCAGATAATAGGGAAAAATTAGCCAGTATCTTAAAGG AG
89	NUF2	2364460	CGTTCAAAGACTGATGATTGTGAAGAAGGAAAAACTT GCCACAGCACAATTCAAAATAAATAAGAAGCATGAAG ATGTTAAGCAATACAAACGCACAGTAATTG
90	NUF2	2364461	AAAAAGAGGTGCTGTCTATGAACGAGTAACCACAATTA ATCAAGA
91	NUF2	2364463	AAAAGTGCTTTGGAGAAATACCACGACGGTATTGAAAA GGCAGCAGAGGACTCCTATGCTAAGATAGATGAGAAG ACAGCTGAACTG
92	NUF2	2364464	AAAAGTTGAAGCGAATGGAAGTATCAGAAGTACCAAA TAATGTTGGCTTCATCAGTTTTTATACACTCTCATAAGT AGTTAATAAGATGAATTTAATGTAGGCTTTTATTAATTT ATAATTAAAATAACTTGTGCAGCTATTCATGTC
93	CENPF	2379864	GCTGCGGGCAGTTTGAATTAGACTCTGGGCTC
94	CENPF	2379865	CGCGCCAGAACTGTACTCTCCGAGAGGTCGTTTTCC
95	CENPF	2379867	TGTCCCAGACCCTACTCGGTCACGGACTCACACTTTAGG GGATCATTTTCTTCCTCCGTAAAAGAATTGGAGATGACT A
96	CENPF	2379878	TTTACAAATGTTGGAGTAATAAAGAAGGCAGAAC
97	CENPF	2379879	GAAAGAAGGGCTGCCTACAAGAGCTCTTCAGAAAATTC AAGAGCTTGAAGGACAGCTTGACAAACTGAAGAAGGA AAAGCAGCAAAGGCAGTTTCAGCTTGACAGTCTCGAGG CTGCGCTGCAGAAGCAAAAA
98	CENPF	2379880	GAAGATTTCTCATGAACTTCAAGTCAAGGAGTCACAAG TGAATTTCCAGGAAGGACAACCTGAATTCAGGCAAAAA CA
99	CENPF	2379881	TATTTTGGGATGGTATTTATAGGGATGATATTTGTATGT ATTAATCAGATGCGTTTGTCTTTTCCTTTAACAATATAA TTATTATACTTTGCAATTTTTTTTCCTGGTAGAATAAGT

			AATGATTCGGTCTCTGTACC
100	CENPF	2379882	GAAGCCAACAAGCTGCGCAGTCTGCAGATG
101	CENPF	2379885	AGACTCTTCCACAAGCCACCATGAATCACCGCGACATT GCCCCGGCATCAGGCTTCATCATCTGT
102	CENPF	2379886	TAGGAGAGATTTCTCTGCATCTTACTTTTCTGGGGAACA AGAGGTGACTCCAAGTCGATCAACTTTGCAAATAGGGA AAAGAGATGCTAATAGCAGTTTCTTTGACAATTCTAGC AGTCCTCATCTTTTGGATCAATTAAGCGCAGAATC
103	CENPF	2379888	ACTGAAAAAATTGACGGAAGATTTGAGTTGTCAGCGAC AAAATGCAGAA
104	CENPF	2379889	GAGCTCTCCCGTCAACAGCGTTCTTTCCAAACACTGGAC CAGGAGTGCATCCAGATGAAGGCCAGACTCACCCAGGA GTTACAGCAAGCCAAGAATATGCACAACGTCCTGCAGG CTG
105	CENPF	2379890	AGAGTTTAAGCAAAAGTTGTGCAGAGCTGAACAGGCGT TCCAGGCGAGTCAGATCAAGGA
106	CENPF	2379895	AAAGGCCAGAGAAGTCTGCCACCTGGAGGCAGAACTC AAGAACATCAAACAGTGTTTAAATCAGAGCCAGAATTT TGCAGAAGA
107	CENPF	2379896	GCCTTGCTGAGTGCTTTAGAGTTAAAAAAGAAAGAATA TGAAGAATTGAAAGAAGAGAAAACCTCTGTTTTCTTGTT GGAAAAGTGAAAACGAAAAACTTTTAACTCAGATGGA ATCAGAAAAGGAAAACCTTGCAGAGTAAAATTAATCACT TGGAACCTTGTCTGAAGACACAGCAAATAAAAAGTCAT GAATACAACGAGAGAGTAAGAACGCTGGAGATGGACA GAGAAAACCTAAGTGTCGAGATCAGAAACCTTCACAAC GTGTTAGACAGTAAGTCAGTGGAGGTAGAGACCCAGAA ACTAGCTTATATGGAGCTACAGCAGAAAGCTGAGTTCT CAGATCAGAAACATCAGAAGGAAATAGAAAATATGTG TTTGAAGACTTCTCAGCTTACTGGGCAAGTTGAAGATCT AGAACACAAGCTTCAGTTACTGTCAAATGAAATAATGG ACAAAGACCGGTGTTACCAAGACTTGCATGCCGAATAT GAGAGCCTC
108	CENPF	2379897	TTTGGCTTTTGATCAGCAGCCTGCCATGCATCATTCTT TGCAAATATAATTGGAGAACAAGGAAGCATGCCTTCAG AGAGGAGTGAATGTCGTTTAGAAGCAGACCAAAGTCCG AAAAATTCTGCCATCCTACAAAATAGAGTTGATTCACTT GAATTTTCATTAGAGTCTCAAAAACAGATGAACTCAGA CCTGCAAAAGCAGTGTGAAGAGTTGGTGCAAATCAAAG GAGAAATAGAAGAAAATCTCATGAAAGCAGAACAGAT GCATCAAAGTTTTGTGGCTGAAACAAGTCAGCGCATT GTAAGTTACAGGAAGACACTTCTGCTCACCAGAATGTT GTTGCTGAAACCTTAAGTGCCCTTGAGAACAAGGAAAA AGAGCTGCAACTTTTAAATGATAAGGTAGAACTGAGC AGGCAGAGATTCAAGAATTAAAAAAGAGCAACCATCT ACTTGAAGACTCTCTAAAGGAGCTACAACCTTTTATCCG AAACCCTAAGCTTGGAGAAGAAAGAAATGAGTTCCATC ATTTCTCTAAATAAAAGGGAAATTGAAGAGCTGACCCA AGAGAATGGGACTCTTAAGGAAATTAATGCATCCTTAA ATCAAGAGAAGATGAACTTAATCCAGAAAAGTGAGAG TTTTGCAAACCTATATAGATGAAAGGGAGAAAAGCATTT

			CAGAGTTATCTGATCAGTACAAGCAAGAAAAACTTATT TTACTACAAAGATGTGAAGAAACCGGAAATGCATATGA GGATCTTA
109	CENPF	2379898	ACTGTGAAATAGATGCGGAAGAAAAGTATATTTTCAGGG CCTCATGAGTTGTCAACAAGTCAAAACGACAATGCACA CCTTCAG
110	CENPF	2379899	TCTGCAAACAACAATGAACAAGCTGAATGAGCTAGAGA AAATATGTGAAATACTGCAGGCTGAAAAGTATGAACTC GTAAGTGAAGCTGAATGATTCAAGGTCAGAATGTATCAC AGCAACTAGGAAAATGGCAGA
111	CENPF	2379900	TGGCTCCATTGGACGAGAGTAATTCCTACGAGCACTTG ACATTGTCAGACAAAGAAGTTCAAATGCACTTTGCCGA ATTGCAAGAGAAATTCTTATCTTTACAAAGTGAACACA AAATTTTACATGATCAGCACTGTCAGATGAGCTCTAAA ATGTCAGAGCTGCAGACCTATGTTGACTCATTAAAGGC CGAAAATTTGGTCTTGTCAACGAATCTGAGAACTTTC AAGGTGACTTGGTGAAGGAGATGCAGCTGGGCTTGGAG GAGGGGCTCGTTCCATCCCTGTCATCCTCTTGTGTGCCT GACAGCTCTAGTCTTA
112	CENPF	2379901	GCTGACAAGCGTGACTCTGGAGATGGAGTCCAAGTTGG CGGCAGAAAAGAAACAGACGGAACAACCTGTCACTTGA GCTGGAAGTAGCACGACTCCAGCTACAAGGTCTGGACT TAAGTTCTCGGTCTTTGCTTGGCATCGACA
113	CENPF	2379902	AGATACCAATTATGAGCCTCCAGGGGAAGATAAAAACCC AGGGCTCTTCAGAATGCATTTCTGAATTGTCATTTTCTG GTCCTAATGCTTTGGTACCTATGGATTTCCTGGGGGAATC AGGAAGATATCCATAATCTTCAACTGCGGGTAAAAGAG ACATCAAATGAGAATTTGAGATTACTTCATGTGATAGA GGACCGTGACAGAAAAGTTGAAAGTTTGCTAAATGAAA TGAAAGAATTAGACTCAAAACTCCATTTACAGGAGGTA CAACTAATGACCAAAAATTGAAGCATGCATAGAATTGGA AAAAATAGTTGGGGAACTTAAGAAAGAAAACCTCAGATT TAAGTGAAAAATTGGAATATTTTTCTTGTGATCACCAGG AGTTACTCC
114	CENPF	2379903	ATTGAGCATGAAGCCCTCTACCTGGAGGCTGACTTAGA GGTAGTTCAAACAGAGAAGCTATGTTTAGAAAAAGACA ATGAAAATAAGCAGAAGGTTATTGTCTGCCTTGAAGAA GAACTCTCAGTGGTCACAAGTGAGAGAAACCAGCTTCG TGGAGAATTAGATACTATGTCAAAAAAAACCACGGCAC TGGATCAGTTGTCTGAAAAAATGAAGGAGAAAACACA AGAGCTTGAGTCTCATCAAAGTGAGTGTCTCCATTGCAT TCAGGTGGCAGAGGCAGAGGTGAAGGAAAAGACGGAA CTCCTTCAGACTTTGTCCTCTGATGTGAGTGAGCTGTTA AAAGACAAAACCTCATCTCCAGGAAAAGCTGCAGAGTTT GGAAAAGGACTCACAGGCACTGTCTTTGACAAAATGTG AGCTGGAAAACCAAATTGCACAACTGAATAAAGAGAA AGAATTGCTTGTCAAGGAATCTGAAAGCCTGCAGGCCA GACTGAGTGAATCAGATTATGAAAAGCTGAATGTCTCC AAGGCCTTGGAGGCCGCACTGGTGGAGAAAGGTGAGTT CGCATTGAGGCTGAGCTCAACACAGGAGGAAGTGCATC AGCTGAGAAGAGGCATCGAGAACTGAGAGTTTCGCATT GAGGCCGATGAAAAGAAGCAGCTGCACATCGCAGAGA

			AACTGAAAGAACGCGAGCGGGAGAATGATTCACTTAA GGATAAAGTTGAGAACCTTGAAAGGGAATTGCAGATGT CAGAAGAAAACCAGGAGCTAGTGATTCTTGATGCC
115	CENPF	2379904	AGAGTCTAGACCCACCAATAGAGGAAGAGCATCAGCTG AGAAATAGCATTGAAAAGCTGAGAGCCCGCCTAGAAG CTGATGAAAAGAAGCAGCTCTGTGTCTTACAACAACCTG AAGGAAAGTGAGCATCATGCAGATTTACTTAAGGGTAG AGTGGAGAACCTTGAAAGAGAGCTAGAGATAGCCAGG ACAAACCAAGAGCATGCAGCTCTTGAGGCAGAGAATTC CAAAGGAGAGGTAGAGACCCTAAAAGCAAAAATAGAA GGGATGACCCAAAGTCTGAGAGGTCTGGAATTA
116	CENPF	2379905	GCTCAATGAGAGAGTGGCAGCCCTGCATAATGACCAAG AAGCCTGTAAGGCCAAAGAGCAGAATCTTAGTAGTCAA GTAGAGTGTCTTGAACCTTGAGAAGGCTCAGTTGCTACA AGGCCTTGATGAGGCCAAAAATAATTATATTGTTTTGC AATCTTCAGTGAATGGCCTCATTCAAGAAGTAGAAGAT GGCAAGCAGAACTGGAGAAGAAGGATGAAGAAATCA GTAGACTGAAAAATCAAATTCAAGACCAAGAGCAGCTT GTCTCTAAACTGTCCCAGGTG
117	CENPF	2379907	AGAGAAAAATAGGCTAGCTGGAGAGTTGC
118	CENPF	2379908	ATAGTGAATTGAAGAAGAGCCTAGATTGCATGCACAAA GACCAGGTGGAAAAGGAAGGGGAAAGTGAGAGAGGAAA TAGCTGAATATCAGCTACGGCTTCATGAAGCTG
119	CENPF	2379909	AATCCAGACATACCGAGAGAAATTGACTTCTAAAGAAG AATGTCTCAGTTCACAGAAGCTGGAGATAGACCTTTTA AAGTCTAGTAAAGAAGAGCTCAATAATTCATTGAAAGC TACTACTCA
120	CENPF	2379910	TCTTCCTTTGGAAATTCATGATGCCATATCAGATGGTTT TAGAATTCTGCACTTTAATAATGTAATGCATATGCCATA TATAATATCCCAGAGGGATCTGCTATAATATTGCATAAT CGAATTCATATTTCTGCAGCAAAATGTGTGGATACTCTC ACAAGGCAGGATAAATAGA
121	CENPF	2379911	TTTTTCCATATGCTTATAAAAAGAAATTCA
122	CENPF	2379912	ATGGACAATCTAAAATATGTAAATC
123	CENPF	2379913	GAAGTTGTTGATCAAATCCTGTAAACAGCTGGAAGAGG AAAAGGAGATACTGCAGAAAGAACTCTCTCAACTTCAA GCTGCACAGGAGAAGCA
124	CENPF	2379914	TCTAAACAAGATTCCCGAGGGTCTCCTTTGCTAGGTCCA GTTGTTCCAGGACCATCTCCAATCCCTTCTGTTACTGAA AAGAGGTTATCATCTGGCCAAAATAAAGCTTCAGGCAA GAGGCAAAGATCCAGTGGAAATATGGGAGAATGGTAGA GGACCAACACCTGCTACCCCAGAGAGCTTTTCTAAAAA AAGCAAGAAAGCAGTCATGAGTGGTATTCACCCTG
125	CENPF	2379915	GACTAGCCCATATATCCTGCGAAGAACAACCATGGCAA CTCGGACCAGCCCCCGCCTGGCTGCACAGAAGTTAGCG CTATCCCCACTGAGTCTCGGCAAAGAAAATCTTGACAGA GTCCTCCAAACCAACAGCTGGTG
126	CENPF	2379918	CTCAGCGGAGCCCAGTAGATTCAAGGCACCATCCTCCGA GAACCCACCACGAAATCCGTCCCAGTCAATAATCTTCC TGAGAGAAGTCCGACTGACAGCCCCAGAGAGGGCCTG AGGGTCAAGCGAGGCCGACTTGTCGCCAGCCCCAAAGC

			TGGACTGGAGTCCAACGGCAGTGAGAAC
127	CENPF	2379919	TTCTCTTTAGTCAGGGCATGCTTTATTAGTGAGGAGAAA ACAATTCCTTAGAAGTCTTAAATATATTGTACTCTTTAG ATCTCCCATGTGTAGGTATTGAAAAAGTTTGGAAGCAC TGATCACCTGTTAGCATTGCCATTCCTCTACTG
128	CENPF	2379920	CTTCCTAGAGGTGTGCTATACCATGCGTCTGTCGTTGTG CTTTTTTCTGTTTTTAGACCAATTTTTTACAGTTCTTTGG TAAGCATTGTCGTATCTGGTGATGGATTAACATATAGCC
129	EXO1	2388223	GGCCATCAGCGCCAGTGCCACTCGCGCCCTCAAG
130	EXO1	2388225	TCGGAGCGGGTTTCTCCAACCGCAATCGGCTCCGCTCA AGGGGAGGA
131	EXO1	2388226	AAACGTGTCGTCTGGAATGGGCTTGGGGGGCCACGCCTG CACATCTCCGCGAGACAGAGGGATAAAGTGAAGATGGT GCTGTTATTGTTACCTCGAGTGCCACATGCGACCTCTGA GATATGTACACAGTCATTCTTACTATCGCACTCAGCCAT TCTTACTACGCTAAAGAAGAAATAATTATTGAGGATA TTTGCCTGGCCC
132	EXO1	2388227	TAGTGAATCCCAGTCACTGAGTGGAGTTGAGAGTCTAA GAACCTCTGAAATTTGAGAACTGCTGGACCAGAGCCTT TAGAGCTCTGATAAGGTGTC
133	EXO1	2388229	TGGGGATACAGGGATTGCTACAATTTATCAAAGAAGCT TCAGAACCCATCCATGTGAGGAAGTATAAAGGGCAGGT AGTAGCTGTGGATACATATTGCTGGCTTCACAAAGGAG CTATTGCTTGTGCTGAAAAACTAGCCAAAGGTGAACCT ACTGATA
134	EXO1	2388230	CTATCTCATGGGATCAAGCCTATTCTCGTATTTGATGGA TGTACTTTACCTTCTAAAA
135	EXO1	2388231	AGACGACAAGCCAATCTTCTTAAGGGAAAGCAACTTCT TCGTGAGGGGAAAGTCTCGGAAGCTCGAGAGTGTTTCA CCCGGTC
136	EXO1	2388232	CTCGTGGCTCCCTATGAAGCTGATGCGCAGTTGGCCTAT CTTAACAAAGCGGGAATTGTGCAAGCCATAATTACAGA GGACTCGGATCTCCTAGCTTTTGGCTGTA
137	EXO1	2388233	TGAAATTGATCAAGCTCGGCTAGGAATGTGCAGACAGC TTGGGGATGTATTCACGGAAGAGAAGTTTCGTTACATG TGTATTCTTTCAGGTTGTGACTACCTGTCATCACTGCGT GGGATTGGA
138	EXO1	2388234	TATCACGGTACCAGAGGATTACATCAACGGGTTTATTC GGGCCAACAATACCTTCTCTATCAGCTAGTTTTTGATC CCATCAAAAGGAACTTATTCCTCTGAACGCCTATGAA GATGATGTTGATCCTGAAACACTAAGCTACGCTGGG
139	EXO1	2388235	TGATGATTCCATAGCTCTTCAAATAGCACTTGGAAATA AAGATATAAATACTTTTGAACAGATCGATGACTACAAT CCAGACACTGC
140	EXO1	2388238	CATAGTTGGGATGACAAAACATGTCAAAGTCAGCTAA TGTTAGCAGCATTTGGCATAGGAATTACTCTCCAGACC AGAGTCGGGTACTGTTTCAGATGCCCCACAATTGAAGG AAAATCCAAGTACTGTGGGAGTGGAACGA

141	EXO1	2388239	ACCTGTTGAGTCAGTATTCTCTTTTCATTTACGAAGAAGA CCAAGAAAAATAGCTCTGAAGGCAATAAATCATTGAGC TTTTCTGAAGTGTTTGTGCCTGACCTGGTAAATGGACCT ACTAACAAAAAGAGTGTAAGCACTCCACCTAGGACGA
142	EXO1	2388240	GTGGTGCAGTTGTGGTTCCAGGGACC
143	EXO1	2388242	GCCTCTGGATGAAACTGCTGTCACAGATAAAGAGAACA ATCTGCATGAATCAGAGTATGGAGACCAAGAAGGCAA GAGACTGGTTGACACAGATGTAGCACGTAATTCAAGTG ATGACATTCCGAATAATCATATTCCAGGTGATCATATTC CAGACAAGGCAACAGTGTTTACAGATGAAGAGTCCTAC TCTTTTGAGAGCAGCAAATTTACAAGGACCATTTCACC ACCCACTTTGGGAACACTAAGAAGTTGTTTTAGTTGGTC TGGAGGTCTTGGAGATTTTTCAAGAACGCCGAGCCCCT CTCCAAGCACAGCATTGCAGCAGTTCCGAAGAAAGAGC GATTCCCCCACCTCTTTGCCTGAGAATAATATGTCTGAT GTGTCGCAGTTAAAGAGCGAGGAGTCCAGTGACGATGA GTCTCATCCCTTACGAGAAGAGGCATGTTCTTCACAGTC CCAGGAA
144	EXO1	2388244	TCTGATTGCAATATTAAGTTACTTGACAGTCAAAGTGAC CAGACCTCCAAGCTACGTTTATCTCATTTT
145	EXO1	2388246	GGCTATATAAGTCCAGTTCTGCAGACTCTCTTTCTACAA CCAAGATCAAACCTCTAGGACCTGCCAGAGCCAGTG CTGAGCAAGAAGCCGGCAAGCATCCAGAAGAGAAAGC ATCATAATGCCGAGAACAAGCCGGGG
146	EXO1	2388248	AGAGATAACATCCAACCTAACTCCAGAAGCGGAAGAGG ATATATTTAACAAACCTGAATGTGGCCGTGTTCAAAGA GCAATATTCCA
147	EXO1	2388253	TCTCGCTGTGTCACAATCTCAGCTCACT
148	EXO1	2388254	TTCTCCATCCTAGGCAGAAATAAAGTCCCAAATCTTTG TTTTTTAACGGGTCATAGAGGACCCATCATCACCTTTA TTCATTCTTGATCATCTCAGGCTAGAGAAGTCTAGGGA TACAGCT
149	UBE2T	2451201	TGTCCTGGTTCATCTTAGTTAATGTGTTCTTTGCCAAGG TGATCTAAGTTGCCTACCTTGAATTT
150	UBE2T	2451202	ACCAGAGGCTGGTGACTCCAGAGTACACAACCTCAACAC AGAAAAGGAAGGCCAGTCAGCTAGTAGGCATAGAAAA
151	UBE2T	2451205	ATTTAAATATAATAAGCCAGCCTTCCTCAAGAAT
152	UBE2T	2451206	GCTCTAACCCTGCAAATCATGTTTTTCT
153	UBE2T	2451207	CTCTGCAACACATATCCTACCTTGTCTATACCGCTAACT CTC
154	UBE2T	2451208	CATCCCTCAACATCGCAACTGTGTTGACCTCTATTCAGC TGCTCATGTGAGAACCCAACCCTGATGACCCGCTCATG GCTGACATA
155	UBE2T	2451210	TGAACCTCCTCAGATCCGATTTCTCACTCCAATTTATCA TCCAAACATTGATTCTGCTGGAAGGATTGTCTGGATGT TCTCAAATTGCC
156	UBE2T	2451214	TGGAGCCAACACACCTTATGAGAAAGGTGTTTTTAAGC TAGAAGTTATCATTCCTGAG
157	UBE2T	2451215	AGAGCTTCACGTCTGAAGAGAGAGCTGCACATGTTAGC CACAGAGCCACCCCCAGGCATCACATGTTGGCAAGATA AAGACCAAATGGATGACCTGCGAGCTC

158	UBE2T	2451216	GTGTGTGGTTCCTTCTACTTGGGGATC
159	RRM2	2469253	TCCCGCGCTGCGCTTGAAAATCGCGCGCGGCCCGCGG CCAGCCTGGGTAGGGGCAAGGCGCAGCCAATGGGAAG GGTCGGAGGCATGGCACAGCCAATGGGAAGGGCCGGG GCACCAAAGCCAATGGGAAGGGCCGGGAGCGCGCGGC GCGGGAGATTTAAAGGCTGCTGGAGTGAGGGGTGCGCC GTGCACCCTGTCCCAGCCGTCCTGTCCTGGCTGCTCGCT CTGCTTCGCTGCGCCTCCACT
160	RRM2	2469254	AGCTGCAGCTCTCGCCGCTGAAGGGGC
161	RRM2	2469255	GACCCGCGTCCTGGCCAGCAAGACCGCGAGGAGGATCT TCCAGG
162	RRM2	2469256	TCTGCTGCGACCCACGGAGTGCGACGGGACAGCCACGT TTTCACATCGGGCCCCGTGAAATTGCCGCCAATGGAAA GGACTTGGTCCAGAAAAACGTTAGTTTCATATGGTTTCG CCCGGTACTTA
163	RRM2	2469257	GCTGCCCCCGGCGTGGAGGATGAGCCGCTGCTG
164	RRM2	2469258	CCCGCCGCTTTGTTCATCTTCCCCATCGAGTACCATGATA TCTGGCAGATGTATAAGAAGGCAGAGGCTTCCTTTTGG ACCGCCGAG
165	RRM2	2469259	ATCGGAGGACCCCAGAAGACCCCTGCAGGG
166	RRM2	2469260	CCCGAGGAGAGATATTTTATATCCCA
167	RRM2	2469261	TGACGATCTGAGGTCGAACTAGTTCGCTTTCCTCGTCTT GTATGTTTTTCCATGCTGAGTGCATCTGTGTGTGTAAGC TGGGTTTTATATTACATGGCATTTCCTGTTTTGTAAACAC TTTGCAGTTCTTTCTTATGGTATTTTCCCGACTCTAGAG AAGCTGAGACAATATTAAGTGGTAGCAATGTGATGACT CTTTGTGGCC
168	RRM2	2469263	AGTCTTCTTATTGACACTTACATAAAAGATCCCAAAGA AAG
169	RRM2	2469266	CCCTGCTGTACTGGACTATGTTTTACTGTCTGTAGACCC TGAAGCTCAATATGAACTACAGAATACCCAAACTTGTA TTAATGTAAATCAAGTGTTGAGGTTTTTAAAAGAACAC TGGAGGGAAAAACTGACCAGTAAAAATAAACATTTCG GTGTGAGTTCTTCCTTTAGGAAGAGGATTGGCAAATAC TTGAATTTGGCCTTTGTCCCAGAGCTCTTATCTAGCAGT TGGTAATCGGAGGTCTTTTACTGTAATGCTTCAATTGCT GATACCGTATGTG
170	RRM2	2469267	AACGATGCCTTGTGTCAAGAAGAAGGCAGACTGGGCCT TGCGCTGGATTGGGGACAAAG
171	RRM2	2469269	TCGATATTCTGGCTCAAGAAACGAGGAC
172	RRM2	2469270	CAACTCGGGCATGCTCTTGTGTTCACTGACGGGGACCT GAGATGCTAGATGGCATATATCCACATTTA
173	RRM2	2469273	ACACCTGGTACACAAACCATCGGAGGAG
174	RRM2	2469275	GCTCATTGGGATGAATTGCACTCTAATGAAGCAATACA TTGAGTTTGTGGCAGACAGACTTATGCTGGAAGTGGGT TTAG
175	RRM2	2469276	AGTAGAGAACCCATTTGACTTTATGGAGAATATTTCACT GGAAGGAAAGACTAACTTCTTTGAGAAGAGAGTAGGC GAGTATCAGAGGATGGGAGTGATGTCAAGTCCAACAGA GAATTCTTTTACCTTGGATGC

176	RRM2	2469277	TGAAGATGTGCCCTTACTTGGCTGATTTTTTTTTTCCATC TCATAAGAAAAATCAGCTGAAGTGTTACCAACTAGCCA CACCATGAATTGTCCGTAATGTTTCATTAAACAGCATCTTT AAAAGTGTGTAGCTACCTCACAACCAGTCCTGTCTGTTT ATAGTGCTGGTA
177	RRM2	2469278	CTTTAGTGAGCTTAGCACAGCGGGATTAAACAGTCCTTT AACCAGCACAGCCAGTTAAAAGATGCAGCCTCACTGCT TCAACGCAGATT
178	RRM2	2469279	AGTCAGTCCTGTGTATACCTAGATATTAGTCAGTTGGTG CCAGATAGAAGACAGGTTGTGTTTTTATCCTGTGGCTTG TGTAAGTGTCTGCTGGGATTCTCTGCCCCCTCTGAGTAGAGT GTTGTGGGATAAAGGAATCTCTCAGGGCAAGGAGCTTC TTAAGTTAAATCACTAGAAATTTAGGGGTGATCTGGGC CTTCATATGTGTGAGAAGCCGTTTCATTTTATTTCTCAC TGTATTTTCCTCAACGTCTGGTTGATGAGAAAAAATTCT TGAAGAGTTTTTCATATGTGGGAGCTAAGGTAGTATTGT AAAATTTCAAGTCATCCTTAAACAAAATGATCCACCTA AGATCTTGCCCCCTGTTAAGTGGTGAAATCAACTAGAGG TGGTTCCTACAAGTTGTTTCATTCTAGTTTTTGTGGTGTA AGTAGGTTGTGTGAGTTAATTCATTTATATTTACTATGT CTGTTAAATCAGAAATTTTTTTATTATCTATGTTCTTCTAG ATTTTACCTGTAGTTCATACTTCAGTCACCCAGTGTCTT ATTCTGGCATTGTCTAAATCTGAGCATTGTCTAGGGGGA TCTTAAACTTTAGTAGGAAACCATGAGCTGTTAATACA GTTTCCATTCAAATATTAATTTTCAGAATGAAACATAATT TTTTTTTTTTTTTTTTGAGATGGAGTCTCGCTCTGTTGCCC AGGCTGGAGTGCAGTGGCGCGATTGTTGGCTCACTGTAA CCTCCATCTCCTGGGTTCAAGCAATTCTCCTGTCTCAGC CTCCCTAGTAGCTGGGACTGCAGGTATGTGCTACCACA CCTGGCTAATTTTTGTATTTTATAGTAGAGATGGAGTTTC ACCATATTGGTCAGGCTGGTCTTGAACCTCCTGACCTCAG GTGATCCACCCACCTCGGCCTCCCAAAGTGCTGGGATT GCAGGCGTGATAAACAAATATTCTTAATAGGGCTACTT TGAATTAATCTGCCTTTATGTTTGGGAGAAGAAAGCTG AGACATTGCATGAAAGATGATGAGAGATAAATGTTGAT CTTTTGGCCCCATTTGTTAATTGTATTTCAGTATTTGAAC GTCGTCCTGTTTATTGTTAGTTTTCTTCATCATTTATTGT ATAGACAATTTTTAAATCTCTGTAATATGATACATTTTC CTATCTTTTAAGTTATTGTTACCTAAAGTTAATCCAGAT TATATGGTCCTTATATGTGTACAACATTAATAAGGAAAG GCTTTGTCTTGCAATTGTGAGGTACAGGCGGAAGTTGGA ATCAGGTTTTAGGATTCTGTCTCTCATTAGCTGA
179	RRM2	2469280	GTCTCAAAATTGAATAATGCACAAGTCTTAAGTGATTA AAATA
180	MLPH	2534256	TGAGCACCCAAAGGCCGGCCCTAGAGTCCAGGAGAAG AGCGCAGCGGCGCGGAGCTCCCAGGCGTTCCCCGCAGC GCGTCCTCGGTCCTGGAACCACCGCGCCGCGCGTCCTG GCTTCCACATCTGCCCCATTTGCCCGCGGATCTTGACTT TTTCTTGGCGGGCAAGGCC
181	MLPH	2534257	GAGAGCCAGGCGCTAACCAGCCGCTCTGCGCCCCGCGC CCTGCTTGCCCCCATTATCCAGCCTTGCCCCGGCGCCCT GACCTGACGCCCTGGCCTGACGCCCTGCTTCGTCGCCTC

			CTT
182	MLPH	2534258	TGCTGGACCAGGGACTGAGCGTCCCCCGGAGAGG
183	MLPH	2534261	TTGGAAGTTGTTCAACGAGATTTTGACCTCCGAAGG
184	MLPH	2534266	CAAACCTGGGGCGTTAGCTCAACTCTTGCCCCCCTGCTG AAGGAGACCAAAACAATGCTTGATCAGGAAACACCATC TGGCTTTGCCCCCAGGATTCTGTGACTGCCCTGGGGAG GGCGCAGTGACCTGCCAACCACAAAATTGGTACAATTGTA AACAGCCACAGAAATGCTTAAATGCAATATCATTTCTA TGAAATTAACGTGTTTCCATTCCATTCCAGCCACCAAAA TTGCCCGTTTGAGCTCAGCCCTCAAAACAAAGATGCCT GTGTGGCTTTGCCCAACGTTGGGTCACTGTTTTCTGCAT A
185	MLPH	2534267	ATGCCCAATATATTTCTTGTTTCTGATATT
186	MLPH	2534268	CGTTGAAGGGCAAGATTAAGAAGGAAAGCTCC
187	MLPH	2534269	AAGAGGGAGCTGCTTTCCGACACTGCCCATCTGAACGA GACCCACTGCGCCCGCTGCCTGCAGCCCTACCAGCTGC TTGTGAATAGCAAAAGGCAGTGCCTGGAATGTGGCCTC TTCACCTGCAAAAGCTGTGGCCGCGTCCACCCGG
188	MLPH	2534271	AGTCGTGAAGATCGGCTCACTGGAGTGGTACTATGAGC ATGTGAAAGCCCGCTTCAAGAGGTTTCGGAAGTGCCAAG GTCATCCGGTCCCT
189	MLPH	2534272	AGTGGAGAGTAAGAACGGCTTTTTTGTTCCCAGGCATTTT AGGAATATTAA
190	MLPH	2534278	ATGGGTGGGTAGGTGAATACATGGATGGATGAGCCACT GATTGAGTGGGTGGATGGGTGGATGAATAGATGGGTGG AGGATAGATAGGTGGGTGTATGGGTGGGTGGATGGATT GATGCATGGATGGATGGGCTGCCCATTTGAGTAGGTGGA TGAGTGGATAAATGGGTGGGTGGGTAGGTGAATAGATG AATAGATTGATAAATAGGGGGATGGGTGGATTGGTAGA TGGGTAGATGGAGGGATACATTGCTGTGTGGATAGGTG GGTGAA
191	MLPH	2534279	GGATGGGTGGATGGGCTGACAAATGGC
192	MLPH	2534280	CTGGGCCTGAACTGATATCTGAAGAGAGAAGTGAGAC AGCGACCAGACAGATGAGGATGGAGAACCTGGCTCAG AGGCCCA
193	MLPH	2534281	AAAAAGCGCCTCCTCTCCGTCCACGACTTCGACTTCGA GGGAGACTCAGATGACTCCACTC
194	MLPH	2534288	TCTGGGTGCCACTCCCATCCGGAAGAGCAGCCGACCAG CATCTCACCTTCCAGACACGGCGCCCTGGCT
195	MLPH	2534290	GGTCGAATGTCATCAGGAATGAGCAGCTGCCCCCT
196	MLPH	2534291	CCGATGTGGACACCTCTGATGAGGAAAGCATCCGGGCT CACGTGATGGCCTCCCACCATTCCAAGCGGA
197	MLPH	2534294	ATCTTTGAGCTGAATAAGCATATTTTCAGCTGTGGAATGC CTGCTGACCTACCTGGAGAACACAGTTGTGCCTCCCTTG GC
198	MLPH	2534296	GTCATTCCCGATCTTTCCACCGAGGGCCTCTGTGATTTG GGGGCTTTGTCAGGAAAGTGGAGCCTCACGGAAAAGCA TACTGGCTAAAACACGCGGCTTCTTCATCGACTCAATCT AATCATCCCCTTGGTGTTTCGTCTGTGAGACCCAGGCAG CCAGCCCTGTGATCTGTCTCAATAGGCTTC
199	MLPH	2534299	GTGCTGGAGTGCGCACGGAGGCCGATGTAG

200	MLPH	2534300	AGGAGGAGGCCCTGAGGAGGAAGCTGGAGGAGCTGAC CAGCAACGTCA
201	MLPH	2534301	CAGGAGACCTCGTCCGAGGAGGAGGAAGCCAAGGACG AAAAGGCAGAGCCCAACAGGGACAAATCAGTTGGGCC TCTC
202	MLPH	2534302	GGCACGGCTGCCCCATCAAACCAACAGACAG
203	MLPH	2534303	CTGGGGACCCCGTCCAGTACAACAGGACCACAGATGAG GAGCTGTCAGAGCTGGAGGACAGAGTGGCAGTGACGG CCTCAGAAGTCCA
204	MLPH	2534304	ATTGAATCCAGGATTGCAGCCCTGAGGGCCGCAGGGCT CACGGTGAAGCCCTCGGGAAAGCC
205	MLPH	2534305	TCTTTATGAGGGGACTCTGAGCCTCTGCTCTGAGGATCT GAAACACACACACCCTGACAGTGTAATAATCCAAAAGG AGCCGCCTGAATCATGTTGCCTCATGTGGAAATCCTTAG TCCGCCGCCACGTG
206	MLPH	2534311	AAGACCACACACCAGTGCAGTGTGATGGGCCTTTCTGC TGCTTCATTAGTGTGAGGATTTCCAGGGCCACAGTGAG GAAGAATGTTAATGCCAGTGCCAGAGCAAAGGAGAAA GAAGTTGGCAAAACTGTTGATTTGCATGACAGCTGAAA TGTAATACTTTTTAAAAAATATGTGATGTGGAAGCTTC TAAAAGGGGATATGTCCATTTTTTTCTACCTTTTAAAT TTCTGAGGAGGCCAAGGCACTTGTTTGGGCTAAGTATG TGATTGATAAAGCACCATCCC
207	MLPH	2534312	ATGATGATTCTTTTGATCGGAAATCAGTGTACCGAGGCT CGCTGACACAGAGAAACCC
208	MLPH	2534313	AGGAGTGGCCCCAACCAATGTGATCAGTCGCAGGAGGC AACCAATCAGAGGCTGAAGGGAAGTTACAAAGTTACAC ATGAAGACTTGGCCGATGACCAG
209	MLPH	2534314	AAACCTGTGGTGGCCCACCAGTCCT
210	MLPH	2534315	ACAGAGCAGCCCTGCACTGTTTTCCCTCCACCACAGCC ATCCTGTCCCTCATTGGCTCTGTGCTTTCCACTATACAC

211	MLPH	2534316	CACCTGCAAGTGGACAGCGACATTCAGTCCTGCACTGC TCACCTGGGTTTACTGATGACTCCTGGCTGCCCCACCAT CCTCTCTGATCTGTGAGAAACAGCTAAGCTGCTGTGACT TCCCTTTAGGACAATGTTGTGTAAATCTTTGAAGGACAC ACCGAAGACCTTTATACTGTGATCTTTTACCCCTTTCAC TCTTGGCTTTCTTATGTTGCTTTCATGAATGGAATGGAA AAAAGATGACTCAGTTAAGGCACCAGCCATATGTGTAT TCTTGATGGTCTATATCGGGGTGTGAGCAGATGTTTGCG TATTTCTTGTGGGTGTGACTGGATATTAGACATCCGGAC AAGTGACTGAACTAATGATCTGCTGAATAATGAAGGAG GAATAGACACCCCAGTCCCCACCCTACGTGCACCCGCT CTGCAAGTTCCCATGTGATCTGTAGACCAGGGGAAATT ACACTGCGGTCAAGGGCAGAGCCTGCACATGACAGCAA GTGAGCATTGATAGATGCTCAGATGCTAGTGCAGAGA GCCTGCTGGGAGACGAAGAGACAGCAGGCAGAGCTCC AGATGGGCAAGGAAGAGGCTTGGTTCTAGCCTGGCTCT GCCCCTCACTGCAGTGGATCCAGTGGGGCAGAGGACAG AGGGTCACAACCAATGAGGGATGTCTGCCAAGGATGGG GGTGCAGAGGCCACAGGAGTCAGCTTGCCACTCGCCCA TTGGTTACATAGATGATCTCTCAGACAGGCTGGGACTC AGAGTTATTTCTAGTATCGGTGTGCCCCATCCAGTTTT AAGTGGAGCCCTCCAAGACTCTCCAGAGCTGCCTTTGA ACATCCTAACAGTAATCACATCTCACCTCCCTGAGGTT CACTTTAGACAGGACCCAATGGCTGCACTGCCTTTGTCA GAGGGGGTGCTGAGAGGAGTGGCTTCTTTTAGAATCAA ACAGTAGAGACAAGAGTCAAGCCTTGTGTCTTCAAGCA TTGACCAAGTTAAGTGTTTCCTTCCCTCTCTCAATAAGA CACTTCCAGGAGCTTTCCAATCTCTCACTTAAACTAAG GTTTGAATCTCAAAGTGTTGCTGGGAGGCTGATACTCCT GCAACTTCAGGAGACCTGTGAGCACACATTAGCAGCTG TTTC
212	GPR160	2651840	CCAGGAGTGGAGCCCGGACGCCCGAGCCTTCCTGCTTC GGGATGGGGATTACCGCGGAGCCTTAGCAACTG
213	GPR160	2651841	ATCCTGGCTGGCTCAAAATTCCCTCTAGATTACCTGCGA CCACCCCCAGGAACCCGGAGACTGAAACTCCT
214	GPR160	2651842	CCTGCAGTCCGGAGACGAACGCACGGACCGGGCCTCCG GAGGCAGGTTCGGCTGGAAGGAACCGCTCTCGCTTCGT CCTACACTTGCGCAAATGTCTC
215	GPR160	2651850	GCTTTGTGCAGTGGCCATTTTCATAGCCAGTGAAGTTTAT CTGAGGCACTTGCTAATTGAAAACCTTTTCTCAATACCCT GCCATGATGAAATATGGTTGGCACTGGCAATTTT
216	GPR160	2651851	ATGTCCAAGTCCCGTGCGGCGGAGGCAGCAGCGGGGGT GACAGCGACGGCCCCGAGCCCGCAGATAGTGGAGCAG AGGGGTCCAGGGAGGCGCTGCACCGACGTTGGGGAGA AT
217	GPR160	2651852	TTCAGGAGGAGAACTCCGTTACACGTCACGAA

218	GPR160	2651853	AAAACCTCCGGCCTCGTCTTGTGATTCCACCAATGCAGC CATCGCCAAGCAAGCCTTGAAATAGCCCATCAAGGGCA AACAGGCCCCCGAAAAAAGCTCAAGGAAAAGTCGCA AACTCACGGATTTCTACCCTGTCCCAAGGAGCTCCAGG AAGGGCAAAGCGGAGCTGCAATTTGAAGAAAGGGAAA GAATAGATGAATTGGTTGAAAGCGGAAAGGAAAGAAG GAGTGAAGACTGACCTCATCAATGACAAAGGCCGGGTG TGAACACCAGAGGGAGCTCTCCCGGGGCGCCTTTGTGG TAGAAAAGCACCGGAGCCTCACGGAGATCACCGACGCC ACGGGACCCCTCCATGGTGGATCTCCGTGGATCTCC
219	GPR160	2651854	GTTGAACGTTTTGTGCTTCCCATGCATGC
220	GPR160	2651864	TGCTCCACTTATCGGGCTCACCAAATACAGCTGCAGTAT GAATTCCATCTTCTACACAACAGTAAACCAGAATG TTC ATGTTACAGCGTTCATCTCCCATCCTGTTGTCTAACGC ACATGGTTTTTTTAACTTTTCTAAGATTGCATGAGATT CTGCAACACAACCTGATTATAAAAACACTTGAAGTTTTT ACCTTTTTTTTTACTTTCCAACCTCTCGTGAATGTACAGA GGACTTTCCA
221	GPR160	2651865	CAGGGGAGAATAAGCTGAACGCAGCTGTTCTCTGACCT TGAGGCAGAGGGCAAGGAGTAGGTACAAGGACGTGTA GGAGAATTTATCTTAAATAGGCTTGTTCACTTGTGTTGT CCAGAAACGACTTTTGATCATCAGCGCGCATGACTGCT CCCTGAAAGGAAGAACAATAATGTTAATTACCCGCAGA CTGTGTTTGCTCCAGGCTTTCGGCATTATGTCTGTACTG AATAAAAGCAAGCAGCTCCAGCTGTTTCGAGGCTGCTCT CTTCTTCAGCCATTAGTGCCGGGCAGCCC
222	GPR160	2651866	AGCTTACTCACATAGCATATTGGTATATCAAAATGAAA TGCAAGGAACCAAAAATAACATAATTGAAGGCAGTAA AAGTGAAATTAAATAGGAAGATCATCAGTCAA
223	GPR160	2651869	GAGCTTCAGGAAAAGACTTAATCTGAAGGATCCTGCAG CTAAAAAGCTTTGAAAACCTGTGTTAAGGGGGCCCCATAA GCATCGCTTCTAACTTCACTGACAAAAGGGACTGGGG TCATGCTGTCTGGAGTCA
224	GPR160	2651870	TGTATTTTCAGCAGGTCTTCTTGAAA
225	GPR160	2651871	TCCAGTTTTCTGACAGCTTGTATAGATTATTGCCTGAA TTTCTCTAAAACAACCAAGCTTTCATTTAAGTGTCAAAA ATTATTTTATTTCTTTACAGTAATTTTAATTTGGATTTC GTCCTTGCTTATGTTTTGGGAGACCCAGCCATCTACCAA AGCCTGAAGGCACAGAATGCTTATTCTCGTCACTGTCCT TTCTATGTCAGCATTTCAGAGTTACTGGCTGTCATTTTTT ATGGTGATGATTTTATTTGTAGCTTTCATAACCTGTTGG GAAGAAGTTACTACTTTGGTACAGGCTATCAGGA
226	GPR160	2651872	TGTTTTACTTAAAGTTCAGATTCCAGCATATATTGAGAT GAATATCCCTGGTTATACTTTGTCAATAGTTTTCTC
227	GPR160	2651873	AAAGACATTGGATTACCTTTGGATCCATTTGTCAACTGG AAGTGCTGCTTCATTCCACTTACAATTCCTAATCTTGAG CAAATTGAAAAGCCTATATCAATAATGATT
228	GPR160	2651874	GTTACAGCTGTCATAAGATCATAATTTTATGAACAGAA AGAACTCAGGACATATTAAAAA

229	GPR160	2651875	CCCTGACTGATAGCATTTCAGAATGTGTCTTTTGAAGGG CTATGATACCAGTTATTAATAAGTGTGTTTTATTTAAAAA CAAAATAATTCCAAGAAGTTTTTATAGTTATTCAGGGA CACTATATTACAAATATTACTTTGTTATTAACACAAAAA GTGATAAGAGTTAACATTTGGCTATACTGATGTTTGTGT TACTCAAAAAAACTACTGGATGCAAACGTGTTATGTAAA TCTGAGATTTCACTGACAACCTTA
230	CCNB1	2813417	GTGCGGGGTTTAAATCTGAGGCTAG
231	CCNB1	2813418	CTCTTCTCGGCGTGCTGCGGCGGAACGGCTGTTGGTTTC TGC
232	CCNB1	2813419	GTAGGTCCTTGGCTGGTCGGGCCTCCGGTGTTCTGCTTC TCCCC
233	CCNB1	2813420	AGCCGCTTCGGACTGCGAACTAACGCGGCCTTCTTAGC TGCTGCCTGCTCTCCCTGCCTCGCCTGCGGGAGCCTCCC GAGCGGGAGAGGGGCCGAGGAGCGATTTGGGGAGGAA GGTGGGAGGGGACTCACCAAGAGAGCGCCGAGGTGGG
234	CCNB1	2813421	TGCTGAAAATAAGGCGAAGATCAACATGGCAGGCGCA AAGCGCGTTCCTACGGCCCCTGCTGCAACCTCCAAGCC CGGACTGAGGCCAAGAACAGCTCTTGGGGACATTGGTA ACAAAGTCAGTG
235	CCNB1	2813422	AAGCAAAACCTTCAGCTACTGGAAAAGTCATTGATAAA AAACT
236	CCNB1	2813425	ACTGGAAACATGAGAGCCATCCTAATTGACTGGCTAGT ACAGGTTCAAATGAAATTCAGGTTGTTGCAGGAGACCA TGTACATGACTGTCTCCATTATTGATCGGTTC
237	CCNB1	2813427	TGTGACTGACAACACTTATACTAAGCACCAAATCAGAC AGATGGAAATGAAGATTCTAAGAGCTTTAACTTTGGT CTGGGTCGGCCTCTACCTTTGCACTTCCTTCGGAGAGCA TCTAAGATTGG
238	CCNB1	2813429	TGATGTGCGAGCAACATACTTTGGCCAAATACCTGATGG AACTAACTATGTTGGACTATGACATGGTGC
239	CCNB1	2813432	AACATTACCTGTCATATACTGAAGAATCTCTTCTTCCAG TTATGCAGCACCTGGCTAAGAATGTAGTCATGGTAAAT CAAGGACTTACAAAGC
240	CCNB1	2813434	TCAAGAACAAGTATGCCACATCGAAGCATGCTAAGATC AGCACTCTACCACAGCTGAATTCTGCACTAGTTCAAG
241	CCNB1	2813435	AAACTTGAGTTGGAGTACTATATTTACAA
242	CCNB1	2813436	ATTACTGTTGCATTTACTTTTAATAAAGCTTGTGG
243	CCNB1	2813437	CCTGGGGATCCAATTGATGTATATGTTTATACTGGGT TCTTGTTTTATATACCTGGCTTTTACTTTATTAATATGAG TTACTGAAGGTGATGGAGGTATTTGAAAATTTTACTTCC ATAGGACATACTGCATGTAAGCCAAGTCATGGAGAATC TG
244	CXXC5	2831352	CCCGGGCAGCGTTCATAGCTCCTGCCCGGGCGGGCGCG CGGCGGCGGCGGCAGAGGCGGCTGAGCCTGAGCGGGG ATGTAGAGGCGGCGGCAGCAGAGGCGGCACTGGCGGC AAGAGCAGACGCCCCGAGCCGAGCGAGAAGAGCGGCAG AGCCTTATCCCCTGAAGCCGGGCCCCGCGTCCCAGCCC TGCCCAGCCCCGCGCCCAGCCATGCGCGCCGCCTGCTGA GTCCGGGCGCCGCACGCTGAGCCCTCCGCCCCGCGAGCC GCGCTCAGCTCGGGGGTGATTAGTTGCTTT

245	CXXC5	2831353	AGTTCGCTGCAAGTCGGCGGAAAGTTTGGCTGCGCGGG TTCCCCCGAAGTTCA
246	CXXC5	2831354	CCTCATCCTCGCAGTAGCTGGGTCTCTCCCAGGGACGCC CCTAGTCAGCCTTGG
247	CXXC5	2831356	GTAATTATGGAATTTTGCTTGGGAAATTAATTTGAAAA AGTTAATTAATTGGTGGTTCCGGAGGTGGCGGGCTCCA CGCCCGGCCAGTCTTGCTGACGTCAGTGCTGACCCACT GGAGACGTGCAGCTTCCG
248	CXXC5	2831357	GGGGTCTGTGACAGCTTGCCCCCAACCACGGAGAGG
249	CXXC5	2831359	TTGTCCAGGGTGGTCTCAAACTCC
250	CXXC5	2831360	CTGAGCAGCGAGGCCACCAGGCATCTCTGTTGTGGGC AGCAGGGCCAGGTCCTGGTCTGTGGACCCTCGGCAGTT GGCAGGCTCCCTCTG
251	CXXC5	2831361	GCTCCCAGGATGCCGGCGGCAGTAGCAG
252	CXXC5	2831362	CAGGAGCAGCAGACAAGAGTGCAGTGGTGGCTGCCGC CGCACCAG
253	CXXC5	2831363	CCCGAGCGTCGGAACAAGAGCGGTATCATCAGTGAGCC CCTCAACAAGAGCCTGCGCCGCTCCCCGC
254	CXXC5	2831364	CCATGGCGGTGGACAAAAGCAACCCTACCTCAAAGCAC AAAAGTGGTGCTGTGGCCAGCCTGCTGAGCAAGGCAGA GCGGGCCACGGAGCTGGCAGCCGAGGGACAGCTGACG CTGCAGCAGTTTGCGCAGTCCACAGAGATGCTGAAGCG CGTGGTGCAGGAGCATCTCCCGCTGATGAGCGAGGCGG GTGCTGGCCTGCCTGACATGGAGGCTGTGGCAGGTGCC GAAGCCCTCAATGGCCAGTCCGACTTCCCCTACCTGGG CGCTTTCCCCATCAACCCAGGCCTCTTCATTATGACCCC GGCAGGTGTGTTCTGGCCGAGAGCGCGCTGCACATGG CGGGCCTGGCTGAGTACCCCATGCAGGGAGAGCTGGCC TCTGCCATCAGCTCCGGCAAGAAGA
255	CXXC5	2831365	TTCAGAAAATGTGAGGAACTCAAAAAGAAGCCTTCCGC TGCTCTGGA
256	CXXC5	2831367	GTGATGCTTCCGACGGGAGCCGCCTTCCGGTGGTTTCA GTGA
257	CXXC5	2831368	AATGTCACTGCTCGTGTGGTCTCCAGCAAGGGATTTCGG GCGAAGACAAACGGATGCACCCGTCTTTAGAACCAAAA ATATTCTCTCACAGATTTTCATTCTGTGTTTTATATATA TTTTTTGTTGTCGTTTTAACATCTCCACGTCCCTAGCATA AAAAG
258	CXXC5	2831369	ATCTATAAAGTACCGAGACTTCCTGGGCAAAGAATGGA CAATCAGTTTCCTTCCTGTGTGCGATGTCGATGTTGTCTG TGCAGGAGATGCAGTTTTTTGTGTAGAGAATGTAAATTTT CTGTAACCTTTTGAAATCTAGTTACTAATAAGCACTACT GTAATTTAGCACAGTTTAACTCCACCCTCATTTAACTT CCTTTGATTCTTTCCGACCATGAAATAG
259	CXXC5	2831370	CCTGGAGAATCCACTCACGTTTCATAAAGAGAATGTTGA TGGCGCCGTGTAGAAGCCGCTCTGTATCCATCCACGCG TGCAGAGC
260	PTTG1	2838203	GGCTTAGATGGCTCCGAGCCCGTTTGAGCGTGGTCTCG GACTGCTAACTGGACCAACGGCAACTGTCTGATGAGTG CCAGCCCCAAACCGCGCGCTGCTCGGGACCTTAGAGCC TCTG

261	PTTG1	2838204	TGTTCCGCTGTTTAGCTCTTGTTTTTTGTGTGGACACTCC TAGGATAGAAAGTTTGGTATGTTGCTATACCTTTGCTTC
262	PTTG1	2838205	GCACCCGTGTGGTTGCTAAGGATGGGC
263	PTTG1	2838206	TATACAAGGCTGCAGTCGGATACACTGGTATTGTGGAC GTGGCCTGGAGCTGGACGAGACATTTAGTGTACTTTTTG GGCAATTGGAGTCGTTTGTATTGGTCCTTTTTTCATTTTT AATATCTTAATGAGATGATTTAAGGAAGTTACTGAATC TCTGCTATTAGGCCTATC
264	PTTG1	2838207	GATCTCAAGTTTCAACACCACGTTTTGGCAAACGTTTCG ATGCCCCACCAGCC
265	PTTG1	2838208	GTAAGTGTGGCTATAAAGACACTGTTTAAACACTTAA GCACTTTTGACTCTTAAAATGACTATTGGCATCATCCTA CGTAGCTTTCTTC
266	PTTG1	2838209	CTGCCTCAGATGATGCCTATCCAGAAATAGAAAAATTC TTTCCCTTCAATCCTCTAG
267	PTTG1	2838210	ATGAGACTGTCTGAATCTGGGTTGCTTTGGACAAGTGT ACTTGTTGATGGAATTATTTGCAAGGTATCATCTTAGGT CAGGAGGGGAATAGGAACAAAGATGTAGAAGACATTG TTCCTGTCTGTAAAAGCTTATCACCTAGAGGAGGTAAG ATGTATTCATGAACATTGAATAAGTCCCATTGTGGACA GTCTTTCTCACAAGGCTT
268	PTTG1	2838211	CTGAAGAGCACCAGATTGCGCACCTCCCCTTGAGTGGA GTGCCTCTCATGATCCTTGACGAGGAGAGAGA
269	PTTG1	2838212	CTGTTGCAGTCTCCTTCAAGCATTCTGTGCGACCCTGGAT GTTGAATTGCCACCTGTTTGCTGTGACATAGATAT
270	PTTG1	2838213	TCTTAGTGCTTCAGAGTTTGTGTGTATTTGT
271	FGFR4	2842913	CCGCCGTCGCGGGTACATTCCTCGCTCCCGGCCGAGGA GCGCTCGGGCTGTCTGCGGACCCTGCCGCGTGCAGGGG TCGCGG
272	FGFR4	2842915	GGCAGTTGGTGGGAAGTCCAGCTTGGGTCCCTGAGAGC T
273	FGFR4	2842916	CCCTGTTGGGGGTCCTGCTGAGTGTGCCTGGGCCTCCAG TCTTGTCCTTGGAGGCCTCTGAGGAAGTGGA
274	FGFR4	2842918	TACAAGGAGGGCAGTCGCCTGGCACCTGCTGGCCGTGT ACGGGGCTGGAGGGGGCCGCCTAGAGATTGCCAGCTTCC TACCTGAGGATGCTGGCCGCTACCTCTGCCTGGCACGA GGCTCCATGATCGTCCTGCAGA
275	FGFR4	2842920	TTGACCTCCAGCAACGATGATGAGGACCCCAAGTCCCA TAGGGACCCCTCGAATAGGCACAGTTACCCCAAGCAA
276	FGFR4	2842921	GCTGCTCATCTGATCACTGAGAAGAGGAGGCCTGTGTG GGAACACACGGTCATTCTAGGGGCCTTCC
277	FGFR4	2842922	CTGCATGCAGTACCTGCGGGGAACACCGTCAAGTTCCG CTGTCCAGCTGCAGGCAACCCACGCCCACCATCCGCT GGCTTAAGGATGGACAGGCCTTTCATGGGGAGAACC
278	FGFR4	2842923	CTGCGCCATCAGCACTGGAGTCTCGTG
279	FGFR4	2842924	ACATACACCTGCCTGGTAGAGAACGCTGTGGGCAGCAT CCGCTATAACTACCTGCTAGAT
280	FGFR4	2842926	CGGCCAACACCACAGCCGTGGTGGGCAGCGACGTGGA GCTGCTGTGCAAGGTGTACAGCGATGCCCAGCCCCACA TCCAGTGGCTGAAGCACATCGTCATCAACGGCAGCAGC TTCGGAGCCGACGGTTTCC

281	FGFR4	2842928	AGGTCCTGTACCTGCGGAACGTGTCAGCCGAGGACGCA GGCGAGTACACCTGCCTCGCAGGCAATTCCATCGGCCT CTCCTACCAGTCTG
282	FGFR4	2842929	AGGAGATGCTGCGAGATGCCCCCTCTGGGCC
283	FGFR4	2842930	GCCCGAGGCCAGGTATACGGACATCATCCTGTACGCGT CGGGCTCCCTGGCCTTGGCTGTGCTCCTGCTGCTGGCCG GGCTGTATCGAGGGCAGGCGCTCCACG
284	FGFR4	2842931	GGCGCATCCCCACCTCACATGTGACAGCCTGACTCCA GCAGGCAGAACCAAGTCT
285	FGFR4	2842932	TTCCGGCAAGTCAAGCTCATCCCTGGTACGAGGCGTGC GTCTCTCCTCCAGCGGGCCCCGCCTTGCTCGCCGGCCTCG TGAGTCTAGATCTACCTCTCGACCCACTATGGGAGTTC
286	FGFR4	2842933	CCCTAGGCGAGGGCTGCTTTGGCCAGGTAGTACGTGCA GAGGCCTTTG
287	FGFR4	2842934	AGGTGATGAAGCTGATCGGCCGACACAAGAACATCATC A
288	FGFR4	2842935	CCCTGTACGTGATCGTGGAGTGCGCCGCCAAGGGAAAC CTGCGGGAGTTCCTGCGGGCCCCGGCGCCCCCAGGCC CGACCTCAGCCCCGACGGTCCTCGGAGCAGTGAGGGGC
289	FGFR4	2842936	CGGCGTCCACCACATTGACTACTATAAGAAAA
290	FGFR4	2842938	GGCCTTGTTTGACCGGGTGTACACACACCAG
291	FGFR4	2842939	TCGGGGGCTCCCCGTATCCTGGCATCCCGGTGGAGGAG CTGTTCTCGCTGCTGCGGGAGGGACATCGGATGGACCG ACCCCCACACTGC
292	FGFR4	2842940	CTGAGGCTCCCTGTGACCCTCCGCCC
293	FGFR4	2842941	ACGGGCTGATGCGTGAGTGCTGGCACGCAGCGCCCTCC
294	FGFR4	2842943	CTCGACCTCCGCCTGACCTTCGGACCCTATTCCCCCTCT GGTGGGGACGCCAGCAGCACCTGCTCCTCCAGCGATTC TGTCTTCAGCCACGACCCCCCTGCCATTGGGATC
295	FGFR4	2842944	CCTGACACAGTGCTCGACCTTGATAGCATGGGGCCCCCT GGCCCAGAGTTGCTGTGCCGTGTCCAAGGGCCGTGCC TTGCCCTTGAGCTGCCGTGCCTGTGTCCTGATGGCCCA AATGTCAGGGTTCTGCTCGGCTTCTTGACCTTGGCGCT TAGTCCCCATCCCGGGTTTGGCTGAGCCTGGCTGGAGA GCTGCTATGCTAAACCTCCTGCC
296	FOXC1	2891769	AGAAGGGCGCCTGCTTGTTCTTTCTTTTGTCTGCTTTCC CCCGTTTGCGCCTGGAAGCTGCGCCGCGAGTTCCTGCA AGGCGGTCTGCCGCGGCCGGGCCCGGCCTTCTCCCCCTC GCAGCGACCCCGCCTCGCGGCCGCGCGGGCCCCGAGGT AGCCCGAGGCGCCGGAGGAGCCAGCCCCAGCGAGCGC CGGGAGAGGCGGCAGCGCAGCCGGACGCACAGCGCAG C
297	FOXC1	2891770	ATGCAGGCGCGCTACTCCGTGTCCAGCCCCAACTCCCT GGGAGTGGTGCCCTACCTCGGCGGCGAGCAGAGCTACT ACCGCGCGGCGGCCGCGGCGGCGGGGGCGGCTACAC CGCCATGCCGGCC
298	FOXC1	2891771	ATGAGCGTGTACTCGCACCCCTGCGCACGCCGAGCAGTA CCCGGGCGGCATGGCCCCGCGCCTACGGGCCCTACACGC CGCAGCCGCAGCCCAAGGACATGGTGAAGCCGCCCTAT AGCTACATCGCGCTCATCACCATGGCCATCCAGAACGC CCCGGACAAGAAGATCACCTGAAC

299	FOXC1	2891772	AGGACAGGCTGCACCTCAAGGAGCCGCCCCCG
300	FOXC1	2891773	GCCGACGGCAACGCGCCCGGTCCGCA
301	FOXC1	2891774	GCGCATCCAGGACATCAAGACCGAGAACG
302	FOXC1	2891775	CGCCGCGGTGCCCAAGATCGAGAGCCCCGACAGCAGCA GCAGCAGCCTGTCCAGCGGGAGCAGCCCCCGGGCAGC CTGCCGTCGGCGCGGGCCGCTCAG
303	FOXC1	2891776	CCGCCGCCGCACCATAGCCAGGGCTTCAGCGTGGACAA CATCATGACGTCGCTGCGGGGGTTCGCCGCAGAGCGCGG CCGCGGAGCTCAGCTCCGGCCTTCTGGCCTCGGCGGCC
304	FOXC1	2891777	GTCCTCGCGCGCGGGGATCGCACCCCCGCTGGCGCTCG GCGCCTACTCGCCCGGCCAGAGCTCCCTCTACAGCTCCC CCTGCAGCCAGACCTCCAGCGCGGGGAGCTCGGGCGGC GGCGGCGGCGGCGCGGGGGGCCGCGGGGGGCGCGGGGCG GCGCCGGGACCTACCACTGCAACCT
305	FOXC1	2891778	ATGAGCCTGTACGCGGCCGGCGAGCGCGGGGGGCCACTT GCAGGGCGCGCCCCGGGGGGCGCGGGGCGGCTCGGCCGTG GACGACCCCTGCCCGACTACTCTCTGCCTCCGGT
306	FOXC1	2891779	GGCCGGCCACCACCCTGCGGCCACCAAGGCCGCCTCA C
307	FOXC1	2891780	ACCTGGGCCACTTGGCGAGCGCGGGCGG
308	FOXC1	2891781	CAGAACTTCCACTCGGTGCGGGAGATGTTCGAGTCACA GAGGATCGGCTTGAACAACCTCTCCAGTGAACGGGAATA GTAGCTGTCAAATGGCCTTCCCTTCCAGCCAGTCTCTGT ACCGCACGTCCGGAGCTTTCGTCTACGA
309	FOXC1	2891782	TGAGAATATTCACCACACCAGCGAACAGAATATCCCTC CAAAAATTAGCTCACCAGCACCAGCACGAAGAAAACCT CTATTTTCTTAACCGATTAATTCAGAGCCACCTCCACTT TGCCTTGTCTAAATAAAACAAACCCGTAAACTGTTTTATA CAGAGACAGCAAAATCTTGGTTTATTAAAGGACAGTGT TACTCCAGATAACACGTAAGTTTCTTCTTGCTTTTCAGA GACCTGCTTTCCCCTCCTCCCGTCTCCCCTCTCTTGCCCTT CTTCCTTGCCCTCTCACCTGTAAGATATTATTTATCCTAT GTTGAAGGGAGGGGGAAAGTCCCCGTTTATGAAAGTCG CTTTCTTTTTATTTCATGGACTTGTTTTAAATGTAAATTG CAACATAGTAATTTATTTTAAATTTGTAGTTGGATGTCG TGGACCAAACGCCAGAAAGTG

310	FOXC1	2891783	GGAGAAACCCTCTGACTAGTCCATGTCAAATTTTACTA AAAGTCTTTTTGTTTAGATTTATTTTCCTGCAGCATCTTC TGCAAAATGTACTATATAGTCAGCTTGCTTTGAGGCTAG TAAAAAGATATTTTTCTAAACAGATTGGAGTTGGCATA TAAACAAATACGTTTTCTCACTAATGACAGTCCATGATT CGGAAATTTTAAGCCCATGAATCAGCCGCGGTCTTACC ACGGTGATGCCTGTGTGCCGAGAGATGGGACTGTGCGG CCAGATATGCACAGATAAATATTTGGCTTGTGTATTCCA TATAAAATTGCAGTGCATATTATACATCCCTGTGAGCCA GATGCTGAATAGATATTTTCCTATTATTTCAAGTCCTTTA TAAAAGGAAAAATAAACCAGTTTTTAAATGTATGTATA TAATTCTCCCCCATTTACAATCCTTCATGTATTACATAG AAGGATTGCTTTTTTAAAAATATACTGCGGGTTGGAAA GGGATATTTAATCTTTGAGAACTATTTTAGAAAATATG TTTGTAGAACAATTATTTTGAAAAAGATTTAAAGCAAT AACAAGAAGGAAGGCGAGAGGAGCAGAACATTTTGGT CTAGGGTGGTTTCTTTTTAAACCATTTTTTCTTGTTAATT TACAGTTAAACCTAGGGGACAATCCGGATTGGCCCTCC CCCTTTTGTAAATAACCCAGGAAATGTAATAAATTCATT ATCTTAGGGTGATCTGCCCTGCCAATCAGACTTTGGGG AGATGGCGATTTGATTACAGACGTTCCGGGGGGGTGGGG GGCTTGCAGTTTGTTTTGGAGATAATACAGTTTCCTGCT ATCTGCCGCTCCTATCTAGAGG
311	ESR1	2931764	AGAAGCTCTTTAACAGGCTCGAAAGGTCCATGCTCCTTT CTCCTGCCCATTTCTATAGCATAAG
312	ESR1	2931765	CAAAGATCTCTTCACATTCTCCGGGACTGCGGTACCAA ATATCAGCACAGCACTTCTTGAAAAAGGATGTAGATTT TAATCTGAACTT
313	ESR1	2931775	ACGAAGTGAGGAGTATTACATTTCACTGGAAACACA TCCCTAGAATGCCAAAACATTTATTCCAAAGTCTGGTTT CCTGGTGCAATCGGAGGCATGGCAATGCCTCTGTTCAG AGA
314	ESR1	2931776	AAGCATAGGGTACTTTCCAGCCTCCAAGGGTAGGGGCA AAGGGGCTGGGGTTTCTCCTCCCCAGTACAGCTTTCTCT GGCTGTGCCACACTGCTCCCTGTGAGCAGACAGCAAGT CTCCCCTCACTCCCCACTGCCATTTCATCCAGCGCTGTGC AGTAGCCCAGCTGCGTGTCTGCCGGGAGGGGGCTGCCAA GTGCCCTGCCTACTGGCTGCTTC
315	ESR1	2931779	GCAGCACATTAGAGAAAGCCGGCCCCTGGATCCGTCTT TCGCGTTTATTTTAAGCCCAGTCTTCCCTGGGCCACCTT TAGCAGATCCTCGTGCGCCCCCGCCCCCTGGCCGTGAA ACTCAGCCTCTATCCAGCAGCGACGACAAGTA
316	ESR1	2931780	CCAATGTCAGGGCAAGGCAACAGTCCCTGGCCGTCCTC CAGCACCTTTGTAATGCATATGAGCTCGGGAGACCAGT ACTTAAAGTTGGAGGCCCGGGAGCCCAGGAGCTGGCGG AGGGCGTTCGTCCTGGGACTGCACTTGCTCCCGTCGGGT CGCCCGGCTTCACCGGACCCGCAGGCTCCCGGGGCAGG GCCGGGGCCAGAGCTCGCGTGTGCGCGGGACATGCGCT GCGTCGCCTCTAACCTCGGGCTGTGCT
317	ESR1	2931781	GTGGCCCGCCGGTTTCTGAGCCTTCTGCCCTGCGGGGAC ACGGTCTGCACCCTGCCCCGCGGCCACGGACC

318	ESR1	2931782	TCTGGGATGGCCCTACTGCATCAGATCCAAGGGAACGA GCTGGAGCCC
319	ESR1	2931783	CCCCTGGGCGAGGTGTACCTGGACAGCAGCAAGCCCGC CGTGTACAACCTACCCCGAGGGCGCCGCCTACGAGTTCA ACGCCGCGGGCCGCCGCCAACGCGCAGGTCTACGGTCAG
320	ESR1	2931784	TGAGGCTGCGGCGTTTCGGCTCCAACGGCCTGGGGGGGT TCCCCCCTCAACAGCGTGTCTCCGAGCCCGCTGATGC TACTGCACCCGCGCCGCGCAGCTGTGCGCCTTTCCTGCAGC CCCACGGCCAGCAGGTGCCCTACTACCTGGAGAACGAG C
321	ESR1	2931791	GTGCTGTCATGTGGACTGTCCTCCCGAGTGTCCCCTGG ATGTTTCAGAGAATTTATGTGAAGGTCACGTCATTTAGC ATTGAGATGCTGTGGTTACCTTCTTCCATTTCTTCCATA ATATGCAGCCACATCTATGTGTGAAGAAATGTAATAGA TAAAATTTCTCTGGACGCATAATAATGTGAGAAAGATT GTCACATGTCCCAGCAA
322	ESR1	2931798	CAAATTCAGATAATCGACGCCAGGGTGGCAGAGAAAG ATTGGCCAGTACCAATGACAAGGGA
323	ESR1	2931799	AATCTGCCAAGGAGACTCGCTACTGTGCAGTGTGCAAT GACTATGCTTCAGGCTACCATTATGGAGTCTGGTCCTGT
324	ESR1	2931812	CAGGCCTGCCGGCTCCGTAAATGCTACGAAGTGGGAAT GA
325	ESR1	2931821	AACCTTTGGCCAAGCCCGCTCATGATCAAACGCTCTAA GAAGAACAGCCTGGCCTTGTCCTGACGGCCGACCAGA TGGTCAGTGCCTTGTTGGATGCTGAGCCCCCGATACTCT ATTCCGAGTATGATCCTACCAGACCCTTCAGTGAAGCTT CGATGATGGGCTTACTGACCAACCTGGCAGA
326	ESR1	2931835	TGGATATATGTGTGATCCTGGGTGTGCCAAATGCTGTG GCTTCCTGAAGCTTAGATTTCCAGCTTGTCACCTTCAAG GTTACCTTGTGAATAGGAC
327	ESR1	2931836	TGACTATGGATTTTGCCTGTTGCTTTGTTTCCACCAACT CTCCCTGAAGATGAGGCGCACAGACAGACAACCTCACAG GCAAGAACAGCCTGGTCCATCTTGAAAGATTCTC
328	ESR1	2931839	GCTTTGTGGATTTGACCCTCCATGATCAG
329	ESR1	2931840	GTCCACCTTCTAGAATGTGCCTGGCTAGAGATCCTGATG ATTGGTCTCGTCTGGCGCTCCATGGAGCACCCAGGGAA GCTACTGTTTGCTCCTA
330	ESR1	2931850	TGGAGATCTTCGACATGCTGCTGGCTACATCATCTCGGT TCCGCATGATGAATCTGCAGGGAGAGGAGTTTGTGTG
331	ESR1	2931859	GAGAAGGACCATATCCACCGAGTCCTGGACAAGATCAC AGA
332	ESR1	2931861	CATGAAGTGCAAGAACGTGGTGCCCCCTCTATGACCTGC TGCTGGAGATGCTGGACGCCACCGCCTACATGCGCCC ACTAGCCGTGGAGGGGGCATCCGTGGAGGAGACGGACC AAAGCCACTTGGCCACTGCGGGCTCTACTTCATCGCATT CCTTG

333	ESR1	2931862	CCTGGCTCCCACACGGTTCAGATAATCCCTGCTGCATTT TACCCTCATCATGCACCACCTTTAGCCAAATTCTGTCTCC TGCATACACTCCGGCATGCATCCAACACCAATGGCTTTC TAGATGAGTGGCCATTCAATTTGCTTGCTCAGTTCTTAGT GGCACATCTTCTGTCTTCTGTTGGGAACAGCCAAAGGG ATTCCAAGGCTAAATCTTTGTAACAGCTCTCTTTCCCCC TTGCTATGTTACTAAGCGTGAGGATTCCCGTAGCTCTTC ACAGCTGAACTCAGTCTATGGGTTGGGGCTCAGATAAC TCTGTGCATTTAAGCTACTTGTAGAGACCCAGGCCTGG AGAGTAGACATTTTGCCTCTGATAAGCACTTTTTTAAATG GCTCTAAGAATAAGCCACAGCAAAGAATTTAAAGTGGC TCCTTTAATTGGTGACTTGGAGAAAGCTAGGTCAAGGG TTTATTATAGCACCCCTCTTGTATTCCTATGGCAATGCAT CCTTTTATGAAAGTGGTACACCTTAAAGCTTTTATATGA CTGTAGCAGAGTATCTGGTGATTGTCAATTCATTCCCCC TATAGGAATACAAGGGGGCACACAGGGAAGGCAGATCC CCTAGTTGGCAAGACTATTTTAACTTGATACACTGCAGA TTCAGATGTGCTGAAAGCTCTGCCTCTGGCTTTCGGGTC ATGGGTTCCAGTTAATTCATGCCTCCCATGGACCTATGG AGAGCAGCAAGTTGATCTTAGTTAAGTCTCCCTATATG AGGGATAAGTTCCTGATTTTTTGTTTTTATTTTTGTGTTAC AAAAGAAAGCCCTCCCTCCCTGAACTTGCAGTAAGGTC AGCTTCAGGACCTGTTCCAGTGGGCACTGTACTTGGATC TTCCCGGCGTGTGTGTGCCTTACACAGGGGTGAACTGTT CACTGTGGTGATGCATGATGAGGGTAAATGGTAGTTGA AAGGAGCAGGGGGCCCTGGTGTTGCATTTAGCCCTGGGG CATGGAGCTGAACAGTACTTGTGCAGGATTGTTGTGGC TACTAGAGAACAAGAGGGGAAAGTAGGGCAGAACTGG ATACAGTTCTGAGGCACAGCCAGACTTGCTCAGGGTGG CCCTGCCACAGGCTGCAGCTACCTAGGAACATTCCTTG CAGACCCCGCATTGCCCTTTGGGGGTGCCCTGGGATCC CTGGGGTAGTCCAGCTCTTCTTCATTTCCCAGCGTGGCC CTGGTTGGAAGAAGCAGCTGTCACAGCTGCTGTAGACA GCTGTGTTCCCTACAATTGGCCCAGCACCCCTGGGGCACG GGAGAAGGGTGGGGACCGTTGCTGTCACTACTCAGGCT GACTGGGGCCTGGTCAGATTACGTATGCCCTTGGTGGTT TAGAGATAATCCAAAATCAGGGTTTGGTTTGGGGGAAGA AAATCCTCCCCCTTCCTCCCCCGCCCCGTTCCCTACCGC CTCCACTCCTGCCAGCTCATTTCTTCAATTTCTTTGAC CTATAGGCTAAAAAAGAAAGGCTCATTCCAGCCACAGG GCAGCCTTCCCTGGGCCTTTGCTTCTCTAGCACAATTAT GGGTACTTCCTTTTTCTTAACAAAAAAGAATGTTTGAT TTCCTCTGGGTGACCTTATTGTCTGTAATTGAAACCCTA TTGAGAGGTGATGTCTGTGTTAGCCAATGACCCAGGTG AGCTGCTCGGGCTTCTCTTGGTATGTCTTGTTTGGAAAA GTGGATTTCAATTCATTTCTGATTGTCCAGTTAAGTGATC ACCAAAGGACTGAGAATCTGGGAGGGCAAAAAAAAAAA AAAAAGTTTTTATGTGCACTTAAATTTGGGGACAATTTT ATGTATCTGTGTTAAGGATATGTTTAAGAACATAATTCT TTTGTTGCTGTTTGTTTAAGAAGCACCTTAGTTTGTTTA AGAAGCACCTTATATAGTATAATATATATTTTTTTGAAA TTACATTGCTTGTTTATCAGACAATTGAATGTAGTAATT
-----	------	---------	--

			CTGTTCTGGATTTAATTTGACTGGGTTAACATGCAAAAA CCAAGGAAAAAATATTTAGTTTTTTTTTTTTTTTTTTGTATA CTTTTCAAGCTACCTTGTCATGTATACAGTCATTTATGC CTAAAGCCTGGTGATTATTCATTTAAATGAAGATCACAT TTCATATCAACTTTTGTATCCACAGTAGACAAAATAGCA CTAATCCAGATGCCTATTGTTGGATACTGAATGACAGA CAATCTTATGTAGCAAAGATTATGCCTGAAAAGGAAAA TTATTCAGGGCAGCTAATTTTGCTTTTACCAAAATATCA GTAGTAATATTTTTGGACAGTAGCTAATGGGTCAGTGG GTTCTTTTAAATGTTTATACTTAGATTTTCTTTTAAAAAA ATTAAAATAAAACAAAAAAAATTTCTAGGACTAGACG ATGTAATACCAGCTAAAGCCAAACAATTATACAGTGGA AGGTTTTACATTATTCATCCAATGTGTTTCTATTTCATGTT AAGATACTACTACATTTGAAGTGGGCAGAGAACATCAG ATGATTGAAATGTTTCGCCCAGGGGTCTCCAGCAACTTT GGAAATCTCTTTGTATTTTTACTTGAAGTGCCACTAATG GACAGCAGATATTTTCTGGCTGATGTTGGTATTGGGTGT AGGAACATGATTTAAAAAAAATCTTGCCTCTGCTTTC CCCCACTCTGAGGCAAGTTAAAATGTAAAAGATGTGAT TTATCTGGGGGGCTCAGGTATGGTGGGGAAGTGGATTC AGGAATCTGGGGAATGGCAAATATATTAAGAAGAGTAT TGAAAGTATTTGGAGGAAAATGGTTAATTCTGGGTGTG CACCAGGGTTCAGTAGAGTCCACTTCTGCCCTGGAGAC CACAAATCAACTAGCTCCATTTACAGCCATTTCTAAAAT GGCAGCTTCAGTTCTAGAGAAGAAAGAACAACATCAGC AGTAAAGTCCATGGAATAGCTAGTGGTCTGTGTTTCTTT TCGCCATTGCCTAGCTTGCCGTAATGATTCTATAATGCC ATCATGCAGCAATTATGAGAGGCTAGGTCATCCAAAGA GAAGACCCTATCAATGTAGGTTGCAAAATCTAACCCCT AAGGAAGTGCAGTCTTTGATTTGATTTCCCTAGTAACCT TGCAGATATGTTTAACCAAGCCATAGCCCATGCCTTTTG AGGGCTGAACAA
334	ESR1	2931877	AGAAGAGAATCCTGAACTTGCATCCTAAAATAT

335	ESR1	2931878	GGCAACTTGTTGACTACCCACTGGTCATTCTCCTCTGGT CTTATTACATACATGGATGCCAGTTTAGATTGTGTTTAT ATAGGAAAAATTAAATGTGTGAGCCTCCTTAAGGAACA TCATCAATACAGATATATCAGATAGTTCTGTCCAGCAA AAAACGTGCTTATTTGCTACAAGTAAATTTTTATTATT TTTCTCACTTCCCTCACTCCTTCAAATTTCCAGGTAAAT AGCTGCCCAGGAGTTGCTTCATCTCTGTCCCAAATACC TAGACAATTGCGGGATAAGGAGAATGGCAGGGAGGGA GTAGTGGCTAAAATCACACCCTTCAAAAGAAAGTGTGT AGGACACACAATTGTGAGAAGTCTGAATGCCATGCACA TAGGGTATGACTCACTTTGAAAATTGTTTATAATCAAGG AAATGAAAATGAGTTAATTTTCGTGCATGCATCATTTAA AGCCAAATGAGAAGAACTTCTAATTTATTTTGTTACTT TTCGGCTAACACTGGCAGTATGTAACAGATTTATTTTGC AGAAACATCTAGATTGTCCGTGATCTTGATCCTGCCCTT ATGTGTCTTGTCTTTGAAACCCAGTGTTTCCTGGATATA TGGTTCAGGAGACAAGTTTCCAGAATCAAGTTAGGACC CAGGTCTTCTTTTTTTTCCAAACCAAACATTCTTGCTAAT CCTAAACTACCTGAGGCAGCCTGTGGTGGCCTCAGCTC TAAAACCATTTGTTTAAAGGCTTCTACCCATCAATGGCCC TTCAGCAGAGTGGTACGGTTAACGGGGTAGGGTCTGGA GTCAGGGGAGACCTGGGTTCAAATCCTACATCTTTACA CCTCTAATCCCCAGTGTCCTTGTCTATAAATTGGGAATA TAGCCATGTCATGGGATTCTTGTGAGGGTTAAATGAGG TAAAACACATACAATGCTTAGCATGTATACAATTAAGC ACTAAATAATTGAAACACATTAAGTACTAAATGAATGT CAGCAGCTTATCACTATTATCTGTATAATGATACCAAGG GTGTGCCGACTCATACCCTTAGGGGT
336	ESR1	2931879	AGGAAGGCCTACCTCAAATAGCAACAGAGA
337	ESR1	2931880	TCTGTGCTGAGGCTCTTTGAATGCTTTGAATAA

338	ESR1	2931881	CCTCTTTCAGTGTTTCGGCCAGTCATTTGCCACTTCTCAT TCCATCTTAGTTCTCTGTAAAGAAGGTGCCAGAGACCT AAGGTGCCCAAGGCAATTTTGCATTTTACAATTCTAAGC TTTAGAATGAAGTCATCAATTTGCTACATCCGGACTACA GTGCAATTATTCCTTTGCCTTGCTGGAAATTGGAGTGAA ATCTTTCTAGCTGTCAATTTCAACTCAGTTGCAGTAGTG TTTTGAAGAATTAATGGCGATAAGGTTAGAAAATTTTA AGTCAAACGTAGGGAAAAAGTACCAGCTAGACCATCAT AAGCATTTGCTTTGAAAGCATGCTTCTAAAGTGTGTTTA ACCTCAAATAACAGTCACAAATATGGTTATTATGAATG TATGCACAGATTTTTATGTTTCTAATTTTAAGAAGTTCT AGGGAGCTCCCTGTAACGATTTAGGGAATCTCTAGATT CTGATATACTGCAAGTCTTTTAATGGTAGGAATCACATT GAATTAATTTTGTAGGCCCGAGGGCCTAAATTTAGTAGG TGTTTCAGTACCTATTGGCATCAATTCATATGTAGGTTTA AAATACTGTATGAAGATACAGAATCACCACCATCAAAT CAAATTGAAATATGTAACAGGCTAGTATAATATTAACA TCTGACTTTAAACAACAACAAAGAAACCAAATGAGTAA CTCCTCCCTTCAAACATAAGTCAGTTTCTTCCAACCTCA GTCTCTTTCTCCTCTCAGGAAGAATGCGTATCTAAAAAT TTCCCATTTGCAGACTGCTGGAAACAACATTCTAAACTAT TTATGCTTCTGCAATAACCTTTCCAATTTGCTGGACCAG TGCAAGATTAAACACGAGATATCTCAAGTCTCAATGTA AAGGAACACCACGACAGCCTGGACTGTGGGTGAAGTTC ATTCTTCCCCAGCAGACTCTGCCTTTCATTCTCGGGGTT GGGTGTGCCCCAACAGAGGTACCGACGGTAACGAAG CCCAAGAATGTTCAACCACAACCTGTCTGTGAAGGTGT TGGATGACGTTTGCCATTCAGGTGAAGATTATTTATGTT CCAGTCCCACCTGAGTAGCAAAGTGAACACTGTGCTGA ATGCTCAGAAAGATGTTAATGAACCGTGCTGGACAGAG CAGAGCTGAAAGGCGCCTTGCGAGTGTCGTAGTGAGAA TGTGGCTGTCCCAGCTGCAAAGCCCTGTTAGGAGGCAT GAGGAAGCACTTGCTGCCCTAAGAAACGATGCCTTCGA CATTTTCAAAAGATCTATGTGGCTGTCTGAAACAATGC GGAGAGCAGATAGACGCAATATTTGGGAACCAAAGAG TGACTGCTGTTGGCGTTGCATCATAACATAAGCGCTTTC CCCCTTCTCGTCACTATCATTTGTATCAACCAAAGAACT GATCTCTGGTATCCTCGAAGGAATGCTGTGGGGATATT CTTCATCTCTGTTTCATGGTACATCAGCAATTTGTGGGGA AAAGATGGACTATATAACACAATGATCTGCCTAAAAGA AACTGTCTCTACTTATAGGGGGGCTGAGCAAACCTTAGA GCATCTGCGGATGCTCGTCATTATCTTC
339	ANLN	2997377	GAAATTCAAATTTGAACGGCTGCAGAGGCCGAGTCCGT CACTGGAAGCCGAGAGGAGAGGACAGCTGGTTGTGGG AGAGTTCCCCCGCCTCAGA
340	ANLN	2997378	ACACACTGAGCTGAGACTCACTTTTCTCTTCCTGAATTT GAACCACCGTTTCCATCGTCTCGTAGTCCGACGCCTGGG
341	ANLN	2997379	GGAGGAAGGCTTTGAGTCTGTCCTAAAAGGCTGTTGCG AGAGGTCTTTCAGC

342	ANLN	2997380	TCCTGGCGCAGCAAGAGTGAGGCGCAGGCCTGCGGAAC GGGTCCCTGCTGGAAGCAGCTGGAATGCCCTGCAGGGCG GGGTCCGGGGCCGGTGACTCAGTGCGGCTGCCGCCGGG AAAGGCAGTAGGATGTGTGATTTGCGGAGTTCACGCAG CCCGCAGGGGAGATGCTAATGAAA
343	ANLN	2997381	AACTGCTGGAGCGAACCCGTGCCAGGCGAGAGAATCTT CAGAGAA
344	ANLN	2997382	CAGCAGCTCCAAGGTCTATGACTCATGCTAAGCGAGCT AGACAGCCACTTTC
345	ANLN	2997384	AGAAATCTTGTACAAAACCATCGCCATCAAAAAAACGC TGTTCTGACAACACTGAAGTAGAAGTTTCTAACTTGGA AAATAACAACCAGTTGAGTCGACATCTGCAAAATCTT GTTCTCCAAGTCCTGTGTCTCCT
346	ANLN	2997385	GCCACAAGCAGCAGATACCATCAGTGATTCTGTTGCTG TCCCGGCATCACTGCTGGGCATGAGGAGAGGGCTGAAC TCAAGATTGGAAGCAACTGCAGCCTCCTCAGTTAAAC ACGTATGCAAAAACCTTGCAAGCAACGGCGCCGTTGGG ATAATGATGATATGA
347	ANLN	2997387	GCTTTCAAATGCCTCGGCAACTCCAGTTGGCAGAAGGG GCCGTCTGGCCAATCTTGCTGCAACTATTTGCTCCTGGG AA
348	ANLN	2997388	GCCTGGTACCGCTTGTTTATCCAAATTTTCCTCTGCAAG TGGAGCATCTGCTAGGATCAATAGCAGCAGTGTTAAGC AGGAAGCTACATTCTGTTCCCAAAGGGATGGCGATGCC TCTTTGAATAAAGCCCTATCCTCAAGTGCTGATGATG
349	ANLN	2997389	TCCAGTGAAATCTACTACATCTATCACTGATGCTAAAA GTTGTGAGGGACAAAATCCTGAGCTACTTCCAAAAACT CCTATTAGTCCTCTGAAAACGGGGGTATCGAAACCAAT TGTGAAGTCAACTTTATCCCAGACAGTTCCATCCAAGG
350	ANLN	2997391	AGCCTTTCCTGGAACGCTTTGGAGAGCGTTGTCAAGAA CATAGCAAAGAAAGTCCAGCTCGTAGCACACCCCACAG AACCCCCATTATTACTCCAAATACAAAGGCCATCCAAG A
351	ANLN	2997393	AGAACTAGCATGTCTTCGTGGCCGATTTGACAAGGGCA ATATATGGAGTGCAGAAAAAGGCGGAAACTCAAA
352	ANLN	2997394	GTTTCAAAAACTCAGTCACTTCCAGTAACAGAAAAGGT GACCGAAAACCAGATAACCAGCCAAAAATTCTAGTACAG
353	ANLN	2997395	CATCAGACCCAAAGGTTGAGCAGAA
354	ANLN	2997396	TCTTCAGTGATGTCCTAGAGGAAGGTGAACTAGATATG GAGAAGAGCCAAGAGGAGATGGATCAAGCATTAGCAG AAAGCAGCGAAGAACAGGAAGATGCACTGAATATCTC CTCAATGTCTTTACTTGCACCATTGGCACAAACAGTTGG
355	ANLN	2997397	AGTTTAGTGTCCACACCTAGACTGGAATTGAAAGACAC CAGCAG
356	ANLN	2997399	TTCAAAGAAACAGAACGTCCATCAATAAAGCAGGTGAT TGTTTCGGAAGGAAGATGTTAC
357	ANLN	2997400	GAACTCAATAACGAAATAAATATGCAACAGACAGTGAT CTATCAAGCTAGCCAGGCTCTTAACTGCTGTGTTGATGA AGAACATGGAAAAGGGTCCCTAGAAGAAGCTGAAGCA GAAAGACTTCTTCTAATTGCA

358	ANLN	2997402	TGCCATCCAAAGGATCAGTTACTTTGTCAGAAATCCGCT TGCCTCTAAAAGCAGATTTTGTCTGCAGTACGGTTCA
359	ANLN	2997403	ATGGTAGCCACACCATTAGCAAGTACTTCAAACCTCTCTT AACGGTGATGCTCTGACATTCACTACTACATTTACTC
360	ANLN	2997406	AAGAAAGATCCCTCAGGCCTTGATAAGAAG
361	ANLN	2997408	GGCCAGTCCAGGAGGTCTTAGTGCTGTGCGAACCAGCA ACTTCGCCCTTGTTGGATCTTACACATTATCATTGTC
362	ANLN	2997409	TAAGAGAGCGAGAGCTACTGGGCTATTTGTTCCAGGAA AA
363	ANLN	2997414	GTTTTGGTGCCTGGCATCGAAGATGGTGTGTTCTTTCTG GAAACTGTATATCTTATTGGACTTATCCAGATGATG
364	ANLN	2997417	TTGGCTGTTGGCTCATGTGTGCCTATATGTGTTTCTTTTC CCATTTTCAGGACCATTGTTGCTCGTGAATGTTTTCTC CACTTTGACTCGTATCATAGGAATTCATGGCTGCCAACA ATCCAGGGCAGTTGTCTGCCCTTATCTTTCATAGATATA TAAAGAAATATTTACACATGAAATCCAATGTCTAGGTT TCCTTTTATAGAAAGGGGAGAAAGTGGGTAAGTTGTAGA TAAAAGGCACTTGAGTGTGTTTCTCATTGTTATAGCTGG TTTTGGTACCTGGGGCTCATTATACTGTTGTTTGTATTTT TTATTTGAAGTTCACCATAATAAAGAGCTTTATAGGATA GTTGGCAAGAGCTACCAGTTGATATTT
365	ANLN	2997418	CATAGGAAGGATAAATCTGGCTAATTGTACCAG
366	ANLN	2997419	GTGCAAGACGCAACACTTTTGAATTAATTACTGTCCGA CCACAAAGAGAAGATGACCGAGAGACTCTTGTCAGCCA ATGCAGGGACACACTCTGTG
367	ANLN	2997422	TGGCTGTCTGCAGATACTAAAGAAGAGCGGGATCTCTG GATGCAAAAACCTCAATCAAGTTCTTGTTGATATTCGCCT CTGG
368	ANLN	2997423	TTGCTACAAACCTATTGGAAAGCCTTA
369	ANLN	2997424	TACGAAAGGGTTTGTGCCAATATTCACTACGTATTATGC AGTATTTATATCTTTTGTATGTAAAACCTTTAACTGATTT CTGTCATTCATCAATGAGTAGAAGTAAATACATTATAG TTGATTTTGCTAAATCTTAATTTAAAAGCCTCATTTTCCT AGAAATCTAATTATTCAGTTATTCATGACAATATTTTTT TAAAAGTAAGAAATTCTGAGTTGTCTTCTTGGAGCTGTA GGTCTTGAAGCAGCAACGTCTTTCAGGGGTTGGAGACA GAAACCCATTCTCCAATCTCAGTAGTTTTTTTCGAAAGGC TGTGATCATTTATTGATCGTGATATGACTTGTTACTAGG GTACTGAAAAAAATGTCTAAGGCCTTTACAGAAACATT TTAGTAATGAGGATGAGAACTTTTTCAAATAGCAAAT ATATATTGGCTTAAAGCATGAGGCTGTCTTCAGAAAAG TGATGTGGACATAGGAGGCAATGTGTGAGACTTGGGGG TTCAATATTTTATATAGAAGAGTTAATAAGCACATGGTT TACATTTACTCAGCTACTATATATGCAGTGTGGTGCACA TTTTACAGAATTCTGGCTTCATTAAGATCATTATTTTT GCTGCGTAGCTTACAGACTTAGCATA
370	BLVRA	2999566	CCGAGAGGAAGTTTGGCGTGGTGGTGGTGGTGGTGGC CGAGCCGGCTCCGTGCGGATGAGGGACTTGCGGAATCC ACACCCTTCCTCAGCGTTCCTGAACCTGATTGGCTTCGT GTCGA

371	BLVRA	2999568	AGCTCGGGAGCATTGATGGAGTCCAGCAGATTTCTTTG GAGGATGCTCTTTCCAGCCAAGAGGTGGAGGTGCGCTA TATCTGCAGTGAGAGCTCCAGCCA
372	BLVRA	2999571	TTCCTTAATGCTGGCAAGCACGTCCTTGTGGAATACCCC ATGACACTGTCATTGGCGGCCGCTCAGGAAGTGTG
373	BLVRA	2999573	GAAAAGTCTTGCACGAGGAGCATGTTGAACTCTTGATG GAGGAATTCGCTTTCCTGAAAAAAGAAGTGGTGGGGAA AGACCTGCTGAAAGGGTCGCTCCTCTTC
374	BLVRA	2999576	AGAAGAGCGGTTTGGCTTCCCTGCATTCAGCGGCATCT CTCGCCTGACCTGGCTGGTCTCCCTCTTTGGGGAGCTTT CTCTTGTGTCTGCCACTTTGGAAGAGCGAAAGGAAGAT CAGTATATG
375	BLVRA	2999577	CCTGGTCTAAAACGAAACAGATATTTAAGCTTCCATTTC AAGTCTGGGTCCTTGGAGAATGTGCCAAATGTAGGAGT GAATAAGAACATATTTCTGAAAGATCAAAATATATTTG TCCAGAAAC
376	BLVRA	2999578	GGTTCTTCTCAAGAGTTGACCATTATCTCTATTCTTAAA ATT
377	EGFR	3002642	GGCTGCGCTCTGCCCCGGCGAGTCGGGGCT
378	EGFR	3002666	ATGATCCTTTGCCTGGACTTTCTAAGTGCCC
379	EGFR	3002667	GTTGCACTTGGCCTAGCATTCACCTCACCTGCCTCAG CTTGTTCAACCTGAAAACCTACCAAGTGAAAGCAAGAG CCACGTGAAGACGCCTTAGTTATATGCACCCACCCAGA CACTTG
380	EGFR	3002717	AACTACAGGCCTTTTGAGAGAGTGCCCTCCTAATGAAT TGAGTACCTATTTCTCCATACACAGTGTCTATCATGACC TACAAACCCTTTTCCCATGAGGTGTAACAGAGAGAGAT TACAGCCTTGGAAGTGGATGTCAGACTCTCCTGGTTTAA GACAATAAGCCATGACATAGAGCCTGAAACCA
381	EGFR	3002729	CAAGCTCACGCAGTTGGGCACTTTTGAAGATCATTTTCT CAGCCTCCAGAGGATGTTCAATAACTGTGAGGTGGTCC TTGGGAATTTGGAAATTACCTATGTGCAGAGGAATTAT GATCTTTCC
382	EGFR	3002731	AGGTGGCTGGTTATGTCCTCATTGCCCTCAACACAGTGG AGCGAATTCCTTTGGAAAACCTGCAGATCATCAGAGGA AATATGTACTACGAAAATTCCTATGCCTTAGCAGTCTTA TCTA
383	EGFR	3002733	GGCGCCGTGCGGTTTCAGCAACAACCCTGCCCTGTGCAA CGTGGAGAGCATCCAGTGGCGGGACATAGTCAGCAGTG ACTTTCTCAGCAACATGTCGATGGA
384	EGFR	3002738	GCCAAAAGTGTGATCCAAGCTGTCCCAATGGGAGCTGC TGG
385	EGFR	3002741	AAAATCATCTGTGCCCAGCAGTGCTCCGGGGCGCTGCCG TGGCAAGTCCCCCAGTGACTGCTGCCACAACCAAGTGTG CTGCAGGCTGCACAGGCCCCCGGGAGAGCGACT
386	EGFR	3002743	CGAAGCCACGTGCAAGGACACCTGCCCCCCTCATGC TCTACAACCCCAACCGTACCAGATGGATGTGAACCCC GAGGGCAAATACAGCTTTGGTGCCACCTGCGTGAAGA
387	EGFR	3002747	TAATTATGTGGTGACAGATCACGGCTCGTGCGTCCGAG CCTGTGGGGCCGACAGCTATGAGATGGAGGAAGACGG CGTCCGCAAGTGTAAGAAGTG

388	EGFR	3002750	TGGATATTCTGAAAACCGTAAAGGA
389	EGFR	3002751	TGTTTTAGAGAGAGAACTTTTCGACATATTTCTGTTCC CTTGGAATA
390	EGFR	3002757	TTTTCTCTTGCGAGTCGTCAGCCTGAACATAACATCCTTG GGATTACGCTCCCTCAAGGAGATAAGTGATGGAGATGT GATAATTTTCAGGAAACAAAAATTTGTGCTATGC
391	EGFR	3002760	CACAGGCCAGGTCTGCCATGCCTTGTGCTCCCCCGAGG GCTGCTGGGGCCCCGGAGCCCAGGGACTGCGTCTCTTGC CGGAATGTCAGCCGAGGCAGGGAATGCGTGGACAAGT GCAACCTTCTGGAG
392	EGFR	3002763	TGTATCCAGTGTGCCCCTACATTGACGGCCCCCACTGC GTCAAGACCTGCCCCGGCAGGAGTCATGGGAGAAAAACA ACACCCTGGTCTGGAAGTACGCAGACGCCGGCCATGTG TGCCACCTG
393	EGFR	3002769	GCCAGGAAATGAGAGTCTCAAAGCCATGTTATTCTGCC TTTTTAACTATCATCCTGTAATCAAAGTAATGATGGCA GCGTGTCCCACCAGAGCGGGAGCCCAGCTGCTCAGGAG TCATGCTTAGGATGGATCCCTTCTCTTCTGCCGTCAGAG TTTCAGCTG
394	EGFR	3002770	GCCTCATGCCTTCACGTGTCTGTTCCCCCGCTTTTCCTT TCTGCCACCCCTGCACGTGGGCGCCAGGTTCCCAAGA GTATCCTACCCATTTCTTCTTCCACTCCCTTTGCCAGT GCCTCTCACCCCAACTAGTAGCTAACCATCACCCCCAG GACTGACCTCTTCCTCCTCGCTGCCAGATGATTGTTCAA AGCACAGAATTTGTCAGAAACCTGCAGGGACTCCATGC TGCCAGCCTTCTCCGTAATTAGCATGGCCCCAGTCCATG CTTCTAGCCTTGGTTCCTTCTGCCCCCTCTGTTTGAAATTC TAGAGCCAGCTGTG
395	EGFR	3002771	GCCAGGTCTTGAAGGCTGTCCAACG
396	EGFR	3002774	AAGCTACATAGTGTCTCACTTTCCA
397	EGFR	3002775	GCCTAAGATCCCGTCCATCGCCACTGGG
398	EGFR	3002776	GTGGCCCTGGGGATCGGCCTCTTCATGCGAAGGCGCCA CATCGTTCGGAAGCGCACGCTG
399	EGFR	3002778	GCCTCTTACACCCAGTGGAGAAGCTCCCAACCAAGCTC TCTTGAGGATCTTGAAGGAACTGAATTCAAAAAGATC AAAGTGCTGGGCTCCGGTGCGTTCGGCACGGTGTAT
400	EGFR	3002779	TTAAAATTCCCGTCGCTATCAAGGAATTAAGAGAAGCA ACATCTCCGAAAGCCAACAAG
401	EGFR	3002786	CTACGTGATGGCCAGCGTGGACAACCCCCACGTGTGCC GCCTGCTGGGCATCTGCCTCACCTCCACCGTGCAGCTCA TCACGCAGCTCATGCCCTTCGGCTGCCTCCTGGACTATG TCCGGGAACACAAAGACAATATTGGCTCCCAGTACCTG CTCAACTG
402	EGFR	3002798	GGCATGAACTACTTGGAGGACCGTCGCTTGGTGCACCG CGACCTGGCAGCCAGGAACGTACTGGTGAAAACACCGC AGCATGTCAAGATCACAGATTTTGGGCTGGCCAAACTG CTGGGTGCGGAAGAGAAAGAATACC
403	EGFR	3002800	GTGCCTATCAAGTGGATGGCATTGGAATCAATTTTACA CAGAATCTATACCCACCAGAGTGA

404	EGFR	3002801	AGTTGATGACCTTTGGATCCAAGCCATATGACGGAATC CCTGCCAGCGAGATCTCCTCCATCCTGGAGAAAGGAGA ACGCCTCCCTCAGCCACCCATATGTACCATCGATGTCTA CA
405	EGFR	3002802	CTGGATGATAGACGCAGATAGTCGCCCAAAGTTCCGTG AGTTGATCATCGAATTCTCCAAAATGGCCCCGAGA
406	EGFR	3002803	GCTTCCATTGGGAAGAGTCCCTCTAATGAGCATCTCATG TCACTGTGTTCTGTACATGCCAGCCTGGCCTCCCTGTG TCCCAGATCGCATTATTAAACCCTCCAGCGCATTAGAG CAAGCCTCAGTAAGGCGCAGGCCACATCGTGA ACTAAG CAGCATCCGTGAGTGGGGGCCCACTCCATCTCCC CCTCCCCGTCTGAACTCTCCTCTGGTGCTCGTCCTCACT GTCCGGCTAG
407	EGFR	3002806	GGGGATGAAAGAATGCATTTGCCAAGTCCTACAGACTC CAACTTCTACCGTGCCCTGATGGATGAAGAAGACATGG ACGACGTGGTGGATGCCGACGAGTACCTCATCC
408	EGFR	3002808	GACAGCTTCTTGACGCGATACAGCTCAGACCCACAGG CGCCTTGACTGAGGACAGCATAGACGACACCTTCCTC
409	EGFR	3002809	TCCTGCTCCTCAACCTCCTCGACCCACTCAGCAG
410	EGFR	3002810	CCTCCAGCATCTCCAGAGGGGGGAAACAGTG
411	EGFR	3002811	GTCAACAGCACATTCGACAGCCCTGCCCACTGGGCCCCA GAAAGGCAGCCACCAAATTAGCCTGGACAACCCTGACT ACCAGCAGGACTTCTTTCCCAAGGAAGCCAAGCCAAAT GGCATCTTTAAGGGCTCCACAGCTGAAAATGCAGAATA CCTAAGGGTTCGCGCCACAAAGCAGTGAAT
412	EGFR	3002812	CCACAGACTGGTTTTTGCAACGTTTACACCGACTAGCCA GGAAGTACTTCCACCTCGGGCACATTTTGGGAAGTTGC ATTCCTTTGTCTTCAAACGTGTAAGCATTTACAGAAACG CATCCAGCAAGAATATTGTCCCTTTGAGCAGAAATTTAT CTTTCAAAGAGGTATATTTGAAAAAAAAAAAAAAGTATA TGTGAGGATTTTTATTGATTGGGGATCTTGGAGTTTTTC ATTGTCGCTATTGATTTTTACTTCAATGGGCTCTTCCAA CAAGGAAGAAGCTTGCTGGTAGCACTTGCTACCCTGAG TTCATCCAGGCCCAACTGTGAGCAAGGAGCACAAGCCA CAAGTCTTCCAGAGGATGCTTGATTCCAGTGGTTCTGCT TCAAGGCTTCCACTGCAAAACACTAAAGATCCAAGAAG GCCTTCATGGCCCCAGCAGGCCGGATCGGTACTGTATC AAGTCATGGCAGGTACAGTAGGATAAGCCACTCTGTCC CTTCCTGGGCAAAGAAGAAACGGAGGGGATGGAATTCT TCCTTAGACTTACTTTTGTA AAAATGTCCCCACGGTACT TACTCCCCACTGATGGACCAGTGGTTTCCAGTCATGAGC GTTAGACTGACTTGTTTGTCTTCCATTCCATTGTTTTGAA ACTCAGTATGCTGCCCCCTGTCTTGCTGTCATGAAATCAG CAAGAGAGGATGACACATCAAATAATAACTCGGATTCC AGCCCACATTGGATTTCATCAGCATTTGGACCAATAGCC CACAGCTGAGAATGTGGAATACCTAAGGATAGCACCGC TTTTGTTCTCGCAAAAACGTATCTCCTAATTTGAGGCTC AGATGAAATGCATCAGGTCCTTTGGGGCATAGATCAGA AGACTACAAAAATGAAGCTGCTCTGAAATCTCCTTTAG CCATCACCCCAACCCCCCAAAATTAGTTTGTGTTACTTA TGGAAGATAGTTTTCTCCTTTTACTTCACTTCAAAAGCT

			TTTTACTCAAAGAGTATATGTTCCCTCCAGGTCAGCTGC CCCCAAACCCCCTCCTTACGCTTTGTACACAAAAAGTG TCTCTGCCTTGAGTCATCTATTCAAGCACTTACAGCTCT GGCCACAACAGGGCATTTTACAGGTGCGAATGACAGTA GCATTATGAGTAGTGTGGAATTCAGGTAGTAAATATGA AACTAGGGTTTGAAATTGATAATGCTTTCACAACATTG CAGATGTTTTAGAAAGGAAAAAAGTTCCTTCCTAAAATA ATTTCTCTACAATTGGAAGATTGGAAGATTCAGCTAGTT AGGAGCCCACCTTT
413	EGFR	3002813	GGCACCTGACCGAGGAAACAGCTGCCAGAGGCCTCCA CTGCTAAAGTCCACATAAGGCTGAGGTCAGTCACCCTA AACAACTGCTCCCTCTAAGCCAGGGGATGAGCTTGGA GCATCCCACAAGTTC
414	EGFR	3002814	GAAATATTTTCAGTCAGAACTGGGAAACAGAAGGACCTA CATTCTGCTGTCACTTATGTGTCAAGAAGCAGATGATCG ATGAGGCA
415	EGFR	3002815	GTCAGTTGTAAGTGAGTCACATTGTAGCATTAAATTCTA GTATTTTTGTAGTTTGAAACAGTAACTTAATA
416	EGFR	3002816	CACAGTTCTGTCTGGTAGAAGCCGCAAAGCCCTTAGCC TCTTCACGGATCT
417	EGFR	3002817	GATAGCCTGGCCTTAATACCCTACAGAAAGCCTGTCCA TTGGCTGTTTCTTCCTCAGTCAGTTCCTGGAAGACCTTA CCCCATGACCCCAGCTTCAGATGTGGTCTTTGGAAACA GAGGTCGAAGGAA

418	EGFR	3002818	CTAGGCCTCTGATTGCACTTGTGTAGGATGAAGCTGGT GGGTGATGGGAACTCAGCACCTCCCCTCAGGCAGAAAA GAATCATCTGTGGAGCTTCAAAAGAAGGGGGCCTGGAGT CTCTGCAGACCAATTCAACCCAAATCTCGGGGGGCTCTTT CATGATTCTAATGGGCAACCAGGGTTGAAACCCTTATTT CTAGGGTCTTCAGTTGTACAAGACTGTGGGTCTGTACCA GAGCCCCCGTCAGAGTAGAATAAAAGGCTGGGTAGGGT AGAGATTCCCATGTGCAGTGGAGAGAACAATCTGCAGT CACTGATAAGCCTGAGACTTGGCTCATTTCAAAAGCGT TCAATTCATCCTCACCAGCAGTTCAGCTGGAAAGGGGC AAATACCCCCACCTGAGCTTTGAAAACGCCCTGGGACC CTCTGCATTCTCTAAGTAAGTTATAGAAACCAGTCTCTT CCCTCCTTTGTGAGTGAGCTGCTATTCCACGTAGGCAAC ACCTGTTGAAATTGCCCTCAATGTCTACTCTGCATTTCT TTCTTGTGATAAGCACACACTTTTATTGCAACATAATGA TCTGCTCACATTTTCCTTGCCTGGGGGGCTGTAAAACCTTA CAGAACAGAAATCCTTGCCTCTTTCACCAGCCACACCT GCCATAACCAGGGGTACAGCTTTGTACTATTGAAGACAC AGACAGGATTTTTTAAATGTAAATCTATTTTTGTAACCTT GTTGCGGGATATAGTTCTCTTTATGTAGCACTGAACCTT GTACAATATATTTTTAGAACTCATTTTTCTACTAAAAC AAACACAGTTTACTTTAGAGAGACTGCAATAGAATCAA AATTTGAAACTGAAATCTTTGTTTAAAAGGGTTAAGTTG AGGCAAGAGGAAAGCCCTTTCTCTCTCTTATAAAAAGG CACAACCTCATTGGGGAGCTAAGCTAGGTCATTGTCAT GGTGAAGAAGAGAAGCATCGTTTTTATATTTAGGAAAT TTTAAAAGATGATGGAAAGCACATTTAGCTTGGTCTGA GGCAGGTTCTGTTGGGGCAGTGTTAATGGAAAGGGCTC ACTGTTGTTACTACTAGAAAAATCCAGTTGCATGCCATA CTCTCATCATCTGCCAGTGTAACCCTGTACATGTAAGAA AAGCAATAACATAGCACTTTGTTGGTTTATATATATAAT GTGACTTCAATGCAAATTTTATTTTTATATTTACAATTG ATATGCATTTACCAGTATAAACTAGACATGTCTGGAGA GCCTAATAATGTTTCAGCACACTTTGGTTAGTTCACCAAC AGTCTTACCAAGCCTGGGCCCAGCCACCCTAGAGAAGT TATTCAGCCCTGGCTGCAGTGACATCACCTGAGGAGCT TTTAAAAGCTTGAAGCCCAGCTACACCTCAGACCGATT AAACGCAAATCTCTGGGGCTGAAACCCAAGCATTCGTA GTTTTTAAAGCTCCTGAGGTCATTCCAATGTGCGGCCAA AGTTGAGAACTACTGGCCTAGGGATTAGCCACAAGGAC ATGGACTTGGAGGCAAATTCTGCAGGTGTATGTGATTC TCAGGCCTAGAGAGCTAAGACACAAAGACCTCCACATC TGTCGCTGAGAGTCAAGAACCTGAACAGAGTTTCCATG AAGGTTCTCCAAGCACTAGAAGGGAGAGTGTCTAAACA ATGGTTGAAAAGCAAAGGAAATATAAAACAGACACCT CTTTCCATTTCCCTAAGGTTTCTCTCTTTATTAAGGGTGG ACTAGTAATAAAATATAATATTCTTGCTGCTTATGCAGC TGACATTGTTGCCCTCCCTAAAG
419	EGFR	3002819	GAAAACGCTGGCCTATCAGTTACATTACAAAA

420	EGFR	3002820	ACTACCTGCAGTGTGTCTCTGAGGCTGCAAGTCTGTCC TATCTGAATTCCCAGCAGAAGCACTAAGAAGCTCCACC CTATCACCTAGCAGATAAACTATGGGGAAAACCTTAA TCTGTGCATACATTTCTGGATGCATTTACTTATCTTTAA AAAAAAAGGAATCCTATGACCTGATTTGGCCACAAAAA TAATCTTGCTGTACAATAACAATCTCTTGGAATTAAGAG ATCCTATGGATTTGATGACTGGTATTAGAGGTGACAAT GTAACCGATTAACAACAGACAGCAATAACTTCGTTTTA GAAACATTCAAGCAATAGCTTTATAGCTTCAACATATG GTACGTTTTA
421	EGFR	3002827	CCAGCTGCTGCTCTTATTGGGCTAAGGGATGAAGACTA CACAGGCTGTGAGTTCTCCTCCAGGATACTCACTGACT CCCAGGTGGCCTACTCTATCAACCCATGAGCATGGTCA GCCCTGAGACACTGTCAGGAAGTGAGAGGCCACTGTAG GAGTGTACGCTAACAGCTAACCCAGCGGCCCCCATGA AGGCTGACGCTTGGCATCCCTGGAGAATGGGTCACACT TTTACCTCATCGCATAGCCATAGTCTCTGCCTCCACAGC CTTCATTTTCTCACTTTTTTCTATCAATGCCCAAGAAAAG AATGTTTTTCCATGCAAAACCCAGCAAAGAAATAAAGT CCCCAAGCCTGTGTGCAGGGTTAAAGGAACCTCATGAG AGTGAAGCACTAGGCTGCGAAGGGGAGAAACCCACTT GGGAAAAGCCCACCCTTCGGGGAACCTGGATGACGGC CCATAGAGCATAGTGCCACAAACAGTGACTCTGAAAGT TCGTGTTCCATGGTTCCAAGATTTGAAGTAGTGTTACTC CTCAGAGGCCTTTGTTACTAATCCCCACGGTGGGCTTTT TCCACCACAGGTTTTTAACCTAGCTTTGAACTATGTTCAA GTCCTATGAGGTTGCAAAGCACCAACCCCAATATTCTTAT ACCTATAACGGGGGCACAGAAGCTACTGAAGCATTGTTGGT AGGGCTGTGGCTGCCTGTGCAGTGGGCTATGTGAAAAT CAACTGGAGTCTCCTGGAGAGTGGGCTCTGGAAGTCTC CTCAGTCATCAACGCAGGCTCTTGACCTCTCGTGCCTA TATGACCAAAGTCTACGCAGGCTATGTGGGCTATTTGC GATTCAAGTCCAGCTATGTGCTGCTTCTAACCCAGGCA GTATTCCAGACTGCAGTCCAGCTGAGCGTGGAATGTGT ATCCTGGTGCCCGGATTCCACACTTCACTGCCTTGGTGA TTCAGCCGACCCTCA
422	EGFR	3002828	GCATTTTGCTAAGTCCCTGAGGGTCACTGGTCCTCAAAG CGGCATGGCGGCATGGCGTGGCTGGTTCTGCCACATGC CAGCTGTGTGACCTCTGAGACTCCACTTCTTCAGTGCTG AAAATAAAGAAGGAGTTTTACTAAGGACCAAACAAGA TAATGAATGTGAAACTGCTCCACGAACCCCAAAGAATT ATGCACATAGATGCGATCATTAAAGATGCGAAGCCATCG AGTTACCACCTGGCATGCTTAAACTGTAAA
423	ACTR3B	3032458	CTGCGGCGGCTCGCGGGAGACGCTGCGCGCGGGGCTAG CGGGCGGCGGAGCGGACGGCGACGGGGCGCTCTCGGG CT
424	ACTR3B	3032459	TCCCTGCCTCCCTGCGTGGTGGACTGTGGCACC
425	ACTR3B	3032468	AACTATCTCCTTCCTGCTGTAATCAGT
426	ACTR3B	3032488	AGGCTCCACCATGTTTCAGGGATTTCGGACGCCGACTGC AGAGGGATTT
427	ACTR3B	3032489	GAGGTCCAGGTGGTCACGCATCACATGCAGCGCTACGC CGTGTGGTTTCGGAGGCTCCATGCT

428	ACTR3B	3032491	AAGGACTATGAAGAGTACGGGCCCAGCATCTGCCGCCA CAACCCCGTCTTTGGAGTCATGT
429	ACTR3B	3032492	TTCGATGGTGTACGTTGGGGAACAAGTGTCTTCAGA ACCCAGAGAAGGCCGCCGTTCTGTAAATAGCGACGTCG GTGTTGCTGCCCAGCAGCGTGCTTGCATTGC
430	ACTR3B	3032493	CCATTTATCCGTGTGCCGACCGCTGTCTGCCAGCCTCCT CCTTCTCCCGCCCTCCTCACCCCTCGCTCTCCCTCCTCCTC CTCCTCCGAGCTGCTAGCTGACAAATACAATTCTGAAG GAATCCAAATGTGACTTTGAAAATTGTTAGAGAAAACA ACATTAGAAAATGGCGCAAAATCGTTAGGTCCCAGGAG A
431	ACTR3B	3032494	GTACAACTGGCTGATACTAAGCACGAATAGATATTGAT GTTATGGAGTGCTGTAATCCAAAGTTTTTAATTGTGAGG CATGTTCTGATATGTTTATAGGCAAACAAATAAAACAG CAAACTTTTTTGCCACATGTTTGCTAGAAAATGATTATA CTTTATTGGAGTGACATGAAGTTTGAACACTAAACAGT AATGTATGAGAATTACTACAGATACATGTATCTTTTAGT TTTTTTTGTGTTGAACTTTCTGGAGCTGTTTTATAGAAGAT GATGGTTTGTGTCGGTGAGTGTTGGATGAAATACTTCC TTGCACCATTGTAATAAAAGC
432	NAT1	3087948	ATTGACCCAGTCGACAGGATCTGAACTTCCAGT
433	NAT1	3087952	GGACCTGTTCCAAGCTCTCACGTTCCACATCACACATGG GACATCTAGTGTCAGGCTCCCAGAGAGCAGGAACCAGG TGAAATATAAGAGCACAGTCCTCCCAGCCGGTGGCATG GGGATAATCGGACAATACAACCTCTC
434	NAT1	3087956	CCCTGAACATGGACTTGCAGAATTCCACAGAAGAGAGG AGACTGGCCTAGACAGACAGCCCCAGGAGCTGAGGGC CCAACAGGCTTTCTACCCTGGATGCTGCTCCCATGCCCT GACATGAGGCCCACTACA
435	NAT1	3087957	CAGCCTGGATGTGAACTGCAACTCCAAAGTGTGTCCAG ACTCAAGGCAAGGGCACTAGGCTTTCCAGACCTCCTAC TAAGTCATTGATCCAGCACTGCCCTGCCAGGACATAAA TCCCTGGCACCTCTTGCTCTCTGCAAAGGAGGGCAAAG CAGCTTCAGGAGCCCTTGGGAGTCCTCCAAAGAGAGTC TAGGGTACAGGTC
436	NAT1	3087958	ACAGAAGGGCCATGCTGTTATTACTCTTACACAAGGAG GCAGCCCTCGAGCCACAGGGTCCAGCTGTTGGCTATAA TAGCCTACCGGTCTCTGATGATCACCATGTTT
437	NAT1	3087960	GCAGCAATCTGTCTTCTGGATTAAAACTGAAGATCAAC CTACTTTCAACTTACT
438	NAT1	3087961	AAATATAGCCATAATTAGCCTACTCAAATCCAAGTGTA AA

439	NAT1	3087962	CCATTGTGGGGATGCCATGGACTTAGGCTTAGAGGCCA TTTTTGATCAAGTTGTGAGAAGAAATCGGGGTGGATGG TGTCTCCAGGTCAATCATCTTCTGTACTGGGCTCTGACC ACTATTGGTTTTTGAGACCACGATGTTGGGAGGGTATGTT TACAGCACTCCAGCCAAAAAATACAGCACTGGCATGAT TCACCTTCTCCTGCAGGTGACCATTGATGGCAGGAACT ACATTGTCGATGCTGGGTTTGGACGCTCATACCAGATGT GGCAGCCTCTGGAGTTAATTTCTGGGAAGGATCAGCCT CAGGTGCCTTGTGTCTTCCGTTTGACGGAAGAGAATGG ATTCTGGTATCTAGACCAAATCAGAAGGGGAACAGTACA TTCCAAATGAAGAATTTCTTCATTCTGATCTCCTAGAAG ACAGCAAATACCGAAAAATCTACTCCTTTACTCTTAAG CCTCGAACAATTGAAGATTTTGAGTCTATGAATACATA CCTGCAGACATCTCCATCATCTGTGTTTACTAGTAAATC ATTTTGTTCCCTTGCAGACCCCAGATGGGGTTCAGTGT GGTGGGCTTCACCCTCACCCATAGGAGATTCAATTATA AGGACAATACAGATCTAATAGAGTTCAAGACTCTGAGT GAGGAAGAAATAGAAAAAGTGCTGAAAAATATATTTA ATATTTCCCTTGCAGAGAAAGCTTGTGCCCAAACATGGT GATAGA
440	NAT1	3087963	ATAAGGAGTAAAACAATCTTGTCTATTTGTCATCCAGCT CACCAGTTATCAACTGACGACCTATCATGTATCTTCTGT ACCCTTACCTTA
441	NAT1	3087964	AAAGATGGCCTGTGGTTATCTTGGAAATTGGTGATTTAT GCTAGAAAGCTTTTA
442	NAT1	3087965	CTTGTGTAGATCTGAGTTGAAATCCTGTGGACACTGGG CGAATTACTTTTTAGATCTGTAGCTCTGACTCCTCAGGC ATAAAATGGGAATAATGCTTTTACAGTTTAGTGGCGGA AC
443	MYC	3115511	TAACGCGCTCTCCAAGTATACGTGGCAATGCGTTGCTG GGTTATTTTAATCATTCTAGGCATCGTTTTCTCCTTATG CCTCTATCATTCCCTCCCTATCTACACTAACATCCCACGC TCTGAACGCGCGCCCATTAATACCCTTCTTTCTCCTCACT CTCCCTGGGACTCTTGATCAAAGCGC
444	MYC	3115512	ATGCGGTTTGTCAAACAGTACTGCTACGGAGGAGCAGC AGAGA
445	MYC	3115513	GTAGGCGCGCGTAGTTAATTCATGCGGCTCTCTTACTCT GTTTACATCCTAGAGCTAGAGTGCTCGGCTGCCCCGGCT GAGTCTCCTCCCCACCTTCCCCACCCTCCCCACCCTCCC CATAAGCGCCCCCTCCCGGGTTCCCAAAGCAGAGGGCGT GGGGGAAAAGAAAAAAGATCCTCTCTCGCTAATCTCCG CCCACCGGCCCTTTATAATGCGAGGGTCTGGACGGCTG AGGACCCCCGAGCTGTGCTGCTCGCGGCCGCCACCGCC GGGCCCCGGCCGTCCCTGGCTCCCCTCCTGCCTCGAGA AGGGCAGGGCTTCTCAGAGGCTTGGCGGGAAAAAGAA CGGAGGGAGGGATCGCGCTGAGTATAAAAGCCGGTTTT C
446	MYC	3115514	CAACCCTTGCCGCATCCACGAACTTTGCCCATAG
447	MYC	3115515	TTACAACACCCGAGCAAGGACGCGACTCTCCCGACGCG GGGAGGCTATTCTGCCCATTTGGGGACACTTCCCCGCC GCTGCCAGGACCCGCTTCTCTGAAAGGCTCTCCTTGCAG

			CTGCTTAGACGCTGGATTTTTT
448	MYC	3115522	AGCCGTATTTCTACTGCGACGAGGAGGAGAACTTCTAC CAGCAGCAGCAGCAGAGCGAGCTGCAGCCCCCGGCGC CCAGCGAGGATATCTGGAAGAAATTCGAGCTGCTGCCC ACCCCGCCCCCTGTCCCCTAGCCGCCGCTCCGGGCTCTGC TCGCCCTCCTACGTTGCGGTCACACCCTTCTCCCTTCGG GGAGACAACGACGGCGGTGGCGGGAGCTTCTCCACGGC CGACCAGCTGGAGATGGTGACCGAGCTGCTGGGAGGA GACATGGTGAACCAGAGTTTCATCTGCGACCCGGACGA CGAGACCTTCATCAAAAACATCATCATCCAGGACTGTA TGTGGAGCGGCTTCTCGGCCGCCGCCAAGCTCGTCTCA GAGAAGC
449	MYC	3115523	GAAGGACTATCCTGCTGCCAAGAGGGTCAAGTTGGACA GTGTCAGAGTCCTGAGACAGATCAGCAACAACCGAAAA TGCACCAGCCCCAGGTCCTCGGACACCGAGGAGAATGT CAAGAGGCGAACACACAACGTCTTGGAGCGCCAGAGG AGGAACGAGCTAAAACGGAGCTTTTTTGGCCTGCGTGA CCAGATCCCGGAGTTGGAAAACAATGAAAAGGCCCCCA AGGTAGTTATCCTTAAAAAAGCCACAGCATACATCCTG TCCGTCCAAGCAGAGGAGC
450	MYC	3115524	TTCCTTCTAACAGAAATGTCCTGAGCAATCACCTATGAA CTTGTTTCAAATGCATGATCAAATGCAACCTCACAACCT TGGCTGAGTCTTGAGACTGAAAGATTTAGCCATAATGT AAACTGCCTCAAATTGGACTTTG
451	MYC	3115525	TCCTAGTATATAGTACCTAGTATTATAGGTACTATAAA
452	SFRP1	3132783	TGTGCAGCTCTCTAAATGGGAATTCTCAGGTAGGAAGC AACAGCTTCAGAAAGAGCTCAAAATAAATTGGAAATGT GAATCGCAGCTGTGGGTTTTACCACCGTCTGTCTCAGAG TCCCAGGACCTTGAGTGTCATTAGTTACTTTATTGAAGG TTTTAGACCCATAGCAGCTTTGTCTCTGTCACATCAGCA ATTTCAGAACCAAAAAGGGAGGCTCTCTGTAGGCACAGA GCTGCACTATCACGAGCCTTTGTTTTTCTCCACAAAGTA TCTAACAAAACCAATGTGCAGACTGATTGGCCTGGTCA TTGGTCTCCGAGAGAGGAGGTTTGCCTGTGATTTCTTAA TTATCGCTAGGGCCAAGGTGGGATTTGTAAAGCTTTAC AATAATCATTCTGGATAGAGTCCTGGGAGGTCCTTGGC AGAACTCAGTTAAATCTTTGAAGAATATTTGTAGTTATC TTAGAAGATAGCATGGGAGGTGAGGATTCCAAAAACAT TTTATTTTTTAAATATCCTGTGTAACTTGGCTCTTGG TACCTGTGGGTAGCATCAAGTTCTCC

453	SFRP1	3132784	GCGCCTGTCAGTAGTGGACATTGTAATCCAGTCGGCTT GTTCTTGCAGCATTCCCGCTCCCTTCCCTCCATAGCCAC GCTCCAAACCCCAGGGTAGCCATGGCCGGGTAAAGCAA GGGCCATTTAGATTAGGAAGGTTTTTAAGATCCGCAAT GTGGAGCAGCAGCCACTGCACAGGAGGAGGTGACAAA CCATTTCCAACAGCAACACAGCCACTAAAACACAAAAA GGGGGATTGGGCGGAAAGTGAGAGCCAGCAGCAAAAA CTACATTTTGCAACTTGTTGGTGTGGATCTATTGGCTGA TCTATGCCTTTCAACTAGAAAATTCTAATGATTGGCAAG TCACGTTGTTTTTCAGGTCCAGAGTAGTTTCTTTCTGTCT GCTTTAAATGGAAACAGACTCATAACCACACTTACAATT AAGGTCAAGCCCAGAAAGTGATAAGTGCAGGGAGGAA AAGTGCAAGTCCATTATGTAATAGTGACAGCAAAGGGA CCAGGGGAGAGGCATTGCCTTCTCTGCCCCACAGTCTTTC CGTGTGATTGTCTTTGAATCTGAATCAGCCAGTCTCAGA TGCCCCAAAGTTTCGGTTCCTATGAGCCCCGGGGCATGA TCTGATCCCCAAGACATGTGGAGGGGGCAGCCTGTGCCT GCCTTTGTGTCAGAAAAAGGAAACCACAGTGAGCCTGA GAGAGACGGCGATTTTCGGGCTGAGAAGGCAGTAGTTT TCAAAACACATAGTTAAAAAAGAAACAAATGAAAAAA ATTTTAGAACAGTCCAGCAAATTGCTAGTCAGGGTGAA TTGTGAAATTGGGTGAAGAGCTTAGGATTCTAATCTCAT GTTTTTTCCTTTTCACATTTTAAAAGAACAATGACAAA CACCCACTTATTTTTCAAGGTTTTTAAAACAGTCTACATT GAGCATTTGAAAGGTGTGCTAGAACAAAGGTCTCCTGAT CCGTCCGAGGCTGCTTCCCAGAGGAGCAGCTCTCCCCA GGCATTTGCCAAGGGAGGCGGATTTCCCTGGTAGTGTA GCTGTGTGGCTTTCCTTCCTGAAGAGTCCGTGGTTGCCC TAGAACCTAACACCCCCCTAGCAAACTCACAGAGCTTT CCGTTTTTTTCTTTCCTGTAAAGAAACATTTCTTTGAAC TTGATTGCCTATGGATCAAAGAAATTCAGAACAGCCTG CCTGTCCCCCGCACTTTTTACATATATTTGTTTCATTTT TGCAGATGGAAAGTTGACATGGGTGGGGTGTCCCCATC CAGCGAGAGAGTTTCAAAGCAAAACATCTCTGCAGTT TTTCCCAAGTACCCTGAGATACTTCCCAAAGCCCTTATG TTAATCAGCGATGTATATAAGCCAGTTCAGTACAGACA ACTTTACCCTTCTTGTCCAATGTACAGGAAGTAGTTCTA AAAAAAATGCATATTAATTTCTTCCCCCAAAGCCGGAT TCTTAATTCTCTGCAACACTTTGAGGACATTTATGATTG TCCCTCTGGGCCAATGCTTATACCCAGTGAGGA
454	SFRP1	3132785	AATGAAAAACCATGAGTGCCCCACCTTTCAGTCCGTGT TTAAGTGA
455	SFRP1	3132786	CTTCCTCATCATGGGCCGCAAGGTGAAGAGCCAGTACT TGCTGACGGCCATCCACAA
456	SFRP1	3132787	AAGTTGGGGCCCATCAAGAAGAAGGACCTGAAGAAGC TTGTGCTGTACCTGAAGAATGGGGCTGACTGTCCCTGCC
457	SFRP1	3132788	AGAAAATGGCGACAAGAAGATTGTCCCCAAG
458	SFRP1	3132808	TGTGTCCTCCCTGTGACAACGAGTTGAAATCTGAGGCC ATCATTGAACATCTCTGTGCCAGCGAGTTTG

459	SFRP1	3132810	GCTCGGCTGCGGAAAAGGTGCTGCAGTCCACAGGGAAC ATGGGGGGATTGGACGGGTTGCCTGAAGAAGAGAGGA AAGAATCCCTCACCCCAGCCCCAAAAGGCTGTGATGG GATGGGGAAACCCCATATCGCTGTCTTCCGGACACCT TTTGCCCCCTTGGCTGCAGTTCCACTGGTCGGCGCCCTTC TCAGCCTGGCTTGGAACCGTCCTCACTCA
460	SFRP1	3132814	TCGGCCAGCGAGTACGACTACGTGAGCTTCCAGTCGGA CATCGGCCCCGTACCAGAGCGGGCGCTTCTACACCAAGC CACCTCAGTGCGTGGACATCCCCGCGGACCTGCGGCTG TGCCACAACGTGGGCTACAAGAAGATGGTGCTGCCCAA CCTGCTGGAGCACGAGACCATGGCGGAGGTGAAGCAG CAGGCCAGCAGCTGGGTGCCCCCTGCTCAACAAGAACTG CCACGCCGGCACCCAGGTCTTCCCTCTGCTCGCTCTTCGC GCCCCGTCTGCCTGGACCGGCCCATCTACCCGTGTCGCTG GCTCTGCGAGGCCGTGCGCGACTCGTGCGAGCCGGTCA TGCAGTTCTTCGGCTTCTACTGGCCCCGAGATGCTTAAGT GTGACA
461	SFRP1	3132815	GTCGCGGAGAACAGGGCGCAGAGCCGGC
462	SFRP1	3132816	TCCCTGGAAGTTTGCGGCAGGACGCGC
463	SFRP1	3132817	TGCAGCCTCCGGAGTCAGTGCCGCGCGCCCCGCCGCCCC GCGCCTTCTGCTCGCCGCACCTCCGGGAGCCGGGGGCG CACCCAGCCCGCAGCGCCGCTCCCCGCCCGCGCCGCC TCCGACCGCAGGCCGAGGGCCGCCACTGGCCGGGGGG ACCGGGCAGCAGCTTGCGGGCCGCGGAGCCGGGGCAACG CTGGGGACTGCGCCTTTTGTCC
464	SFRP1	3132819	AATGGATCCAACCTGCTTGCCCCGTCATCCCAGATGGCT AGGCCCCCATTCATCCCCTCTCGCTCTCCTACTGGAGGA ACTGCTGTATGAATCATAAAGCTCTGGGTAGGGAAGCA GGGAGCAGGTTCCAGGCAGAGCTGACAAGTGACTTCAC TTTTGAGCATCGGTTGAACCAG
465	MELK	3168509	AAGCGGCCACAACCCGGCGATCGAAAAGATTCTTAGGA ACGCCGTACCAGCCGCGTCTCTCAGGACAGCAGGCCCC TGTCTTCTGTGCGGGCGCCGCTCA
466	MELK	3168510	CCCAGTTTGCTCCTGGCTCTCGGGAGACTGGAGGATTTC ATCGGAGCCCCGCGCTTTACCAGCCCTGTTCCCTGGATA AGATATTTGACCTTTCGACCCGCG
467	MELK	3168511	TTCTAATTCCAAATAAACTTGCAAGAGGACT
468	MELK	3168512	TGAAAGATTATGATGAACTTCTCAAATATTATGAATTAC ATGAA
469	MELK	3168513	AAAGGTCAAACCTTGCCATATCCTTACTGGAGAGA TGGTAGCTATAAAAATC
470	MELK	3168514	CCCGGATCAAAACGGAGATTGAGGCCTTGAAGAACCTG AGACATCAGCATATATGTCAACTCTACCATGTGCTAGA GACAGCCAACAAAATATTCATGGTTCTTG
471	MELK	3168515	TACTGCCCTGGAGGAGAGCTGTTTGACTATATAATTTCC CAG
472	MELK	3168516	CAGAAGAGGAGACCCGGGTTGTCTTCCGTCAGATAGTA TCTGCTGTTGCTTATGTGCACAGCCAGGGC
473	MELK	3168518	ACAAGGATTACCATCTACAGACATGCTGTGGGAGTCTG GCTTATGCAGCACCTGAGTTAATACAAGGCAAATCATA TC

474	MELK	3168519	GCAGATGTTTGGAGCATGGGCATACTGTTATATGTTCTT A
475	MELK	3168522	AAGTGGCTCTCTCCCAGTAGCATTCTGCTTCTTCAA
476	MELK	3168523	GACCCAAAGAAACGGATTTCTATGA
477	MELK	3168524	GCAAGATTACAACCTATCCTGTTGAGTGGCAAAGCAAGA
478	MELK	3168525	TTTATTACCTCGATGATGATTGCGTAACAGAACTTTCT GTACATCACAGAAACAACAGGCAAACAATGGAGGATT
479	MELK	3168526	TGGCAGTATGATCACCTCACGGCTACCTATCTTCTGCTT CTAGCCAAGAAGGCTCGGGGAAAACCAGTTCGTTTAAG GCTTTCTTCTTTCTCCTGTGGACAAGCCAGTGCT
480	MELK	3168528	TGGAAGATGTGACCGCAAGTGATAAAAATTATGTGGCG GGATTAATAGACTATGATTGGTGTGAAGATGATTTATC AACAGGTGCTGCTACTCCCCGAACATCA
481	MELK	3168529	GGGGTGGGAATCTAAATCATTAACCTCCAGCCTTATGCAG AACACCTGCAAATAAATTAAAGAACAAAGAAAATGTAT ATACTCCTAAGTCTGCTGTAAAGAATGAAGAGTACTTT ATGTTTCCTGAGCCAAAGACTCCAGTTAATA
482	MELK	3168530	GAAACCAGTGCCTGAAAGAAACTCCAATTAATAATACCA GTAAATTCAACAGGAACAGACAAGTTAATGACAGGTGT CATTAGCCC
483	MELK	3168531	TGGATCTCAACCAAGCACATATGGAGGAGACTCCAAAA AGAAAGGGAGCCAAAGTGTTTGGGAGCCTTGAAAGGG GGTTGGATAAGGTTATCACTGTGCTCACCAGGAGCAAA AGGAAGGGTTCTGCCAGAGACGGGCCCAGAAGA
484	MELK	3168533	CTTCACTATAACGTGACTACAACCTAGATTAGTGAATCC AGATCAACTGTTGA
485	MELK	3168535	ATACACTGAAGTGTCAAACACAGTCAGATTTTGGGAAA GTGACAATGCAATTTGAATTAGAAGTGTGCCAGCTTCA AAAA
486	MELK	3168536	CTTAAGGGCGATGCCTGGGTTTACAAAAGATTAGTGGA AGACATCCTATCTAGCTGCA
487	MELK	3168537	ATGGATTCTTCCATCCTGCCGGATGAGTGTGGGTGTGAT ACAGCCTACATAAAGACTGTTATGATCGCTTTGATTTTA AAGTTCATTGGAACCTACCAACTTGTTTCTAAAGAGCTAT CTTAAGACCAATATCTCTTTGTTTTTAAACAAAAGATAT TATTTTGTGTATGAATCTAAATCAAGCCCATCTGTCATT ATGTTACTGTC
488	CDC20	3177818	GAGGGGGCACCAGTGATCGACACATTTGCATCTGGAAC GTGTGCTCTGGGGCCTGTCTGAGTGCCGTGGATGCCC
489	CDC20	3177820	TTATTTGGAAGTACCCAACCATGGC
490	BAG1	3203483	CGGACCTATGTCCTACCTGTTTCATGCAGTTGTCCATATC CAGTGGGATGTCCTAGGGGCTCAACTGTCCACAAACAT CACTGCCCCCACAAGAACTGGTACAGACCCCCAAACCA CCCATCTCAGCCCATGAAACCACTGGCCACCCAAGCCC ACAAATCAGAAACCAGTATGCTGCCTCCTTCCCCTCAG CCTTTACATACAGTCACATACCAAGCCTGTCAATTCCAC TCCCAATGTACCTCCTAACCATGAGTCTTTG
491	BAG1	3203484	ACCTTCTCAGGAGCTGTAGTGTACCATTCAGGGACCTG GCACAGTCCATCCAGACATCCTGCTGAGCGTCGCCAC ATATGCAGT

492	BAG1	3203486	TCTTTCAGGTCCTCAGATGCACTGCACCCTCTCCTGCCT GGGGGTCTTTGCTCCTGCTACTACCTCTGCTTGAACAGC TCCTCACCTTCCTTCCTCCAACCCTACCCTTGTATAGGT GACTTTTGTTCATCCTTCAGAATTCAACTCACATGTCTC TTGCATGGAGAACCCTCACCTACTGTGTTGAGACCCTGT CCAGCCCCCAGGTGGGATCCTCTCTCGACTTCCCATAACA TTTCTTTCACAGCATTTACATAGTCCATGATAGTTTACT TGTGGGATTATTTGGTTAATCTTTGCCTTTAACACCAGG GTTCTTGGGTGAAGGAGCTTCTTTATC
493	BAG1	3203487	AGAGTCGTTGAAGTCCCAGGAATTCAGGACTGGGCAGG TTAAGACCTCAGACAAGGTAGTAGAGGTAGACTTGTGG ACAAGGCTCGGGTCCCAGCCCACCGCACCCCAACTTTA ATCAGAGTGGTTCACTATTGATCTATTTTTGTGTGATAG CTGTGTGGCGTGGGCCACAACATTTAATGAGAAGTTAC TGTGCACCAAACCTGCCGAACACCATTCTAAACTATTCT ATATATTAGTCATTTAATTCTTACATAACTTGAGAGGTA GACAGATATCCTTATTTTAGAGATGAGGAAACCAAGAG AACTTAGGTCATTAGCGCAAGGTTGTAGAGTAAGCGGC AAAGCCAAGACACAAAGCTGGGTGGTTTGGTTTCAGAG CCAGTGCTTTTCCCCTCTACTGTACTGCCTCTCAACCAA CACAGGGTTGCACAGGCCCATCTCTGATTTTTTTCCTC TTGTCCTCTGCCTCTCCCTCTAGCTCCCCTTCTCTCTG CTCTAGTTCATTTTCTTTAGAGCAGCCCGAGTGATCATG AAGTGCAAATCTTGCCATGTCAGTCCCCTGCTTAGAACC CTCCAATGGCTCACTTTCTCTTTAGGCA
494	BAG1	3203488	CTTCTGTCTCTGTGGTTGTACTGTCCAGCAATCCACCTT TTCTGGAGAGGGCCACCTCTGCCCAAATTTTCCCAGCTG TTTGGACCTCTGGGTGCTTTCTTTGGGCTGGTGAGAGCT CTAATTTGCCTTGGGCCAGTTTCAGGTTTATAGGCCCCC TCAGTCTTCAGATACATGAGGGCTTCTTTGCTCTTGTGA TCGTGTAGTCCCATA
495	BAG1	3203489	TTTCCTACTCTCACACTGGTTCTCAATGAAAA
496	BAG1	3203490	AATGGCGCCACCAGCTCTGCCGTCTCTGGAGCGGAATT TACCTGATTTCTTCAGGGCTGCTGGGGGCAACTGGCCAT TTGCCA
497	BAG1	3203493	TTCAAAGACAGTAGATTGAAAAGGAAAGGCT
498	BAG1	3203495	GAAGCTCTCTGCAAACCTTGATAGGAGAGTAAAAGCCAC AATAGAGCAGTTTATGA
499	BAG1	3203496	AGCTCTTGCTACGTGTTGTGAAATCTGTGTCTGTAGCTC GTGGCTGTGATAAACATCCTCAGAGATCCCTGCTATCC AACTCTTGTCACCAGCTAACTGGTCATTAGGCCAAGCT GTGTGAGTGAACCATTAGACAATTTGATAAAAATAAGC ACTGCTGCCATTCTTTAGCATGCGTCTGTGCCACAAGTT AGTGACACATGTACATATATCCCTTTACCTCACAGTAA CCATCTAGGGTGTGGGCATCATAATCTTCATTTTTTAAAA TGAGGGTACTGAGGCATGAATAGGCTAAATAATTTGCT CAAGATCACAAGTTAGTAAATGGCAGTCAGTTTTTCAGG CGTAGGCTTTGAAGACTCTAAACCTGTGCTTTTAAACATC TGCCTCTTCTTGTGACTGGGGGCTTCACTGGAGCCAAGC CTCAGGAGGCATTTGCAGCCACAGTGGGTCATGCGAGG TAGAGCAGACTGCAACCTGATAGAATTCTTGGACTGGC CCACGGCCAGCCTTTTTTAATTTTTCCAAGAGTTAAAGTT

			GTGGATCTGAGATGTGGCCTGGCCTGCCAGGGCTATGG TGGGCTCAGTGTGATTGCATCATTAGTATTGTGGCATGG AGTCTTCCGTCAGCCTCAGAGA
500	BAG1	3203497	AGTCCACAGGAAGAGGTTGAACTAAAGAAGTTGAAAC ATTTGGAGAAGTCTGTGGAGAAGATAGCTGACCAGCTG GAAGAGTTGAATAAAGAGCTTACTGGAATCCAGCA
501	BAG1	3203498	CTAAATTTCTTGCTTCAGGGTCAGGGAGAATGGTGATG GGCAACAGGCAGAACCAAAGAGTCAAGTTTGAAGAAA CTATAGGACTTTTACTTGGAGCTGACACAGAGCGTATG GAGCGAAGTGTGAACTCAAGGAAGGCACCATGGCACA TGCCTATTGTCCCAGCAAGTTGGGAGTCTGAGACAGGA GGATCACTTGAGTCCAGGGGTTTGAGGCTGCAGTGAGT TATGATCATGCCTGTAAACAGCCACTGCACTCCAACCT GGGAACCGTAGTGAGACCCTATCTCAAAAAAGAAAAA AGTCTGAACTTAAGTCTAATCTACCTCTTTTGGACTGTG TGATCTCATGTTACTTTACTACATTAAGCCTCAGTTTCA TCATCTGTAAACAGCAGTACTTCCCTGATGGAGTTGTG GTAAGGCTTAAAAAATAGGTAAGGTGCTTAGGATAGTG TGTGGCATGTAGGAAGTGTTCAATAAAAGTATTCATCG TTGTTAACCAGCATCACATTAAACAGGAGCGCTCAATT GGAGGCTGCCATTTAGGAATTCCATTTAAAGGAATGGT AGAATTCCACCTTTCTTGCCATTCTGGACTCCTCACAAG TGTTTACTG
502	BAG1	3203499	GGAAATGGAAACACCGTTGTCAGCACTTGGAATACAAG ATGGTTGCCGGGT
503	BAG1	3203500	GACCTGCTAGGTATTGGACACTCTCAAACACCTGGACA GGTGTCAGATTTGAAGTCTTATGATGATGGCAGAAATC TCACCATTTTCGATGAAGCTCATGGGCAGTCTTC
504	BAG1	3203501	GAGAAGCACGACCTTCATGTTACCTCCCAGCAGGGCAG CAGTGAACCAGTTGTCCAAGACCTGGCCCAGGTTGTTG AAGAGGTCATAGGGGTTCCACAGTCTTTTC
505	BAG1	3203504	GGCAGCTGGGCTCACCGTGACTGTCACCCAC
506	BAG1	3203505	GAGGCGACCCAGGGCGAAGAGATGAATCGGAGCCAGG AGGTG
507	BAG1	3203506	AGTTGACCCTGAGTGAGGAAGCGACCTGGAGTGAAGA GGCGACCCAGAGTGAG
508	BAG1	3203507	ACCCGGCGCCGCTCGACCCGGAGCGAGGA
509	BAG1	3203508	TGGGCGTCCACCTGCCCCGAGTACTGCCAGCGGGCATG ACCGACCCACCAGGGGCGCCGC
510	BAG1	3203509	CTGGGTTCCTCGGCTGCGCGCCCTTCGGCCAG
511	BAG1	3203510	GCGGGGTGTGAGACGCCGCGCTCAGCTTCCATCGCTG GGCGGTCAACAAGTGCG
512	CEP55	3258448	TGTGACTCGGCCGACGCGAGCGCCGCGCTTCGCTTCAG CTGCT
513	CEP55	3258449	GGAGGCGACCGCGGAGGGTGGCGAGGGGGCGGCCAGGA CCCGCAGCCC
514	CEP55	3258450	GGCAGATCGCGTCCGCGGGATTCAATCTCTGCCCGCTCT GATAACAGTCCTTTTCCCTGGCGCTCACTTCGTGCCTGG CACCCGGCTGGGCGCCTCAAGACCGTTGTCTCTTCGATC GCTTCTTTGGACTTGG
515	CEP55	3258451	ATGTCTTCCAGAAGTACCAAAGATTTAATTA

516	CEP55	3258452	TAAGTGGGGATCGAAGCCTAGTAACTCCAAATCCGAAA CTACATTAGAAAAATTAAAGGGAGAAATTGCACACTTA AAGACATCAGTGGATGAAATCACAAGTGGGAAAGGAA AGCTGACTGATAAAGAGAGACACAGACTT
517	CEP55	3258453	GCGACTGAGAGACCAACTGAAGGCCAGATATAGTACTA CCACATTGCTTGAACAGCTGGAAGAGACAACGAGAGA AGGAGAAAGGAGGGGAGCAGGTGTTGAAAGCCTTATCT GAAGAGAAAGACGTATTGAAACAACAGTTGTCTGCTGC AACCTCA
518	CEP55	3258454	CTGTGGCTCCAAACTGCTTCAACTCATCAATAAATAAT
519	CEP55	3258455	TCTGGAGAAAAATCAGCAGTGGCTCGTGTATGATCAGC AGCGGGAAGTCTATGTAAAAGGACTTTTAGCAAAGATC TTTGAGTTGGAAAAGAAAACGGAAACAGCTGCTCATTC ACTCCCACAGCAGACAAAAAAGC
520	CEP55	3258456	GAAGCAGAAATGTTACAACGATCTCTTGGCAAGTGCAA AAAAAGATCTTGAGGTTGAACGACAAACCATAACTCAG
521	CEP55	3258457	AGCTGTTGTATTACAAAGAAGGGCAGATGTGCAACAT CTGGAAGATGATAGGCATAAAACAGAGAAGATACAAA AACTCAGGGAAGAGAATGATATTGCTAGGGGAAAACCTT GAAGAAGAGAAGAAGAGATCCGAAGAGCTCTTATCTC
522	CEP55	3258459	CTTTACACATCTCTGCTAAAGCAGCAAGAAGAACAAAC AAGGGTAGCTCTGTTGGAACAACAG
523	CEP55	3258460	ACTCATTCGGGTTGCTTCTAAATTCAATTCTGCCTGTTA GAAAATGCAGTTTTTTCCTCATGTTTATGCTGTTCTATGG AGAACTGTTTGAAAGTTGTGAAAAGTGTCT
524	CEP55	3258461	TGAAAAACTCGACCGTCAACATGTGCAGCATCAATTGC ATGTAATTCTTAAGGAGCTCCGAAAAGCAAGAAATCAA ATAACACAGTTGGAATCCTTG
525	CEP55	3258462	TCCGAACCTTAGGAGGATACAGCTTAACACACAGCTAGC TGTATCTCAAATCAGTAGGTAGAGCCTCTGCCTCATTTG AAGCAACTGCCCTTTGAGCATCAATTCAGAGGACATGA AAGAGGGACATGATCACATCTGGAAACA
526	CEP55	3258463	CAGAGCCATTAGTCACTTTCCAAGGAGAGACTGAAAAC AGAGAAAAAGTTGCCGCCTCACCAAAAAGTCCCCTGC TGCACTCAATGAAAGCCTGGTGGGAATGTCCCAAGTGCA ATATACAGTATCCAGCCACTGAGCATCGCGATCTGCTT GTCCATG
527	CEP55	3258464	TACCTTTGACACTCCAGCATGCTAGTGAATCATGTATCT TTTAGGCTGCTGTGCATTTCTCTTGGCAGTGATACCTCC CTGACATGGTTCATCATCAGGCTGCAATGACAGAATGT GGTGAGCAGCGTCTACTGAGACTACTAACATTTTGCAC TGTCAAAATACTTGGTGAGGAAAAGATAGCTCAGGTTA TTGCTAATGGGTTAATGCACCAGCAAGCAAAATATTTT ATGTTTTTGGGGGTTTTTGA AAAAATCAAAGATAATTAACC AAGGATCTTAACTGTGTTCGCATTTTTTTATCCAAGCACT TAGAAAACCTACAATCCTAATTTTGTATGTCCATTGTAA GAGGTGGTGATAGATACTATTTTTTTTTTCATATTGTAT AGCGGTATTAGAAAAGTTGGGGATTTTCTTGATCTTTA TTGCTGCTTACCATTGAAACTTAACCCAGCTGTGTTCCC CAACTCTGTTCTGCGCACGAAACAGTATCTG

528	CEP55	3258465	TCAGATCTTTGTTTGTCTGAACAGGTATTTTTATACATG CTTTTTGTAAACCAAAAACCTTTTAAATTTCTTCAGGTTT TCTAACATGCTTACCACTGGGCTACTGTAAATGAGAAA
529	MKI67	3312496	ACTCGTGAGCACATCTTTAGGGACCAAGAGTGACTTTC TGTAAGGAGTGACTCGTGGCTTGCCTTGGTCTCTTGGGA ATACTTTTCTAACTAGGGTTGCTCTCACCTGAGACATTC TCCACCCGCGGAATCTCAGGGTCCCAGGCTGTGGGCCA TCACGACCTCAAACCTGGCTCCTAATCTCCAGCTTTCCTG TCATTGAAAGCTTCGGAAGTTTACTGGCTCTGCTCCCGC CTGTTTTCTTTCTGACTCTATCTGGCAGCCCGATGCCAC CCAGTACAGGAAGTGACACCAGTACTCTGTAAAGCATC ATCATCCTTGGAGAGACTGAGCACTCAGCACCTTCAGC CACGATTTCAGGATCGCTTCCTTGTGAGCCGCTGCCTCC GAAATCTCCTTTGAAGCCCAGACATCTTTCTCCAGCTTC AGACTTGTAGATATAACTCGTTCATCTTCATTTACTTTC CACTTTGCCCCCTGTCCTCTCTGTGTTCCCCAAATCAGA GAATAGCCCGCCATCCCCCAGGTACCTGTCTGGATTCC TCCCCATTACCCACCTTGCCAGGTGCAGGTGAGGATG GTGCACCAGACAGGGTAGCTGTCCCCCAAATGTGCCC TGTGCGGGCAGTGCCCTGTCTCCACGTTTGTTCCTCCAG TGTCTGGCGGGGAGCCAGGTGACATCATAAATACTTGC TGAATGAATGCAGAAATCAGCGGTACTGACTTGTACTA TATTGGCTGCCATGATAGGGTTCTCACAGCGTCATCCAT GATCGTAAGGGGAGAATGACATTCTGCTTGAGGGAGGGA ATAGAAAGGGGGCAGGGAGGGGACATCTGAGGGCTTCA CAGGGCTGCAAAGGGTACAGGGATTGCACCAGGGCAG AACAGGGGAGGGTGTTC AAGGAAGAGTGGCTCTTAGCA GAGGCACTTTGGAAGGTGTGAGGCATAAATGCTTCCTT CTACGTAGGCCAACCTCAAACTTTCAGTAGGAATGTT GCTATGATCAAGTTGTTCTAACACTTTAGACTTAGTAGT AATTATGAACCTCACATAGAAAAATTCATCCAGCCAT ATGCCTGTGGAGTGGAATATTCTGTTTAGTAGAAAAAT CCTTTAGAGTTCAGCTCTAACCAGAAATCTTGCTGAAGT ATGTCAGCACCTTTTCTCACCTGGTAAGTACAGTATTT CAAGAGCACGCTAAGGGTGGTTTTTCATTTTACAGGGCT GTTGATGATGGGTAA AAAATGTTTCATTTAAGGGCTACC CCCGTGTTTAATAGATGAACACCACTTCTACACAACCCT CCTTGGTACTGGGGGAGGGAGAGATCTGACAAATACTG CCCATTCCCCTAGGCTGACTGGATTTGAGAACA
530	MKI67	3312497	ATGAGCGCACGGATGAATGGAGCTTACAAGATCTGTCT TTCCAATGGCCGGGGGGCATTGTGGTCCCCAAATTAAGGC TATTGGACATCTGCACAGGACAGTCCTATTTTTTGATGTC
531	MKI67	3312498	AGGAACAACATCCTCGTCTGTCCCAACACTGAGCAGG CACTCGGTAAAC
532	MKI67	3312499	ATTTGCTGGGTCTGAATCGGCTTCATAAACTCCACTGGG AGCACTGCTGGGCTCCTGGACTGAGAATAGTTGAACAC CGGGGGCTTTGTGAAGGAGTCTGGGCCAAGGTTTGCCC TCAGCTTTGCAGAATGAAGCCTTGAGGTCTGTCACCAC CCACAGCCACCCTACAGCAGCCTTA ACTGTGACACTTG CCACACTGTGTCGTCGTTTGTTCCTATGTCCTCC
533	MKI67	3312500	GGACAATGTGTGTGTCAAGAAAATAAGAACCAGAAGTC ATAGGGACAGTGAAGATATTTG

534	MKI67	3312502	CAGAAGAGTGCGAAGGTTCTCATGCAGAATCAGAAAG GGAAAGGAGAAGCAGGAAATTCAGACTCCATGTGCCTG AGATCAAGAAAGACAAAAAGCCAGCCTGCAGCAAGCA CTTTGGAGAGCAAATCTGTGCAGAGAGTAACGCGGAGT GTCAA
535	MKI67	3312503	GAGCCCGGAAACCCATACCTAGAGACAAAG
536	MKI67	3312504	TATCCCTGCGCTCCAGACGCCAAAAT
537	MKI67	3312506	AAGAGGCTGCGCTGCATGCCAGCACCAGAGGAAATTGT GGAGGAGCTGCCAGCCAGCAAGAAGCAGAGGGTTGCT CCCAGGGCAAGAGGCAAATCATCCGAACCCGTGGTCAT CATGAAGAGAAGTTTGAGGACTTCTGCAAAAAGAATTG AACCTGCGGAAGAGCTGAACAGCAACGACATGAAAAC CAACAAAGAGGAACACAAATTACAAGACTCGGTCCCTG
538	MKI67	3312507	CCCGTGCTCTAGAAGACCTGGTTGACTTCAAAGAGCTC TTCTCAGCACCAGGTCACACTGAAGAGTCAATGACTAT TGACAAAAACACAAAAATTCCCTGCAAATCTCCCCAC CAGAACTAACAGACACTGCCACGAGCACAAAGAGATG CCCCAAGACACGTCCCAGGAAAGAAGTAAAAGAGGAG CTCTCAGCAGTTGAGAGGCTCACGCAAACATCAGGGCA AAGCACACACACACAAAGAACCAGCAAGCGGTGAT GAGGGCATCAAAGTATTGAAGCAACGTGCAAAGAAGA AACCAAACCCAGTAGAAGAGGAACCCAGCAGGAGAAG GCCAAGAGCACCTAAGGAAAAGGCCCAACCCCTGGAA GACCTGGCCGGCTTCACAGAGCTCTCTGAAACATCAGG TCACACTCAGGAATCACTGACTGCTGGCAAAGCCACTA AAATACCCTGCGAATCTCCCCCACTAGAAGTGGTAGAC ACCACAGCAAGCACAAAGAGGCATCTCAGGACACGTGT GCAGAAGGTACAAGTAAAAGAAGAGCCTTCAGCAGTC AAGTTCACACAAACATCAGGGGAAACCACGGATGCAG ACAAAGAACCAGCAGGTGAAGATAAAGGCATCAAAGC ATTGAAGGAATCTGCAAAACAGACACCGGCTCCAGCAG CAAGTGTA ACTGGCAGCAGGAGACGGCCAAGAGCACC CAGGGAAAGTGCCCAAGCCATAGAAGACCTAGCTGGCT TCAAAGACCCAGCAGCAGGTCACACTGAAGAATCAATG ACTGATGACAAAACCACTAAAATACCCTGCAAATCATC ACCAGAACTAGAAGACACCGCAACAAGCTCAAAGAGA CGGCCCAGGACACGTGCCCAGAAAGTAGAAGTGAAGG AGGAGCTGTTAGCAGTTGGCAAGCTCACACAAACCTCA GGGGAGACCACGCACACCGACAAAGAGCCGGTAGGTG AGGGCAAAGGCACGAAAGCATTTAAGCAACCTGCAAA GCGGAAGCTGGACGCAGAAGATGTAATTGGCAGCAGG AGACAGCCAAGAGCACCTAAGGAAAAGGCCCAACCCC TGGAAGATCTGGCCAGCTTCCAAGAGCTCTCTCAAACA CCAGGCCACACTGAGGAACTGGCAAATGGTGCTGCTGA TAGCTTTACAAGCGCTCCAAAGCAAACACCTGACAGTG GAAAACCTCTAAAAATATCCAGAAGAGTTCTTCGGGCC CCTAAAGTAGAACCCGTGGGAGACGTGGTAAGCACCAG AGACCCTGTA

539	MKI67	3312508	GGAGAACTCTTAGCGTGCAGGAATCTAATGCCATCAGC AGGCAAAGCCATGCACACGCCTAAACCATCAGTAGGTG AAGAGAAAGACATCATCATATTTGTGGGAACTCCAGTG CAGAAACTGGACCTGACAGAGAACTTAACCGGCAGCA AGAGACGGCCACAACTCCTAAGGAAGAGGGCCAGGC TCTGGAAGACCTGACTGGCTTTAAAGAGCTCTTCCAGA CCCCTGGTCATACTGAAGAAGCAGTGGCTGCTGGCAAA ACTACTAAAATGCCCTGCGAATCTTCTCCACCAGAATC AGCAGACACCCCAACAAGCACAGAAGGCAGCCCAAG ACACCTTTGGAGAAAAGGGACGTACAGAAGGAGCTCTC AGCCCTGAAGAAGCTCACACAGACATCAGGGGAAACC ACACACACAGATAAAGTACCAGGAGGTGAGGATAAAA GCATCAACGCGTTTAGGGAACTGCAAAACAGAACTG GACCCAGCAGCAAGTGTAAGTGGTAGCAAGAGGCACCC AAAAACTAAGGAAAAGGCCCAACCCCTAGAAGACCTG GCTGGCTTGAAAGAGCTCTTCCAGACACCAGTATGCAC TGACAAGCCCACGACTCACGAGAAAACCTACCAAAATAG CCTGCAGATCACAAACCAGACCCAGTGGACACACCAACA AGCTCCAAGCCACAGTCCAAGAGAAGTCTCAGGAAAGT GGACGTAGAAGAAGAATTCTTCGCACTCAGGAAACGAA CACCATCAGCAGGCAAAGCCATGCACACACCCAAACCA GCAGTAAGTGGTGAGAAAAACATCTACGCATTTATGGG AACTCCAGTGCAGAACTGGACCTGACAGAGAACTTAA CTGGCAGCAAGAGACGGCTACAAACTCCTAAGGAAAA GGCCCAGGCTCTAGAAGACCTGGCTGGCTTTAAAGAGC TCTTCCAGACACGAGGTCACACTGAGGAATCAATGACT AACGATAAAACTGCCAAAGTAGCCTGCAAATCTTCACA ACCAGACCCAGACAAAAACCCAGCAAGCTCCAAGCGA CGGCTCAAGACATCCCTGGGGAAAGTGGGCGTGAAAG AAGAGCTCCTAGCAGTTGGCAAGCTCACACAGACATCA GGAGAGACTACACACACACACAGAGCCAACAGGAG ATGGTAAGAGCATGAAAGCATTTATGGAGTCTCCAAAG CAGATCTTAGACTCAGCAGCAAGTCTAACTGGCAGCAA GAGGCAGCTGAGAACTCCTAAGGGAAAGTCTGAAGTCC CTGAAGACCTGGCCGGCTTCATCGAGCTCTTCCAGACA CCAAGTCACACTAAGGAATCAATGACTAACGAAAAAAC TACCAAAGTATCCTACAGAGCTTCACAGCCAGACCTAG TGGACACCCCAACAAGCTCCAAGCCACAGCCCAAGAGA AGTCTCAGGAAAGCAGACACTGAAGAAGAATTTTTAGC ATTTAGGAAACAAACGCCATCAGCAGGCAAAGCCATGC ACACACCCAAACCAGCAGTAGGTGAAGAGAAAGACAT CAACACGTTTTTTGGGAACTCCAGTGCAGAACTGGACC AGCCAGGAAATTTACCTGGCAGCAATAGACGGCTACAA ACTCGTAAGGAAAAGGCCCAGGCTCTAGAAGAACTGAC TGGCTTCAGAGAGCTTTTCCAGACACCATGCACTGATA ACCCACGACTGATGAGAAAACCTACCAAAAAAATACTC TGCAAATCTCCGCAATCAGACCCAGCGGACACCCCAAC AAACACAAAGCAACGGCCCAAGAGAAGCCTCAAGAAA GCAGACGTAGAGGAAGAATTTTTAGCATTTCAGGAACT AACACCATCAGCAGGCAAAGCCATGCACACGCCTAAAG CAGCAGTAGGTGAAGAGAAAGACATCAACACATTTGTG GGGACTCCAGTGGAGAACTGGACCTGCTAGGAAATTT
-----	-------	---------	--

			ACCTGGCAGCAAGAGACGGCCACAAACTCCTAAAGAA AAGGCCAAGGCTCTAGAAGATCTGGCTGGCTTCAAAGA GCTCTTCCAGACACCAGGTCACACTGAGGAATCAATGA CCGATGACAAAATCACAGAAGTATCCTGCAAATCTCCA CAACCAGACCCAGTCAAAACCCCAACAAGCTCCAAGCA ACGACTCAAGATATCCTTGGGGAAAGTAGGTGTGAAAG AAGAGGTCCTACCAGTCGGCAAGCTCACACAGACGTCA GGGAAGACCACACAGACACACAGAGAGACAGCAGGAG ATGGAAAGAGCATCAAAGCGTTTAAGGAATCTGCAAAG CAGATGCTGGACCCAGCAAACCTATGGAACTGGGATGGA GAGGTGGCCAAGAACACCTAAGGAAGAGGCCCAATCA CTAGAAGACCTGGCCGGCTTCAAAGAGCTCTTCCAGAC ACCAGACCACACTGAGGAATCAACAACCTGATGACAAA ACTACCAAATAGCCTGCAAATCTCCACCACCAGAATC AATGGACACTCCAACAAGCACAAAGGAGGCGGCCCAAA ACACCTTTGGGGAAAAGGGATATAGTGGAAGAGCTCTC AGCCCTGAAGCAGCTCACACAGACCACACACACAGACA AAGTACCAGGAGATGAGGATAAAGGCATCAACGTGTTC AGGGAAACTGCAAAACAGAACTGGACCCAGCAGCAA GTGTAACCTGGTAGCAAGAGGCAGCCAAGAACTCCTAAG GGAAAAGCCCAACCCCTAGAAGACTTGGCTGGCTTGAA AGAGCTCTTCCAGACACCAATATGCACTGACAAGCCCA CGACTCATGAGAAAACCTACCAAATAGCCTGCAGATCT CCACAACCAGACCCAGTGGGTACCCCAACAATCTTCAA GCCACAGTCCAAGAGAAGTCTCAGGAAAGCAGACGTA GAGGAAGAATCCTTAGCACTCAGGAAACGAACACCATC AGTAGGGAAAGCTATGGACACACCCAAACCAGCAGGA GGTGATGAGAAAGACATGAAAGCATTTATGGGAACTCC AGTGCAGAAATTGGACCTGCCAGGAAATTTACCTGGCA GCAAAAGATGGCCACAAACTCCTAAGGAAAAGGCCCA GGCTCTAGAAGACCTGGCTGGCTTCAAAGAGCTCTTCC AGACACCAGGCACTGACAAGCCCACGACTGATGAGAA AACTACCAAATAGCCTGCAAATCTCCACAACCAGACC CAGTGGACACCCCAAGCAAGCACAAAGCAACGGCCCAA GAGAAACCTCAGGAAAGCAGACGTAGAGGAAGAATTT TTAGCACTCAGGAAACGAACACCATCAGCAGGCAAAGC CATGGACACACCAAAACCAGCAGTAAGTGATGAGAAA AATATCAACACATTTGTGGAAACTCCAGTGCAGAACT GGACCTGCTAGGAAATTTACCTGGCAGCAAGAGACAGC CACAGACTCCTAAGGAAAAGGCTGAGGCTCTAGAGGAC CTGGTTGGCTTCAAAGAA
540	MKI67	3312509	AACAACAGTTGAAGGCATCCCTGGGGAAAGTAGGTGTG AAAGAAGAGCTCCTAGCAGTCGGCAAGTTCACACGGAC GTCAGGGGAGACCACGCACACGCACAGAGAGCCAGCA GGAGATGGCAAGAGCATCAGAACGTTTAAGGAGTCTCC AAAGCAGATCCTGGACCCAGCAGCCCGTGTAACCTGGAA TGAAGAAGTGGCCAAGAACGCCTAAGGAAGAGGCCCA GTCACTAGAAGACCTGGCTGGCTTCAAAGAGCTCTTCC AGACACCAGGTCCCTCTGAGGAATCAATGACTGATGAG AAAACCTACCAAATAGCCTGCAAATCTCCACCACCAGA ATCAGTGGACACTCCAACAAGCACAAAGCAATGGCCTA AGAGAAGTCTC

541	MKI67	3312510	TGCAAACAGGTCAGGAAGGTCTACAGAGTTCAGGAATA TACAGAAGCTACCTGTGGAAAGTAAGAGTGAAGAAAC AAATACAGAAATTGTTGAGTGCATCCTAAAAAGAGGTC AGAAGGCAACACTACTACAACAAAGGAGAGAAGGAGA GATGAAGGAAATAGAAAGACCTTTTGAGACATATAAGG AAAATATTGAATTAAAAGAAAACGATGAAAAGATGAA AGCAATGAAGAGATCAAGAAGCTTGGGGGCAGAAATGT GCACCAATGTCTGACCTGACAGACCTCAAGAGCTTGCC TGATACAGAAGTCATGAAAGACACGGCACGTGGC
542	MKI67	3312511	CCCAGTGAAGGAGCAACCGCAGTTGACAAGCACATGTC ACATCGCTATTTCAAATTCAGAGA
543	MKI67	3312513	TAAAAACGTAGTCTTAGATCTTATAAATCTTTTGACTCT ACTGTTTTTTACTGTGTTAATGTTTGTGTTTGCTAACTTTG TTTATCTGCTG
544	MKI67	3312514	CGCAAACCTCTCCTTGTACCATAATAATAGGGAAAGCTC ATACTGAAAAAGTACATGTGCCTGCTCGACCCTACAGA GTGCTCAA
545	MKI67	3312515	AGCCTGTGGGCGAAGTTCACAGTCAA
546	MKI67	3312516	CATGGGCAGATGTAGTAAACTTGGTGCAAAACAAACA CAAACCTAAAGTCATAAAACATGGTCCTCAAAGGTC
547	MKI67	3312517	AAGAGAGTGTCTATCAGCCGAAGTCAACATGATATTTT ACAGATGATATGTTCCAAAAGAAGAAGTGGTGCTTCGG AAGCAAAT
548	MKI67	3312518	AAACAAGAGTCAGGTTTCAGAAATCCATGTGGAAGTGAA GGCACAAAGCTTGGTTATAAGCCCTCCAGCTCCTAGTC CTAGGAAAACCTCCAGTTGCCAGTGATCAACGCCGTAGG TC
549	MKI67	3312519	CCTTTGAAAAGAAGGCGTGTGTCCTTTGGTGGGCACCT AAGACCTGAACTATTTGATGAAAACCTTGCCTCCTAATA CGCCTCTCAAAGGGGAGAAGCCCCAACCAAAAGAAA GTCTCTGGTAATGCACACTCC
550	MKI67	3312520	GGACAGATGTGCTCTGGGTTACCTGGTCTTAGTTCAGTT GATATCAACAACCTTTGGTGATTCCATT
551	MKI67	3312521	TTGAGAGGAAGATCCAAAAGGATTCCCTCAG
552	MKI67	3312522	GAAGCTTTCAACTAGAAATCGAACACCAGCTAAAGTTG AAGATGCAGCTGACTCTGCCACTAAGCCAGAAAATCTC TCTTCCAAAACCAGAGGAAGTATTCCTACAGATGTGGA AGTTCTGCCTACGGAAACTGAAATTCACAATGAGC
553	MKI67	3312523	CCAGCGTTAAATTAGTGAGCCGTTATGGAGAATTGAAG TCTGTTCCCACTACACAATGTCTTGACAATAGCAAAAA AAATGAATCTCCCTTTTGGAAGCTTTATGAGTCAGTGAA GAAAGAGTTGGATGTAAAATCACAAAAAGAAAATGTC CTACAGTATTGTAGAAAATCTGGATTACAACTGATTA CGCAACAGAGAAAGAAAGTGCTGATGGTTTACAGGGG GAGACCCAACCTGTTGGTCTCGCGTAAGTCAAGACCAAA ATCTGGTGGGAGCGGCCACGCTGTGGCAGAGCCTGCTT CACCTGAACAAGAGCTTGACCAGAACAAAGGGGAAGGG AAGAGACGTGGAGTCTGTTTCAGACTCCCAGCAAGGCTG TGGGCGCCAGCTTTCCTCTCTATGAGCCGGCTAAAATG
554	MKI67	3312524	AGCCAGCACGTCGTGTCTCAAGATCTAGCTTCT
555	MKI67	3312526	TTCAGAATGGAAGGAAGTCAACTGAATTTC

556	MKI67	3312527	CCAACACAAGTAAATGGGTCTGTTATTGATGAGCCTGT ACGGCTAAAACATGGAGATGTAATAACTATTATTGATC GTTCTTCAG
557	MKI67	3312528	TGTGACATCCGTATCCAGCTTCCTGTTGTGTCAAAACAA CATT
558	MKI67	3312530	CCTGAGCCTCAGCACCTGCTTGTTTGGAAG
559	MKI67	3312531	CCCACGAGACGCCTGGTTACTATCAA
560	MKI67	3312532	TTTGCTTCTGGCCTTCCCCTACGGATTATACCTGGCCTT CCCCTACGGATTATACTCAACTTACTGTTTAGA
561	MKI67	3312533	GACTCGGTGGGAGCCGCTAGAGCCGGGCGCCCGGGGA CGTAGCCTGTAGGGCCACCGGGTCCCCGTCAGAGGCGG CGGCGGGAGCAGCGGGGACTGCAGGCCGGGGGTGCAGC GAACGCGACCCCGCGGGCTGCGGCCCGGTGTGTGCGGA GCGTGGCGGGGCGCAGCTTACCGGGCGGAGGTGAGCGC GGCGCCGGCTCCTCCTGCGGCGGACTTTGGGTGCGACT TGACGAGCGGTGGTTCGACAAGTGGCCTTGCGGGCCGG AT
562	TMEM45 B	3356039	TGCAGACGGCTGCGAGGCGCTGGGC
563	TMEM45 B	3356044	GCAGGGCTGAGACTATCTTCTGCTCAGGAA
564	TMEM45 B	3356053	TCTCATGTTTTTCTATAAGCAGTTAAGAGAAGCCACACA GCATCCTGAACACTTTGCTTTCT
565	TMEM45 B	3356054	ATGGCAAATTTCAAGGGCCACGCGCTTCCAGGGAGTTT CTTCCTGATCATTGGGCTGTGTTGGTCAGTGAAGTACCC GCT
566	TMEM45 B	3356055	GTACTIONTAGCCACACGCGGAAGAACAGCCCACTACATT ACTATCAG
567	TMEM45 B	3356056	CGTCTCGAGATCGTCGAAGCCGCAATTAGGACTTTGTTT TCCGTCCTG
568	TMEM45 B	3356057	GTCATTTGGTCTAGGGAATCTCCTCATCATACCCAGAAC CTTTAATTCATTTTCTGAGCCCTGTGAAATAGATGTTCC CACTGGCAGAGATAATAGGGCAACAATTCCTGATGGC CACTAGACTATTTTATCGTAACATCCATTGTGTACAGAG CTTTATAATACTAACGGTTGACAGCTCTCACATCATG
569	TMEM45 B	3356058	CACCATGTACCTATTCTTTGCAGTCTCAGGAATTGTTGA CATGCTCACCTATCTGGTCAGCCACGTTCCCTTGG
570	TMEM45 B	3356061	AACCGGCCTCCGCTGGACCAGCACATCCACTCACTCCT GCTGTATGCTCTGTTTCGGAGGGTGTGTTAGTATCTCCCT AGAGGTGATCTTCCGGGACCACATTGTGCTGGAACCTTT CCGAACCAGTCTCATC
571	TMEM45 B	3356063	ATTGGGTTTGTGCTGTTCCACCTTTTGGAACACCCGAA TGGGACCAGAAGGATGATGCCAACCTCATGTTTCATCAC CATGTGCTTCTGCTGGCACTACCTGGCTGCCCTCAGCAT TGTGGCCGTCAACTATTCTCTTG
572	TMEM45 B	3356065	CCTTTTGACTCGGATGAAGAGACACGGAAGGGGAGAA ATCATTGGAATTCAGAAGCTGAATTCAGATGACACTTA CCAGACCGCCCTCTTGAGTGGCTCAGA

573	TMEM45 B	3356066	TAAAGTCTGTGTTGGTATAGTACCCTTCATAAGGAAAA ATGAAGTAATGCCTATAAGTAGCAGGCCTTTGTGCCTC AGTGTCAAGAGAAATCAAGAGATGCTAAAAGCTTTACA ATGGAAGTGGCCTCATGGATGAATCCGGGGGTATGAGCC CAGGAGAACGTGCTGCTTTTGGTAACTTATCCCTTTTTC TCTTAAGAAAGCAGGTACTTTCTTATTAGAAATATGTTA GAATGTGTAAGCAAACGACAGTGCCTTTAGAATTACAA TTCTAACTTACATATTTTTTTGAAAGTAAAATAATTCACA AGCTTTGGTATTTTAAAATTATTGTTAAACATATCATAA CTAATCATACCAGGGTACTGCAATACCACTGTTTATAA GTGACAAAATTAGGCCAAAGGTGATTTTTTTTTTAAATCA GGAAGCTGGTTACTGGCTCTACTGAGAGTTGGAGCCCT GATGTTCTGATTCTTCAAAGTCACCCTAAAAGAAGATCT GACAGGAAAGCTGTATAATGAGATAGAAAAACGTCAG GTATGGAAGGCTTTCAGTTTTAATATGGCTGAAAGCAA AGGATAACGAATTCAGAATTAGTAATGTAAAATCTTGA TACCCTAATCTTGCTTCTGGATCTGTTCTTTTTTTAAAAA AACTTCCTTCACCGCGCCTATAATCCTAGCACTTTGGGA GGCCGAGGCAGGCAGATCACGGGGTCAGGAGATCAAG ACCATCCTGGCTAACATGGTGAAACCCCGTCTCTACTG AAAATACAAAAAATTAGCCGGGTGTGGTGGCGGGCGCC TGTAGTTCCAGCTACTCGGGAGGCTGAGGCAAGAGAAT GGCATGAACCCGGTAGGGGAGCTTGCAGTGAGCCCAGA TCATGCCACTGTACTCCAGCCTAGGTGACAGAGCAAGA CTCTGTCTCAAAAACAAGCAAACAGACTTCCTTCAACA AATATTTATTAAATATCCACTTTGCAACAGCACTGAAAT GGCTGTAAGGACTCCTGAGATATGTGTCCAGCAAGG
574	PGR	3388371	AGTGTTCCCGTCTTCTCCGAGCTTAGAGTTGGATGGGGA ATAAAGACAGGTAAACAGATAGCTACAATATTGTACTG TGAATGCTTATGCTGGAGGAAGTACAGGGAAGTATTGG AGCACCTAAGAGGAGCACCTACCTTGAATTTAGGGGTT AGCAGAGGCATCCTGAAAAAAGTCAAAGCTAAGCCAC AATCTATAAGCAGTTTAGGAATTAGCAGAACGTGCGTG GTGAGGAGATGCCAAAGGCAAGAAGAGAAGAGTATTC CAAACAGGAGGGATTCCAAAGAGAGAAGAGTATCCCA AACAAACATTTGCACAAACCTGATGGGGAGAGAGAATGT GGGGTGGGGATGGATGATGAGACTGAAGAAGAAAGCC AGGTCTAGATAATCAGTGGCCTTGTACACCATGTTAAA GAGTGTAGACTTGATTCTGTTGTAAACAGGAAAGCAGC ACAATTCATATGAATATTTTAGAAGACTCCCCTGGAA TATGGAGAATAAAAGTTGGAGATGACTAATCCTGGAAGC AGGGAGAACATTTTTGAGGAAGTTGCACTATTTTGGTG AAAATGATGATCATAAACATGAAGAATTGTAGGTGATC ATGACCTCCTCTCTAATTTTCCAGAAGGGTTTTGGAAGA TATAACATAGGAACATTGACAGGACTGACGAAAGGAG ATGAAATACACCATATAAATTGTCAAACACAAGGCCAG ATGTCTAATTATTTTGCTTATGTGTTGAAATTACAAATT TTTCATCAGGAAACCAAAAACCTACAAAACCTTAGTTTTC CCAAGTCCCAGAATTCTATCTGTCCAAACAATCTGTACC ACTCCACCTATATCCCTACCTTTGCATGTCTGTCCAACC TCAAAGTCCAGGTCTATACACACGGGTAAGACTAGAGC AGTTCAAGTTTCAGAAAATGAGAAAGAGGAACTGAGTT

			GTGCTGAACCCATACAAAATAAACACATTCTTTGTATA GATTCTTGGAACCTCGAGAGGAATTCACCTAACTCATA GGTATTTGATGGTATGAATCCATGGCTGGGCTCGGCTTT TAAAAAGCCTTATCTGGGATTCCCTTCTATGGAACCAAGT TCCATCAAAGCCCATTATAAAAGCCTACATTAAAAACAA AATTCTTGCTGCATTGTATACAAATAATGATGTCATGAT CAAATAATCAGATGCCATTATCAAGTGGAATTACAAAA TGGTATACCCACTCCAAAAAAAAAAAAAAAAAGCTAAATT CTCAGTAGAACATTGTGACTTCATGAGCCCTCCACAGC CTTGGAGCTGAGGAGGGAGCACTGGTGAGCAGTAGGTT GAAGAGAAAACCTTGGCGCTTAATAATCTATCCATGTTTT TTCATCTAAAAGAGCCTTCTTTTTTGGATTACCTTATTCA ATTTCCATCAAGGAAATTGTTAGTTCCACTAACCAGAC AGCAGCTGGGAAGGCAGAAGCTTACTGTATGTACATGG TAGCTGTGGGAAGGAGGTTTCTTTCTCCAGGTCCTCACT GGCCATACACCAGTCCCTTGTTAGTTATGCCTGGTCATA GACCCCCGTTGCTATCATCTCATATTTAAGTCTTTGGCT TGTGAATTTATCTATTCTTTTCAGCTTCAGCACTGCAGAG TGCTGGGACTTTGCTAACTTCCATTTCTTGCTGGCTTAG CACATTCCTCATAGGCCCAGCTCTTTTCTCATCTGGCCC TGCTGTGGAGTCACCTTGCCCCCTTCAGGAGAGCCATGG CTTACCACTGCCTGCTAAGCCTCCACTCAGCTGCCACCA CACTAAATCCAAGCTTCTCTAAGATGTTGCAGACTTTAC AGGCAAGCATAAAAAGGCTTGATCTTCCTGGACTTCCCTT TACTTGTCTGAATCTCACCTCCTTCAACTTTCAGTCTCA GAATGTAGGCATTTGTCCTCTTTGCCCTACATCTTCCTT CTTCTGAATCATGAAAGCCTCTCACTTCCTCTTGCTATG TGCTGGAGGCTTCTGTCAGGTTTTAGAAATGAGTTCTCAT CTAGTCCTAGTAGCTTTTGATGCTTAAGTCCACCTTTTA AGGATACCTTTGAGATTTAGACCATGTTTTTTCGCTTGAG AAAGCCCTAATCTCCAGACTTGCCTTTCTGTGGATTTC AAGACCAACTGAGGAAGTCAAAAGCTGAATGTTGACTT TCTTTGAACATTTCCGCTATAACAATTCCAATTCTCCTC AGAGCAATATGCCTGCCTCCAAGTACCAGGAGAAAGG TCCAGTGCCAAAGAGAAAAACACAAAGATTAATTATTT CAGTTGAGCACATACTTTCAAAGTGGTTTGGGTATTTCAT ATGAGGTTTTCTGTCAAGAGGGTGAGACTCTTCATCTAT CCATG
575	PGR	3388372	GCCTTGTAAGTAGCCATGGAATGTCAACCTGTAACCTTA AATTATCCACAGATAGTCATGTGTTTGATGATGGGCACT GTGGAGATAACTGACATAGGACTGTGCCCCCCTTCTCT GCCACTTACTAGCTGGATGAGATTAAGCAAGTCATTTA ACTGCTCTGATTAAACCTGCCTTTCCCAAGTGCTTTGTA ATGAATAGAAATGGAAACCAAAAAAAAAACGTATACAGG CCTTCAGAAATAGTAATTGCTACTATTTTGTTTTTCATTA AGCCATAGTTCTGGCTATAATTTTATCAAACCTCACCAGC TATATTCTACAGTGAAAGCAGGATTCTAGAAAGTCTCA CTGTTTTATTTATGTCACCATGTGCTATGATATATTTGGT TGAATTCATTTGAAATTAGGGCTGGAAGTATTCAAGTA ATTTCTTCTGCTGAAAAAATACAGTGTTTTGAGTTTAGG GCCTGTTTTATCAAAGTTCTAAAGAGCCTATCACTCTTC CATTGTAGA

576	PGR	3388373	GTCCTATCTACTAATGTCTCCATTACTATTTAGTCATCA TAACCATTATCTTCATTTTACATGTCGTGTTCTTTCTGGT AGCTCTAAAATGACACTAAATCATAAGAAGACAGGTTA CATATCAGGAAATACTTGAAGGTTACTGAAATAGATTTC TTGAGTTAATGAAAATATTTTCTGTAAAAAGGTTTGAA AAGCCATTTGAGTCTAAAGCATTATACCTCCATTATCAG TAGTTATGTGACAATTGTGTG
577	PGR	3388374	GCAGTAATTTGCCTTCTCCTAGAGTTTACCTGCCATTTT GTGCACATTTGAGTTACAGTAGCATGTTATTTTACAATT GTGACTCTCCTGGGAGTCTGGGAGCCATATAAAGTGGT CAATAGTGTTTGCTGACTGAGAGTTGAATGACATTTTCT CTCTGTCTTGGTATTACTGTAGATTTTCGATCATTCTTTGG TTACATTTCTGCATATTTCTGTACCCATGACTTTATCACT TTCTTCTCCCATGCTTTATCTCCATCAATTATCTTCATTA CTTTTAAATTTTCCACCTTTGCTTCCTACTTTGTGAGATC TCTCCCTTTACTGACTATAACATAGAAGAATAGAAGTG TATTTTATGTGTCTTAAGGACAATACTTTAGATTCCTTG TTCTAAGTTTTTAAACTGAATGAATGGAATATTATTTCT CTCCCTAAGCAAAATTCCACAAAACAATTATTTCTTATG TTTATGTAGCCTTAAATTGTTTTGTACTGTAAACCTCAG CATAAAAACCTTTCTTCATTTCTAATTTCAATCAACAAAT ATTGATTGAATACCTGGTATTAGCACAAAGAAAATGTG CTAATAAGCCTTATGAGAATTTGGAGCTGAAGAAAGAC ATATAACTCAGGAAAGTTACAGTCCAGTAGTAGGTATA AATTACAGTGCCTGATAAATAGGCATTTTAATATTTGTA CACTCAACGTATACTAGGTAGGTGCAAAACATTTACAT ATAATTTTACTGATACCCATGCAGCACAAAGGTACTAA CTTTAAATATTAAATAACACCTTTATGTGTCAGTAATTC ATTTGCATTAAATCTTATTGAAAAGGCTTTCAATATATT TTCCCCACAAATGTCATCCCAAGAAAAAAGTATTTTAA ACATCTCCCAAATATAATAGTTACAGGAAATCTACCTCT GTGAGAGTGACACCTCTCAGAATGAACTGTGTGACACA AGAAAATGAATGTAGGTCTATCCAAAAAAAACCCCAAG AAACAAAAACAATATTATTAGCCCTTTATGCTTAAGTG ATGGACTC
578	PGR	3388375	TAGGTAACCTCCCTTTGTGTCAATTATATTTCCAAAAATG AACCTTTAAAATGGTATGCAAAATTTTGTCTATATATAT TTGTGTGAGGAGGAAATTCATAACTTTCCTCAGATTTTC AAAAGTATTTTAAATGCAAAAAATGTAGAAAGAGTTTA AAACCACTAAAATAGATTGATGTTCTTCAAACCTAGGCA AAACAACCTCATATGTTAAGACCATTTTCCAGATTGGAA ACACAAATCTCTTAGGAAGTTAATAAGTAGATTCATAT CATTATGCAAATAGTATTGTGGGTTTTGTAGGTTTTTAA AATAACCTTTTTTGGGGAGAGAATTGTCCTCTAATGAG GTATTGCGAGTGG
579	PGR	3388376	CAAACAACCTTCATCTGTACTGCTTGAATACATTTATCCA GTCCCGGGCACTGAGTGTTGAATTTCCAGAAATGATGT CTGAAGTTATTGCTGCACAATTACCCAAGATATTG
580	PGR	3388377	ATGAGGTCAAGCTACATTAGAGAGCTCATCAAGGCAAT TGGTTTGAGGCAAAAAGGAGTTGTGTGCGAGCTCACAGC GTTTCTATCAACTTA
581	PGR	3388378	TGGAAGGGCTACGAAGTCAAACCCA

582	PGR	3388379	CAGGAGTTTGTCAAGCTTCAAGTTAGCCAAGAA
583	PGR	3388382	TATTTTGCACCTGATCTAATACTAAATGA
584	PGR	3388383	CTTACATATTGATGACCAGATAACTCTCATTTCAGTATTC TTGGATGAGCTTAATGGTGTGTTGGTCTAGGATGGA
585	PGR	3388387	CAGCCAGTGGGCGTTCCAAATGAAAGCCAAGCCCTAAG CCAGAGATTCACTTTTTTCACCAGGTCAAGACATACAGTT GATTCCACCACTGATCAACCTGTTAATGAGCATTGAAC CAGATGTGATCTATGCAGGACATGACAACACAAAACCT GACACCTCCAGTTCTTTGCTGACAAGTCTTAATCAACTA GGCGAGAGGCAACTTCTTTCAGTAGTCAAGTGGTCTA
586	PGR	3388388	ATGGAGTTTATATATATTTACATGAATTTCTTTTTTTTCT TCTCTG
587	PGR	3388389	AGACCATTGGCGTACCACCAGTTTGTGGAGGGAAGTGG AAAAACTGGAATACACATGCCCCATCCAAAAGCAACCA TTGCAACTAAACTTTAACAGATTGTTGCCACCTAAGTAA TTCACGGATGGTCTCATAATTCTGGTCAGCATTGTCTGA GCCAAACAAAATGTATCTATGGGCATGATCAGATACTA GAGCCAGCAGATTGCAACCTCTGCTTAGATAAATTGCAG GTATCAGCCTTCCCTTGGCTAAACAGCTACTTCATACTG ATAAGTAGCCCTTGCCTGGCACAAGCAGGTGGGGCTG AATCCAGCCTGATATCACATCACCACAACCTTTCTCTAAT TCTCCTCAAGGCGTCTGTGAACTACCA
588	PGR	3388393	TGACTGCATCGTTGATAAAATCCGCAGAAAAAACTGCC CAGCATGTGCGCCTTAGAAAGTGCTG
589	PGR	3388407	CAGGCTGTCATTATGGTGTCTTACCTGTGGGAGCTGTA AGGTCTTCTTTAAGAGGGCAATGGAA
590	PGR	3388408	AGCCAGAGCCCACAATACAGCTTCGAGTCATTACCTCA GAAGATTTGTTTA
591	PGR	3388410	TCGGCTACCAGGCCGCGGTGCTCAAGGAGGGCCTGCCG CAGGTCTACCCGCCCTATCTCAACTACCTGA
592	PGR	3388411	GCCGCCCTGCAAGGCGCCGGGCGCGAGCGGCTGCCTGC TCCCGCGGGACGGCCTGCCCTCCACCTCCGCCTCTGCCG CCGCCGCCGGGGCGGCCCCCGCGCTCTACCCTGCACTC GGCCTCAACGGGCTC
593	PGR	3388412	GTGCCTCAGTCTCGTCTGCGTCCTCCTCGGGGTCGACCC TGGAGTGCATCCTGTACAAAGCGGAGGGGCGCG
594	PGR	3388413	CTGCCTCTCAATCACGCCTTATTGGCAGCCCGCACTCGG CAGCTGCTGGAAGACGAAAGTTACGACGGCGGGGCCG GGGCTGCCAGCGCCTTTGCCCCGCCGCGGAGTTCACCC TGTGCCTCGTCCACCCCGGTGCTGTAGGCGACTTCCCC GACTGCGCGTACCCGCCCGACGCCGAGCCCAAGGACGA CGCGTACCCTCTCTATAGCGACTTCCAGCCGCCCGCTCT AAAGATAAAGG

595	PGR	3388414	TTGCCTGAAGTTTCGGCCATACCTATCTCCCTGGACGGG CTACTCTTCCCTCGGCCCTGCCAGGGACAGGACCCCTCC GACGAAAAGACGCAGGACCAGCAGTCGCTGTCGGACG TGGAGGGCGCATATTCCAGAGCTGAAGCTACAAGGGGT GCTGGAGGCAGCAGTTCTAGTCCCCCAGAAAAGGACAG CGGACTGCTGGACAGTGTCTTGGACACTCTGTTGGCGC CCTCAGGTCCCGGGCAGAGCCAACCCAGCCCTCCCGCC TGCAGAGGTCACCAGCTCTTGGTGCCTGTTTGGCCCCGAA CTTCCCGAAGATCCACCGGCTGCCCCCGCCACCCAGCG GGTGTGTGTCCTCGCTCATGAGCCGGTCCGGGTGCAAGG TTGGAGACAGCTCCGGGACGGCAGCTGCCCATAAAGTG CTGCCCCGGGGCCTGTACCAGCCCGGCAGCTGCTGCT CCCGGCCTCTGAGAGCCCTCACTGGTCCGGGGGCCCCAG TGAAGCCGTCTCCGCAGGCCGCTGCGGTGGAGGTTGAG GAGGAGGATGGCTCTGAGTCCGAGGAGTCTGCGGGTCC GCTTCTGAAGGGCAAACCTCGGGCTCTGGGTGGCGCGG CGGCTGGAGGAGGAGCCGCGGCTGTCCCGCCGGGGGC GGCAGCAGGAGGCGTCGCCCTGGTCCCCAAGGAAGATT CCCGCTTCTCAGCGCCCAGGGTCGCCCTGGTGGAGCAG GACGCGCCGATGGCGCCCCGGGCGCTCCCCGCTGGCCAC CACGGTGATGGATTTCATCC
596	PGR	3388415	TGAAATCTACAACCCGAGGCGGCTAGTGCTCCCGCACT ACTGGGATCTGAGATCTTCGGAGATGACTGTGCCCCGC AGTACGGAGCCAGCAGAAGTCCGACCCTTCCTGGGAAT GGGCTGTACCGAGAGGTCCGACTAGCCCCAGGGTTTTA GTGAGGGGGCAGTGGAACCTCAGCGAGGGACTGAGAGC TTCACAGCATGCACGAGTTTGATGCCAGAGAAAAAGTC GGGAGATAAAGGAGCCGCGTGTCCTAAATTGCC
597	MDM2	3421302	CGCACCGAGGCACCGCGGCGAGCTTGGCTGCTTCTGGG GCCTGTGTGGCCCTGTGTGTCGGAAAGATGGAGCAAGA AGCCGAGCCCGAGGGGCGGCCGCGACCCCTCTGACCGA GATCCTGCTGCTTTCGCAGCCAGGAGCACCGTC
598	MDM2	3421303	GTACGAGCGCCAGTGCCCTGGCCCGGAGAGTGGA
599	MDM2	3421304	GAGGCCCAGGGCGTCGTGCTTCCGCGCGCCCCGT
600	MDM2	3421305	ACTCCAAGCGCGAAAACCCCGGATGGTGAGGAGCA
601	MDM2	3421306	TTCAGTGGCGATTGGAGGGTAGACCTGTGGGCACGGAC GCACGCCACTTTTTCTCTG
602	MDM2	3421307	TGTACCTACTGATGGTGCTGTAACCACCTC
603	MDM2	3421310	ACCAAAGCCATTGCTTTTGAAGTTATTAAA
604	MDM2	3421311	GTCTGTTGGTGCACAAAAAGACACTTATACTATGAAA
605	MDM2	3421312	GACTTCTTGGGCATCCCTGGATCCCAGGTTAAGAAGCTC TGCACTAGAGATACATGA
606	MDM2	3421313	GTACAGTATACTGATCTTTCTGGGATAG
607	MDM2	3421314	GGGCTCAAGGGATCTGCTTACCTCGGCCTCCTAA
608	MDM2	3421315	TATGACTAAACGATTATATGATGAGAA
609	MDM2	3421316	CTTCTAGGAGATTTGTTTGGCGTGCCAAGCTTCTCT
610	MDM2	3421317	ATTGTAAAAAGCCATCTGGGCTAACATTTC
611	MDM2	3421321	AGGTAAATTGCATAAGGGTTTGTGTTAGACTGATAGC ATATCTACTGAGTAGCGCCCCGCGCCCCCGCCCCACC ACCAAGTTTCTGATCCTTTT
612	MDM2	3421322	AATCATCGGACTCAGGTACATCTGTGA

613	MDM2	3421323	GTGAGAACAGGTGTCACCTTGAAGGTGGGAG
614	MDM2	3421325	TCACATTTGGTTTCTAGACCATCTACCTCATCTAGAAGG AGAGCAATTAGTGAGACA
615	MDM2	3421326	ATATTTATTTGACGCATTCACACAGCTTTTTTGATATTCTT TCTCTAATGAAATTAGTGCTTTTAGACTTAAT
616	MDM2	3421328	TCAGATGAATTATCTGGTGAACGACAAAGAAAACGCCA CAAATCTGATAGT
617	MDM2	3421329	AAAGCCTGGCTCTGTGTGTAATAAGGGAGATATGTTGT GAAAGAAGCAGTAGCAGTGAATCTACAGGGACGCCA
618	MDM2	3421334	TTCAGTTTCAGATCAGTTTAGTGTAGAATTTGAAGTTGA ATCTCTCGACTCAGAAGATTATAGCCTTAGTGAAGA
619	MDM2	3421336	TGCAATGAAATGAATCCCCCCCCTTCCATCACATTGCAAC AGATGTTGGGCCCTTCGTGAGAATTGGCTTCCTGAAGA
620	MDM2	3421337	CTATAGTGAATGATTCCAGAGAGTCATGTGTTGAGGAA AATGATGATAAAATTACACAAGCTTCACAAT
621	MDM2	3421338	TCTCAGCCATCAACTTCTAGTAGCA
622	MDM2	3421339	AAGAGAGTGTGGAATCTAGTTTGCCCCTTAATGCCATT GAA
623	MDM2	3421340	TCAAGGTCGACCTAAAAATGGTTGCATTGTCC
624	MDM2	3421341	ATATTTCTAACTATATAACCCTAGGA
625	MDM2	3421342	ACCGCGTCCGGCCTAAATGTCACTTAGTACCTTTGATAT AAAGAGAAAATGTGTGAAAGATTTAGTTTTTTGTTTTT TGTTTGTTTGTTTGTTTGTTTGTTTGAGATGAGTCTCTC TGTCGCCCAGGCTGGAGTGCAGTGTGATGATCTAGCAG TCTCCGCTTCCCGGGTTCAAGCCATTCTCCTGGCTCAGC CTCTGGAGCAGCTGGGATTACAGGCATGCACCACCATG CCCAGCTAATTTTTGTATTTTAGTAGAGATAGGGTTTC ACCATGTTGGCCAGGCTGGTCACGAACTCCTGACCTCA AGTGAGGTCACCCGCCTCGGCCTCCCGAAGTGCTGGGA TTGCAGATGTGAGCCACCATGTCCAGCCAAGAATTAGT ATTTAAATTTTAGATACTCTTTTTTTTTTTTTTTTTTT TTTTTGAGACAGAGTCTTGCTCCATCACCCATGCTAGAG TGCAGTGGAGTGATCTCGGCTCACTGCAACTTCCGCCTT CTGGGTTCAGCTATTCTCCTGCCTCAGCCTTCCAAGTA ACTGGGATTACAGGCATGTACCACCATAACCAGCTGATT TTTTTGATTTTTTAGTAAAGACAGGGTTTCACCATGTTA GCCAGGCTGATCTTGAATCCTAAACTCAAGTGATCTA CTCACCTCAGCCTCCCAAAATGCTGGGATTACAGATGT GAGGCACCTGGCCTCAGATTTTTGA
626	MDM2	3421343	TGGAGGCCCATCCGAGCTCAGCACTGA
627	MDM2	3421344	ACAAGCCTGTCAAATATCTGCAAGAACTATGGAATAAA ACTACTGATGCAGTGAAGACAGTTGAAAAGATCAAACA AATGCCAAGCTATATTTATAATGAACAAATTCAAGAAA AAGGACTACGGAAAGTTCAGGACATCAAAGAAGTCAG GCAAACTCATCTTGACCCCTGTTGCAGGCAAAGGAAC GCAGCTGGAAGAAAAGATGATATAACAGTTAACAGGA TGCAGACATGGCAGAGGTTTCCTAAAAATCTCATTATCT ATAACCATTTCTATATTTACATTTGAAAATCTCCTTTGG AGACTTAGAACCTCTAAATTATTGACTTATTTTTTATAT AAGGTCACCTCCGATGAAAGGTGATTACA

628	MDM2	3421345	TGAGAGCCGAATAAGGTTTGCCTGAAATAACTGACACT ATATAATTTCTGCTTTGGCAAATACTAAGTTCTAACTTG TCATTCCTGGTAGAACAAGCTTTATTTTTTCGAGCCTAGC AATGATCTAGAAGCAGATGTTATCTCAGTGCCTTTTG
629	MDM2	3421346	CTGATGGGTGTGCTAATTACACTGATTTGATCAATACCC ATTGTATGTGAAACAGTACATACACCATATTTACAATTA TGTATTTAACATTTAAAATTTCTAATATAAGTATCTCTC AAACTGTGGATTAACTTCTTGATTTATATTTAAATATGA ATCTTAAGCAAAACAGTGAAAATAACCATCTTGATTTA GTGTTTTTCTCCCATATGTGAATTGTATATAC
630	MDM2	3421347	GCTTAGAATAGGACTGAGGTAATTCTGCACAGCAACTT TACTAATGGTA
631	MDM2	3421348	GTCCTCCAAGCATTATTTGGAGTTGATAATACTTCAGCT ACAACCAAGCAGAATCTCTTTTTTTTGGGA
632	MDM2	3421349	GATAATACTTCAGCTTCAATTTGGAGTTGATAATATTTT AGCTAGAACCTAGTAGAATC
633	MDM2	3421350	CACTTGATATATGGAGGCAGTGACAGCTATTTTTACAA AATTTAAATCTGCAAATGGATTCAACATGTTTATGGGTT ATTAAAATTGTCTGATTTCTTAGGTTCTTTATAGTACAC GTGTTGA
634	MDM2	3421351	TGGGAGCCTCCAATGAGAGCAACTTGAGAGAATGATGT TGCAAGTTAGTAGGAGTAAGAAATGCTGTGTTCTCCCT GTCTTCTCTTAGGTCACATGGCAGCCTGGCCTAAGTGAT CGTGAATGGTCTATAAGGGAGGTAGCTGGGACAGGGA GGGGAGTTTGGGCTAGCCACCGTACCACTTGTCAGCGT GAAAAGTAAGATTGTAATTGCCTGTTTAGTTTTCTGCCT CATCTTTGAAAGTTCCACCAAGCTGGGAACCTCTTGATT GTGAGGCACAAATGTAAGTACATCAGAAAAAAACAAA AAAAGTGGCTTTAAAGCAGGAGCTTGTGGGCCCTAAG CCAGACGGGGACTAGCTTTTGGCATTATATAATTAAGA TTTTTTAAATCCTTAATAAGGGTTTTATTTTATTTTATT TATTTTTTGAGACGGAGTCTTGCTCTGTGGCTCAGGCTG GAGTACAGTGGTGCAATCTTGGCTCACTGCAACCTCTG CCTCCTGGCTGTGTTCAAGTGGTTCT
635	MDM2	3421359	GAAACATTAAGAATACCATATGAGTAAATTAAACACTT TGGCTCTTTTCGGAAAAAACAGATGAGCTCTTATATTT TAAAGTTTGGTTTTGACAGAAAAAAATTCCTAGATTTTT TGGTTAATAAAAACTTTATTAGATAGATTAAATTGTGAT G
636	MDM2	3421361	AGGGAACCTTCTGCTTAAGAGGCTTCTATGTAATGAAAT TCTCTTGAAAACAGAGAAACTATTTCCCTGTTTATTTTCT AAATTGAGACGTCACTTTTTTAAAAATTGGTACCTGTAAT TTAGCCATTTCTACTCAGCAATGTCTCATTTAAACTAT TATTTGTTTAGCGTGTTTCAAAGAGCAGATGTAAGCTTG AGCCCATCCTCTGTCCTATGACTAAGTCGATATTAGCAG GGGTTAGGACTGTTAGTTTTCCAGTTCCTACTGGAGGCA AATTCTT
637	KRT5	3455207	CCTTTTCTGGAGAGTAGTCTAGACCAAGCCAATTGCAG AACCACATTCTTTGGTTCCCAGGAGAGCCCCATTCCCAG CCCCTGGTCTCCCGTGCCGCAGTTCTATATTCTGCTTCA AATCAGCCTTCAGGTTTCCCACAGCATGGCCCCCTGCTGA

			CACGAGAACCCCAAAGTT
638	KRT5	3455208	TCTTGCCGGAGGTAGCAGTGGAAGCTACTACTCCAGCA GCAGTGGGGGTGTCGGCCTAGGTGGTGGGCTCAGTGTG GGGGGCTCTGGCTTCAGTGCAAGCAGTGGCCGAGGGCT GGGGGTGGGCTTTGGCAGTGGCGGGGGTAGCAGCTCCA GCGTCAAATTTGTCTCCAC
639	KRT5	3455211	ACTCAGTGGAGAAGGAGTTGGACCAGTCAACATCT
640	KRT5	3455212	AGGTCAATCCCTCTTCATTGGAAAATCCCTCTGGAGAGT TCTCCCTTCCTTTAACTTAAGCAGCTTTTGGGTGTACAG ACTCCTGGCTTATGGAATGAACTCGAATCATGAGGATG GGAGTTAGCCACATAGACTAATGCTGTCTTTTTGGGAG CTGTAAACCCTTAATTCA
641	KRT5	3455214	CAAGATGGCCTTCAGCTGATAAAGCGAAGCTGCTCTAC TGTGGGGTGTACAACACACATACATGAGATCAGTGACT TGTGCGTGATAATGACACATCATCAACACTATTTTCAGTC TGACTCATGGCCATATAGCTGACCTCAACTCACTTTTCT GGTCTCTTTTCCCCCACC GGTTTCCTGGGCACTGGCTG TCCTCCAAGCACCTGAGCAACTCAGCAATCTTCTTGACA CTTGTGCCTTTTCTGCTTTTGCTCACGTCCTTTGCTCAAC CTCAATATCCATGTCATG
642	KRT5	3455215	TGCGCCAATCTGCAGAACGCCATTGCGGATGCCGAGC
643	KRT5	3455216	CTTTTGCTAAACACACGCAGCTAGATCCAGTACCAGTG TTTCAGTGTCTGCCACCCACGATGTACTGGTTTCTCTC TGGGATTCATGATAGTTTGGTTTGTCTGACCCAGAACT CAG
644	KRT5	3455217	AGCTGGCCGGCATGGCGATGACCTCCGCAACACCAAGC ATGAGATCTCTGAGATGAACCGGATGATCCAGAGGCTG AGAGCCGAGATTGACAATGTCAAGA
645	KRT5	3455219	CAGATGCAGACGCATGTCTCTGACACCTCAGTGGTCCT CTCCATGGACAACAACCGCAACCTGGACCTGGATAGCA TCATCGCTGAGGTCAAGGCCCAGTATGAGGAGATTGCC AACCGCAGCCGGACAGAAGCCGAGTCCTGGTATCAGAC CAAG
646	KRT5	3455220	CAGAACCAGATGACCGACTCCAAATCTCCCTG
647	KRT5	3455222	GGCCAAGGTTGATGCACTGATGGATGAGATTA ACT
648	KRT5	3455223	GCAGCCTGCAGCTATGCTCTCTAAGCGTGGAGCTCACTT GAGTAGGGTGACGGTGTG
649	KRT5	3455224	TGAAATCAACAAGCGTACCACTGCTGAGAATGAG
650	KRT5	3455225	AAAAGAACA CTAGAGAAATTGACTAG
651	KRT5	3455228	GTGGACACGTTCTGAATTAGACTGGCAGCTGGGAAG
652	KRT5	3455229	CAACCTGCAAATCGACCCCAGCATCCAGAGGGTGAGGA CCGAGGAGCGCGAGCAGATCAAGA
653	KRT5	3455230	GAGGTGGTGCCGGTAGTGGATTTGGTTTCGGCGGTGGA GCTGGTGGT
654	KRT5	3455231	GGCAGCTTCAGGAACCGGTTTGGTGCTGGTGC
655	KRT5	3455232	GGGCTCCAAGAGGATATCCATCAGCACTAGTG
656	KRT5	3455233	TGTGGAGTGGGTGGCTATGGCAGCCGGAGCCTCTACAA CCTGGG
657	KRT5	3455234	TGGTGGCTTCGGCAGGGTCAGCCTTGCGG
658	KRT5	3455235	TCAAGTGTGTCCTTCCGGAGCGGGGGCAGTCGTAGCTT CAGCACCGCCTCTGCCATCACCCCGTCTGTCTCCCGCAC

			CAG
659	KRT5	3455236	ACAGCTCGACAGCTCTCTCGCCCAGCCCAGTTCTGGAA GGGATAAAAAGGGGGGCATCACCGTTCCTGGGGTAACAGA GCCACCTTCTGCGTCCTGCTGAGCTCTGTTCTCTCCAGC ACCTCCCAACCCACTAGTGCCT
660	KRT5	3455237	CCCAGCCTCTATGGTGAAGACATACTTGCTAGCAGCGT CACCAACTTGCTGCCAAGAGATCAGTGCTGCAAGGCAA GGTTATTTCTAACTGAGCAGAGCCTG
661	FOXA1	3561726	CAGGTCTGTGGCAATACTCTTAACCATAAGAATTGAAA TGGTGAAGAAACAAGTATACACTAGAGGCTCTTAAAAG TATTGAAAGACAATACTGCTGTTATATAGCAAGACATA AACAGATTATAAACATCAGAGCCATTTGCTTCTCAGTTT ACATTTCTGATACATGCAGATAGCAGATGTCTTTAAATG AAATACATGTATATTGTGTATGGACTTAATTATGCACAT GCTCAGATGTGTAGACATCCTCCGTATATTTACATAACA TATAGAGGTAATAGATAGGTGATATACATGATACATTC TCAAGAGTTGCTTGACCGAAAGTTACAAGGACCCCAAC CCCTTTGTCCTCTCTACCCACAGATGGCCCTGGGAATCA ATTCCTCAGGAATTGCCCTCAAGAACTCTGCTTCTTGCT TTGCAGAGTGCCATGGTCATGTCATTCTGAGGTCACATA ACACATAAAATTAGTTTCTATGAGTGTATACCATTTAAA GAATTTTTTTTTTCAGTAAAAGGGAATATTACAATGTTGG AGGAGAGATAAGTTATAGGGAGCTGGATTTCAAACGT GGTCCAAGATTCAAAAATCCTATTGATAGTGGCCATTTT AATCATTGCCATCGTGTGCTTGTTTCATCCAGTGTTA
662	FOXA1	3561727	GTGTGTATTCCAGACCCGTCCTAAACACTTCCTAG
663	FOXA1	3561728	TCGGAGCAGCAGCATAAGCTGGACTTCAAGGCATACGA ACAGGCACTGCAATACTCGCCTTACGGCTCTACGTTGCC CGCCAGCCTGCCTCTAGGCAGCGCCTCGGTGACCACCA GGA
664	FOXA1	3561729	GGGCGCCTCGGAGTTGAAGACTCCAGCCTCCTCAACTG CGCCCCCATAA
665	FOXA1	3561730	GGCGGCCCTGAGAGCCGCAAGGACCCCTCTGGCGCCTC TAACCCCAGCGCCGACTCGCCCCCTCCATCGGGGTGTGC ACGGGAAGACCGGCCAGCTA
666	FOXA1	3561731	AGGCGCCCAGCAAGATGCTCACGCTGAGCGAGATCTAC CAGTGGATCATGGACCTCTTCCCCTATTACCGGCAGAA CCAGCAGCGCTGGCAGAACTCCATCCGCCACTCGCTGT CCTTCAATGACTGCTTCGTCAAGGTGGCACGCTCCCCGG ACAAGCCGGGCAAGGGCTCCTACTGGACGCTGCACCCG GACTCCGGCAACATG
667	FOXA1	3561732	TACGCGCCGTCCAACCTGGGCCGCAGCCGCGCGGGCGG CGGCGGCGACGCCAAGACGTTCAAGCGCAG
668	FOXA1	3561733	TCCGTCCCGGTCAGCAACATGAACTCAGGCCTGGGCTC CATGAACTCCATGAACACCTACATGACCATGAACACCA TGACTACGAGCGGCAACATGACCCCGGCGTCCTTCAAC ATGTCCTATGCCAACCCGGGCCTAGGGGGCCGGCCTGAG TCCCGGCGCAGTAGCCGGCATGCCGGGGGGGCTCGGCGG GCGCCATGAACAGCATGACT
669	FOXA1	3561736	TGGAAGGGCATGAAACCAGCGACTGGAACAGCTACTAC GCAGACACGCAGGAG

670	FOXA1	3561738	CTTTGTGCGGCGGACAAATGGGGAGAG
671	FOXA1	3561741	TCATAAAGATATAAAACCGGTGCTGTGACTCACCTGCTCT TAGCCGCAG
672	ORC6	3658927	GGGGTCGGAGCTGATCGGGCGCCTAGCCCCGCGCCTGG GCCTCGCCGAGCCCGACATGCTGAG
673	ORC6	3658928	GTGAGTTCGGCCGCGCAAGACCAGGGCTGGGCTTCCGC CTCGCGGCCCTGGGC
674	ORC6	3658931	CTCTCACCAGAGGATATGACCTTCATTCCCAGCCCCAG ATAAACGAGCCACAGGAGTTAGGCTTAGTGTGAAGCTA ACCAGGCTGTATT
675	ORC6	3658932	AAGCAGAGGAGTACTTGCGCCTGTCCCGGGTGAAGTGT GTCGGCCTCTCCGCACGCACCACGGAGACCAGCAGTG
676	ORC6	3658934	GATCTTGACTTATCCAGGCCACTTTTCAC
677	ORC6	3658935	GCCAAGTGACTATATTCCCAGTTTATCCCATAATGTAGC TAACAACCTTGGAAGTAGTGTTGCCAGAATTCCACTAGC AAATAGCAGCTGTATATATATGCTGGGAATTCTGATTTC AGTCTGCCTTTTGTAAAGAGATGATATC
678	ORC6	3658937	AAGTCATGAAGCACTACAGCAAATGTCTTTTATGTGCC CCTTTTGTATATAAAATAGATCCCATGTGCATTTTAACTC TCAGTCCAATAAACAACCTAAACAACCTAGCATAGATAA TAACATGTTTGGGAATGAAGGAAAAAACTAGACAGAG GCTCTGGAAGCATGGTCAAAAAGAAAATAAGTTGATTA TCTGGTTGCCCAGAGAAGAAAACCTGTACAGGTCTTGAG AAAAGC
679	ORC6	3658938	GATTCTAAAGCTGAAAGTGGATAAAAAACAA
680	ORC6	3658939	AAAAAGCTATATTTGATCGACTGTGTAAACAACCTAGAG AAGATTGGACAGCAGGTCGACA
681	ORC6	3658940	TTATTTGTGATCCAAAACATGCCCAAATACTGAAATTG AG
682	ORC6	3658941	ACCTGGAGATGTAGCTACTCCACCACGGAAGAGAAAGA AGATAGTGGTTGAAGCCC
683	ORC6	3658943	AAGGTAGAGGAGATGCCACATAAACCACAGAAAGATG AAGATCTGACACA
684	ORC6	3658944	TTGGAAAATGCTGCCAGTGCTCAAAAGGCTACAGCAGA GTG
685	ORC6	3658945	TCTCCAGGAAGACTTGACGGCTTTGGGATTTTGTTTAAA CTTTTATAATAAGGATCCTAAGACTGTTGCCTTTAAATA GCAAAGCAGCCTACCTGGAGGCTAAGTCTGGGCAGTGG GCTGGCCCCTGGTGTGAGCATTAGACCAGCCACAGTGC CTGATTGGTATAGCCTTATGTGCTTTCCTACAAAATGGA ATTGGAGGCCGGGCGCAGTGGCTCACGCCTGTAATCCC AGCACTTTGGGAGGCCAAGGTGGGTGGATCACCTGAGG TCAGGAGCTCGAGACCAGCCTGGCCAACATGGTGAAAC CCCATCTCTACTAAAAATACAAAAATTAGCCAGGTGTG ATGGTGCATGCCTGTAATCCCAGCTCCTCAGTAGGCTG AGACAGGAGCATCACTTGAACGTGGGAGGCAGAGGTT GCAGTGAGCCGAGATTGCACCACCGCACTCCAGCCTGG GTGACAGAGCGAGACTTATCTCATAAATAAATAGATAG ATACTCCAGCCTGG

686	ORC6	3658946	TGGAGCCATTTTGGCTTTAAGTGAATGGCAGTCCCTTGTC TTATTCAGAATATAAAAATTCAGTCTGAATGGCATCTTAC AGATTTTACTTCAATTTTTGTGTACGGTATTTTTTTATTTG ACTAAATCAATATATTGTACAGCCTAAGTTAATAA
687	CDH3	3666367	CGGAGCCTCCGTTTTTCAGTCGACTTCAGATGTGTCTCCA CTTTTTTCCGCTGTAGCCGCAAGGCAAGGAAACATTTCT CTTCCCGTACTGAGGAGGCTGAGGAGTGCAGTGGGTGT TCTTTTCTCCTCTAACCCAGAACTGCGAGACAGAGGCTG AGTCCCTGTA
688	CDH3	3666368	ATGGGGCTCCCTCGTGGACCTCTCGCGTCTCTCCTC
689	CDH3	3666369	GCTGGCTGCAGTGCGCGGCCTCCGAGCCGTGCCGGGCG GTCTTCAGGGAGGCTGAAGTGACCTTGGAGGC
690	CDH3	3666376	AAGAGCCAGCTCTGTTTAGCACTGATAATGATGACTTC ACTGTGCGGAATGGCGAGACAGTCC
691	CDH3	3666380	GATCTTCCCATCCAAACGTATCTTACGAAGACACA
692	CDH3	3666381	TGGGTGGTTGCTCCAATATCTGTCC
693	CDH3	3666382	TTTCTACAGCATCACGGGGCCGGGGGCAGACAGCCCCC CTGAGGGTGTCTTCGCTGTAGAGAAGGAGACAGGCTGG TTGTTGTTGAATAAGCCACTGGACCGGGAGGA
694	CDH3	3666384	CTCAGTGGAGGACCCCATGAACATCTCCATCATCGTGA CCGACCAGAATGACCACAAGCCCAAGTTTACCCAGGAC ACCTTCCGAGGGAGTGTCTTAGAGGGAGTCCTACCA
695	CDH3	3666385	TGACAGCCACGGATGAGGATGATGCCATCTACACCTAC AATGGGGTGGTTGCTTACTCCATCCATAGCCAAGAACC AAAGGACCCACACGACCTCATGTTTCACCATTCACCGGA GCACAGGCACCATCAG
696	CDH3	3666387	AGGCCCATGTGCCTGAGAATGCAGTGGGCCATGAGGTG CAGAGGCTGACGGTCACTGATCTGGACGCCCCCACTC ACCAGCGTGGCGTGCCACCTACCTTATCATGGGCGGTG ACGACGGGGACCATTTTACCATC
697	CDH3	3666388	CCAGCACACCCTGTACGTTGAAGTGACCAACGAGGCCC CTTTTGTGCTGAAG
698	CDH3	3666389	ACAGCCACCATAGTGGTCCACGTGGAGGATGTGAATGA GGCACCTGTGTTTGTCCCACCCTCCAAAGTCGTTGAGGT CCAGGA
699	CDH3	3666390	GCTGTGGGCACCCTCGACCGTGAGGAT
700	CDH3	3666394	ACGGGAACCCTTCTGCTAACACTGATTGATGTCAATGA CCATGGCCCAGTCCCTGAGCCCCGTCAGATCACCATCT GCAACCAAAGCCCTGTGCGCCAGGTGCTGAACATCACG GACAAGGACCTGTCTCCCCACACCTCCCCTTTCCAGGCC CAGCTCACAGATGACTCAGACATCTACTGGACGGC
701	CDH3	3666395	GTGGTCTTGTCCCTGAAGAAGTTCCTGAAGCAGGATAC ATATGACGTGCACCTTTCTCTGTCTGACCATGGCAACAA AGAGCAGCTGACGGTGATCAGGGCCACT
702	CDH3	3666396	GTGTGCGACTGCCATGGCCATGTTCGAAACCTGCCCTGG
703	CDH3	3666397	CTCCCAGAAGATGACACCCGTGACAACGTCTTCTACTA TGGCGAAGAGGGG
704	CDH3	3666398	CACCCAGCTCCACCGAGGTCTGGAGGCCAGGCCGGAGG TGGTTCTCCGCAATGACGTGGCACCAACCATCATCCCG ACACCCATGTACCGTCCTCGGCCAGCCAACCCAGATGA AATC

705	CDH3	3666400	GCAAGAGGCAGGACCCGCCGCTCCTAACTACCTGTTCTCTG
706	CDH3	3666401	ACCTGAAGGCGGCTAACACAGACCCACAGCCCCGCCCTACGACACCCTCTTGGTGTTCGACTATGAGGGCAGCGGCTCCGACGCCGCGTCCCTGAGCTCCCTCACCTCCTCCGCCTCCGACCAAGACCAAGATTACGATTATCTGAACGAGTGGGGC
707	CDH3	3666402	TCTGACGTTAGAGTGGTGGCTTCCTTAGCCTTTCAGGATGGAGGAATGTGGGCAGTTTGACTTCAGCACTGAAAACCTCTCCACCTGGGCCAGGGTTGCCTCAGAGGCCAAGTTTCCAGAAGCCTCTTACCTGCCGTAAAATGCTCAACCCTGTGTCCTGGGCCTGGGCCTGCTGTGACTGACCTACAGTGGACTTTCTCTCTGGAATGGAACCTTCTTAGGCCTCCTGGTGCAACTTAATTTTTTTTTTTAATGCTATCTTCAAACGTTAGAGAAAGTTCTTCAAAGTGAGAGCCAGAGCTGCTGGGCCACTGGCCGTCCTGCATTTCTGGTTTCCAGACCCCAATGCCTCCCATTCGGATGGATCTCTGCGTTTTTATAC
708	CDH3	3666404	AGAGAACCTACCCAAGATGTCAGTGAAATTGGAACATTCCTGACAATACCAGGGCATAAATGCAGGAATCAGGAATAGGCAGCAGTGATAGAACAATTCTGTTTGTGCCCTTGTTAACGTGAAGTTCAA
709	ERBB2	3720403	TTCCCGGATTTTTTGTGGGCGCCTGCCCCGCCCTCGTCCCCCTGCTGTGTCCATATATCGAGGCGATAGGGTTAAGGGAAGGCGGACGCCTGATGGGTAAATGAGCAAACCTGAA GTGTTTTCCATGATCTTTT
710	ERBB2	3720404	CGCAATTGAAGTACCACCTCCCGAGGGTGATTGCTTCCCATGCGGGGTAGAACCTTTGC
711	ERBB2	3720406	CCAGTGGTCTATACCTCCAGCAGCAAGTCGAGTGAGCAAGTGATGTCCTGAAAGGCCCAGTGGATCAGTGGAATGAAGCGGGCAGGAAGACTTAGTGCTCCTGAAACAAGGAATCCAGAATCCAGGAGAAGGATGGCTCAGTGGGGCTTTCAAGGGACAAGTATGGGGGTGAAGGGGTCACTGTCCCTATACC
712	ERBB2	3720407	GGCAAAGCAAAGCTATATTCAAGACCACATGCAAAGCTACTCCCTGAGCAAAGAGTCACAGATAAAACGGGGGCA CCAGTAGAATGGCCAGGACAAACGCAGTGCAGCA
713	ERBB2	3720408	GATGAGAGTGACATGTACTGTTGTGGACATGC
714	ERBB2	3720410	TGCCCCGGGGGTCCTGGAAGCCACA
715	ERBB2	3720411	AGAATGAAGTTGTGAAGCTGAGATTCCCCTCCATTGGGACCGGAGAAACCAGGGGAGCCCCCGGGCAGCCGCGCGCCCCTTCCCACGGGGCCCTTTACTGCGCCGCG
716	ERBB2	3720412	CAGCCGGAGCCATGGGGCCGGAGCCG
717	ERBB2	3720413	GAGCTGGCGGCCTTGTGCCGCTGGGGGCTCCTCCTCG
718	ERBB2	3720417	TGTGCACCGGCACAGACATGAAGCTGCGGCTCCCTGCCAGTCCCGAGACCCACCTGGACATGCTCCGCCACCTTACCAGGGCTGCCAGGTGGTGCAGGGAAACCTGGAACCTCACCTACCTGCCCCACCAATGCCAGCCTGT
719	ERBB2	3720419	TTGGGAGCAGTTGTGAAGCTCAGAAGAGAAATGTCTGTGAAAAGGTTATGAACAGGAGGGAGAGTGGAACCAACCTGCTGGATCGTGTCCACAGACCCTGGAATGGGGCCACATGCTTGGTTTGTCAAATTGCAGACGCCGGCCGGGT

720	ERBB2	3720420	CAGGGCTACGTGCTCATCGCTCACAACCAAGTGAGGCA GGTCCCCTGCAGAGGCTGCGGATTGTGCGAGGCACCC AGCTCTTTGAGGACAACCTATGCCCTGGCCGTGCTAGAC AATGGAGACCCGCTGAACA
721	ERBB2	3720421	AGGGGAAAGGGTCCTCTGATCATTGCTCACCC
722	ERBB2	3720422	GGTCTTGATCCAGCGGAACCCCCAGCTCTGCTACCAGG ACACGATTTTGTGGAAGGACATCTTCCACAAGAACAAC CAGCTGGCTCTCACACTGATAGACACCAACCGCTCTCG GGCC
723	ERBB2	3720425	GCCACTGCCCCACTGACTGCTGCCATGAGCAGTGTGCTG CCGGCTGCACGGGC
724	ERBB2	3720427	TGGTCACCTACAACACAGACACGTTTGAGTCCATGCCC AATCCCGAGGGGCCGGTATACATTTCGGCGCCAGCTGT
725	ERBB2	3720428	ACCTTTCTACGGACGTGGGATCCTGCACCCTCGTCTGCC CCCTGCACAACCAAGAGGTGACAGCAGAGGATGGAAC ACAGCGGTGTGAGAAGTGCAGCAAGCCCTGT
726	ERBB2	3720429	TGCAGTTCCTGTCCCTCTGCGCATGCAGCCTGGCCCAGC CCACCCTGTCCTATCCTTC
727	ERBB2	3720430	TACAAGTGTCCCTATATCCCCTGTCAGTGTGGGGAGGG GCCCCGACCCTGATGCTCATGTGGC
728	ERBB2	3720431	GGCATGGAGCACTTGCGAGAGGTGAGGGCAGTTACCAG TGCCAATATCCAGGAGTTTGCTGGCTGCAAGAAGATCT TTGGGA
729	ERBB2	3720432	AACACTGCCCCGCTCCAGCCAGAGCAGCTCCAAGTGTT TGAGACTCTGGAAGAGATC
730	ERBB2	3720434	GGCGCCTACTCGCTGACCCTGCAAGGGCTGGGCATCAG CTGGCTGGGGCTGCGCTCACTGAGGGAACTGGGCAGTG GACTGGCCCTCATCCACCATAACACCCACCTCTGCTTCG TGCACACGGTGCCCTGGGACCAGCTCTTTCGGAACCCG CA
731	ERBB2	3720435	AGCAGCGTTCTTGGACTTGTGCAGACTGCCCCGTCTCTGT GCACCCTTCTTGACTCAGCACAGCTCTGGCTGGCTTGGC CTCTTGGCATGGCTTCTCTAGCTGGGTCCTACCTGCCTT GGCATCCTTCCCTCCCCCTCTGTTTCTGAAATCTCAGAA CTCTTCCTCTCCCTACATCGGCCCCACCTGTCCCCACCC CTCCAGCCCACAGCCATGCCACAGCCAGTTCCCTGGTT CACTTGGACCTG
732	ERBB2	3720436	GCCACCAGCTGTGCGCCCCAGGGGCACTGCTGGGGTCCA GGGCCCACCCAGTGTGTCAACTGCAGCCAGTTCCTTCG GGGCCAGGAGTGCGTGGAGGAATGCCGA
733	ERBB2	3720437	TGGCTGGAGGGGTGCATGGGGCTCCTCTCAGACCCCCCT CACCCTGT
734	ERBB2	3720438	GCTCCCCAGGGAGTATGTGAATGCCAGGCACT
735	ERBB2	3720439	ACTCGCTGTTACACCTTAGGTAATGCGTTTTCTCTCTG GGTGCCTCCCATTTTCTGGCTCAAGTCCCTGCCCAGGAT CAAGCTTGGAGGAGGGCCCCGAGGGAGGGGGCCACAGA GACTGGGTGAAGAGCAAGGGTGTTTGTCCCAGGAGCAT GGCGAAAATTGCTGCTGGGTGGCCTTGGGAAGCACAAA GGGGACCCAACTAAGGGCCTGATCCTACTGCC

736	ERBB2	3720440	GTGGCCTGTGCCCCACTATAAGGACCCTCCCTTCTGCGTG GCCCCGCTGCCCCAGCGGTGTGAAACCTGACCTCTCCTA CATGCCCATCTGGAAGTTTCCAGATGAGGAGGGCGCAT GCCA
737	ERBB2	3720441	GTGAGTCCAACGGTCTTTTCTGCAGAAAGGAGGACTTT CCTTTCAGGGGTCTTTCTGGGGCTCTTACTATAAAAG
738	ERBB2	3720442	GGGCTGCCCCGCCGAGCAGAGAGCC
739	ERBB2	3720443	TTCCACTGTGGAACCTCCTGTCATTTTCCACTTCACCAA GTGACAGAGGACCTGCTCAGATGCTGAGGGGAGGGGA CTGCAAGGAAAGATGGCTAGGAAACCCAGTCCCTCCAC ACCCTAGAGTAACTTGATGCCTTGTGAGGGACACAGGC AAAGTTCAATTC
740	ERBB2	3720444	GTGGTCTTTGGGATCCTCATCAAGCGACGGCAGCAGAA GATCCGGAAGTACACGATGCGGAGACTGCTGCAGG
741	ERBB2	3720446	AGCGATGCCCAACCAGGCGCAGATGCGGATCCTGAAAG AGACGGAGCTGAGGAAGGTGAAGGTGCTTGGATCTGGC GCTTT
742	ERBB2	3720447	GCATCTGGATCCCTGATGGGGAGAATGTGAAAATTCCA GTGGCCATCAAAGTGTTGAGGGAAAACACATCCCCCAA AGCCAACAAAGAAATCTTAG
743	ERBB2	3720449	TGGGCATCTGCCTGACATCCACGGTGCAGCTGGTGACA CAGCTTATGCCCTATGGCTGCCTCTTAGACCATGTCCGG GAAAACCGCGGACGCCTGGGCTCCCAGGACCTGCTGAA CTGGTGTATGCAGATTGCCA
744	ERBB2	3720452	ATGTGCGGCTCGTACACAGGGACTTGGCCGCTCGGAAC GTGCTGGTCAAGAGTCCCAACCATGTCAA AATTACAGA CTTCGGGCTGGCTCGGCTGCTGGACATTGACGAGACAG AGTA
745	ERBB2	3720453	CTGGGTGGAGTGGTGTCTAGCCCATGGGAGAACTCTG
746	ERBB2	3720454	CTGGAGTCCATTCTCCGCCGGCGGTTACCCACCAGAG TGA
747	ERBB2	3720455	ACTGTGTGGGAGCTGATGACTTTTGGGGCCAAACCTTA CGATGGGATCCCAGCCCCGGGAGATCCCTGACCTGCTG
748	ERBB2	3720456	GTGCGTGGCTGAGCTGTGCTGGCTGCCTGGA
749	ERBB2	3720457	GTTGGATGATTGACTCTGAATGTCGGCCAAGATTCCGG G
750	ERBB2	3720458	GTTGGTGTCTGAATTCTCCCGCATGGCCAGGGACCCCC AGCGCTTTGTGGT
751	ERBB2	3720460	TCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC CTGGTG
752	ERBB2	3720462	GTGGGGACCTGACACTAGGGCTGGAGCCCTCTGAAGAG GAGGCCCCCAGGTCTCCACTGGCACCCCTCCGAAGGGGC TGGCTCCGATGTATTTGATGGTGACCTGGGAATGGGGG CAGCCAAGGGGCTGCAAAGCCTCCCCACACATGACCCC AGCCCTCTACAGCGGTACAGTGAGGACCCACAGTACC CCTGCCCTCTGAGACTGATGGCTACGTTGCCCCCCTGA
753	ERBB2	3720463	ATGTGAACCAGCCAGATGTTTCGGCCCCAGCCC
754	ERBB2	3720464	AGCCTTCGACAACCTCTATTACTGGGACCAGGACCCAC CAGAGCGGGGGGCTCCACCCAGCACCTTCAAAGGGACA CCTACGGCAGAGAACCCAGAGTACCTGGGTCTGGACGT GCCAGTGT

755	ERBB2	3720465	AGAAGGCCAAGTCCGCAGAAGCCCT
756	ERBB2	3720466	CGACCACTTCCAGGGGAACCTGCCATGCCAGGAACCTG T
757	ERBB2	3720467	CTTCCTGCTTGAGTTCCCAGATGGCTGGAAGGGGTCCA GCCTCGTTGGAAGAGGAACAGCACTGGGGAGTCTTTGT GGATTCTGAGGCCCTGCCCAATGAGACTCTA
758	ERBB2	3720468	GGTACTGAAAGCCTTAGGGAAGCTGGCCTGAGAGGGG AAGCGGCCCTAAGGGAGTGTCTAAGAACAAAAGCGAC CCATTCAGAGACTGTCCCTGAAACCTAGTACTGCCC
759	ERBB2	3720469	AGTATCCAGGCTTTGTACAGAGTGCTTTTCT
760	GRB7	3720477	CCTCCCTGAAGACGTGGTCCCAGCCGGGTGTC
761	GRB7	3720478	GGAGAGGGATCCTCTAAATTGTCGAGGCTTCATCTCTCC AGATTGTATGCCCTTCTC
762	GRB7	3720481	CTGGTTCGGTTAAGCCCCCTCTCTTG
763	GRB7	3720482	ATCTTAGCAGCTCTCCGGAAGACCTTTGCCCAGCCCCCTG GGACCCCTCCTGGGACTCCCCGGCCCCCTGATACCCCTC TGCCTG
764	GRB7	3720483	GTAAAGAGGTCCCAGCCTCTCCTCAT
765	GRB7	3720485	GAAACTTCGAGAGGAGGAGAGGCGTGCCACCTCCCTCC
766	GRB7	3720486	TCTCGGGGGCCCCCTCCAGTGCAAGGGGGGCTGCTCCCC GCGATGCCAGCCGCCCCCA
767	GRB7	3720487	TGGGAGATACACAGCCGCTTCCATGGAGGCAGGGGATC TTGGTTAGGAGTCCCTGAGGGTCTAGCAGGTGCGGAAA GGGAATGAATCAC
768	GRB7	3720488	GCCACAGCTCGCCACGTGTGTGAAATGCTGGTGCAGCG AGCTCACGCCTTGAGCGACGAGACCTG
769	GRB7	3720490	ACCACGAGTCCGTGGTGGAAGTGCAGGCTGCCTGGCCC GTGGGCGGAGATAGCCGCTTCGTCTTCCGGAAAACTT CGCCAAGTACGAAGTGTCAAGAGCTCCC
770	GRB7	3720491	TCTGGGCGCTGGGATGCCCTGATCCTCAACCTGGATGCT GGAGCCCTGATCCCTGACACTTGTCTACCCACAG
771	GRB7	3720492	TCCAGCTGTCTCGATGCACACACTGGTATATCCCATGAA GACC
772	GRB7	3720494	TCAGGACGGAAGCTTTGGAAACGCTTTTTTCTGCTTCTTG CGCCGATCTGGCCTCTATTACTCCACCAAGGGCACCTCT A
773	GRB7	3720495	CAGTCCCTGGTCCTTTTAGAAGTTGCCCCCTTCTCTGCTG GAACCTCTGAGCCCTTCTCCCCCTGGGCCCCCCCAGGCCA GCCACCTCCAGTTTACCATCTCTCCCTACATCCTTGCCT AGCTCACCTGCCCAG
774	GRB7	3720496	ATCCGAGGCACCTGCAGTACGTGGCAGATGTGAACGAG TCCAACGTGTACGTGGTGACGCAGGGCCGCAAGCTCTA CGGGATGCCCACTGACTTCGGTTTCTGTGTC
775	GRB7	3720498	CAACAAGCTTCGAAATGGCCACAAGGGGCTTCGGATCT TCTGCAGTGAAGATGAGCAGAGCCGCACCTGCTGGCTG
776	GRB7	3720501	TACGGGGTGCAGCTGTACAAGAATTACCAGCAGGCACA GTCTCGCCATCTGCATCCATCTTGTTTGGGCTCCCCACC
777	GRB7	3720502	AGAAGTGCCTCAGATAATACCCTGGTGGCCATGGACTT CTCTGGCCATGCTGGGCGTGTCAATTGAGAACCCCCGGG AGGCTCT

778	GRB7	3720505	CCATCCACCGCACCCAACTCTGGTTCCACGGGCGCATTT CCCGTGAGGAGAGCCAGCGGCTTATTGGACAGCAGGGC T
779	GRB7	3720507	CTGTTCCCTGGTCCGGGAGAGTCAGCGGAACCCCCAGGG CTTTGTCCTCTCTTTGTGCCACCTGCAGAAAGTG
780	GRB7	3720510	AGGAGGGCCGCCTGTACTTCAGCATGGATGATGGCCAG ACCCGCTTCACTGACCTGCTGCAGCTCGTGGAGTTCCAC CAGCTGAACCGCGGCATCCTGCCGTGCTTGCTGCGCCA TTGCTGCACGCGG
781	GRB7	3720511	CCCATCCAGTGGACTCTGGGGCGCGGCCACAGGGGACG GGATGAGGAGCGGGAGGGTTCGCCACTCCAGTTTTCT CCTCTGCTTCTTTGCCTCCCTCAGATAGAAAACAGCCCC CACTCCAGTCCACTCCTGACCCCTCTCCTCAAGGGAAG GCCTTGGGTGGCCCCCTCTCCTTCTCCTAGCTCTGGAGG TGCTGCTCTAGGGCAGGGAATTATGGGAGAAGTGGGGG CAGCCCAGGCGGTTTCACGCCCCACACTTTGTACAGAC CGAGAGGCCAGTTGATCTGCTCTGTTTTA
782	CDC6	3720897	TGGCCTCACAGCGACTCTAAGACTTGGGGCTCTCTCATT GGCTGTAACCTTCCACTGGATTGGTAGCAAAAAAAGA GGCGGTGCCCAAGGCGAAAGGCTCTGTGACTACAGCCA ATCAGAATCGAGGCCGGGCTTT
783	CDC6	3720900	CTGTCTCGGGCATTGAACAAAGCTAAAAACTCCAGTGA TGCCAAACTAGAACCAACAAATGTCCAAACCGTAACCT GTTCTCCTCGTGTAAGGCCCTGC
784	CDC6	3720901	GCGATGACAACCTATGCAACACTCCCCATTTACCTCCTT GTTCTCCACCAAAGCAAGGCAAGAAAGAGAATGGTCCC CCTCACTCACATACTTAAGGGACGAAGATTGGTATT TGACAATCAGCTGACAATTAAGTCTCCTAGCAAAAGAG AACTAGCCAAAGTTCACCAAAACAAAATACTTTCTTCA GTTAGAAAAAGTCAAGAGATCACAAACAATTCTGAGCA GAGATGTCCACTGAAGAAAGAATCTGCATGTGTGAGAC TATTCAAGC
785	CDC6	3720902	TGCTACCAGCAAGCAAAGCTGGTCCTGAACACAGCTGT CCCAGATCGGCTGCCTGCCAGGGAAAGGGAGATGGATG TCATCAGGAATTTCTTGAGGGAACACATCTGTGGGAAA AAAGCTGGAAGCCTTTACCTTTCTGGTGCTCCTGGA ACTGGAAAACTGCCTGCTTAAGCCGGA
786	CDC6	3720903	TTTAAACTATCATGCTGAATTGCATGTCCTTGAGGACT GCCAGGCTGTATTCCCAGCTATTGCTCAGGAGATTTGT CAGGAAGAGGTATCCAGGCCAGC
787	CDC6	3720904	GACAGCAAAGGCCAGGATGTATTGTACACGCTATTTGA ATGGCCATGGCTAAGCAATTCTC
788	CDC6	3720905	GTATTGCTAATACCCTGGATCTCACAGATAGAATTCTAC CTAGGCTTCAAGCTAGAGAAAAATGTAAGCCACAGCTG TTGAACTTCCCACCTTATACCAGAAATCAGATAGTCACT ATTTTGCAAGATCGACTTA
789	CDC6	3720906	GTATCTAGAGATCAGGTTCTGGACAATGCTGCAGTTCA ATTCTGTGCCCGCAAAGTCTCTGCT
790	CDC6	3720907	GAGATGTTGCGCAAAGCACTGGATGTTTGCA
791	CDC6	3720908	GTGAGTTACGGCTCTGTTGCATTCTT
792	CDC6	3720910	AGATGTCAAAGCCAGACTATTCTCAA

793	CDC6	3720913	GTAAATCACCTTCTGAGCCTCTGATTCCCAAG
794	CDC6	3720914	TATCCCAAGTCATCTCAGAAGTTGATGGTAACAGGATG ACCTTGAGCCAAGAAGGAGCACAAGATTCCTTCCCTCT TCAGCAGAAGATCTTGGTTTGCTCTTTGATGCTCTTGAT CAGGCAGTTGAAAATCAAAGAGGTCACCTCTG
795	CDC6	3720916	TACAGTAAAGTCTGTCGCAAACAGCAGGTGGCGGCTGT GGACCAGTCAGAGTGTTTGTCACCTTTCAGGGGCTCTTGGA AGCCAGGGGGCATTTTAGGATTAAAGA
796	CDC6	3720917	GAAATAGAACATGCTCTGAAAGATA
797	CDC6	3720918	CCCGAAAGTATTCAGCTGGCATTTAGAGAGCTACAGTC TTCATTTTAGTGCTTTACACATTCGGGCCTGAAAACAAA TATGACCTTTTTTACTTGAAGCCAATGAATTTTAATCTA TAGATTCTTTAATATTAGCACAGAATAATATCTTTGGGT CTTACTATTTTTTACCCATAAAAAGTGACCAGGTAGACCCT TTTTAATTACATTCACTACTTCTACCACTTGTGTATCTCT AGCCAATGTGCTTGCAAGTGTACAGATCTGTGTAGAGG AATGTGTGTATATTTACCTCTTCGTTTGCTCAAACATGA GTGGGTATTTTTTTGTTTGTTTTTTTTTGTTGTTGTTGTTTT TGAGGCGCGTCTCACCTGTTGCCCAGGCTGGAGTGCA ATGGCGCGTTCTCTGCTCACTACAGCACCCGCTTCCCAG GTTGAAGTGATTCTCTTGCCTCAGCCTCCCGAGTAGCTG GGATTACAGGTGCCCACCACCGCGCCCAGCTAATTTTTT AATTTTTAGTAGAGACAGGGTTTTACCATGTTGGCCAG GCTGGTCTTGAACCTCTGACCCTCAAGTGATCTGCCCAC CTTGGCCTCCCTAAGTGCTGGGATTATAGGCGTGAGCC ACCATGCTCAGCCATTAAGGTATTTTGTTAAGAACTTTA AGTTTAGGGTAAGAAGAATGAAAATGATCCAGAAAAA TGCAAGCAAGTCCACATGGAGATTTGGAGGACACTGGT TAAAGAATTTATTTCTTTGTATAGTATACTATGTTTCATG GTGCAGATACTACAACATTGTGGCATTTTAGACTCGTTG AGTTTCTTGGGCACTCCCAAGGGCGTTGGGGTTCATAAG GAGACTATAACTCTACAGATTGTGAATATATTTATTTTC AAGTTGCATTCTTTGTCTTTTTTAAGCAATCAGATTTCAA GAGAGCTCAAGCTTTCAGAAGTCAATGTGAAAATTCCT TCCTAGGCTGTCCCACAGTCTTTGCTGCCCTTAGATGAA GCCACTTG
798	MAPT	3723688	GCCGGCCTCAGGAACGCGCCCTCTTCGCCGGCGCGCGC CCTCGCAGTCACCGCCACCCACCAGCTCCGGCACCAAC AGCAGCGCCGCTGCCACCGCCCACCTTCTGCCGCCGCC ACCACAGCCACCTTCTCCTCCTCCGCTGTCCTCTCCCGT CCTCGCCTCTGTCGACTATCA

799	MAPT	3723690	TAAGGTACTGGTGCTTCGGCCACACCCATCTTTCTGAG CCCACTGGACTGGGCGCAGAGGGGGGATTGCCATGGAA ACCACAGGTGTCCGGAGAGGGGATCTTGGGGCTGGCCT CACCCCTTCCCTGCGGAGATTGGGGACCCTGGGGTAGG GGGAGCCGCGCCCAGTCGGCCTCCTGGAGGACACGGGA GGAAGCCCCGAACCCCCGCGCCTGAGGCTGTTTCTGAT TGGCCCCTGGAGGCCGCGACACGCGAGATAGGCGGCCC TGGGTGTATTTTTATTAATATTATGTCCGTACTGATTAA TATTATTTATCTTAAATAAATTTACCCCGTGTCCAAGTT CACCGCGCCCCCAAACCGAGTCTGGGGCGGCAGGGG GAACTCCTGGCCAACGAATCCATGCCTCGCCCTCCTGTG ATGAACCTGGTACGCACGGTTTTCTGGTTAATTCTATCG CTGAAAACCTGGTGCGGGGGGGCGCACTTCTGAGACGGAA GAGCATCTAGGAGCTGAATCCTCCACGCGGGTCGCCCA GGTTGATCTGAATTTCTGGGGAATGGCTTGGCTGCCCCG CCGGGACCAGGCCGACCCTCCTTGACGGTGGCGTAGAG GGCTGGAGCCTGGGTACTGCGAGGCTCCTCGCATGGCT GGGCCCGCCGCGAGGGGGTTGCAGAGCGGCTCAGGGATC GATTCAAGCATCGTCTCTCCTCCCTCGCCCCCAGACAGA GCTGGGCGCGGGGGTTCCCCTTCCAGATGGAGCGAGGGT CTCGGGGTGGCCCCCGGAAAAGGGGAGCCCCGCGGCCAC GGCTACGTATTGCCATCTCGCGAGCAGAGATGTCACCT CCTGCCTTTGGAGGAAAGGGAGCCCGGTGGGGATGAGC GCATTTAGCCCAATGCTGGGAACAAAGCGCACTCCGCG CTTCTGCGATTTTCGCTCCATTTTGAAATGTGTTGGCGCT TTGGTGGGGCCGCTGCGGTGGGCAAGGCCGGGGGCGCT GTTAATGGAGGAACCTCAGGGGGACGGTCCTTCGTAGG AAACCTCTATCCTGGCTCTGCGCGCGCTTTAAGGAAATG GC
800	MAPT	3723691	ACCTCGAGGGATGCAGCTTTTTCGCGCGGATGACGGTGGG GTGCTGAACCAGCCGGTGCGCCTCTGGAAATGTCTGGG CACGGATCCTGGGGCCATCGACGACTCCTCCCCATTCCC AGCAGGCGGGAGCTCTTACATTCCGAG
801	MAPT	3723692	GAAATGTCTTTCCTACCGCGGTTGATTCTGGGGGTGTCAT TTTGTGTTTTGTGATGGCTGCTTATATTTACTGTATAAG CATTGTATTTACTGTATAAGCATTGTATTATAATTACTG TATAAGCTGCTTATATTTACTGTATAAGCATCTCCAAAT CCTCCCTCTACGTAAACAAATTAATGGATAAACAGATA AGTGTATCCCCTGCCCCCACCCTGCTACGCAGGTCCGG AGTGACTCTTGAAGCTCATACATTCCTTGGCCAAGTTTG CTTCTCTAACAGATGTTTATATAGCAATAACCTGGCTTG GCTCTTGGGTTCACCTTTGGACGATTTGGGGAAGGGGC TTGTTGGCTTTGCTGGGTTTTGGATGAGTGACAGTCCAT GACTGTTCTGCTGGAAGGGCGTGACTTTTAAGTGGTTT CTAATATCAGGCATTGCTCCTCCGACAGGAACAAAAGA AATGGATACTGCCATAAATTGTTAGAAAACCTTAGAAT CGCTTTGATTGAGGAAAGGTTAGATTTATTCCGGTTGGA AAAAGTGGCCTTTCTATTAAACGTGCCCTTTGACCCTCA TGCCCTTGGAGGTCGGTGCCAGCCTGGAGATGGGATAA GATTGTGGTTTTCTTCTGCCTTTTTTAACATCTGTTGTTA CAGTCCATTTGTTGAAAATTTAAAGAAACTGTTTTATTC CACTTCCCTCAGCATTTATGTGTGTGGTTTCAGTAGCT

			CTGTGGCTATATGTACGAACACGTGTTATTTTTCCAATT GGACATGTGATAATTTTCCAACCTGGACCTTGCCTTCTAT TGATGTA
802	MAPT	3723707	CCCGCCAGGAGTTCGAAGTGATGGAAGATCACGCTGGG ACGTACGGGTGTTGGGGGACAGGAAAGATCAGGGGGGGCT ACACCATGCACCAAGACCAA
803	MAPT	3723712	TGTGACAGCACCTTAGTGGATGAGGGAGCTCCCGGCA AGCAGGCTGCCGCGCAGCCCCACACGGAGATCCCAGAA GGAACC
804	MAPT	3723713	GCCAGTCCCATGTGACAGTCAAAGCTTCTAACTCCATTC AAAGTTGCAGCCATTCCCCTCGAGGGCTGGCAGGGAGG GGAGGGGTAAAGAGAAACAGGAAGGTTCTTACTGAGTTG GTCCTGGTGTGAGCTGCGTCACACTCCCTGCAGAGGTTT CAAGGAGACTCTCTCTCTCTGTCTCCATGGGGACCTT ATTTGAATTCTTCTACTCTTACCCCAGCCTGCCATCTCC AGCTATCCTCCCCTGAAGAGCCCTTCTGCTGCGCTGGAT TCTGGTGGCCATGTCATCTCCTCGGCCCCGTGGGAGTCT GAAGATCTGGCTGCAGCCTCACCTCTGAGGTCCTGCTA GTTGCCACCTCTTAAA
805	MAPT	3723714	AGCCTGGAAGACGAAGCTGCTGGTCACGTGACCCAAG
806	MAPT	3723715	CTGGAATTGCCTGCCATGACTTGGGGGTGGGGGGAGG GACATGGGGTGGGCTCTGCCCTGAAAAGATCATTTGGA CCTGAGCTCTAATTCACAAGTCCAGGAGATTTTAGGGA GTTGGTTCTTATCAAAGGTTGGCTACTCA
807	MAPT	3723716	GCGATTCTCACTGCAGGCTGCCCTGTGGCTGATCCAGG AGCAAGGCCTTAACCATGTCATCCCCAAGCGATTGCTT GTAAACTTTCTTCTGTGCAGCCTTCAACCCTTATTATGA TTTTCTTCTCAGGAACCAAACTGCTGTATTCAAGAAAGG CAGCTTTGTGTAATCATTTATCATAAATATCTTAAGAAA AATCCTAGAGATTCTTAATTTTAGGAAATGGGAGACCT ATGGTACTGATATAATGTGGGCTGGGCTTGTCTTCTGTC ATTTGCTAGATAAATGAACTTGAGAGCCTACTGTAAAA TGTGGAAGCTTCTAGATTGCAGAAGGGCTGGAAAGACA CTGTTCTTTTCTCCCGAGTGATGGGATCTGTCCAGTATT TAGAGCTGCCTCTGAGGCCATCTGATTCTAGGAGACTCT GCCTCGTTGAGGATATTTTGAGGCCTAACTACACATTCC TGCCCCCAGAGAGGTCACAGCCTATAGCAGGCTGATGT TTCTCATGTAC
808	MAPT	3723717	TAAGCTATGGGAAGGCCTGTATACGAGGGGTGGACTTT TCTTCTGTAAGTGTCCAGAGACCAGGCCTCCTGAAGAG GGCATGGGGGGCTTAACTTACCTGGACTACTGTG
809	MAPT	3723720	GCCAATGAGATTAGCGCCCACGTCCAGCCTGGACCCTG CGGAGAGGCCTCTGGGGTCTCTGGGGCCGTGCCTCGGGG AGAAAGAGCCAGAAGCTCCCGTCCCGCTGACCGCGAGC CTTCCTCAGCACCGTCCCGTTTGCCCAGCGCCTCCTCCA ACAGGAGGCCCTCAGGAGCCCTCCCTGGAGTGGGGACA AAAAGGCGGGGACTGGGCCGAGAAGGGTCCGGCCTTTC CGAAGCCCGCCACCACTGCGTATCTC
810	MAPT	3723721	CTCATGTCCGGCATGCCTGGGGCTCCCCTCCTGCCTGAG GGCCCCAGAGAGGCCACACGCCAACCTTCGGGGGACAG GACCTGAGGACACAGAGGGCGGCCGCCACGCCCTGA

			GCTGCTCAAGCACCAGCTTCTAGGAGACCTGCA
811	MAPT	3723722	ATGAAGACCGCGACGTCGATGAGTCCTCCCCCAAGAC TCCCCTCCCTCCAAGGCCTCCCCAGCCCAAGATGGGCG GCCTCCCCAGACAGCCGCCAGAGAAGCCACC
812	MAPT	3723725	ACGGGACTGGAAGCGATGACAAAAAAGCCAA
813	MAPT	3723731	ACATCCACACGTTCTCTGCTAAACCTTGAA
814	MAPT	3723732	CTCAGACCCTCTGATCCAACCCTCCAG
815	MAPT	3723733	TCTTCTGTCACTTCCCGAACTGGCAG
816	MAPT	3723735	GGGCTGATGGTAAACGAAGATCGCCACACCGCGG
817	MAPT	3723736	CCAGGCCAACGCCACCAGGATTCCAGCAAAAACCCCGC CCGCTCCAAAGACACCACCCA
818	MAPT	3723737	CCAAGTCGCCGTCTTCCGCCAAGAGCCGCCTGCAGACA GCCCCCGTGCCCATGCCAGACCTGAAGAATGTCAAGTC CAAGATCGGCTCCACTGAGAACCTGAAGCACCAGCCGG GAGGCG
819	MAPT	3723740	AGAAGCTGGATCTTAGCAACGTCCAGTCCAAGTGTGGC TCAAAGGATAATATCAAACACGTCCCGGGAGGC
820	MAPT	3723743	TAGTCTACAAACCAGTTGACCTGAGCAAGGTGACCTCC AAGTGTGGCTCATTAGGCAACATCCATCATA
821	MAPT	3723746	CAGAGTCCAGTCGAAGATTGGGTCCCTGGACAATATCA CCCACGTCCCTGGCGGAGGAAAT
822	MAPT	3723747	TCGTGTACAAGTCGCCAGTGGTGTCTGGGGACACGTCT CCACGGCATCTCAGCAATGTCTCCTCCACCGGCAGCAT CGACATGGTAGACTCGCCCCAGCTCGCCACGCTAGCTG ACGAGGTGTCTGCCTCCC
823	MAPT	3723748	CCCTGGGGCGGTCAATAATTGTGGAGAGGAGAGAATGA GAGAGTGTGGAAAAAAAAAAGAATAATGACCCGGCCCC CGCCCTCTGCCCCCAGCTGCTCCTCGCAGTTCGGTTAAT TGGTTAATCACTTAACCTGCTTTTGTCACTCGGCTTTGG CTCGGGACTTCAAAATCAGTGATGGGAGTAAGAGCAAA TTTCATCTTTCCAAATTGATGGGTGGGCTAGTA
824	MAPT	3723749	ACATGGCCACATCCAACATTTCTCAGG
825	MAPT	3723750	TGCTTCTGGGGGATTTCAAGGGACTGGGGGTGCCAACC ACCTCTGGCCCTGTTGTGGGGGTGTCACAGAGGCAGTG GCAGCAACAAAGGATTTGAAACTTGGTGTGTTTCGTGGA GCCACAGGCAGACGATGTCAACCTTGT
826	MAPT	3723751	CCTCCTTGCCGCTGGGAGAGCCAAGGCCTATGCCACCT GCAGCGTCTGAGCGGCCGCCTGTCCTTGGTGGCCGGGG GTGGGGGCCTGCTGTGGGTCAGTGTGCCACCCTCTGCA GGGCAGCCTGTGGGAGAAGGGACAGCGGGTAAAAAGA GAAGGCAAGCTGGCAGGAGGGTGGCACTTCGTGGATG ACCTCCTTAGAAAAGACTGACCTTGATGTCTTGAGAGC GCTGG

827	MAPT	3723752	TTGCAGACCTGGGACTTTAGGGGCTAACCAGTTCTCTTTG TAAGGACTTGTGCCTCTTGGGAGACGTCCACCCGTTTCC AAGCCTGGGGCCACTGGCATCTCTGGAGTGTGTGGGGGT CTGGGAGGCAGGTCCCGAGCCCCCTGTCCTTCCCACGG CCACTGCAGTCACCCCGTCTGCGCCGCTGTGCTGTTGTC TGCCGTGAGAGCCCAATCACTGCCTATACCCCTCATCAC ACGTCACAATGTCCCGAATTCCCAGCCTCACCACCCCTT CTCAGTAATGACCCTGGTTGGTTGCAGGAGGTACCTAC TCCATACTGAGGGTGAAATTAAGGGAAGGCAAAGTCCA GGCACAAGAGTGGGACCCCAAGCCTCTCACTCTCAGTTC CACTCATCCAATGAGGACCCCTCACCACGAATCTCATGA TCTGATTTCGGTTCCCTGTC
828	MAPT	3723753	CCACTTGCACCCTAGCTTGTAGCTGCCAACCTCCCAGAC AGCCCAGCCCGCTGCTCAGCTCCACATGCATAGTATCA GCCCTCCACACCCGACAAAGGGGAACACACCCCTTGG AAATGGTTCTTTTCCCCCAGTCCCAGCTGGAAGCCATGC TGTCTGTTCTGCTGGAGCAGCTGAACATATACATAGAT GTTGCCCTGCCCTCCCCATCTGCACCCTGTTGAGTTGTA GTTGGATTTGTCTGTTTATGCTTGGATTACCA
829	MAPT	3723754	TTCTAGCAGCTAAGGAGGCGTTCAGCTGTGACGAAGG CCTGAAGCACAGGATTAGGACTGAAGCGATGATGTCCC CTTCCCTACTTCCCCTTGGGGGCTCCCTGTGTTCAGGGCAC AGACTAGGTCTTGTGGCTGGTCTGGCTTGCGGCGCGAG GATGGTTCTCTCTGGTCATAGCCCGAAGTCTCATGGCAG TCCCAAAGGAGGCTTACAACCTCCTGCATCACAAGAAAA AGGAAGCCACTGCCAGCTGGGGGGGATCTGCAGCTCCCA GAAGCTCCGTGAGCCTCAGCCACCCCTCAGACTGGGTT CCTCTCCAAGCTCGCCCTCTGGAGGGGGCAGCGCAGCCT CCCACCAAGGGCCCTGCGACCACAGCAGGGATTGGGAT GAATTGCCTGTCCTGGATCTGCTCTAGAGGCCCAAGCT GCCTGCCTGAGGAAGGATGACTTGACAAGTCAGGAGAC ACTGTTCCCAAAGCCTTGACCAGAGCACCTCAGCCCGC TGACCTTGACAAACTCCATCTGCTGCCATGAGAAAAG GGAAGCCGCCTTTGCAAAACATTGC
830	MAPT	3723756	GTGTCTGCTGCTCCCTAGTCTGGGCC
831	MAPT	3723757	CCGGCCCTCATTGAATGCGGGGGTTAATTTAACTCAGCCT CTGTGTGAGTGGATGATTCAGGTTGCCAGAGACAGAAC CCTCAGCTTAGCATGGGAAGTAGCTTCCCTGTTGACCCT GAGTTCATCTGAGGTTGGCTTGGAAGGTGTGGGCACCA TTTGGCCCAGTTCTTACAGCTCTGAAGAGAGCAGCAGG AATGGGGCTGAGCAGGGAAGACAACCTTCCATTGAAGG CCCCTTTCAGGGCCAGAACTGTCCCTCCCACCCTGCAGC TGCCCTGCCTCTGCCCATGAGGGGTGAGAGTCAGGCGA CCTCATGCCAAGTGTA
832	BIRC5	3736291	GGGTGGACCGCCTAAGAGGGGCGTGCGCTCCCGAC
833	BIRC5	3736292	GCGGCGCGCCATTAACCGCCAGATTTGAATCGCGGGAC CCGTTGGCAG
834	BIRC5	3736293	TGCCCCGACGTTGCCCCCTGCCTGGCA
835	BIRC5	3736294	TTTCTCAAGGACCACCGCATCTCTACATTCAAGAACTGG CCCTTCTTG

836	BIRC5	3736295	TGGCTTCATCCACTGCCCCACTGAGAACGAGCCAGACT TGGCCCAGTGTTTCTTCTGCTTCAAGGAGCTGGAAGGCT GGGAGCCAGATGACGACCCC
837	BIRC5	3736296	CCTCGATGGGCTTTGTTTTGAACTGAGTTGTCAAAAGAT TTGAGTTGCAAAGACACTTAGTATGGGAGGGTTGCTTT CCACCCTCATTGCTTCTTAAACAGCTGTTGTGAACGGAT ACCTCTCTATATGCTGGTGCCTTGGTGATG
838	BIRC5	3736298	GCTTGGGCAAAGCACTGATGCCATCAACTTCAGACTTG ACGTCTTACTCCTGAGGCAGAGCAGGGTGTGCCTGTGG AGGGCGTGGGGAGGTGGCCCGTGGGGAGTGGACTGCC GCTTTAATCCCTTCAGCTGCCTTTCCGCTGTTGTTTTGAT T
839	BIRC5	3736299	ACATAAAAAGCATTTCGTCCGGTTGCGCTTTCCTTTCTGT CAAGAAGCAGTTTGAAGAATTAACCCTTGGTGAATTTT TGAAACTGGACAGA
840	BIRC5	3736301	AAGAATTTCTGTTCGAGGAAGAGCCTGATGTTTGCCAG GGTCTGTTTAACTGGACATGAA
841	BIRC5	3736303	AGAATTTGAGGAAACTGCGGAGAAAGTGCGCCGTGCCA TCGAGCAGCTG
842	BIRC5	3736304	GGCTGCACCACTTCCAGGGTTTATTCCCTGGTGCCACCA GCCTTCCTGTGGGCCCCCTTAGCAATGTCTTAGGAAAGG AGATCAACATTTTCAAATTAGATGTTTCAACTGTGCTCT TGTTTTGTCTTGAAAGTGGCACCAGAGGTGCTTCTGCCT GTGCAGCGGGTGCTGCTGGTAACAGTGGCTGCTTCTCTC TCTCTCTCTCTTTTTTTGGGGGCTCATTTTTGCTGTTTTGA TTCCCGGGCTTACCAGGTGAGAAGTGAGGGAGGAAGA AGGCAGTGTCCCTTTTGCTAGAGCTGACAGCTTTGTTCG CGTGGGCAGAGCCTTCCACAGTGAATGTGTCTGGACCT CATGTTGTTGA
843	BIRC5	3736305	GGTTCCTTATCTGTACACCTGTGCCTCCTCAGAGGACA GTTTTTTTTGTTGTTGTGTTTTTTTTTTTTTTTGGT AGATGCATGACTTGTGTGTGATGAGAGAATGGAGACAG AGTCCCTGGCTCCTCTACTGTTTAACAACATGGCTTTCT TATTTTGTTTGAATTGTTAATTCACAGAATAGCACAAAC TACAATTA
844	BIRC5	3736306	AACGGGGTGAACCTTCAGGTGGATGAGGAGACAGAATA GAGTGATAGGAAGCGTCTGGCAGATACTCCTTTTGCCA CTGCTGTGTGATTAGACAGGCCCAGTGAGCCGCGGGGC ACATGCTGGCCGCTCCTCCCTCAGAAAAAGGCAGTGGC CTAAATCCTTTTTTAAATGACTTGGCTCGATGCTGTGG
845	BIRC5	3736307	CGTGTGTCTGTCAGCCCAACCTTCACATCTGTCACGTTC TCCACACGGGGGAGAGACGCAGTCCGCCCAGGTCCCCG CTTTCTTTGGAGGCAGCAGCTCCCGCAGGGCTGAAGTC TGGCGTAAGATGATGGATTTGATTTCGCCCTCCTCCCTGT CATAGAGCTGCAGGGTGGATTGTTACAGCTTCGCTGGA AACCTCTGGAGGTCATC
846	BIRC5	3736308	TGTTCCCTGAGAAATAAAAAGCCTGTCATTTTC

847	BIRC5	3736309	GTTTTTCATCGTCGTCCCTAGCCTGCCAACAGCCATCTG CCCAGACAGCCGCAGTGAGGATGAGCGTCCTGGCAGAG ACGCAGTTGTCTCTGGGCGCTTGCCAGAGCCACGAACC CCAGACCTGTTTGTATCATCCGGGCTCCTTCCGGGCAGA AACAACTGAAAATGCACTTCAGACCCACTTATTTCTGCC ACATCTGAGTCGGCCTGAGATAGACTTTTCCCTCTAAAC TGGGAGAATATCACAGTGGTTTTTGTTAGCAGAAAATG CACTCCAGCCTCTGTACTCATCTAAGCTGCTTA
848	BIRC5	3736310	CTGTGCTGTGGGCAGGGCTGAGCTGGAGCCGCCCCTCT CAGCCCCG
849	BIRC5	3736311	ATCCTTAAAACCAGACCCTCATGGCTACCAGCACCTGA AAGCTTCCTCGACATCTGTTAATAAAGCCGTAGGCCCTT GTCTAAGTGC
850	BIRC5	3736312	CCGCCTAGACTTTCTTTCAGATACATGTCCACATGTCCA TTTTTCAGGTTCTCTAAGTTGGAGTGGAGTCTGGGAAGG GTTGTGAATGAGGCTTCTGGGCTATGGGTGAGGTTCCA ATGGCAGGTTAGAGCCCCCTCGGGCCAACCTGCCATCCTG GAAAGTAGAGACAGCAGTGCCCGCTGCCCAGAAGAGA CCAGCAAGCCAAACTGGAGCCCCCATTGCAGGCTGTCTG CCATGTGGAAAGAGTA
851	KRT14	3757155	TAGGAGGCCCCCGTGTGGACACAG
852	KRT14	3757156	TCCAGCCGCCAAATCCGCACCAAGGTCATGGA
853	KRT14	3757157	TGAGCTCTAGTGCTGTCACCCAGTTTCCCTTGTGAACCT CCTTGGGTGGAAGAAGCTATTTTCTAAACCCTCCTTAGG GCTAGGAGAGGCAGCCCCCACCTCTTGCTTCTACGTGG TGTCTGTGGCAGATCCTATTGCTGTTGTGGTCAGCACCA TGAACAGGGCCCTACAGGGCTCTTCCCCTGAGACCAC TCCATTGGGTGAATATGGATGGAACCAGCCAGGTGTGA GCTCTTAGGAAGCTCTAATCTGAGGGCAAAGACTCTGT CTCTGACCTTTGGGAGCCCTCGTCTGAAAGAAATG
854	KRT14	3757160	CTGGAGGAGACCAAAGGTCGCTACTGCATGCAGCTGGC CCAGATCCAGGAGATGATTGGCAGCGT
855	KRT14	3757162	CAAGAGCGAGATCTCGGAGCTCCGGCGCACCATGCAGA AC
856	KRT14	3757164	GGAGATGGACGCTGCACCTGGCGTGGACCTGAGCCGCA TTCTGAACGAGATGCGTGACCAGTAT
857	KRT14	3757167	GATGGGTGTCTCATACCTTTTCTCTGGGGTTCATTCCAG
858	KRT14	3757169	AGCCACAGTGGACAATGCCAATGTCCTTCTGCAGATTG ACAATGCCCGTCTGGCCGCGGATGACTTCCGCACCAA
859	KRT14	3757172	TGGCCTTGGTGCTGGCTTGGGTGGTGGCTTTGGTGGTGG CTTTGCTGGTG
860	KRT14	3757174	ACCCGAGCACCTTCTCTTCACTCAGCCAACTGCTCGCTC GCTCA
861	KRT14	3757199	GAGAAGGTGACCATGCAGAACCTCAATGACCGCCTGGC C
862	KRT17	3757215	GGACTCAGCTACCCCGGGCCGGCCAC
863	KRT17	3757218	CCAGGAATACAAAATCCTGCTGGAT
864	KRT17	3757219	AAGAGTGAGATCTCGGAGCTCCGGCGCACC
865	KRT17	3757221	AGGTGGGTGGTGAGATCAATGTGGAGATGGACGCTGCC CCAGGCGTGGACCTGAGCCGCATCCTCAACGAGATGCG TGAC

866	KRT17	3757222	GTGCACCGGGATTAGTCACCTTAGAGGGCTTCCCTGTCT GCAGAGCCCTGATCCTTGGGGTCCAGTGTGCAGGGCAG ACTCCTCTTTGTACCACACTGCTTCTCTGTACACAAGGA ACCTC
867	KRT17	3757223	CTGGCCAGAGCCGACCTGGAGATGCAGATTGAGAACCT CAAGGAG
868	KRT17	3757224	CCCTGCGCCTGAGTGTGGAGGCCGACATCAATGGCCTG
869	KRT17	3757227	GTCTGGCTGCTGATGACTTCCGCAC
870	KRT17	3757228	GGTACTGAGTATCGGGGGAAGAAGA
871	KRT17	3757230	GGCAGCAGCTTTGGGGGTGTTGATGGGCTGCTGGCTGG AGGTGAGAAGGCCACCATGCAG
872	KRT17	3757231	GTCCCGCACCTCCTGCCGGCTGTCTGGCGGCCTGGGTGC CGGCTCCTGCAGGCTGGGATCTGCTGGCGGCCTGGGCA GCACCCTCGGGGGTAGCAGCTACTCCAGCTGCTACAGC TTTGGCTCTGGTGGTG
873	KRT17	3757234	ACACGCACGGCACTCAGCACGAGGATTTGGAGA
874	TYMS	3775844	TTGGCCTGCCTCCGTCCCGCCGCGCCAC
875	TYMS	3775845	CTGCCTCCGTCCCGCCGCGCCACTT
876	TYMS	3775846	GCCTGTGGCCGGCTCGGAGCTGCCGC
877	TYMS	3775850	CGCTTCGCAGCGTTTTTCAAAAACCTGGAGCGAAAGTGAT GTGGGCGGGGCAAAGGCGGGCGGGAAGAGGAGAGCACT GAAGCTGGCGCGGGAACTTGGTTTCCTGGTGGCCTCCC ATCCAATCCCCACGAACCAGCTTTCCTCTTAAACCTTGA AAAGAGAAATTCGGGAGTTCGAGTATAAGTTCTTAGTC GTCCTTTCCTCTTTCCTTTCCGACAGGAGCACCCCAGGC AAAAAATGTCTCGCGGGTCATTGGCGCCAGGCTTTCAG GGGACAGTGGGGCGGGGCGGGGTGGGCACAGGACGTT AGGCAGCCGTTGGC
878	TYMS	3775851	CGTCCTGCCGTCCTGGATCCTGCGCCAGCTGCG
879	TYMS	3775853	CTCTGCTGACAACCAAACGTGTGTTCTGGAAGGGTGTT
880	TYMS	3775855	GCTGTCTTCCAAGGGAGTGAAAATCTGGGATGCCAATG GATCCCGAGACTTTTTGGACAGCCTGGGATTCTCCACCA GA
881	TYMS	3775856	AGGACAGGGAGTTGACCAACTGCAAAGAGTGATTGAC ACCATCAAAACCAACCCTGACGACAGAAGAATCATC
882	TYMS	3775857	AAGCAATCTGGTTTTTGTGCAGAGGCACCTGAGGGAGGC AGGACCCTGGGAACTTCCCCCAGCCACATGGTTGATTG TGTGACGTTGG
883	TYMS	3775861	CTCTGCCAGTTCTATGTGGTGAACAGTGAGCTGTCCTGC CAGCTGTACCAGAGATCGGGAGACATGGGCCTCGGTGT GCCTTTCAACATCGCCAGCTACGCCCTGCTCACGTACAT GATTGCGCACATCACGGGCCTGAA
884	TYMS	3775862	GGAGATGCACATATTTACCTGAATCACATCGAGCCACT GAAAATT
885	TYMS	3775864	CCAAAGCTCAGGATTCTTCGAAAAGTTGAGAAAATTGA TGACTTCAAAGCTGAAGACTTTCAGATTGAAGGGTACA ATCCGCATCCAACCTATTAATAATGGA
886	TYMS	3775865	AGGAGCTCGAAGGATATTGTCAGTCTTTAGGGGTTGGG CTGGATGCCGAGGTAAAAGTTCTTTTTGCTCTAAAAGA AAAAGGAAGTAGGTCAAAAATCTGTCCGTGACCTATCA GTTATTA

887	TYMS	3775866	CACTGAGGGTATCTGACAATGCTGAGGTTATGAACAAA GTGAGGAGAATGAAATGTATGTGCTCTTAGCAAAAACA TGTATGTGCATTTCAATCCCACGTACTTATAAAGAAGGT TGGTGAATTTTACAAGCTATTTTTGGAATATTTTTAGAA TATTTTAAGAATTTTACAAGCTATTCCTCAAATCTGAG GGAGCTGAGTAACACCATCGATCATGATGTAGAGTGTG GTTA
888	TYMS	3775867	TTGTTTATTCTGTACTGCCACTTATCTGCTCAGTTCCTTC
889	NDC80	3776145	AGCGCCGGCGGAGAATTTCAAATTCGAACGGCTTTGGC GGGCCGAGGAAGGACCTGGTGTGTTTGATGACCGCTGTC CTGTCTAGCAGATACTTGCACGGTTTACAGAAATTCGGT CC
890	NDC80	3776147	ATGAAGCGCAGTTCAGTTTCCAGCGGTGGTGCTGGCCG CCTCTCCATGCAGGAGTTAAGATCCCAGGATGTAAATA AACAAGGCCTCTATACCCCTCA
891	NDC80	3776149	GTGGACATGGATCCCGGAATAGTCAACTTGGTATATTTT CCAGTTCTGAGAAAATCAAGGACCCGAGACCACTTAAT GACAAAGCATTTCATTC
892	NDC80	3776150	CTTACAGAAAATGGTTATGCACATAATGTGTCCATGAA ATCTCTACAAGCTCCCTCTGTAAAGACTTCCTGAAGAT CTTACATTTCTTTATGGCTTCCTGTGCCCCCTCATACGA ACTTCCTGACACAAAGT
893	NDC80	3776151	CTCCTCATACATGGCCTCACATTGTGGCAGCCTTAGTTT GGCTAATAGACTGCATCAAG
894	NDC80	3776152	TGAAATGTATACATGGGAAAGGGTTTTTTTCCTCAAAA AAAATATTTTCTCTCCCAGTCTTTTGACAGTATTCTCAA AGTCTGCTTCAGAGTTTTTCATTTTTTCAAAGCACATTTGA TTTAAAG
895	NDC80	3776154	ATGAAAGAAAGCTCACCTTTATTTGATGATGGG
896	NDC80	3776155	CTACACCATAAAATGCTATGAGAGTTTTATGAGTGGTG CCGACAGCTTTGATGAGAT
897	NDC80	3776156	GCTTTTAAGCTGGAATCATTAGAAGCAAAAAACAGAGC ATTGAATGAACAGATTGCAAGATTGGAACAAGA
898	NDC80	3776157	AATCGTCTAGAGTCGTTGAGAAAACCTGAAGGCTTCCTT ACAAGGAGATGTTCAAAAGTATCAGGCATACATGAGCA ATTTGGAGTCTCATTCAGCCATTCTTGACCAGAAATTAA ATGGTCTCAATGAGGAAATTGC
899	NDC80	3776159	AACCAGAAGTACTCAGTTGCAGACATTGAGCGAATAAA TCATGAAAGAAATGAATTGCAGCAGACTATTAATAAAT TAACCAAGGACCTGGAAGCTGAACAACAGAAGTTGTGG AATGAGGAGTTA
900	NDC80	3776161	CAGAGTATCACAAATTGGCTAGAAAATTAAACTTATT CCTAAAGGTGCTGAGAATTCCAAAGGTTATGACTTTGA AATTAAGTTTAATCCCGAGGCTGGTGCCAACTGCCTTGT CAAATACA
901	NDC80	3776162	GTACCTCTTAAGGAACTCCTGAATGAAACTGAAGAAGA AATTAATAAAGCCCTAAATAAAAAAATGGGTTTGGAGG ATACTTTAGAACA
902	NDC80	3776163	TTGAATGCAATGATAACAGAAAGCAAGAGAAGTGTGA GAACTCTGAAAGAAGAAGTTCAAAAGCTGGATGATCTT TACCAACAAAAA

903	NDC80	3776165	ACCTGCTAGAAAGTACTGTTAACCAGGGGCTCAGTGAA GCTATGAATGAATTAGATGCTGTTC
904	NDC80	3776166	TAGTTGTGCAAACCACGACTGAAGAAAGACGAAAAGT GGGAAATAACTTGCAACGTCTGTTAGAGATGGTTGCTA CACATGTTG
905	NDC80	3776167	CTGGGGTGAAGCAGCCGCATGCTAAGGAACACCAAGG ACTGCCAGGAGCCGCCAGCAACTGGGGAGAGACGAAG AAGGATTCTTCCCTAGAGCCTTCAGAGAGACCATGGCC CTGCTGACGTCTTGATTTCAAACCTCCGGCCTCCAGAGC TGAAAGAGTACATTTCTGTGTGTTTAAAGCCACCTAGTTT GTGGCAATTTGTTACAGTATCAGTATTTGAAATCGCAA AAAAATCAACAAAAACAACAAGAAAAAATAATGTGGC ATGTTAGTTTCCCA
906	NDC80	3776168	AACATCTTGAGGAGCAGATTGCTAAAGTTGATAGAGAA TATGAAGAATGCATGTCAGAAGATCTCTCGGAAAATAT TAAAGAGATTAGAGATAAGTATGAGAAGAAAGCTACTC TAATTAAGTCTTCTGAAG
907	NDC80	3776169	TATATCCATAGTGAATAAAATTGTCTCAGTAAA
908	SLC39A6	3804200	CAAAATGTTTCGTGCGGGTATATACCAGATGAGTACAGT GAGTAGTTTTATGTATCACCAGACTGGGTTATTGCCAAG TTATATATCACCAAAGCTGTATGACTGGATGTTCTGGT TACCTGGTTTACAAAATTATCAGAGTAGTAAACTTTG ATATATATGAGGATATTA AAACTACACTAAGTATCATTT GATTTCGATTTCAGAAAGTACTTTGATATCTCTCAGTGCTT CAGTGCTATCATTGTGAGCAATTGTCTTTTATATACGGT ACTGTAGCCATACTAGGCCTGTCTGTGGCATT
909	SLC39A6	3804201	AGAACTGCTGGTGTTTAGGAATAAGAAT
910	SLC39A6	3804202	AGTTTCAGTAGGTCATAGGGAGATGAGTTTGTATGCTG TACTATGCAGCGTTTAAAGTTAGTGGGTTTTGTGATTTT TGTATTGAATATTGCTGTCTGTTACAAAGTCAGTTAAAG GTACGTTTTAATATTTAAGTTATTCTATCTTGGAGATAA AATCTGTATGTGCAATTCACCGGTATTA
911	SLC39A6	3804203	AGAATGCTGGGATGCTTTTGGGTTTTGGAATTATGTTAC TTATTTCCATATTTGAACATAAAATCGTGTTTCGTATAA ATTTCTAG
912	SLC39A6	3804204	ATGCTGCACAATGATGCTAGTGACCATGGATGTAGCCG CTGG
913	SLC39A6	3804206	GCATGACCGTTAAGCAGGCTGTCCTTTATAATGCATTGT CAGCCATGCTGGCGTATCTTGGAATGGCAACAGGAATT TTCATTGGTCATTATGCTGAAAATGTTTCTATGTGGATA TTTGCACCTACTGCTGGCTTATTCATGTATGTTGCTCTG GTTGATATG
914	SLC39A6	3804207	GTTGCTGTGTTCTGTTCATGAGTTGCCTCATGAATT
915	SLC39A6	3804208	GAGCTGAAAGATGCCGGCGTCGCCACTCTGGCCTGGAT GGTGATAATGGGTGATGGCCTGCACAATTCAGCGATG GCCTAGCAATTG
916	SLC39A6	3804209	ACCATCATATTCTCCATCATCACCACCACCAAAACCACC ATCCTCACAGTCACAGCCAGCGCTACTCTCGGGAG
917	SLC39A6	3804210	CCACAGGAAGTCTACAATGAATATGTACCCAGAGGGTG CAAGAATAAATGCCATTACATTTCCACGATACACTCG GCCAGTCAGACGATCTCATTACCA

918	SLC39A6	3804212	TGATGTGGAGATTAAGAAGCAGTTGTCCAAGTATGAATCTCAACTTTCAACAAATGAGGAGA
919	SLC39A6	3804213	TGCCTATTTTGATTCCACGTGGAAGGGTCTAACAGCTCTAGGAGGCCTGTATTTTCATGTTTCTTGTTGAACATGTCCTCACATTGATCAAACAATTTA
920	SLC39A6	3804214	TCAGTCATCTGTCTTCTCAAAACATA
921	SLC39A6	3804217	GTTTTATAGCCATTTCCATCATCAGTTTCCTGTCTCTGCTGGGGGTATCTTAGTGCCTCTCATGAATCGGGTGTTTTTCAAATTTCTCCTGAGTTTCCTTGTGGCACTGGCCGTTGGGACTTTGAGTGGTGATGCTT
922	SLC39A6	3804218	GAATGCAACAGAGTTCAACTATCTCTGTCCAGCCATCATCAACCAAATTGATGCTAGATCTTGTCTGATTCATACAA GTGAAAAGAAGGCTGAAATCCCTCCAAAGACCTATTCA TTACA
923	SLC39A6	3804219	GCATCAAAGCTACTGACATCTCATGGC
924	SLC39A6	3804221	TGAGCCGGCTGGCTGGTAGGAAAACAAATGAATCTGTGAGTGAGCCCCGAAAAGGCTTTATGT
925	SLC39A6	3804222	ACTCAGATAGTTCAGGTAAAGATCCTAGAAACAGCCAGGGGAAAGGAGCTCACCGACCAGAACATGCCAGTGGTAGAAGGAATGTCAAGGACAGTGTTAGTGCTAGTGAAGTGACCTCAACTGTGTACAACACTGTCTCTGAAGGAACTCACTTTCTAGAGACAATAGAGACTCCAAGACCTGGAAAAC TCTTCCCCAAAGATGTAAGCAGCTCCACTCCACCCAGT GTCACATCAAAGAGCCGG
926	SLC39A6	3804223	CGCAATGGCGAGGAAGTTATCTGTAATCTTGATCCTGACCTTTGCCCTCTCTGTCACAAATCCCCTTCATGAACTAA AAGCAGCTGCTTTCCCCCAGACCACTGAGAAAATTAGT CCGAATTGGGAATCTGGCATTAAATGTTGACTTGGCAATT TCCACACGGCAATATCATCTACAACAGCTTTTCTACCGC TATGGAGA
927	SLC39A6	3804226	TGTGGAACCAAACCTGCGCGCGTGCGCCGGGCGGTGGGA CAACGAGGCCGCGGAGAC
928	SLC39A6	3804227	AGATTTCTCGAAGACACCAGTGGGCCCCG
929	SLC39A6	3804228	CTGCGCGCGGCGGTAATTAGTGATTGTCTTCCAGCTTCG CGAAGGCTAGGGGCGCGGCTGCCGGGTGGCTGCGCGGC GCTGCCCCCGGACCGAGGGGCAGCCAACCCAATGAAAC CACCGCGTGTTTCGCGCCTG
930	BCL2	3811353	TGAAGAAAAATAAAGTACAGTGTGAG
931	BCL2	3811354	TGTATTGAAAGCTTTTGTATCAAGATTTTCATACTTTT ACCTTCCATGGCTCTTTTTTAAGATTGATACTTTTAAGAG GTGGCTGATATTCTGCAACACTGTACACATAAAAAATA CGGTAAGGATACTTTACATGGTTAAGGTAAAGTAAGTC TCCAGTTGGCCACCATTAGCTATAATGGCACTTTGTTTG TGTGTTGGAAAAAGTCACATTGCCATTAACTTTCCTT GTCTGTC
932	BCL2	3811355	CTGTAGTGTAGATACTGAGTAAATCCATGCACCTAAAC CTTTTGGAAAATCTGCCGTGGGCCCTCCAGATAGCTCAT TTCATTAAGTTTTTCCCTCCAAGGTAGAATTTGCA
933	BCL2	3811356	GGAGGATGGAAAGGCTCGCTCAATCAAGAAAATTC

934	BCL2	3811357	GACCTTGGACAATCATGAAATATGCATCTCACTGGATG CAAAGAAAATCAGATGGAGCATGAATGGTACTGTACCG GTTTCATCTGGACTGCCCCAGAAAAATAACTTCAAGCAA ACATCCTATCAACAACAAGGTTGTTCTGCATACCAAGC TGAG
935	BCL2	3811358	CCTGTGCTGCTATCCTGCCAAAATCATTTTAATGGAGTC AGTTTGCAGTATGCTCCACGTGGTAAGATCCTCCAAGCT GCTTTAGAAGTAACAATGAAGAACGTGGACGTTTTTAA TATAAAGCCTGTTTTGTCTTTTGTGTTGTTCAAACGGG ATTCACAGAGTATTTGAAAAATGTATATATATTAAGAG GTCACGGGGGGCTAATTGCTGGCTGGCTGCCTTTTGTCTGT GGGGTTTTGTTACCTGGTTTTAATAACAGTAAATGTGCC CAGCCTCTTGGCCCCAGAACTGTACAGTATTGTGGCTGC ACTTGCTCTAAGAGTAGTTGATGTTGCATTTTTCCTTATT GTTAAAAACATGTTAGAAGCAATGAATGTATATAAAAG CCTCAACTAGTCATTTTTTTTCTCCTCTTCTTTTTTTTCATT ATATCTAATTATTTTGCAGTTGGGCAACAGAGAACCAT CCCTATTTTGTATTGAAGAGGGGATTCACATCTGCATCTT AACTGCTCTTTATGAATGAAAAAACAGTCCTCTGTATGT ACTCCTCTTTACACTGGCCAGGGTCAGAGTTAAATAGA GTATATGCACTTTCCAAATTGGGGACAAGGGCTCTAAA AAAAGCCCCAAAAGGAGAAGAACATCTGAGAACCTCC TCGGCCCTCCCAGTCCCTCGCTGCACAAATACTCCGCAA GAGAGGCCAGAATGACAGCTGACAGGGTCTATGGCCAT CGGGTCGTCTCCGAAGATTTGGCAGGGGGCAGAAAACCTC TGGCAGGCTTAAGATTTGGAATAAAGTCACAGAATTAA GGAAGCACCTCAATTTAGTTCAAACAAGACGCCAACAT TCTCTCCACAGCTCACTTACCTCTCTGTGTTTCAGATGTG GCCTTCCATTTATATGTGATCTTTGTTTTTATTAGTAAATG CTTATCATCTAAAGATGTAGCTCTGGCCCAGTGGGAAA AATTAGGAAGTGATTATAAATCGAGAGGAGTTATAATA ATCAAGATTAAATGTAAATAATCAGGGCAATCCCAACA CATGTCTAGCTTTACCTCCAGGATCTATTGAGTGAACA GAATTGCAAATAGTCTCTATTTGTAATTGAACTTATCCT AAAACAAATAGTTTATAAATGTGAACTTAACTCTAAT TAATTCCAACCTGTACTTTTAAGGCAGTGGCTGTTTTTAG ACTTTCTTATCACTTATAGTTAGTAATGTACACCTACTC TATCAGAGAAAAACAGGAAAGGCTCGAAATACAAGCC ATTCTAAGGAAATTAGGGAGTCAGTTGAAATTCTATTCT GATCTTATTCTGTGGTGTCTTTTGCAGCCCAGACAAATG TGGTTACACACTTTTTAAGAAATACAATTCTACATTGTC AAGCTTATGAAGGTTCCAATCAGATCTTTATTGTTATTC AATTTGGATCTTTCAGGGATTTTTTTTTTTAAATTATTATG GGACAAAGGACATTTGTTGGAGGGGTGGGAGGGAGGA AGAATTTTTAAATGTAAAACATTCCCAAGTTTGGATCA GGGAGTTGGAAGTTTTTCAGAATAACCAGAACTAAGGGT ATGAAGGACCTGTATTGGGGTCGATGTGATGCCTCTGC GAAGAACCTTGTGTGACAAATGAGAAACATTTTGAAGT TTGTGGTACGACCTTTAGATTCCAGAGACATCAGCATG GCTCAAAGTGCAGCTCCGTTTGGCAGTGCAATGGTATA AATTTCAAGCTGGATATGTCTAATGGGTATTTAAACAAT AAATGTGCAGTTTTAACTAACAGGATATTTAATGACAA

			CCTTCTGGTTGGTAGGGACATC
936	BCL2	3811359	CGTCCCTGGGCAATTCCGCATTTAATTCATGGTATTCAG GATTACATGCATGTTTGGTTAAACCCATGAGATTCATTC AGTTAAAAATCCAGATGGCAAATGACCAGCAGATTCAA ATCTATGGTGGTTTGACCTTTAGAGAGTTGCTTTACGTG GCCTGTTTCAACACAGACCCACCCAGAGCCCTCCTGCC CTCCTTCCGCGGGGGGCTTTCTCATGGCTGTCCTTCAGGG TCTTCCTGAAATGCAGTGGTGCTTACGCTCCACCAAGA AAGC
937	BCL2	3811360	TAGGCCCGTTTTTCACGTGGAGCATGGGAGCCACGACCC TTCTTAAGACATGTATCACTGTAGAGGGAAGGAACAGA GGCCCTGGGCCCTTCCTATCAGAAGGACATGGTGAAGG CTGGGAACGTGAGGAGAGGCAATGGCCACGGCCCATTT TGGCTGTAGCACATGGCACGTTGGCTGTGTGGCCTTGG CCACCTGTGAGTTTAAAGCAAGGCTTTAAATGACTTTG GAGAGGGTCACAAATCCTAAAAGAAGCATTGAAGTGA GGTGTCATGGATTAATTGACCCCTGTCTATGGAATTACA TGTA AACATTATCTTGTCACCTGTAGTTTGGTTTTATTT GAAAACCTGACAAAAAAAAAAGTTCCAGGTGTGGAATAT GGGGGTATCTGTACATCCTGGGGCATT
938	BCL2	3811361	CAACAGGGCAGTGTGGTCTCCGAATGTCTGGAAGCTGA T
939	BCL2	3811362	CACCTGGATGTTCTGTGCCTGTAAACATAGATTCGCTTT CCATGTTGTTGGCCGGATCACCATCTGAAGAGCAGACG GATGGAAAAAGGACCTGATCATTGGGGAAGCTGGCTTT CTGGCTGCTGGAGGCTGGGGAGAAGGTGTTCACTACT TGCATTTCTTTGCCCTGGGGGCTGTGATATTAACAGAGG GAGGGTTCCTGTGGGGGGGAAGTCCATGCCTCCCTGGCC TGAAGAAGAGACTCTTTGCATATGACTCACATGATGCA TACCTGGTGGGAGGAAAAGAGTTGGGAACTTCAGATGG ACCTAGTACCCACTGAGATTTCCACGCCGAAGGACAGC GATGGGAAAAATGCCCTTAAATCATAGGAAAGTATTTT TTTAAGCTACCAATTGTGCCGAGAAAAGCATTTTAGCA ATTTATACAATATCATCCAGTACCTTAAGCCCTGATTGT GTATATTCATATATTTTGGATACGCACCCCCCAACTCCC AATACTGGCTCTGTCTGAGTAAGAAACAGAATCCTCTG GAACTTGAGGAAGTGAACATTTCCGGTGACTTCCGCATC AGGAAGGCTAGAGTTACCCAGAGCATCAGGCCGCCACA AGTGCCTGCTTTTAGGAGACCGAAGTC
940	BCL2	3811363	GTGGGAGCTTGCATCACCTGGGTGCCTATCTGGGCCA CAA
941	BCL2	3811364	TGTGGAAGTGTACGGCCCCAGCATGCGGCCTCTGTTTG ATTTCTCCTGGCTGTCTCTGAAGACTCTGCTCAGTTTGG CCCT

942	BCL2	3811433	GCAATACCATTCTCATGCCAGTGTACAAATTACATGAA AGAGCATCATTTTTCTAGTGTCTGAGGATTGGCTGCTTA TGGCCAATTTTGGCAGCAAGACGATAGGATTAAAAATA GCTTGAAGATGATCTAGTCTTAAATAATATATTTTCATGA TGAACCTTTCCTTGGGAAAGTGCATCTTTCTGCCTACAAG AATCACATGACCCCTTTCAATAATTTATGTAGTAGAGA AAAACACACTATTTCTCATAGAGTTTTTCAGTCATGTGCT GTGGTGTGATTGTTTCTGGACATTCATAAAATTTTATAG TTAACTGAATTCTCTTTTCTGTTTTTGTGCTATTTAACGT CCATTGAAAACATGGCTTTCTTTTGCGCATTCTGTTACT TTCAGCTGTACTTTCTAATAAGAATGGATTGCCCTTTTT AGCAATCTTTGATTGAACTGGTACATTTTCAGATTACTTA AATGTCATCAGGCCACACAGCATAACCAGG
943	BCL2	3811441	ACTTCGCCGAGATGTCCAGCCAGCTGCACCTGACGCCC TTCACCGCGCGGGGACGCTTTGCCACGGTGGTGGAGGA GCTCTTCAGGGACGGGGTGAAGTGGGGGAGGATTGTGG CCTTCTTTGAGTTCGGTGGGGTCATGTGTGTGGAGAGCG TCAACCGGGAGATGTCGCCCCCTGGTGGACAACATCGCC CTGTGGATGACTGAGTACC
944	BCL2	3811442	GCCACCTGTGGTCCACCTGACCCTC
945	BCL2	3811443	CCCGCACCGGGCATCTTCTCCTCCCAGCCCCGGGCACAC GCCCCATCCAGCCGCATCCCGGGACCCGGTCGCCAGGA CCTCGCCGCT
946	BCL2	3811444	GTACGATAACCGGGAGATAGTGATGAAGTACATCCATT ATAAGCTGTCGCAGAGGGGCTACGA
947	BCL2	3811445	CACAGAGGAAGTAGACTGATATTAACAATACTTACTAA TAATAACGTGCCTCATGAAATAAAGATCCGAAAGGAAT TGGAATAAAAATTTCTGCATCTCATGCCAAGGGGGAA ACACCAGAATCAAGTGTTCCGCGTGATTGAAGACACCC CCTCGTCCAAGAATGCAAAGCACATCCAATAAAATAGC TGGATTATAACTCCTCTTCTTT
948	BCL2	3811446	TGTAACCTTCAATGGAAACCTTTGAGATTTTTTACTTAA AGTGCATTTCGAGTAAATTTAATTTCCAGGCAGCTTAATA CATTCTTTTTAGCCGTGTTACTTGTAGTGTGTATGCCCT GCTTTCACTCAGTGTGTACAGGGAAACGCACCTGATT
949	BCL2	3811447	GGCGCGTCCTGCCTTCATTTATCCAGCAGCTTTTCGGAA AATGCATTTGCTGTTTCGGAGTTTAATCAGAAGAGGATT CCTGCCTCCGTCCCCGGCTCCTTCATCGTCCCCTCTCCC CTGTCTCTCTCCTGGGGAGGCGTGAAGCGGTCCCGTGG ATAGAGATTCATGCCTGTGCCCGCGCGTGTTGTGCGCGC GTGTAAATTGCCGAGAAGGGGAAAACATCACAGGACTT CTGCGAATACCGGACTGAAAATTGTAATTCATCTGCCG CCGCCGCTGCCTTTTTTTTTTCTCGAGCTCTTGAGATCTC CGGTTGGGATTCTGCGGATTGACATTTCTGTGAAGCA GAAGTCTGGGAATCGATCTGGAAATCCTCCTAATTTTAA CTCCCTCTCCCCGCGACTCCTGATTCATTGGGAA
950	BCL2	3811448	GGAGGCGGCCGTAGCCAGCGCCGCCGC
951	BCL2	3811449	TGCCGGGGCTCCGGGCCCTCCCTGCCGGCGGCCGTCAG
952	BCL2	3811450	CCGCCGCTCTCCGTGGCCCCGCCGCGCTGCC
953	CCNE1	3828126	TTTTAAATGTCCCGCTCTGAGCCGG
954	CCNE1	3828128	GACGGCGGCGCGGAGTTCTCGGCTCGCTCCAGGAAGAG

			G
955	CCNE1	3828129	GAAATGGCCAAAATCGACAGGACGGCGAGGGACCAGT GTGGGAGCC
956	CCNE1	3828130	TCTAATGCAGCCACAGCCCATATGGCCCAGCACTGTAC CTGTCAGTGGGCACTGGCCTCTGCCAGTCCTGGGATTCC AGGAAGCTTGGTGTTCCTGACTGGCACCGTCTGAGATT ACAGATATGTGCCTAGCCTGGAAGA
957	CCNE1	3828131	AGAAGATGATGACCGGGTTTACCCAAACTCAACGTGCA AGCCTCGGATTATTGCACCATCCAGAGGCT
958	CCNE1	3828132	AAAGACATACTTAAGGGATCAGCACTTTCTTGAGCAAC ACCCTCTTCTGCAGCCAAAAATGCGAGCAATTCTTCTGG ATTGGT
959	CCNE1	3828133	GGGAGACCTTTTACTTGGCACAAGATTTCTTTGACCGGT ATATGGCGACACAAGAAAATGTTGTAAAACTCTTTTA CAGCTTATTGGGATTTTCATCTTTAT
960	CCNE1	3828134	GAAATCTATCCTCCAAAGTTGCACCAGTTTGCGTATGTG ACAGATGGAGCTTGTTTCAGGAGATGAAATTCTCACCAT GGAATT
961	CCNE1	3828135	TGGCGTTTAAGTCCCCTGACTATTGTGTCCTGGCTGAAT GTATACATGCAGGTTGCATATCTAAATGACTTACATGA AGTGCTACTGCCGCAGTATCCC
962	CCNE1	3828136	CTGGATGTTGACTGCCTTGAATTCCTTATGGTATACTT GCTGCTTCGGCCTTGTATCATTTCTCGTCATCTGAATTG ATGCAAAAGG
963	CCNE1	3828137	CTGTGTCAAGTGGATGGTTCCATTTGCCATGGTTATAAG GGAGACGGGGAGCTCAAAACTGAAGCACTTCAGGGGC GTCGCTGATGAAGATGCACACAACATA
964	CCNE1	3828138	GACAAAGCCCGAGCAAAGAAAGCCATGTTGTCTGAACA AAATAGGGCTTCTCCTC
965	CCNE1	3828139	GTAAGAAGCAGAGCAGCGGGCCGGAAATGGCGTGA
966	CCNE1	3828140	GCGTGCGTTTGCTTTTACAGATATCTGAATGGAAGAGT GTTTCTTCCACAACAGAAGTATTTCTGTGGATGGCATCA AACAGGGCAAAGTGTTTTTTATTGAATGCTTATAGGTTT TTTTTAAATAAGTGGGTCAAGTACACCAGCCACCTCCA GACACCAGTGCGTGCTCCCGATGCTGCTATGGAAGGTG CTACTTGACCTAAGGGACTCCCA
967	CCNE1	3828141	TGGGCTCCGTTGTACCAAGTGGAGCAGGTGGTTGCGGG CAAGCGTTGTGCAGAGCCCATAGCCAGCTGGGCAGGGG GCTGCCCTCTCCACATTATCAGTTGACAGTGTACAATGC CTTTGATGAACTGTT
968	CCNE1	3828142	GTAAGTGCTGCTATATCTATCCATTTTTTTAATAAAG
969	MIA	3833795	TCTAGGTGGTGTGGGCGAAGTTTGGGACTGGTTTAGGG CGGGGACAAGACCAAGAACAAGTTTCCTTGTACTAC GGGAGAGAGGGA
970	MIA	3833796	GGTCCCTGGTGTGCCTTGGTGTGCATCATCTTGCTGTCTG
971	MIA	3833798	TTCAGGACTACATGGCCCCCGACTGCCGATTCCTGACC ATTCACCGGGGCCAAGTGGT
972	MIA	3833799	GCCGTGGGCGGCTCTTCTGGGGAGG
973	MIA	3833800	CATTTAAGCTGAGATTCATATGACAAGGATGGAGCAGT TATGTGGAGATCAGGGAGAAGGGAGAATGCAAAGGCC TTCAGCAGGCACAAGCTTGCCATCTTCCCAGACCCTAG

			CTTTTAACTCCTCTTCCCCAG
974	MIA	3833801	G TTCAGGGAGATTACTATGGAGATCTGGCTGCTCGCCT GGGCTATTTCCCCAGTAGCATTGTCCGAGAGGACCAGA CCC
975	MYBL2	3886226	AAAGTGCTTCAACCCGCGCCGGCGGGCGACTGCAGTTCC TGCGAGCGAGGAGCGCGGGACCTGCTGACACGCTGACG CCTTCGAGCGCGGCCC
976	MYBL2	3886229	GCTGCACTACCAGGACACAGATTTCAGATGTGCCGGAGC AGAGGGATAGCAAGTGCAAGGTCAAATGGACCCATGA GGA
977	MYBL2	3886231	CCCTGGTGAGGCAGTTTGGACAGCAGGACTGGAAGTTC CTGGCCAGCCACTTCC
978	MYBL2	3886232	TCCAGACCTTGTCAAGGGGCCATGGACCAAAGAGGA
979	MYBL2	3886235	TGATTGCCAAGCACCTGAAGGGCCGGCTGGGGGAAGCAG TGCCGTGAACGCTGGCACAACCACCTCAACCCTGAGGT GAAGAAGTCTTGCTGGACCGAGGAGGAGGACCGCATC ATCTGCGAGGCCCAACAAGGTGCTGGGCAACCGCTGGGC CGAGATCGCCAAGATGTTGCCAGGG
980	MYBL2	3886237	ACACAGGAGGCTTCTTGAGCGAGTCCAAAGACTGCAAG CCCC
981	MYBL2	3886238	GCAGCCACCACATCGAAGGAACAGGAGCCCATCGGTAC AGATCTGGACGCAGTGCGAACACCAGAGCCCTTGGAGG AATTCCCGAAGCGTGAGGACCAGGAAGGCTCCCCACCA GAAACGAGCCTGCCTTACAAGTGGGTGGTGGAGGCAGC TAACCTCCTCATCCCTGCTGTGGGTCTAGCCTCTCTGA AGC
982	MYBL2	3886239	CTGATGCTTGGTGTGACCTGAGTAAATTTGACCTCCCTG AGGA
983	MYBL2	3886240	GTATCAACAACAGCCTAGTGCAGCTGCAAGCGTCACAT CAGCAGCAAGTCCT
984	MYBL2	3886241	CAGTGTGACCGAGTACCGCCTGGATGGCCACACCATCT CAGACCTGAGCCGGAGCAGCCGGGGCGAGCTGATCCCC ATCTCCCCCAGCACTGAAGTCGGGGGGCTCTGGCATTTGG CACACCGCCCTCTGTGCTCAAGCGGCAGAGGAAGAGGC GTGTGGCTCTGTCCCCTGTCACTGAGAATAGCACCAGTC TGTCCCTTCCTGGATTCTGTAAACAGCCTCACGCCCAAGA GCA
985	MYBL2	3886242	TTTCTGAACTTCTGGAACAAACAGGACACATTGGAGCT GGAGAGCCCCCTCGCTGACATCCACCCCAGTGTGCAGCC AGAAGGTGGTGGTCACCACACCACTGCA
986	MYBL2	3886245	CTCCATGGACAACACTCCCCACACGCCAACCCCGTTCA AGAACGCCCTGGAGAAGTACGGACCCCTGAAGCC
987	MYBL2	3886248	ACTTGAAGGAGGTGCTGCGTTCTGAGGCTGGCATCGAA CTCATCATCGAGGACGACATCAGGCCCGAGAAGC
988	MYBL2	3886250	CCGACA ACTGCCCCTTCAA ACTCTTCCAG
989	MYBL2	3886251	CCTCACCTGT CAGGTATCAAAGAAGACAAC
990	MYBL2	3886252	CTTGCTCAACCAGGGCTTCTTG CAGGCCAAGCCCGAGA AGGCAGCAGTGGCCCAGAAGCCCCGAAGCCACTTCACG ACACCTGCCC

991	MYBL2	3886254	CAGCCACACATCTCGGACCCTCATCTTGTCTGA
992	MYBL2	3886255	GTGTCACGAGCCCATTCTCATGTTTACAGGGGTTGTGGG GGCAGAGGGGGTCTGTGAATCTGAGAGTCATTCAGGTG ACCTCCTGCAGGGAGCCTTCTGCCACCAGCCCCTCCCCA GACTCTCAGGTGGAGGCAACAGGGCCATGTGCTGCCCT GTTGCCGAGCCCAGCTGTGGGCGGCTCCTGGTGCTAAC AACAAAGTTCCACTTCCAGGTCTGCCTGGTTCCCTCCCC AAGGCCACAGGGAGCTCCGTCAGCTTCTCCCAAG
993	UBE2C	3887050	GTCCTGCAGTTGCAGTCGTGTTCTCCGAGTTCCTGTCTC TCTGCCAACGCCGCC
994	UBE2C	3887051	TGGCTTCCCAAACCGCGACCCAGCCGCCACTAGCGTC GCCGCCGCCCGTAAAGGAGCTGAGCCGA
995	UBE2C	3887054	GAGCTCAGACCGCTCTTTGAGACTCTCCCGAAGGAGAA TGGGAGGGTAGGGGCGCTGCCAGACTCCTTCCCTGGTG GGCCTAGATGAAGACGCTCAAGGACCCTCGTGACTTGG CCGAGACAGGGGAAGGGAGAAGTTGAGTCGGGCAAGG AAGAGATGCTAAAGCCTGGGGAATTAAGAACATGCCA GAATCATCCCGAGGGAGTCTGGAATTAGGGAGGGTGAG GACTCGCTAGGATCGTCCTGTGGATC
996	UBE2C	3887059	ATGTCTGGCGATAAAGGGATTTCTGCCTTCCCTGAATCA GACAACCTTTTCA
997	UBE2C	3887061	CAGTTTGTCTACTGTCCGGTCCCAG
998	UBE2C	3887062	ACTCAAGATTCTAGCAAGCCCCTTGTGTGGGGCT
999	UBE2C	3887063	GGTATAAGCTCTCGCTAGAGTTCCCCAGTGGCTACCCTT ACAATGCGCCCACAGTGAAGTTCCTCACGCCCTGCTAT CACCCCAACGTGGA
1000	UBE2C	3887066	ACACACATGCTGCCGAGCTCTGGAAAAACCCCA
1001	UBE2C	3887067	GTACCTGCAAGAAACCTACTCAAAGCAGGTCACCAGCC AGGAG
1002	UBE2C	3887068	GTGATTTCTGTATAGGACTCTTTATCTTGAGCTGTG
1003	MMP11	3939471	GGCCTTTACGCGACATCCGAGCAGCGTGTCTATCCCAA AGGCCTAGGAGCATTTGCCCCGGCTCGGTCAAATCTAGC GCAAGTTTGAAGCCTGCGGCCTCGCAATTTTAGCAGCTT C
1004	MMP11	3939472	GTGGAGTCTTCTTGAATAAGCTGTGAAACATTTCCCCAC CCGCTTCCCTTTCTTGGCCCAGGCTTCCTGACCACAGCC TCACCTTTGAGCAGCTCAGAGCCCTGCCTGCCAGGATG CGAGCCACTGCCTGGATCGTGGCTCTGCAG
1005	MMP11	3939473	GGCCCGGAGCGGCCCCAGCAAGCCCAGCAGCCC
1006	MMP11	3939474	GGCTCCGGCCGCCTGGCTCCGCAGCGCGGCCGCGCGCG CCCTCCTGCCCCCGA
1007	MMP11	3939475	CATGCAGCCCTGCCAGTAGCCCGGCACCTGCC
1008	MMP11	3939476	GAAGCCCCCGGCCTGCCAGCAGCCTCAG
1009	MMP11	3939477	CTGTGGCGTGCCCGACCCATCTGATGGGCTGAGTGCCC GCAACCGACAGAAGAG
1010	MMP11	3939478	GCGCTGGGAGAAGACGGACCTCACCTACAG

1011	MMP11	3939479	CAGGGAGGTCATCTATGGGCAAACCCCCTGAAACCCCA ACTTAGACACATACACATATGGAGACCCTCCCTCAGCA GAGGGGCAGAGCCTCCGTCATCATGCAAAGAGTCGCAG CACATGCCTGCGGACGGGTGTTCACTCACTCAGGCAGC CTTTACAAGAGACCTGTGAGGACCAGGCTCTGGGACTC CACGGTGAATGAGGCAGACACAGCCCCATCCTCTGTGT CAGTCTGAGGTGGGTGTCAGCCATGTCATTGTCCAATC TACCATCACAACCTTGGGCTTCGAGCAGGTGGAGACAGT GGTAAGCGGGGAGAGGCAATAGTGGGCATCTCACTGG GTGACCTGGGAGGACCCTGGGCAGGTGATGGGGGAAGCT GAGGCTCACACATCCTGCGGGTGGGGACCCAGCCTGAA GAATGGGCTGGTGTACACAGCATTGGAGCTGAGACTG GGGTCTTTAGAATTTCTAGGTGGGGGCTGGGAACCA ACAGGGGCTCAAGGAACCAAGGTGTCCCCACAGTAAGT GGCACTGTCAGGTCTAGGATGGGGGTCTCGGGACCCCT GGTCCTGGTTCTTTCCACTGAATTC
1012	MMP11	3939480	TTCGGTTCCCATGGCAGTTGGTGCAGGAGCAGGTGCGG CAGACGATGGCAGAGGCCCTAAAGGTATGGAGCGATGT GACGCCACTCACCTTTACTGAGGTGCACGAGGGCCGTG CTGACATCATGATCGACTTCGCCA
1013	MMP11	3939481	GGACGACCTGCCGTTTGATGGGCCTGGGGGGCATCCTGG CCCATGCCTTCTTCCCCAAGACTCACCGAGAAGGGGAT GTCCACTTCGACTATGATGA
1014	MMP11	3939482	AGGTGGCAGCCCATGAATTTGGCCA
1015	MMP11	3939483	TACACCTTTCGCTACCCACTGAGTCTCAGCCCAGATGAC TGCAGGGGCGTTCAACACCTATATGGCCAGCCCTGGCC CACTGTCACCTCCAGGACCCAGCCCTGGGCCCCCAGG CTGGGATAGACACCAATGA
1016	MMP11	3939484	ACTGTGACTGCAGCATATGCCCTCAGCATGTGTC
1017	MMP11	3939485	CCGAGGCGAGCTCTTTTTCTTCAAAGCGGGCTTTGTGTG GCGCCTCCGTGGGGGGCCAGCTGCAGCCCGGCTACCCAG CATTGGCCTCTCGCCACTGGCAGGGACTGCCCAGCCCT GTGGACGCTGCCTTCGAGGATGCCCAGGG
1018	MMP11	3939486	GGAGCATTGCAGATGCCAGGGACTTCACAAATGAAGGC ACAGCATGGGAAACCTGCGTGGGTTCAGGGGCAG
1019	MMP11	3939487	TTTGTCACAGCCAAATGCCAGTGGAAGGAGCAGCCGCC CAGGCAGCCCTCTACTGATGAGAGTAACCTCACCCGTG CACTAGTTTACAGAGCATTCCTGCCCCAGCTTATCCCA GGCCTCCCGCTTCCCTCTGCGGGTGGGGTGCTGAGCAG GCATTATTGGCCTGCATGTTTTACTGA
1020	MMP11	3939488	CTCAGTACTGGGTGTACGACGGTGAAAAGCCAGTCCTG GGCCCCGCACCCCTCACCGAGCTGGGCCTGGTGAGGTT CCCGGTCCATGCTGCCTTGGTCTGGGGTCCCGAGAAGA ACA
1021	MMP11	3939489	AGCACCCGGCGTGTAGACAGTCCCGTGCCCCGCAGGGC CACTGACTGGAGAGGGGTGCCCTCTGAGATCGACGCTG CCTTCCAGGAT
1022	MMP11	3939491	GCTATGCCTACTTCCTGCGCGGGCCGCTCTACTGGAAGT TTGACCCTGTGAAGGTG
1023	MMP11	3939492	TCCTGACTTCTTTGGCTGTGCCGAGCCTGCCAACACTTT CC

1024	MMP11	3939493	CTGCCAGGCCACGAATATCAGGCTAGAGACCCATGGCC ATCTTTGTGGCTGTGGGCACCAGGCATGGGACTGAGCC CATGTCTCCTCAGGGGGATGGGGTGGGGTACAACCACC ATGACAACCTGCCGGGAGGGGCCACGCAGGTCGTGGTCAC CTGCCAGCGACTGTCTCAGACTGGGCAGGGAGGCTTTG GCATGACTTAAGAGGA
1025	MMP11	3939494	GAGTGTCCTTGCTGTATCCCTGTTGTGAGGTTCCCTCCA GGGGCTGGCACTGAAGCAAGGGTGCTGGGGCCCCATGG CCTTCAGCCCTGGCTGAGCAACTGGGCTGTAGGGCAGG GCC
1026	MMP11	3939495	GCCTTCTGGCTGACAATCCTGGAAATCTGTTCTCCAGAA TCCAGGCCAAAAAGTTCACAGTCAAATGGGGAGGGGTA TTCTTCATGCAGGAGACCCCAGGCCCTGGAGGCTGCAA CATACTCAATCCTGTCCCAGGCCGGATCCTCCTGAAGC CCTTTTCGCAGCACTG
1027	MDM2	3979479	CTGATGGGTGTGCTAATTACACTGATTTAATCGATACCC ATTGTATGTGAAACAGTATATACACCATATTTACAATTA TGTATCAGTTTAACATTTAAAAAAACATTTCTAATATAA GTATCTCTCAAACCTGTGGATTAACCTTCTTGATTTATATT TAAATATGAATCTTGAGGAAAATAGTGAAAATAACCAT CTTGATTTAGTGTATTTCTCCCATATGTGAATTGTATAT AC
1028	RRM2	4006364	AACGATGCCTTGTGTCAAGAAGAAGGCAGATTGGGCCT TGCGCTGGATTGGGGACAAAG
1029	RRM2	4006368	AGCTGCAGCTCTCGCCGCTGAAGGGGC

Table 9. Gene Targets

Gene
CDC20
KIF2C
PHGDH
NUF2
CENPF
EXO1
UBE2T
RRM2
MLPH
GPR160
CCNB1
CXXC5
PTTG1
FGFR4
FOXC1
ESR1
ANLN
BLVRA
EGFR
ACTR3B
NAT1
MYC
SFRP1
MELK
BAG1
CEP55
MKI67
TMEM45B
PGR
MDM2
KRT5
FOXA1
ORC6
CDH3
ERBB2
GRB7
CDC6
MAPT
BIRC5
KRT14
KRT17

TYMS
NDC80
SLC39A6
BCL2
CCNE1
MIA
MYBL2
UBE2C
MMP11

CLAIMS

What is claimed is:

1. A method comprising:
 - a) providing a biological sample from a subject having prostate cancer;
 - b) measuring levels of expression in the biological sample of a plurality of genes selected from Table 8, Table 9 or SEQ ID NOs: 1-1029; and
 - c) subtyping the prostate cancer of the subject according to a genomic subtyping classifier based on the levels of expression of the plurality of genes, wherein said subtyping comprises assigning the prostate cancer to one of three subtypes selected from the group consisting of a luminal A subtype, a luminal B subtype, and a basal subtype.
2. The method of claim 1, further comprising administering androgen deprivation therapy to the subject if the subtyping indicates that the subject has the luminal B subtype.
3. The method of claim 1, wherein the method is performed prior to treatment of the patient with the androgen deprivation therapy.
4. The method of claim 1, wherein the subject is undergoing androgen deprivation therapy.
5. The method of claim 1, wherein the biological sample is a biopsy.
6. The method of claim 1, wherein the biological sample is a urine sample, a blood sample or a prostate tumor sample.
7. The method of claim 6, wherein the blood sample is plasma, serum, or whole blood.
8. The method of claim 1, wherein the subject is a human.
9. The method of claim 1, wherein the level of expression is increased or reduced compared to a control.
10. The method of claim 1, wherein said measuring the level of expression comprises performing *in situ* hybridization, a PCR-based method, an array-based method, an immunohistochemical method, an RNA assay method, or an immunoassay method.
11. The method of claim 10, wherein said measuring the level of expression comprises using a reagent selected from the group consisting of a nucleic acid probe, one or more nucleic acid primers, and an antibody.
12. The method of claim 11, wherein said measuring the level of expression comprises measuring the level of an RNA transcript.
13. The method of claim 11, further comprising administering at least one cancer treatment selected from the group consisting of surgery, radiation therapy, immunotherapy,

biological therapy, neoadjuvant chemotherapy, and photodynamic therapy after the androgen deprivation therapy.

14. A method for determining a treatment for a subject who has prostate cancer, the method comprising:

- a) providing a biological sample from the subject;
- b) measuring levels of expression in the biological sample of a plurality of genes selected from Table 8, Table 9 or SEQ ID NOs: 1-1029;
- c) subtyping the prostate cancer in the subject according to a genomic subtyping classifier based on the levels of expression of the plurality of genes, wherein said subtyping comprises assigning the prostate cancer to one of three subtypes selected from the group consisting of a luminal A subtype, a luminal B subtype, and a basal subtype; and
- d) determining whether or not the subject is likely to be responsive to androgen deprivation therapy based on the subtype of the prostate cancer in the subject; and
- a) prescribing androgen deprivation therapy to the subject if the patient is identified as likely to be responsive to androgen deprivation therapy, or prescribing a cancer treatment other than androgen deprivation therapy to the subject if the subject is not identified as likely to be responsive to androgen deprivation therapy.

15. A kit for predicting response of a subject to androgen deprivation therapy, the kit comprising agents for measuring levels of expression of a plurality of genes, wherein said plurality of genes comprises one or more genes selected from Table 8, Table 9 or SEQ ID NOs: 1-1029.

16. The kit of claim 15, wherein the kit comprises agents for measuring the levels of expression of the genes listed in Table 8 or Table 9.

17. The kit of claim 15, wherein said agents comprise reagents for performing *in situ* hybridization, a PCR-based method, an array-based method, an immunohistochemical method, an RNA assay method, or an immunoassay method.

18. The kit of claim 15, wherein said agents comprise one or more of a microarray, a nucleic acid probe, a nucleic acid primer, or an antibody.

19. The kit of claim 15, wherein the kit comprises at least one set of PCR primers capable of amplifying a nucleic acid comprising a sequence of a gene selected from Table 8 or Table 9 or its complement.

The kit of claim 15, wherein the kit comprises at least one probe capable of hybridizing to a nucleic acid comprising a sequence of a gene selected from Table 8 or Table 9 or its complement.

20. The kit of claim 15, further comprising information, in electronic or paper form, comprising instructions on how to determine if a subject is likely to be responsive to androgen deprivation therapy.
21. The kit of claim 15, further comprising one or more control reference samples.
22. A probe set for predicting benefit from androgen deprivation therapy in a subject who has prostate cancer, the probe set comprising a plurality of probes for detecting a plurality of target nucleic acids, wherein the plurality of target nucleic acids comprises one or more gene sequences, or complements thereof, of genes selected from Table 8 or Table 9.
23. The probe set of claim 23, wherein at least one probe is detectably labeled.
24. A kit for predicting response of a subject to androgen deprivation therapy comprising the probe set of claim 23.
25. A system for analyzing a prostate cancer to predict response of a subject to androgen deprivation therapy, the system comprising:
- a) the probe set of claim 23; and
 - b) a computer model or algorithm for analyzing an expression level or expression profile of the plurality of target nucleic acids hybridized to the plurality of probes in a biological sample from a subject who has prostate cancer and subtyping the prostate cancer of the subject according to a genomic subtyping classifier based on the expression level or expression profile, wherein said subtyping comprises assigning the prostate cancer to one of three subtypes selected from the group consisting of a luminal A subtype, a luminal B subtype, and a basal subtype.
26. A kit for predicting response of a subject to androgen deprivation therapy comprising the system of claim 26.
27. The kit of claim 27, further comprising a computer model or algorithm for designating a treatment modality for the subject.
28. The kit of claim 27, further comprising a computer model or algorithm for normalizing the expression level or expression profile of the plurality of target nucleic acids.
29. A method for treating a subject with prostate cancer, the method comprising: a) providing a biological sample from a subject having prostate cancer; b) detecting the presence or expression level in the biological sample for a plurality of targets selected from Table 8, Table 9 or SEQ ID NOs: 1-1029; and c) administering a treatment to the subject, wherein the treatment is selected from the group consisting of androgen deprivation therapy or an anti-cancer treatment.

30. The method of claim 30, wherein the anti-cancer treatment is selected from the group consisting of surgery, chemotherapy, radiation therapy, immunotherapy, biological therapy, hormonal therapy, and photodynamic therapy.

31. The method of claim 30, further comprising subtyping the prostate cancer in the subject according to a genomic subtyping classifier based on the presence or expression levels of the plurality of targets, wherein said subtyping comprises assigning the prostate cancer to one of three subtypes selected from the group consisting of a luminal A subtype, a luminal B subtype, and a basal subtype.

32. A method comprising: a) providing a biological sample from a subject having prostate cancer; b) detecting the presence or expression level in the biological sample for a plurality of targets selected from the group consisting of CDC20, KIF2C, PHGDH, NUF2, CENPF, EXO1, UBE2T, RRM2, MLPH, GPR160, CCNB1, CXXC5, PTTG1, FGFR4, FOXC1, ESR1, ANLN, BLVRA, EGFR, ACTR3B, NAT1, MYC, SFRP1, MELK, BAG1, CEP55, MKI67, TMEM45B, PGR, MDM2, KRT5, FOXA1, ORC6, CDH3, ERBB2, GRB7, CDC6, MAPT, BIRC5, KRT14, KRT17, TYMS, NDC80, SLC39A6, BCL2, CCNE1, MIA, MYBL2, UBE2C, and MMP11; and c) subtyping the prostate cancer in the subject according to a genomic subtyping classifier based on the presence or expression levels of the plurality of targets, wherein said subtyping comprises assigning the prostate cancer to one of three subtypes selected from the group consisting of a luminal A subtype, a luminal B subtype, and a basal subtype.

33. The method of claim 33, further comprising administering androgen deprivation therapy to the subject if the subtyping indicates that the subject has the luminal B subtype and administering an anti-cancer treatment other than the androgen deprivation therapy to the subject if the subtyping indicates that the subject has the luminal A subtype or the basal subtype, wherein the anti-cancer treatment other than androgen deprivation therapy is selected from the group consisting of surgery, chemotherapy, radiation therapy, immunotherapy, biological therapy, neoadjuvant chemotherapy, and photodynamic therapy.



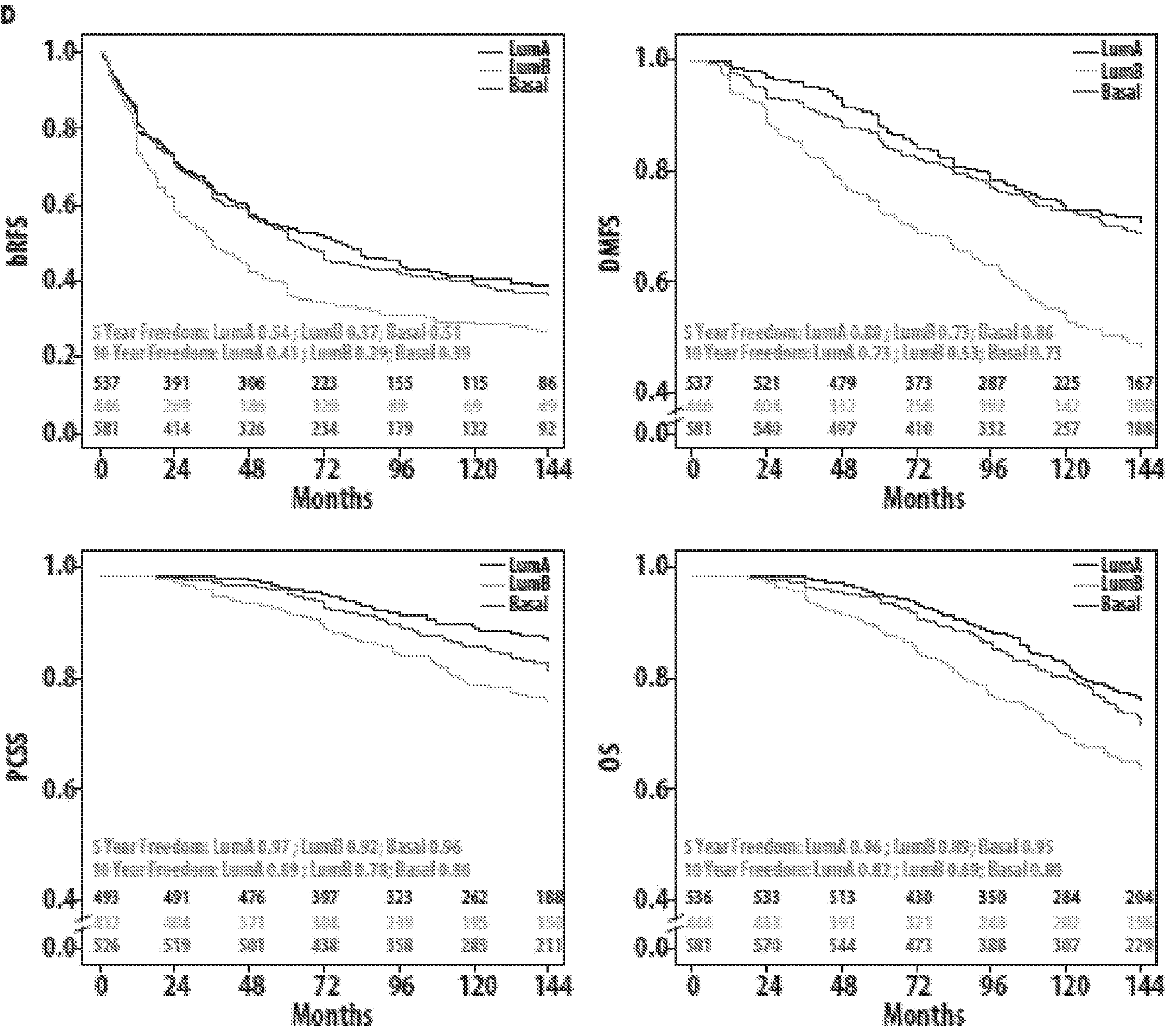


FIGURE 1B

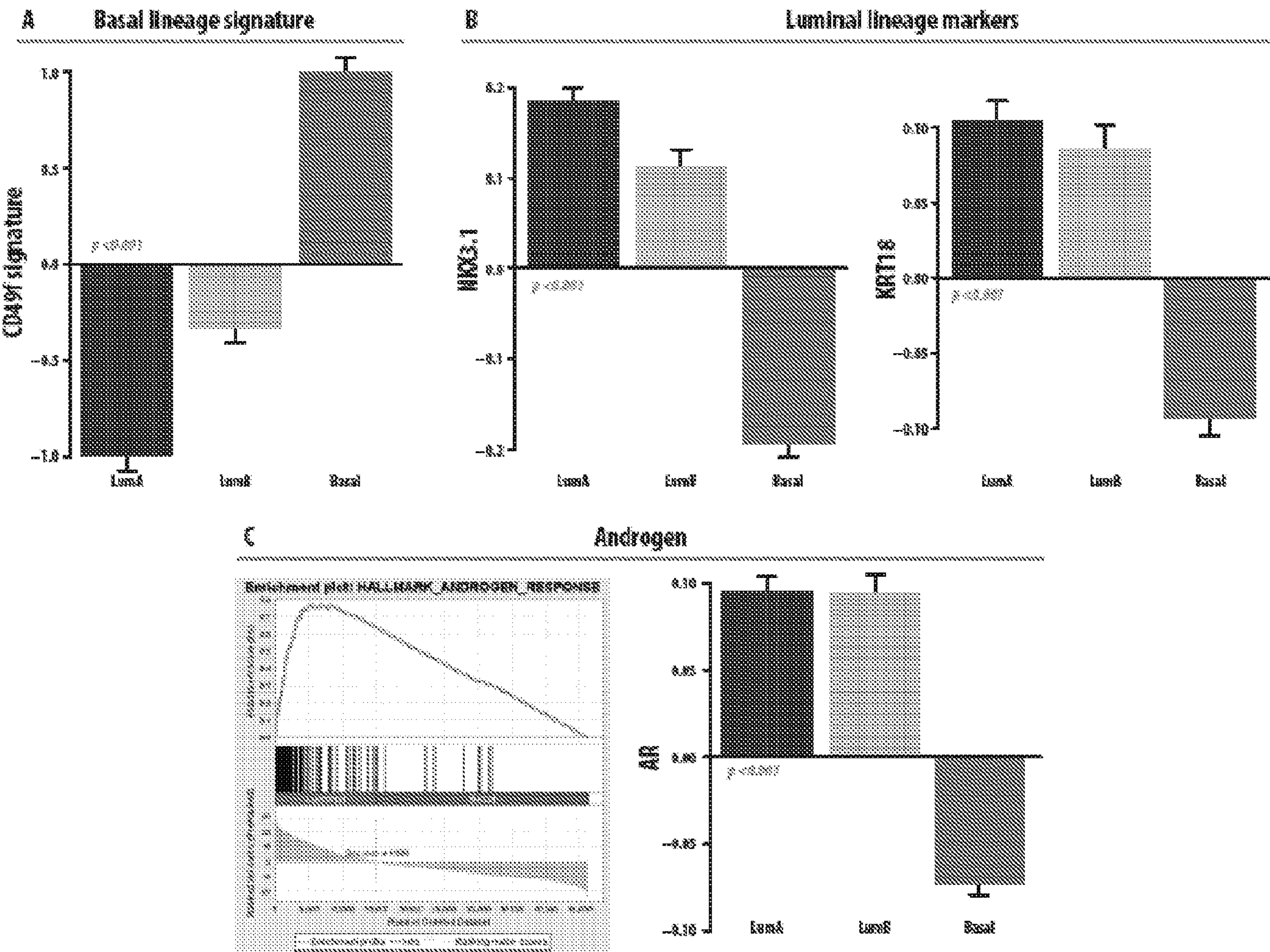


FIGURE 2

Prospective Validation Cohort (GRID) (n=2215)
Commercially run prostatectomy samples on a CLIA-certified platform

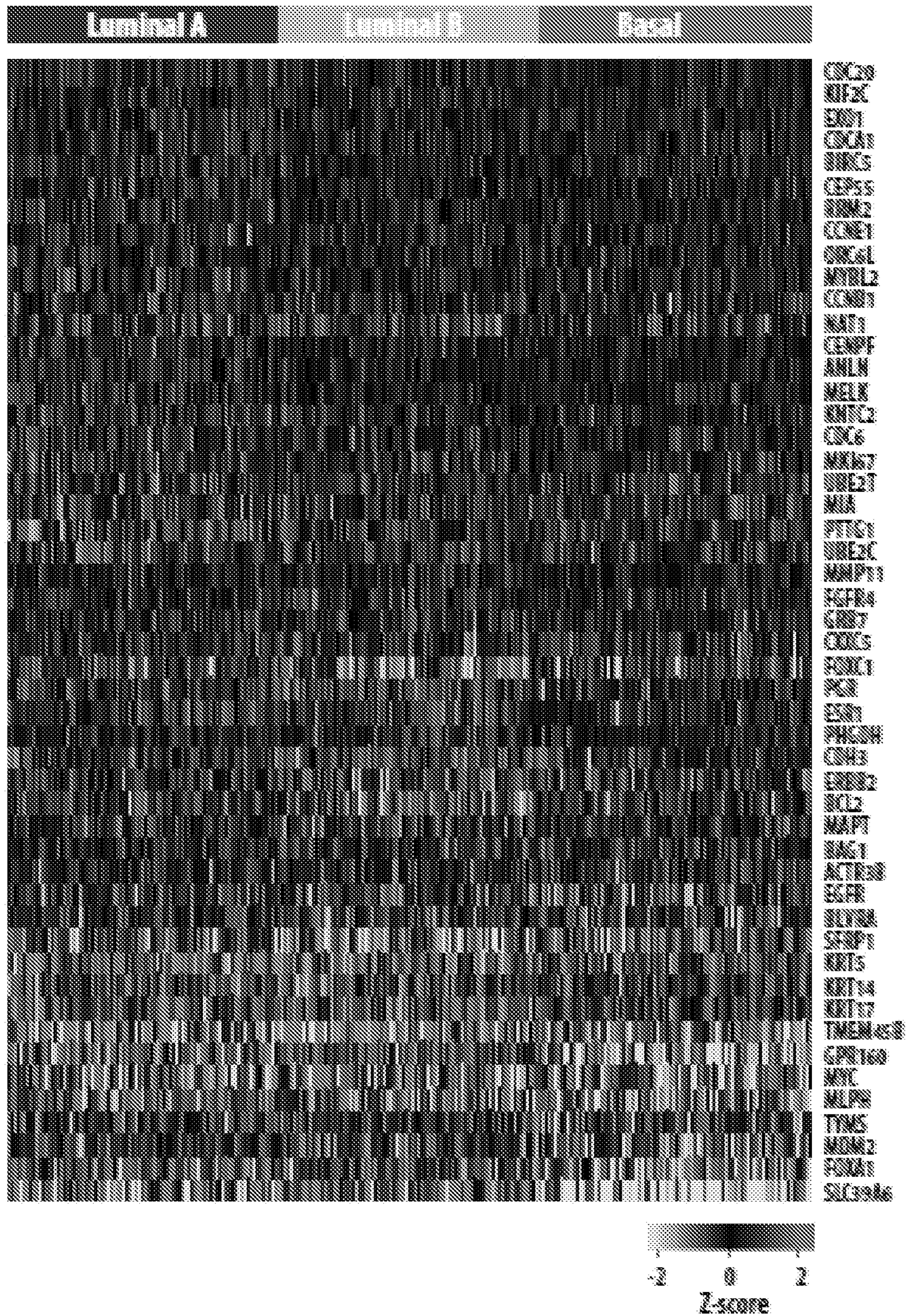
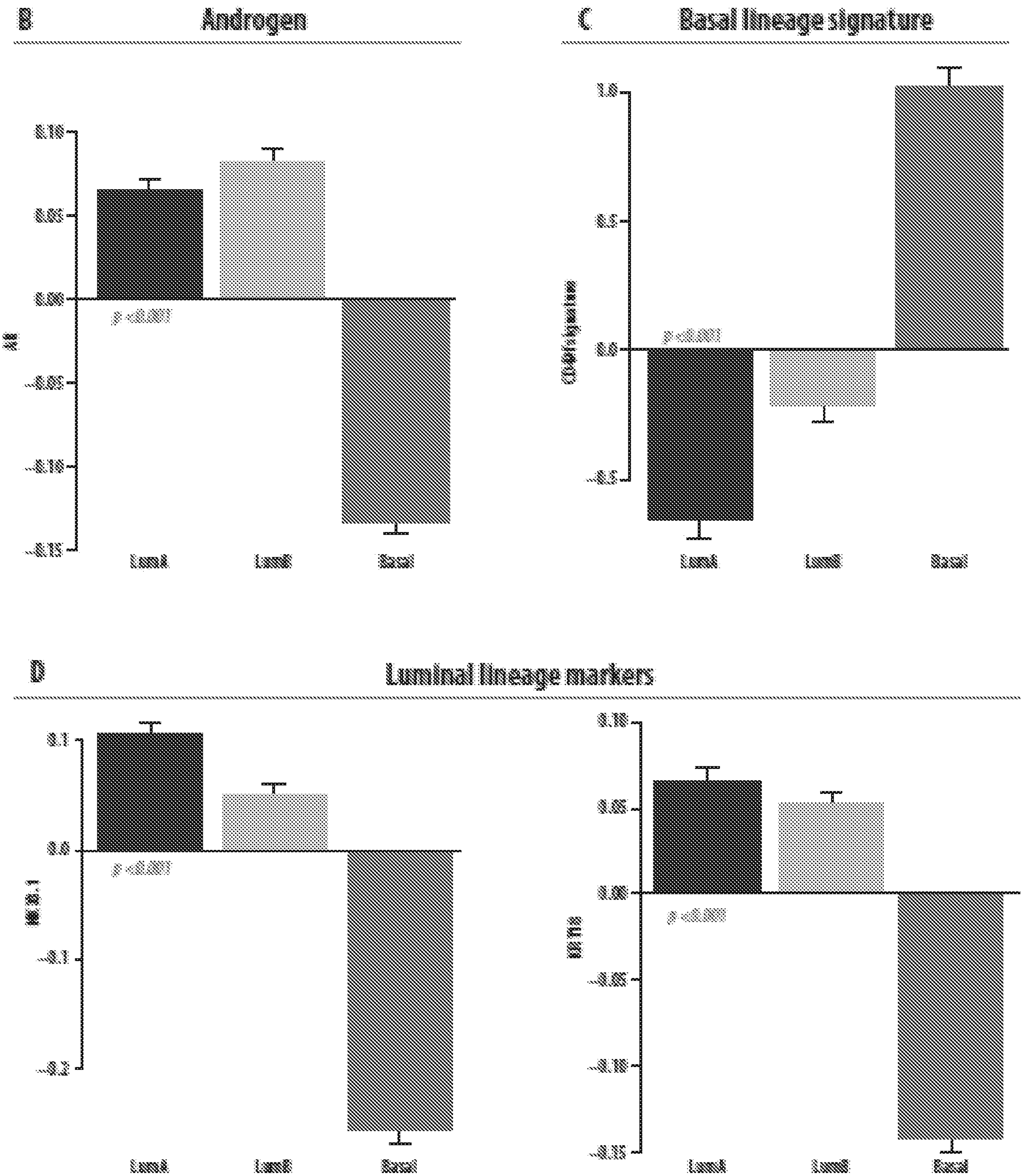


FIGURE 3A



FIGURES 3B-3D

6/14

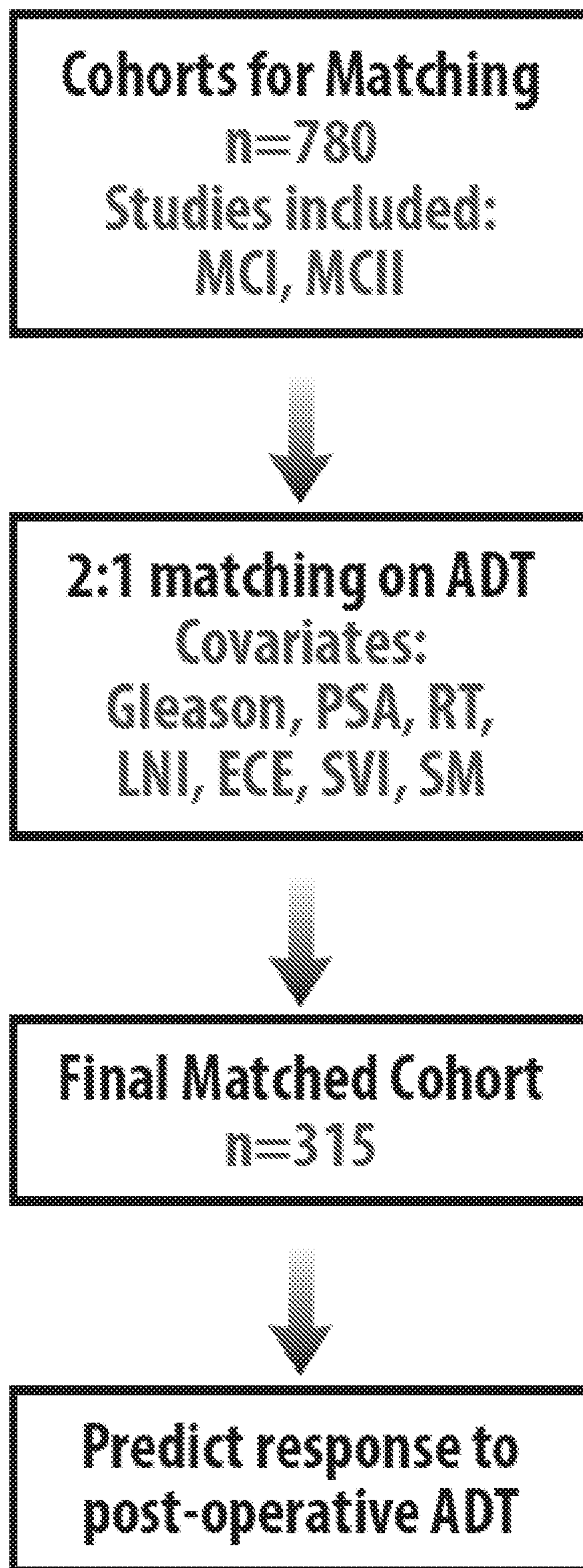


FIGURE 4A

7/14

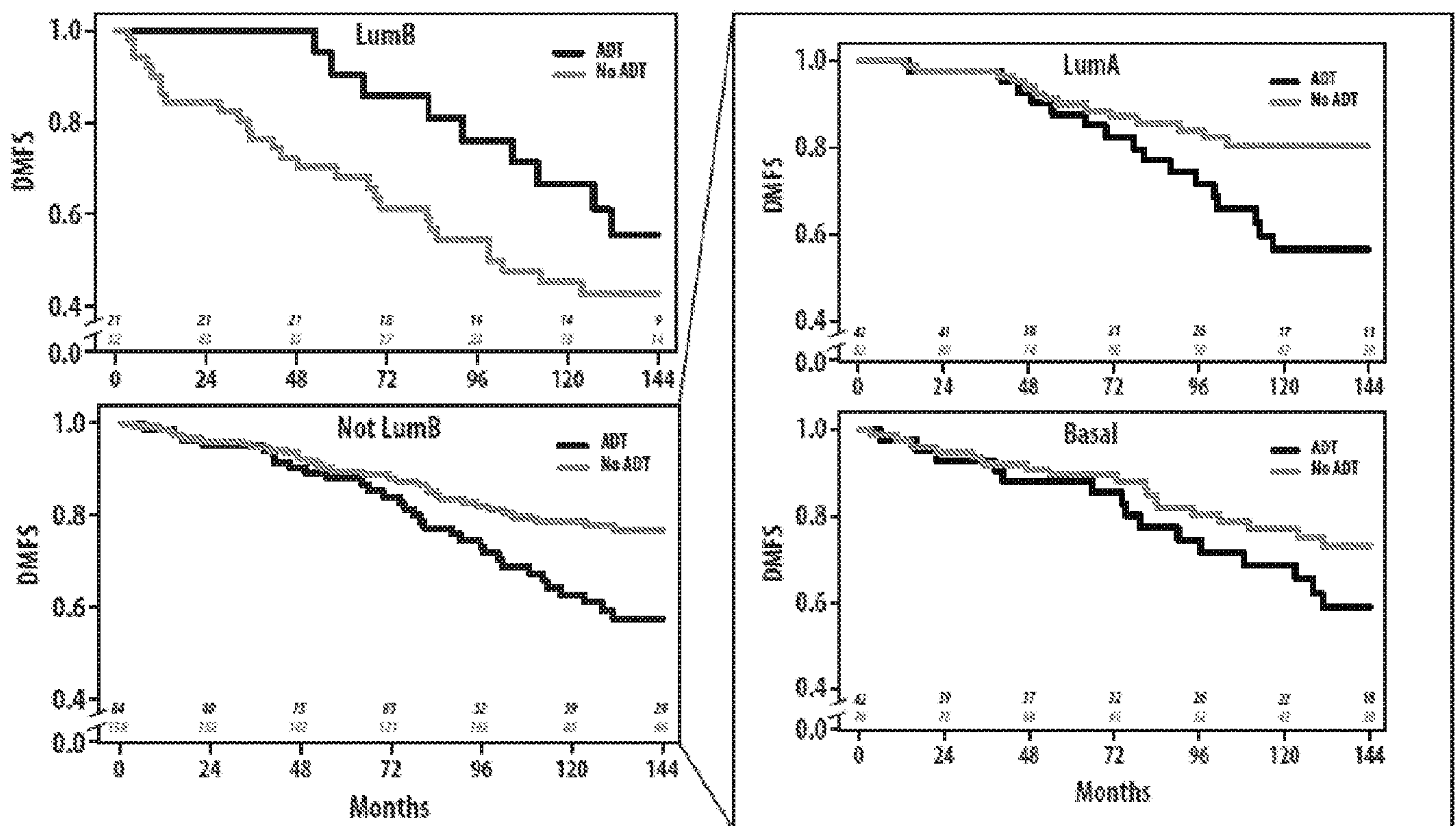


FIGURE 4B

8/14

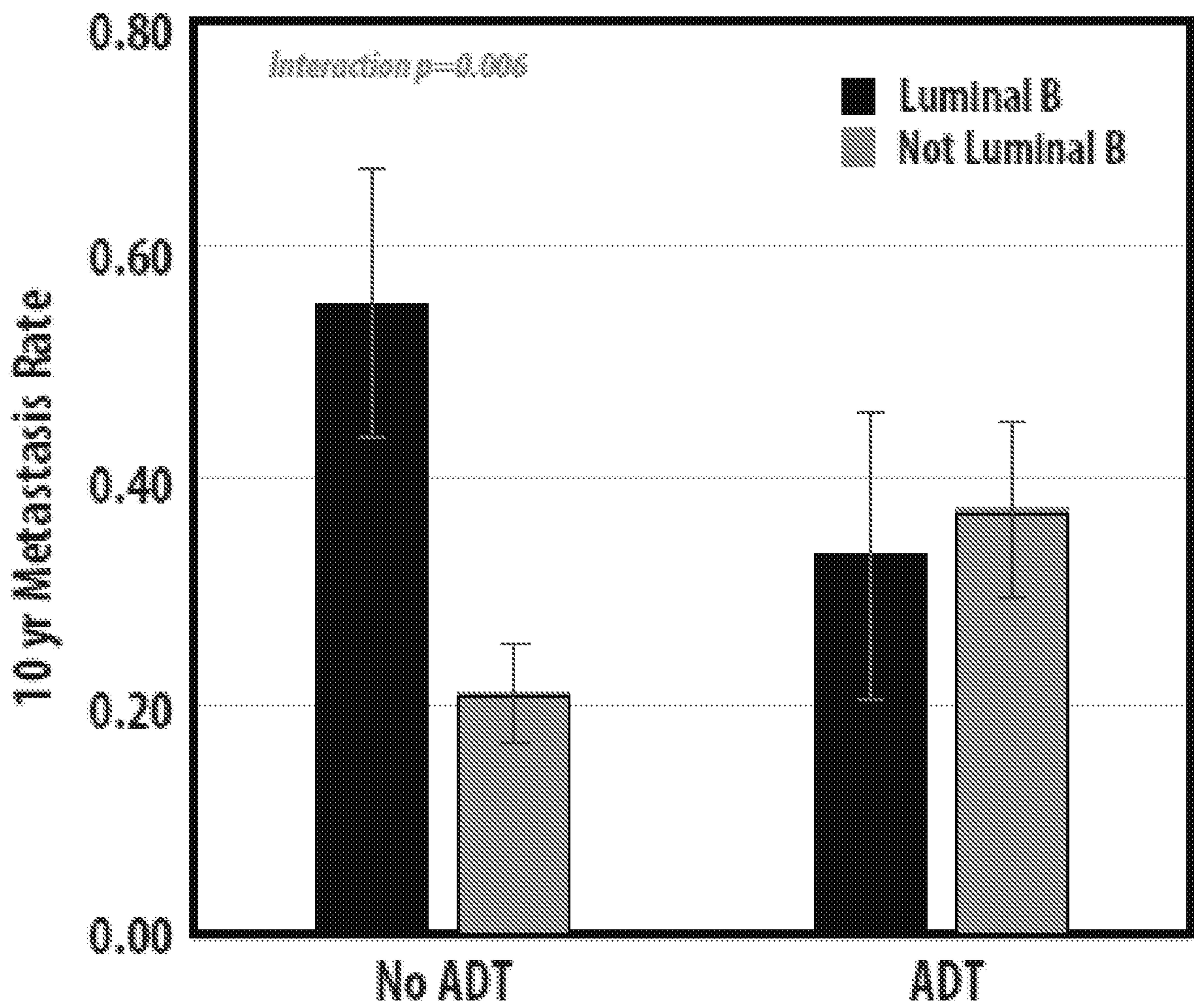


FIGURE 4C

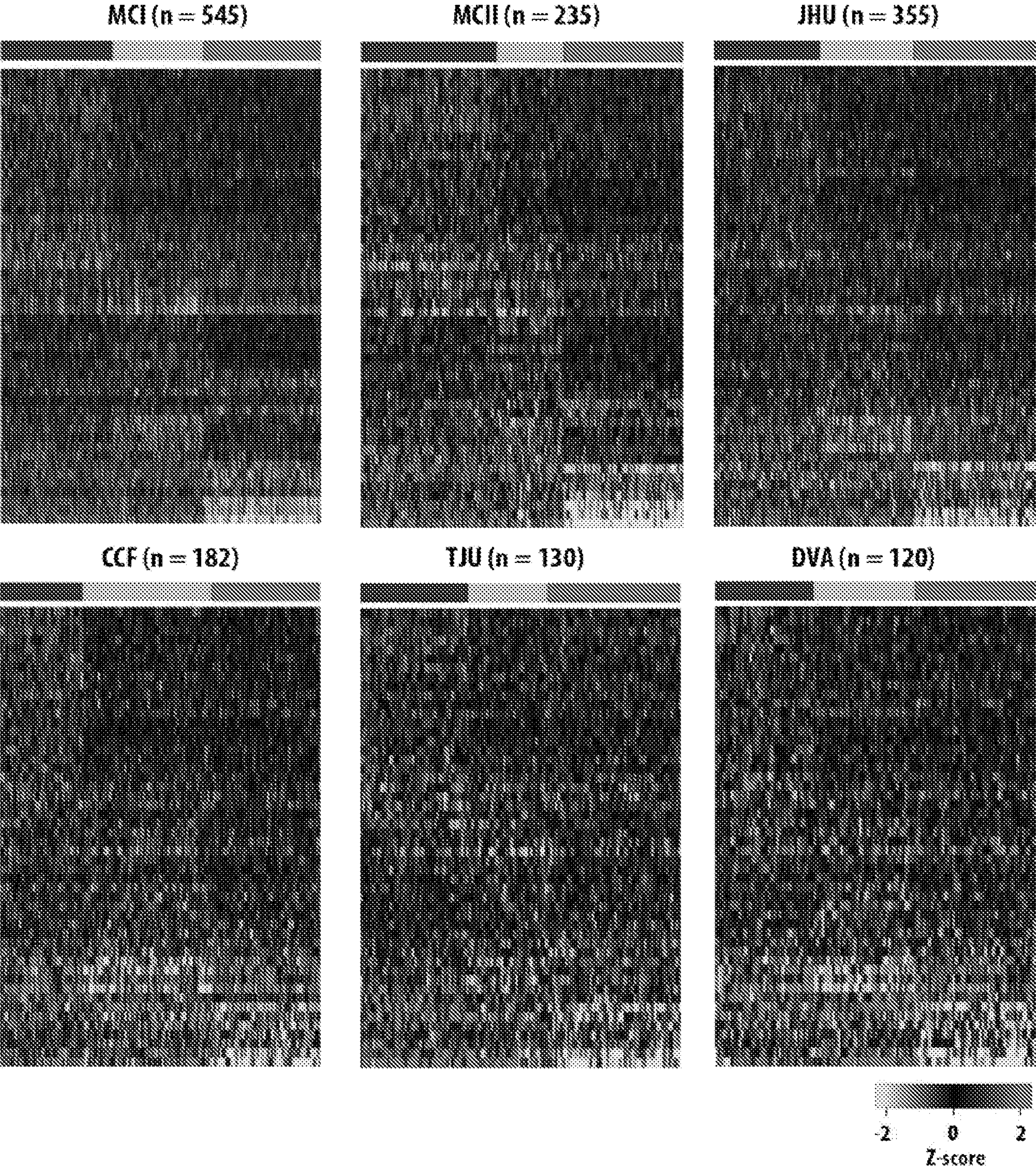


FIGURE 5

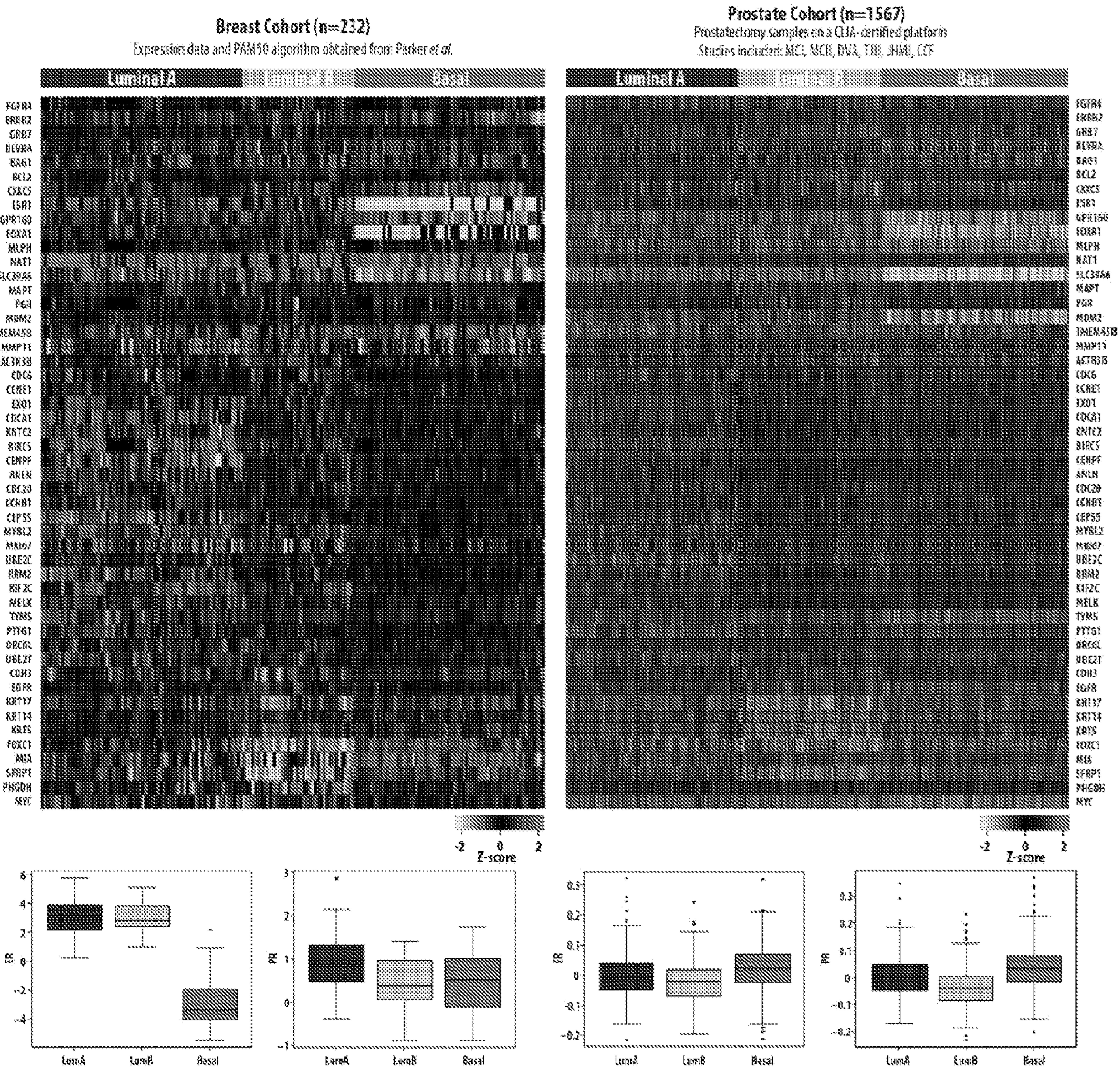


FIGURE 6

Retrospective Cohorts

Prospective GRID Cohort

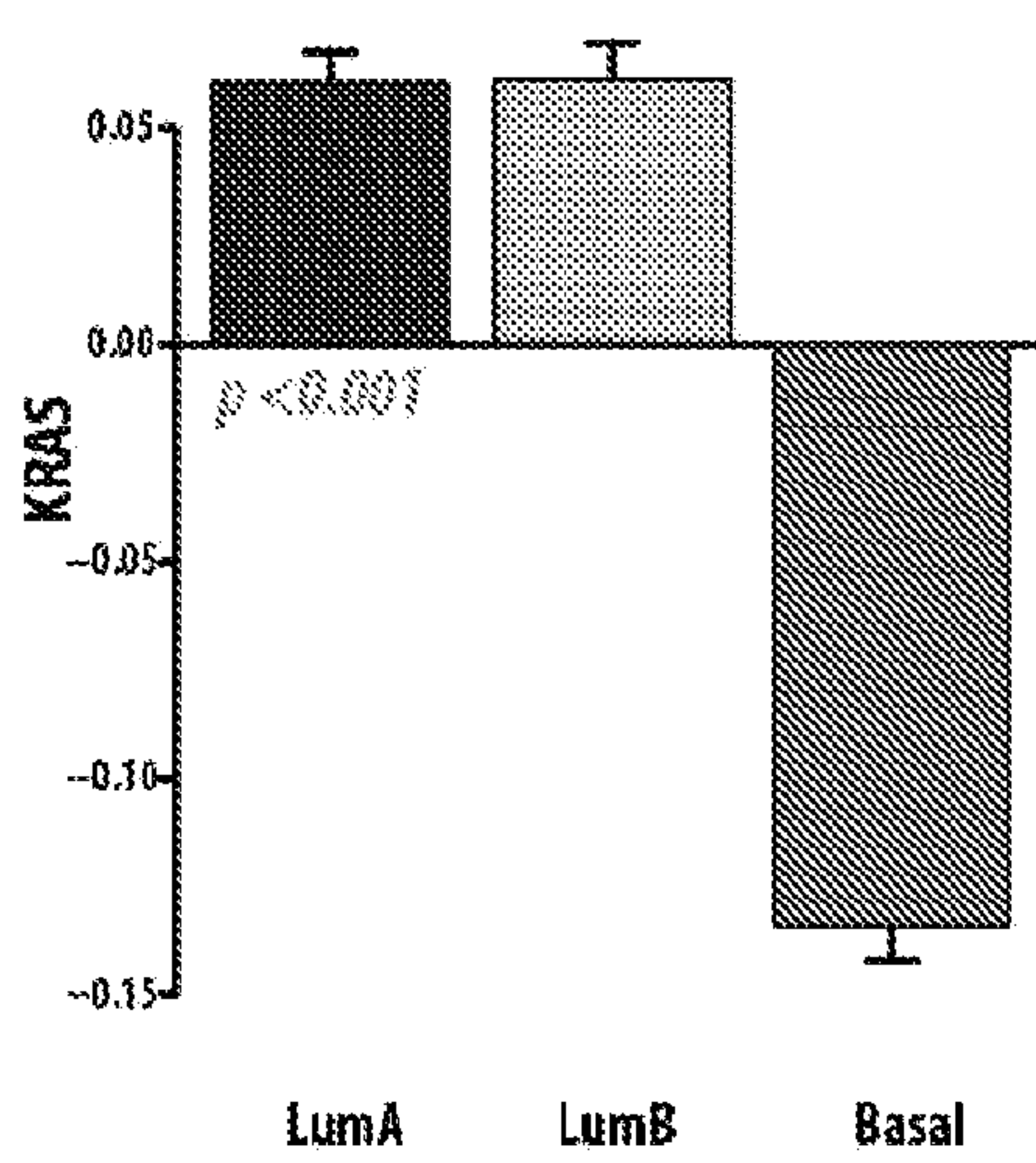
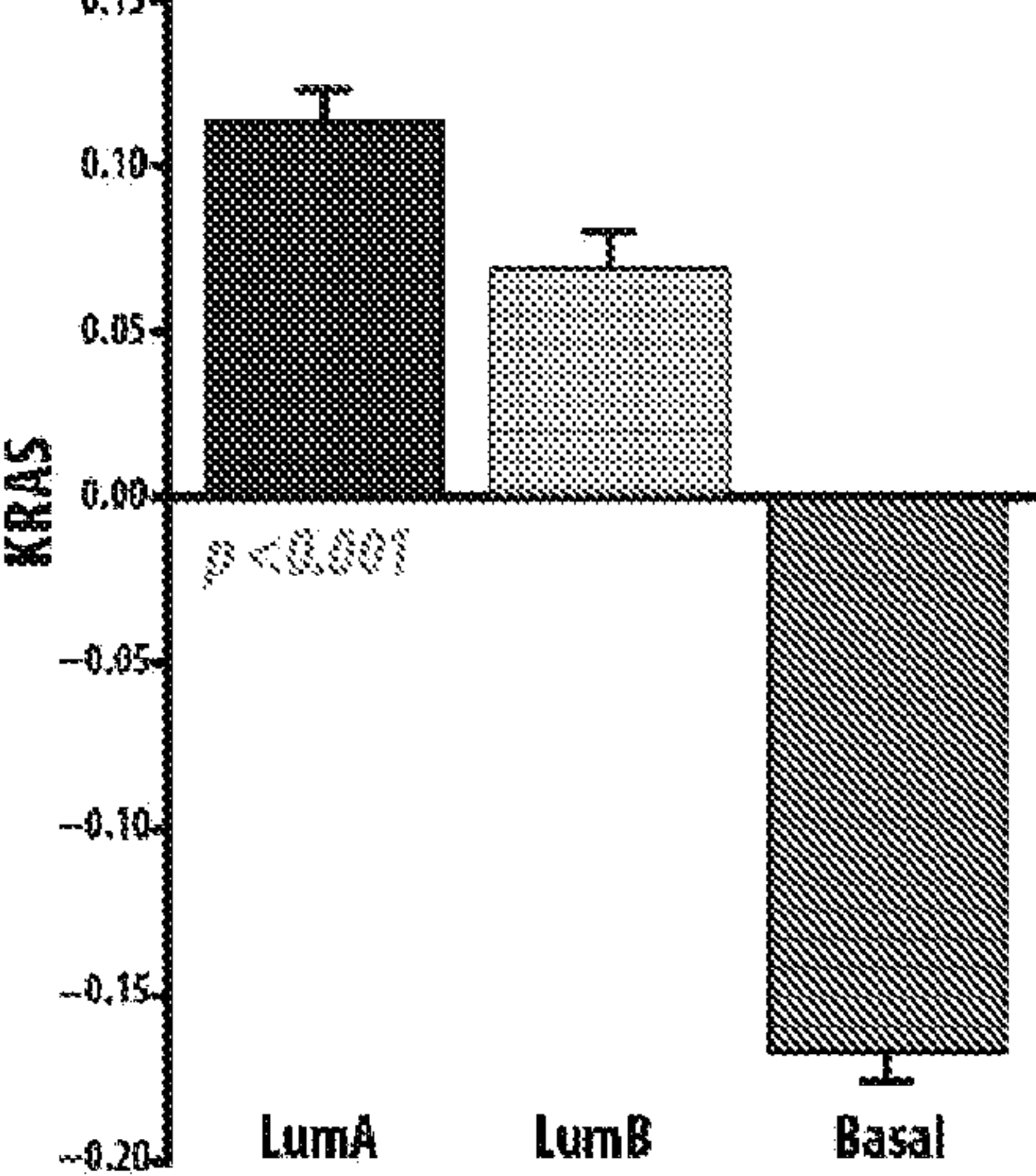
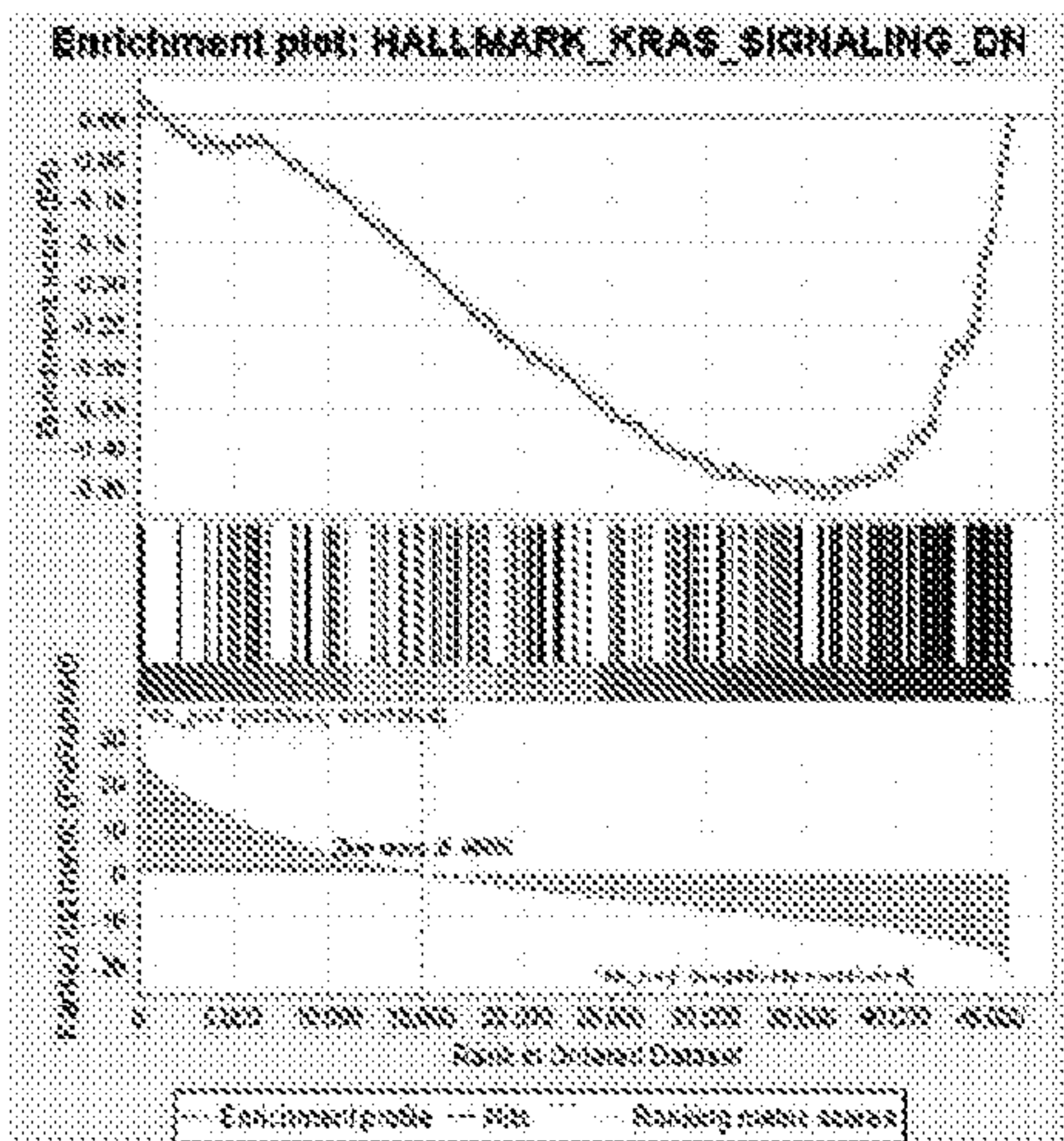
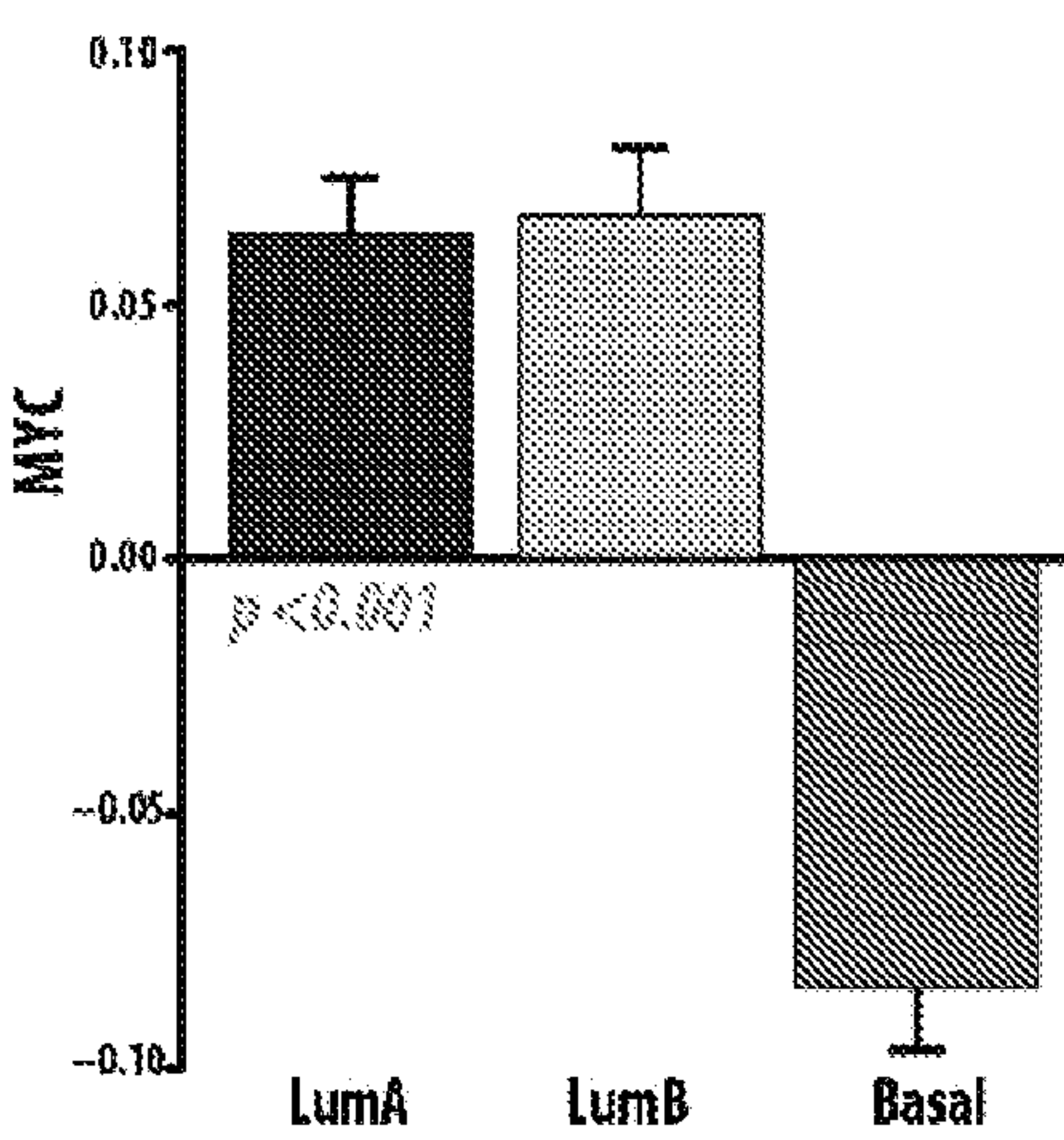
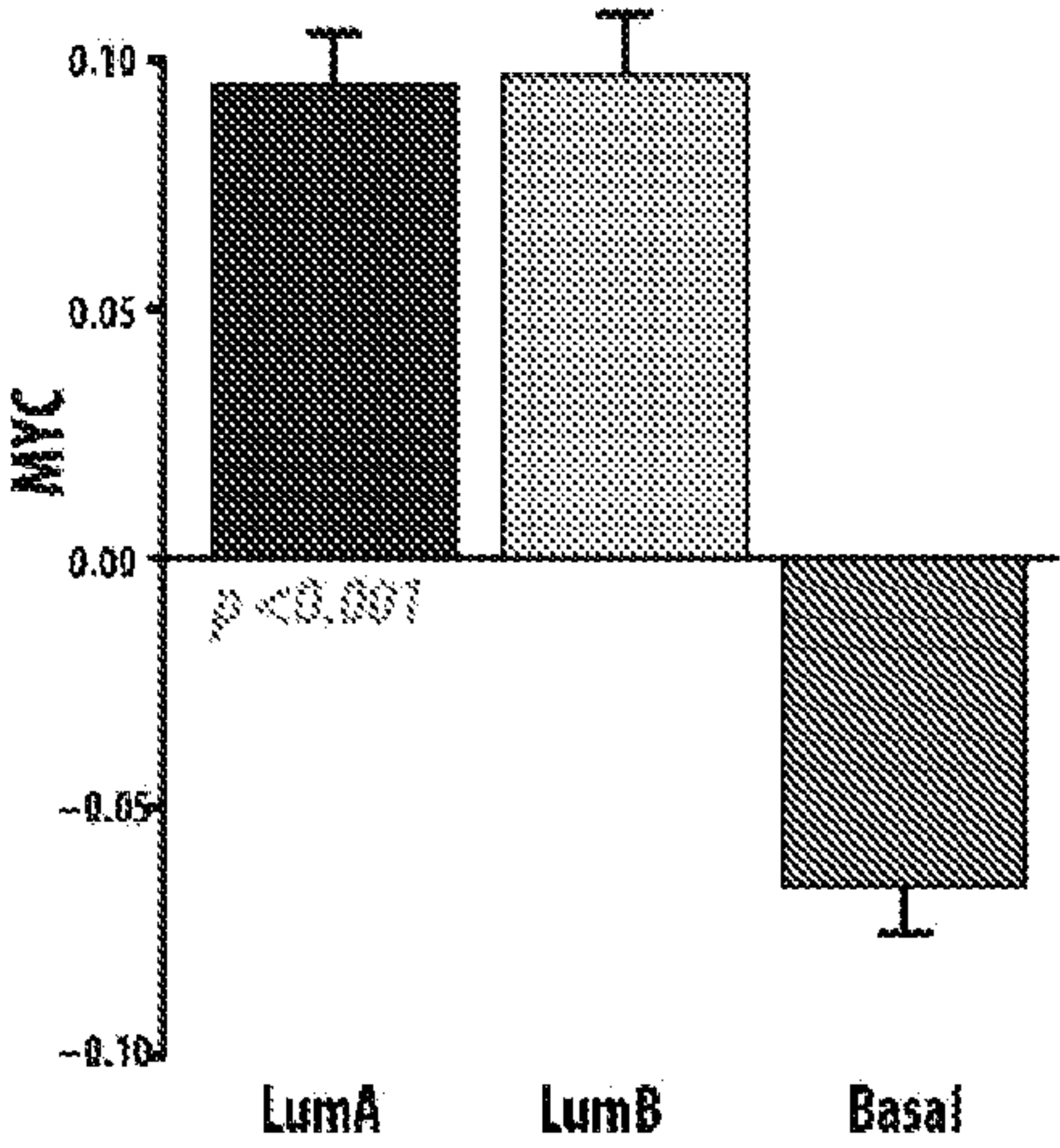
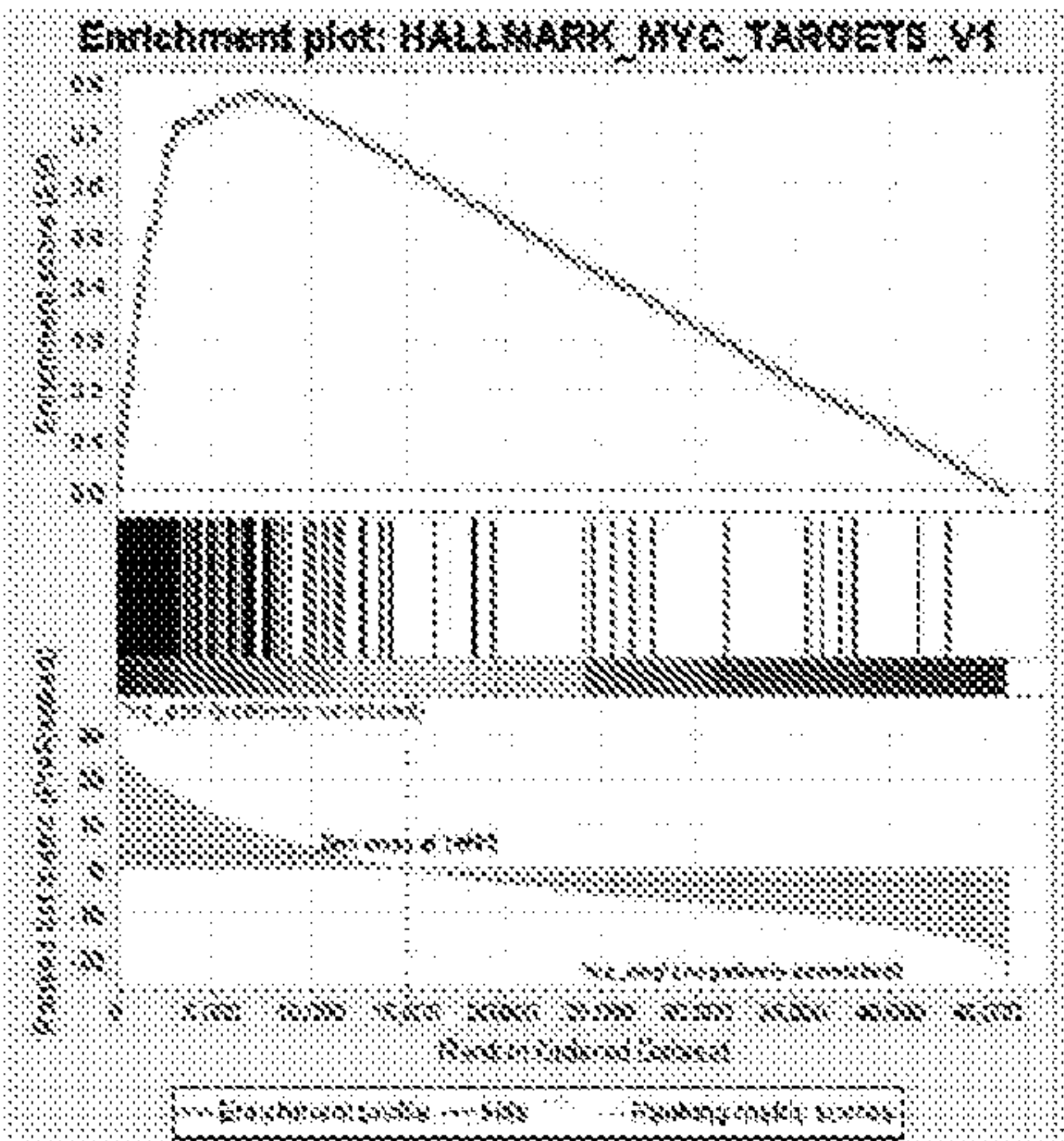


FIGURE 7

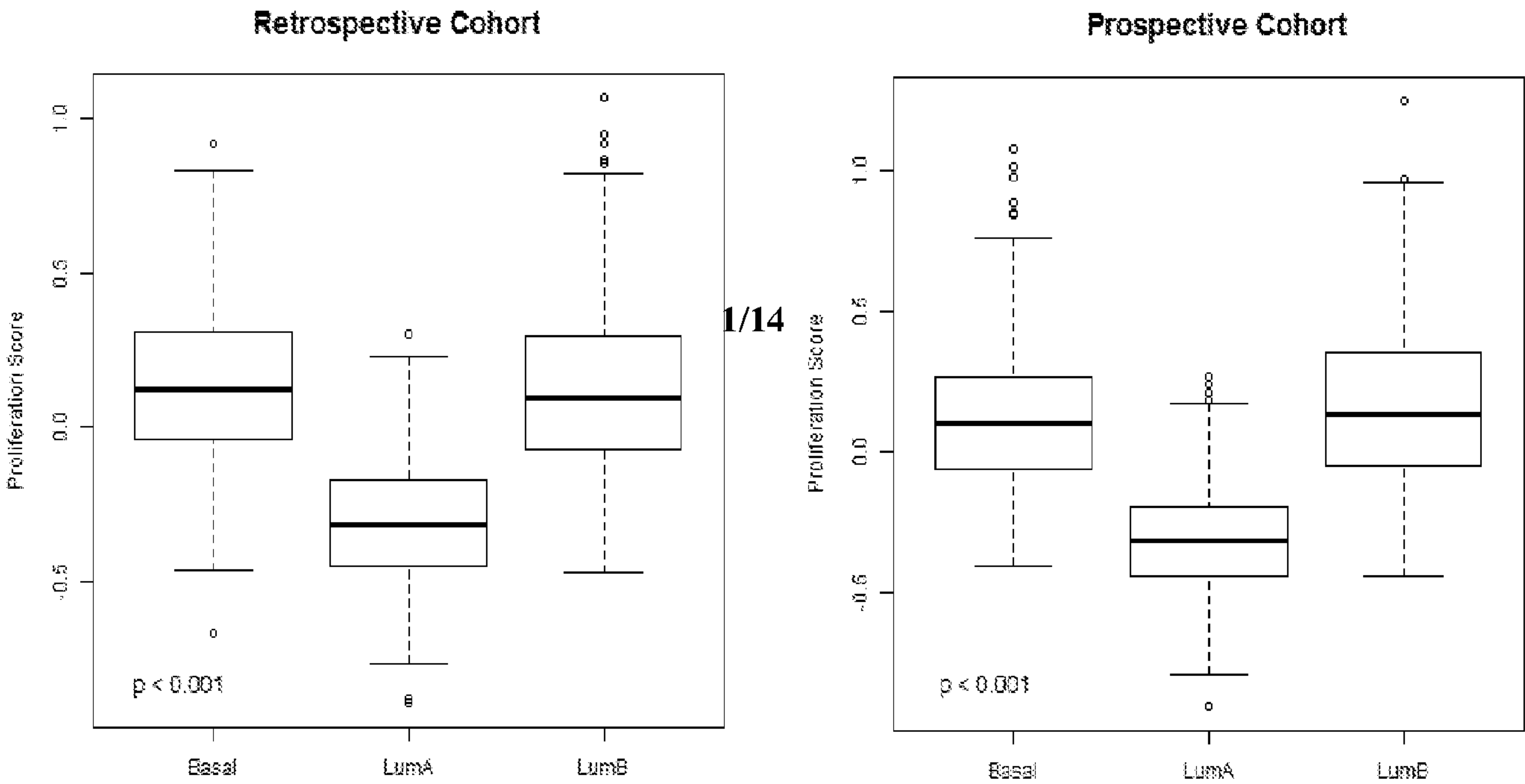


FIGURE 8

13/14

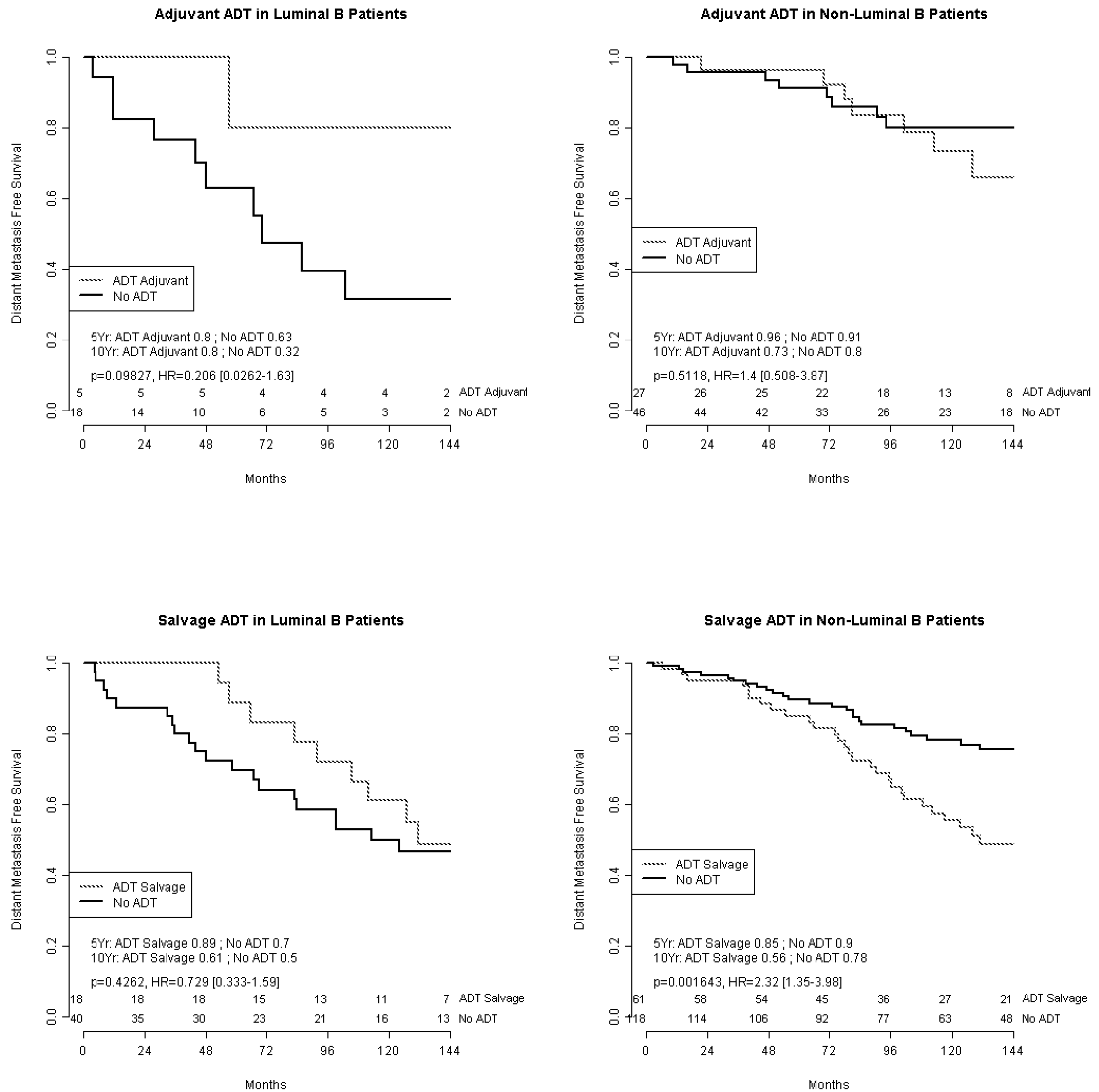


FIGURE 9

14/14

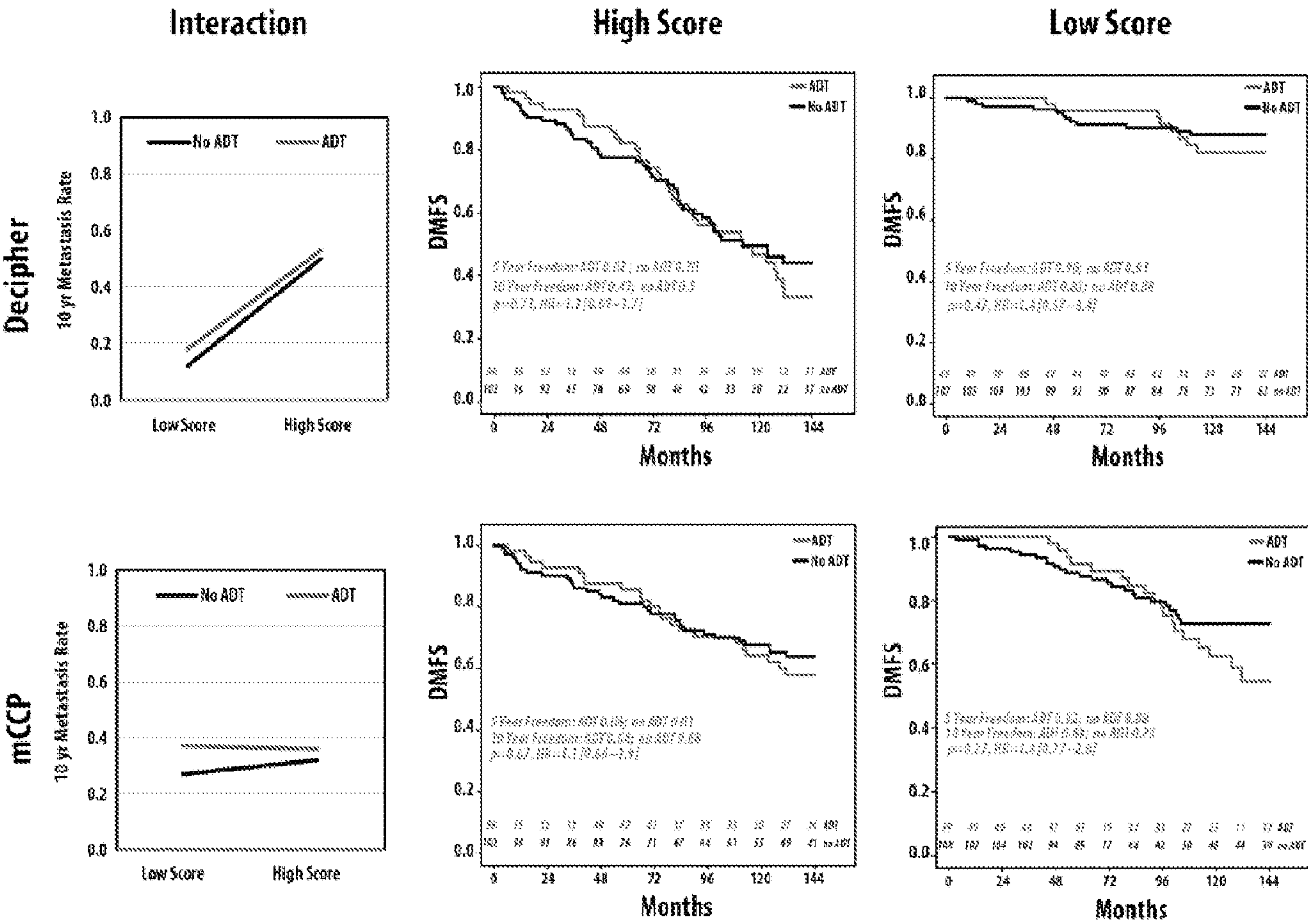


FIGURE 10

