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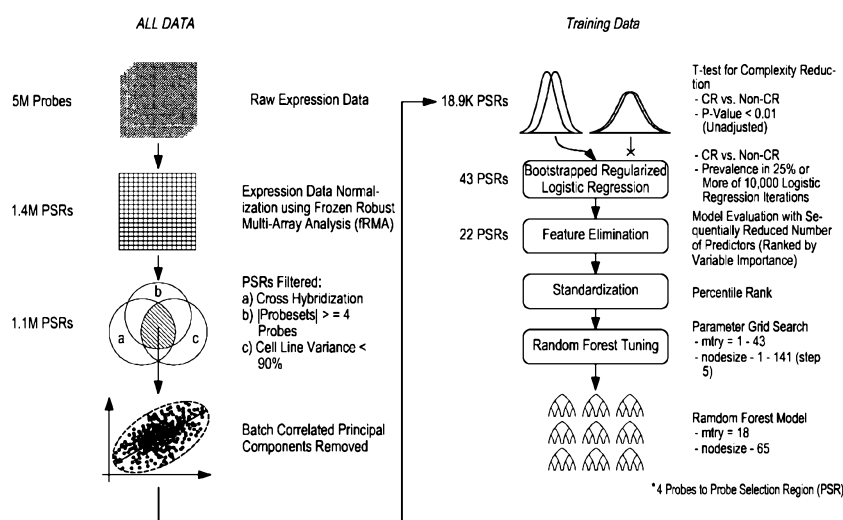


FIG. 3

(57) Abstract: Disclosed herein, in certain instances, are methods, systems and kits for the diagnosis, prognosis and determination of cancer progression of a cancer in a subject. Further disclosed herein, in certain instances, are methods, systems and kits for determining the treatment modality of a cancer in a subject. The methods, systems and kits comprise expression-based analysis of biomarkers. Further disclosed herein, in certain instances, are probe sets for use in assessing a cancer status in a subject.



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CANCER DIAGNOSTICS USING BIOMARKERS

BACKGROUND OF THE INVENTION

[0001] 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, breast cancer, lung cancer, colon cancer, prostate cancer, pancreatic cancer, thyroid cancer). Cancer is not confined to humans; animals and other living organisms can get 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 breast cancer cells spread to a bone (or anywhere else), it can mean that the individual has metastatic breast cancer.

[0002] 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, disclosed herein are methods, compositions and systems for the analysis of coding and non-coding targets for the diagnosis, prognosis, and monitoring of a cancer.

[0003] 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

[0004] Disclosed herein in some embodiments is a method of diagnosing, prognosing, determining progression the cancer, predicting a therapeutic regimen or predicting benefit from therapy in a subject, comprising (a) assaying an expression level in a sample from the subject for a plurality of targets, wherein the plurality of targets comprises more than one target selected from Tables 2, 4, 11 or 55; and (b) diagnosing, prognosing, determining progression the cancer, predicting a therapeutic regimen or predicting benefit from therapy in a subject based on the expression levels of the plurality of targets. In some embodiments, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In some embodiments, cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas. In some embodiments, the cancer is a prostate cancer. In some embodiments, the cancer is a pancreatic cancer. In some embodiments, the cancer is a thyroid cancer. In some embodiments, the cancer is a bladder cancer. In some embodiments, the plurality of targets comprises a coding target. In some embodiments, the coding target is a coding antisense sequence an exonic sequence. In some embodiments, the plurality of targets comprises a non-coding target. In some embodiments, the non-coding target comprises an intronic sequence or partially overlaps an intronic sequence. In some embodiments, the non-coding target comprises an intronic sequence or partially overlaps an intronic sequence. In some embodiments, the non-coding target comprises a sequence within the UTR or partially overlaps with a UTR sequence. In some embodiments, the non-coding target comprises an antisense sequence or partially overlaps with an antisense sequence. In some embodiments, the non-coding target comprises an intergenic sequence. In some embodiments, the target comprises a nucleic acid sequence. In some embodiments, the nucleic acid sequence is a DNA sequence. In some embodiments, the nucleic acid sequence is an RNA sequence. In some embodiments, the plurality of targets comprises at least 5 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 10 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 15 targets selected from Tables 2, 4,

11 or 55. In some embodiments, the plurality of targets comprises at least 20 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 22 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 30 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 35 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 40 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 5 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets is selected from SEQ ID NOs:1-43. In some embodiments, the plurality of targets is selected from SEQ ID NOs:1-22. In certain embodiments, the plurality of targets is selected from the group consisting of: PBX1, MYBPC1, LASP1, CAMK2N1, RABGAP1, UBE2C, PCAT-32, NF1B, TNFRSF19, PCDH7, ANO7, GLYATL1P4/PCAT-80, C6orf10, IQGAP3, THBS2, EPPK1, NUSAP1, ZWILCH, S1P4, SENP7, ANLN, C10orf116, PPP6R3, PDS5B, TOP2A, IL1RAP, CENPE, GALNT8, KCNQ1, C6orf155, LUZP2, HEATR3, TMEM108, CFBXXbac-BPG116M5.17, ECHDC2, and ARNTL. In other embodiments the plurality of targets is selected from the group consisting of: PBX1, MYBPC1, LASP1, CAMK2N1, RABGAP1, UBE2C, PCAT-32, NF1B, TNFRSF19, PCDH7, ANO7, GLYATL1P4/PCAT-80, C6orf10, IQGAP3, THBS2, EPPK1, NUSAP1, ZWILCH, and S1P4. In some embodiments, the diagnosing, prognosing, determining progression the cancer, predicting a therapeutic regimen or predicting benefit from therapy includes determining the malignancy of the cancer. In some embodiments, the diagnosing, prognosing, determining progression the cancer, predicting a therapeutic regimen or predicting benefit from therapy includes determining the stage of the cancer. In some embodiments, the diagnosing, prognosing, determining progression the cancer, predicting a therapeutic regimen or predicting benefit from therapy includes assessing the risk of cancer recurrence. In some embodiments, the diagnosing, prognosing, determining progression the cancer, predicting a therapeutic regimen or predicting benefit from therapy includes assessing the grade of the cancer. In some embodiments, determining the treatment for the cancer includes determining the efficacy of treatment. 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.

[0005] Disclosed herein in some embodiments is a method of determining a treatment for a cancer in a subject, comprising (a) assaying an expression level in a sample from the subject for a plurality of targets, wherein the plurality of targets comprises more than one target selected from Tables 2, 4, 11 or 55; and (b) determining the treatment for the cancer based on the expression level of the plurality of targets. In some embodiments, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In some embodiments, cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas. In some embodiments, the cancer is a prostate cancer. In some embodiments, the cancer is a bladder cancer. In some embodiments, the cancer is a pancreatic cancer. In some embodiments, the cancer is a thyroid cancer. In some embodiments, the plurality of targets comprises a coding target. In some embodiments, the coding target is a coding antisense sequence or an exonic sequence. In some embodiments, the plurality of targets comprises a non-coding target. In some embodiments, the non-coding target comprises an intronic sequence or partially overlaps an intronic sequence. In some embodiments, the non-coding target comprises an intergenic sequence. In some embodiments, the non-coding target comprises a sequence within the UTR or partially overlaps with a UTR sequence. In some embodiments, the target comprises a nucleic acid sequence. In some embodiments, the nucleic acid sequence is a DNA sequence. In some embodiments, the nucleic acid sequence is an RNA sequence. In some embodiments, the plurality of targets comprises at least 5 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 10 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 15 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 20 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets

comprises at least 22 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 30 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 35 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 40 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 5 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets is selected from SEQ ID NOs:1-43. In some embodiments, the plurality of targets is selected from SEQ ID NOs:1-22. In certain embodiments, the plurality of targets is selected from the group consisting of: PBX1, MYBPC1, LASP1, CAMK2N1, RABGAP1, UBE2C, PCAT-32, NF1B, TNFRSF19, PCDH7, ANO7, GLYATL1P4/PCAT-80, C6orf10, IQGAP3, THBS2, EPPK1, NUSAP1, ZWILCH, S1P4, SENP7, ANLN, C10orf116, PPP6R3, PDS5B, TOP2A, IL1RAP, CENPE, GALNT8, KCNQ1, C6orf155, LUZP2, HEATR3, TMEM108, CFBXXbac-BPG116M5.17, ECHDC2, and ARNTL. In other embodiments the plurality of targets is selected from the group consisting of: PBX1, MYBPC1, LASP1, CAMK2N1, RABGAP1, UBE2C, PCAT-32, NF1B, TNFRSF19, PCDH7, ANO7, GLYATL1P4/PCAT-80, C6orf10, IQGAP3, THBS2, EPPK1, NUSAP1, ZWILCH, and S1P4. In some embodiments, the diagnosing, prognosing, determining progression the cancer, predicting a therapeutic regimen or predicting benefit from therapy includes determining the malignancy of the cancer. In some embodiments, the diagnosing, prognosing, determining progression the cancer, predicting a therapeutic regimen or predicting benefit from therapy includes determining the stage of the cancer. In some embodiments, the diagnosing, prognosing, determining progression the cancer, predicting a therapeutic regimen or predicting benefit from therapy includes assessing the risk of cancer recurrence. In some embodiments, determining the treatment for the cancer includes determining the efficacy of treatment. 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 amplifying the plurality of targets. In some embodiments, assaying the expression level may also comprise quantifying the plurality of targets.

[0006] Further disclosed herein in some embodiments is a probe set for assessing a cancer status of a subject comprising a plurality of probes, wherein the probes in the set are capable of detecting an expression level of a plurality of targets selected from Tables 2, 4, 11 or 55, wherein the expression level determines the cancer status of the subject with at least 40% specificity. In some embodiments, the plurality of targets comprises at least 5 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 10 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 15 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 20 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 22 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 30 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 35 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 40 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 5 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets is selected from SEQ ID NOs:1-43. In some embodiments, the plurality of targets is selected from SEQ ID NOs:1-22. In certain embodiments, the plurality of targets is selected from the group consisting of: PBX1, MYBPC1, LASP1, CAMK2N1, RABGAP1, UBE2C, PCAT-32, NF1B, TNFRSF19, PCDH7, ANO7, GLYATL1P4/PCAT-80, C6orf10, IQGAP3, THBS2, EPPK1, NUSAP1, ZWILCH, S1P4, SENP7, ANLN, C10orf116, PPP6R3, PDS5B, TOP2A, IL1RAP, CENPE, GALNT8, KCNQ1, C6orf155, LUZP2, HEATR3, TMEM108, CFBXXbac-BPG116M5.17, ECHDC2, and ARNTL. In other embodiments the plurality of targets is selected from the group consisting of: PBX1, MYBPC1, LASP1, CAMK2N1, RABGAP1, UBE2C, PCAT-32, NF1B, TNFRSF19, PCDH7, ANO7, GLYATL1P4/PCAT-80, C6orf10, IQGAP3, THBS2, EPPK1, NUSAP1, ZWILCH, and S1P4. In some embodiments, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In some embodiments, the cancer is

selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas. In some embodiments, the cancer is a prostate cancer. In some embodiments, the cancer is a bladder cancer. In some embodiments, the cancer is a pancreatic cancer. In some embodiments, the cancer is a thyroid cancer. In some embodiments, the probe set further comprises a probe capable of detecting an expression level of more than one coding target. In some embodiments, the coding target is a coding antisense sequence or an exonic sequence. In some embodiments, the probe set further comprises a probe capable of detecting an expression level of more than one non-coding target. In some embodiments, the non-coding target is an intronic sequence or partially overlaps with an intronic sequence. In some embodiments, the non-coding target is an intergenic sequence. In some embodiments, the non-coding target is a UTR sequence or partially overlaps with a UTR sequence. In some embodiments, assessing the cancer status includes assessing cancer recurrence risk. In some embodiments, assessing the cancer status includes determining a treatment modality. In some embodiments, assessing the cancer status includes determining the efficacy of treatment. In some embodiments, the target is a nucleic acid sequence. In some embodiments, the nucleic acid sequence is a DNA sequence. In some embodiments, the nucleic acid sequence is an RNA sequence. In some embodiments, the probes are between about 15 nucleotides and about 500 nucleotides in length. In some embodiments, the probes are between about 15 nucleotides and about 450 nucleotides in length. In some embodiments, the probes are between about 15 nucleotides and about 400 nucleotides in length. In some embodiments, the probes are between about 15 nucleotides and about 350 nucleotides in length. In some embodiments, the probes are between about 15 nucleotides and about 300 nucleotides in length. In some embodiments, the probes are between about 15 nucleotides and about 250 nucleotides in length. In some embodiments, the probes are between 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 25 nucleotides in length. In some embodiments, the expression level determines the cancer status of the subject with at least 50% specificity. In some embodiments, the expression level determines the cancer status of the subject with at least 60% specificity. In some embodiments, the expression level determines the cancer status of the subject with at least 65% specificity. In some

embodiments, the expression level determines the cancer status of the subject with at least 70% specificity. In some embodiments, the expression level determines the cancer status of the subject with at least 75% specificity. In some embodiments, the expression level determines the cancer status of the subject with at least 80% specificity. In some embodiments, the expression level determines the cancer status of the subject with at least 85% specificity. In some embodiments, the non-coding target is a non-coding RNA transcript and the non-coding RNA transcript is non-polyadenylated.

[0007] Further disclosed herein in some embodiments is a system for analyzing a cancer, comprising: (a) a probe set comprising a plurality of target sequences, wherein (i) the plurality of target sequences hybridizes to more than one target selected from Tables 2 or 4; or (ii) the plurality of target sequences comprises more than one target sequences selected from Table 11; and (b) 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 a cancer. In some embodiments, the system further comprises an electronic memory for capturing and storing an expression profile. In some embodiments, the system further comprises a computer-processing device, optionally connected to a computer network. In some embodiments, the system further comprises a software module executed by the computer-processing device to analyze an expression profile. In some embodiments, the system further comprises a software module executed by the computer-processing device to compare the expression profile to a standard or control. In some embodiments, the system further comprises a software module executed by the computer-processing device to determine the expression level of the target. In some embodiments, the system further comprises a machine to isolate the target or the probe from the sample. In some embodiments, the system further comprises a machine to sequence the target or the probe. In some embodiments, the system further comprises a machine to amplify the target or the probe. In some embodiments, the system further comprises a label that specifically binds to the target, the probe, or a combination thereof. In some embodiments, the system further comprises a software module executed by the computer-processing device to transmit an analysis of the expression profile to the individual or a medical professional treating the individual. In some embodiments, the system further comprises a software module executed by the computer-processing device to transmit a diagnosis or prognosis to the individual or a medical professional treating the individual. In some embodiments, the plurality of targets comprises at least 5 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the

plurality of targets comprises at least 10 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 15 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 20 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 30 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 35 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 40 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 22 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 30 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 35 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 40 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 5 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets is selected from SEQ ID NOs:1-43. In some embodiments, the plurality of targets is selected from SEQ ID NOs:1-22. In certain embodiments, the plurality of targets is selected from the group consisting of: PBX1, MYBPC1, LASP1, CAMK2N1, RABGAP1, UBE2C, PCAT-32, NF1B, TNFRSF19, PCDH7, ANO7, GLYATL1P4/PCAT-80, C6orf10, IQGAP3, THBS2, EPPK1, NUSAP1, ZWILCH, S1P4, SENP7, ANLN, C10orf116, PPP6R3, PDS5B, TOP2A, IL1RAP, CENPE, GALNT8, KCNQ1, C6orf155, LUZP2, HEATR3, TMEM108, CFBXXbac-BPG116M5.17, ECHDC2, and ARNTL. In other embodiments the plurality of targets is selected from the group consisting of: PBX1, MYBPC1, LASP1, CAMK2N1, RABGAP1, UBE2C, PCAT-32, NF1B, TNFRSF19, PCDH7, ANO7, GLYATL1P4/PCAT-80, C6orf10, IQGAP3, THBS2, EPPK1, NUSAP1, ZWILCH, and S1P4. In some embodiments, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In some embodiments, the cancer is selected from the group consisting of bladder, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas. In some embodiments, the system further comprises a sequence for sequencing the plurality of targets.

In some embodiments, the system further comprises an instrument for amplifying the plurality of targets. In some embodiments, the system further comprises a label for labeling the plurality of targets.

[0008] Further disclosed herein in some embodiments is a method of analyzing a cancer in an individual in need thereof, comprising: (a) obtaining an expression profile from a sample obtained from the individual, wherein the expression profile comprises more than one target selected from Tables 2, 4, 11 or 55; and (b) comparing the expression profile from the sample to an expression profile of a control or standard. In some embodiments, the plurality of targets comprises at least 5 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 10 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 15 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 20 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 30 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 35 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 40 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 22 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 30 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 35 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 40 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 5 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets is selected from SEQ ID NOs:1-43. In some embodiments, the plurality of targets is selected from SEQ ID NOs:1-22. In certain embodiments, the plurality of targets is selected from the group consisting of: PBX1, MYBPC1, LASP1, CAMK2N1, RABGAP1, UBE2C, PCAT-32, NF1B, TNFRSF19, PCDH7, ANO7, GLYATL1P4/PCAT-80, C6orf10, IQGAP3, THBS2, EPPK1, NUSAP1, ZWILCH, S1P4, SENP7, ANLN, C10orf116, PPP6R3, PDS5B, TOP2A, IL1RAP, CENPE, GALNT8, KCNQ1, C6orf155, LUZP2, HEATR3, TMEM108, CFBXXbac-BPG116M5.17, ECHDC2, and ARNTL. In other embodiments the plurality of targets is selected from the group consisting of: PBX1, MYBPC1,

LASP1, CAMK2N1, RABGAP1, UBE2C, PCAT-32, NF1B, TNFRSF19, PCDH7, ANO7, GLYATL1P4/PCAT-80, C6orf10, IQGAP3, THBS2, EPPK1, NUSAP1, ZWILCH, and S1P4. In some embodiments, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In some embodiments, the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas. In some embodiments, the cancer is a prostate cancer. In some embodiments, the cancer is a pancreatic cancer. In some embodiments, the cancer is a breast cancer. In some embodiments, the cancer is a thyroid cancer. In some embodiments, the cancer is a lung cancer. In some embodiments, the method further comprises a software module executed by a computer-processing device to compare the expression profiles. In some embodiments, the method further comprises providing diagnostic or prognostic information to the individual about the cardiovascular disorder based on the comparison. In some embodiments, the method further comprises diagnosing the individual with a cancer if the expression profile of the sample (a) deviates from the control or standard from a healthy individual or population of healthy individuals, or (b) matches the control or standard from an individual or population of individuals who have or have had the cancer. In some embodiments, the method further comprises predicting the susceptibility of the individual for developing a cancer based on (a) the deviation of the expression profile of the sample from a control or standard derived from a healthy individual or population of healthy individuals, or (b) the similarity of the expression profiles of the sample and a control or standard derived from an individual or population of individuals who have or have had the cancer. In some embodiments, the method further comprises prescribing a treatment regimen based on (a) the deviation of the expression profile of the sample from a control or standard derived from a healthy individual or population of healthy individuals, or (b) the similarity of the expression profiles of the sample and a control or standard derived from an individual or population of individuals who have or have had the cancer. In some embodiments, the method further comprises altering a treatment regimen prescribed or administered to the individual based on (a) the deviation of the expression profile of the sample from a control or standard derived from a healthy individual or population of healthy individuals, or (b) the similarity of the expression profiles of the sample and a control or standard derived from an individual or population of

individuals who have or have had the cancer. In some embodiments, the method further comprises predicting the individual's response to a treatment regimen based on (a) the deviation of the expression profile of the sample from a control or standard derived from a healthy individual or population of healthy individuals, or (b) the similarity of the expression profiles of the sample and a control or standard derived from an individual or population of individuals who have or have had the cancer. In some embodiments, the deviation is the expression level of more than one target from the sample is greater than the expression level of more than one target from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of more than one target from the sample is at least about 30% greater than the expression level of more than one target from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of more than one target from the sample is less than the expression level of more than one target from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of more than one target from the sample is at least about 30% less than the expression level of more than one target from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the method further comprises using a machine to isolate the target or the probe from the sample. In some embodiments, the method further comprises contacting the sample with a label that specifically binds to the target, the probe, or a combination thereof. In some embodiments, the method further comprises contacting the sample with a label that specifically binds to a target selected from Tables 2, 4, 11 or 55, or a combination thereof. In some embodiments, the method further comprises amplifying the target, the probe, or any combination thereof. In some embodiments, the method further comprises sequencing the target, the probe, or any combination thereof. In some embodiments, the method further comprises quantifying the expression level of the plurality of targets. In some embodiments, the method further comprises labeling the plurality of targets. In some embodiments, assaying the expression level of a plurality of targets may comprise the use of a probe set. In some embodiments, obtaining 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, obtaining the expression level may also comprise sequencing the plurality of targets.

[0009] Disclosed herein in some embodiments is a method of diagnosing cancer in an individual in need thereof, comprising (a) obtaining an expression profile from a sample obtained from the individual, wherein the expression profile comprises more than one target selected from Tables 2, 4, 11 or 55; (b) comparing the expression profile from the sample to an expression profile of a control or standard; and (c) diagnosing a cancer in the individual if the expression profile of the sample (i) deviates from the control or standard from a healthy individual or population of healthy individuals, or (ii) matches the control or standard from an individual or population of individuals who have or have had the cancer. In some embodiments, the plurality of targets comprises at least 5 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 10 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 15 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 20 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 30 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 35 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 40 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 22 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 30 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 35 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 40 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 5 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets is selected from SEQ ID NOs:1-43. In some embodiments, the plurality of targets is selected from SEQ ID NOs:1-22. In certain embodiments, the plurality of targets is selected from the group consisting of: PBX1, MYBPC1, LASP1, CAMK2N1, RABGAP1, UBE2C, PCAT-32, NF1B, TNFRSF19, PCDH7, ANO7, GLYATL1P4/PCAT-80, C6orf10, IQGAP3, THBS2, EPPK1, NUSAP1, ZWILCH, S1P4, SENP7, ANLN, C10orf116, PPP6R3, PDS5B, TOP2A, IL1RAP, CENPE, GALNT8, KCNQ1, C6orf155, LUZP2, HEATR3, TMEM108, CFBXXbac-BPG116M5.17, ECHDC2, and ARNTL. In other embodiments the plurality of targets is selected from the group consisting of: PBX1, MYBPC1,

LASP1, CAMK2N1, RABGAP1, UBE2C, PCAT-32, NF1B, TNFRSF19, PCDH7, ANO7, GLYATL1P4/PCAT-80, C6orf10, IQGAP3, THBS2, EPPK1, NUSAP1, ZWILCH, and S1P4. In some embodiments, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In some embodiments, the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas. In some embodiments, the cancer is a prostate cancer. In some embodiments, the cancer is a pancreatic cancer. In some embodiments, the cancer is a breast cancer. In some embodiments, the cancer is a thyroid cancer. In some embodiments, the cancer is a lung cancer. In some embodiments, the method further comprises a software module executed by a computer-processing device to compare the expression profiles. In some embodiments, the deviation is the expression level of more than one target targets from the sample is greater than the expression level of more than one target from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of more than one target from the sample is at least about 30% greater than the expression level of more than one target from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of more than one target from the sample is less than the expression level of more than one target from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of more than one target from the sample is at least about 30% less than the expression level of more than one target from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the method further comprises using a machine to isolate the target or the probe from the sample. In some embodiments, the method further comprises contacting the sample with a label that specifically binds to the target, the probe, or a combination thereof. In some embodiments, the method further comprises contacting the sample with a label that specifically binds to a target selected from Tables 2, 4, 11 or 55, or a combination thereof. In some embodiments, the method further comprises amplifying the target, the probe, or any combination thereof. In some embodiments, the method further comprises sequencing the target, the probe, or any combination thereof. In some embodiments, the method further comprises quantifying the

expression level of the plurality of targets. In some embodiments, the method further comprises labeling the plurality of targets. In some embodiments, obtaining 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, obtaining the expression level may also comprise sequencing the plurality of targets.

[0010] Further disclosed herein in some embodiments is a method of predicting whether an individual is susceptible to developing a cancer, comprising (a) obtaining an expression profile from a sample obtained from the individual, wherein the expression profile comprises more than one target selected from Tables 2, 4, 11 or 55; (b) comparing the expression profile from the sample to an expression profile of a control or standard; and (c) predicting the susceptibility of the individual for developing a cancer based on (i) the deviation of the expression profile of the sample from a control or standard derived from a healthy individual or population of healthy individuals, or (ii) the similarity of the expression profiles of the sample and a control or standard derived from an individual or population of individuals who have or have had the cancer. In some embodiments, the plurality of targets comprises at least 5 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 10 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 15 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 20 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 30 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 35 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 40 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 22 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 30 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 35 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 40 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 5 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the

plurality of targets is selected from SEQ ID NOs:1-43. In some embodiments, the plurality of targets is selected from SEQ ID NOs:1-22. In certain embodiments, the plurality of targets is selected from the group consisting of: PBX1, MYBPC1, LASP1, CAMK2N1, RABGAP1, UBE2C, PCAT-32, NF1B, TNFRSF19, PCDH7, ANO7, GLYATL1P4/PCAT-80, C6orf10, IQGAP3, THBS2, EPPK1, NUSAP1, ZWILCH, S1P4, SENP7, ANLN, C10orf116, PPP6R3, PDS5B, TOP2A, IL1RAP, CENPE, GALNT8, KCNQ1, C6orf155, LUZP2, HEATR3, TMEM108, CFBXXbac-BPG116M5.17, ECHDC2, and ARNTL. In other embodiments the plurality of targets is selected from the group consisting of: PBX1, MYBPC1, LASP1, CAMK2N1, RABGAP1, UBE2C, PCAT-32, NF1B, TNFRSF19, PCDH7, ANO7, GLYATL1P4/PCAT-80, C6orf10, IQGAP3, THBS2, EPPK1, NUSAP1, ZWILCH, and S1P4. In some embodiments, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In some embodiments, the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas. In some embodiments, the cancer is a prostate cancer. In some embodiments, the cancer is a pancreatic cancer. In some embodiments, the cancer is a breast cancer. In some embodiments, the cancer is a thyroid cancer. In some embodiments, the cancer is a lung cancer. In some embodiments, the method further comprises a software module executed by a computer-processing device to compare the expression profiles. In some embodiments, the deviation is the expression level of more than one target from the sample is greater than the expression level of more than one target from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of more than one target from the sample is at least about 30% greater than the expression level of more than one target from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of more than one target from the sample is less than the expression level of more than one target from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of more than one target from the sample is at least about 30% less than the expression level of more than one target from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the method further comprises using a machine to isolate the target or the probe from the sample. In some embodiments, the

method further comprises contacting the sample with a label that specifically binds to the target, the probe, or a combination thereof. In some embodiments, the method further comprises contacting the sample with a label that specifically binds to a target selected from Tables 2, 4, 11 or 55, or a combination thereof. In some embodiments, the method further comprises amplifying the target, the probe, or any combination thereof. In some embodiments, the method further comprises sequencing the target, the probe, or any combination thereof. In some embodiments, obtaining 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, obtaining the expression level may also comprise sequencing the plurality of targets. In some embodiments, obtaining the expression level may also comprise amplifying the plurality of targets. In some embodiments, obtaining the expression level may also comprise quantifying the plurality of targets.

[0011] Further disclosed herein in some embodiments is a method of predicting an individual's response to a treatment regimen for a cancer, comprising (a) obtaining an expression profile from a sample obtained from the individual, wherein the expression profile comprises more than one target selected from Tables 2, 4, 11 or 55; (b) comparing the expression profile from the sample to an expression profile of a control or standard; and (c) predicting the individual's response to a treatment regimen based on (a) the deviation of the expression profile of the sample from a control or standard derived from a healthy individual or population of healthy individuals, or (b) the similarity of the expression profiles of the sample and a control or standard derived from an individual or population of individuals who have or have had the cancer. In some embodiments, the plurality of targets comprises at least 5 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 10 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 15 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 20 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 30 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 35 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 40 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 22 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 30 targets selected from Tables 2, 11

or 55. In some embodiments, the plurality of targets comprises at least 35 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 40 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 5 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets is selected from SEQ ID NOs:1-43. In some embodiments, the plurality of targets is selected from SEQ ID NOs:1-22. In certain embodiments, the plurality of targets is selected from the group consisting of: PBX1, MYBPC1, LASP1, CAMK2N1, RABGAP1, UBE2C, PCAT-32, NF1B, TNFRSF19, PCDH7, ANO7, GLYATL1P4/PCAT-80, C6orf10, IQGAP3, THBS2, EPPK1, NUSAP1, ZWILCH, S1P4, SENP7, ANLN, C10orf116, PPP6R3, PDS5B, TOP2A, IL1RAP, CENPE, GALNT8, KCNQ1, C6orf155, LUZP2, HEATR3, TMEM108, CFBXXbac-BPG116M5.17, ECHDC2, and ARNTL. In other embodiments the plurality of targets is selected from the group consisting of: PBX1, MYBPC1, LASP1, CAMK2N1, RABGAP1, UBE2C, PCAT-32, NF1B, TNFRSF19, PCDH7, ANO7, GLYATL1P4/PCAT-80, C6orf10, IQGAP3, THBS2, EPPK1, NUSAP1, ZWILCH, and S1P4. In some embodiments, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In some embodiments, the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas. In some embodiments, the cancer is a prostate cancer. In some embodiments, the cancer is a pancreatic cancer. In some embodiments, the cancer is a breast cancer. In some embodiments, the cancer is a thyroid cancer. In some embodiments, the cancer is a lung cancer. In some embodiments, the method further comprises a software module executed by a computer-processing device to compare the expression profiles. In some embodiments, the deviation is the expression level of more than one target from the sample is greater than the expression level of more than one target from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of more than one target from the sample is at least about 30% greater than the expression level of more than one target from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the

expression level of more than one target from the sample is less than the expression level of more than one target from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of more than one target from the sample is at least about 30% less than the expression level of more than one target from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the method further comprises using a machine to isolate the target or the probe from the sample. In some embodiments, the method further comprises contacting the sample with a label that specifically binds to the target, the probe, or a combination thereof. In some embodiments, the method further comprises contacting the sample with a label that specifically binds to a target selected from Tables 2, 4, 11 or 55, or a combination thereof. In some embodiments, the method further comprises amplifying the target, the probe, or any combination thereof. In some embodiments, the method further comprises sequencing the target, the probe, or any combination thereof. In some embodiments, the method further comprises quantifying the target, the probe, or any combination thereof. In some embodiments, the method further comprises labeling the target, the probe, or any combination thereof. In some embodiments, obtaining 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, obtaining the expression level may also comprise sequencing the plurality of targets. In some embodiments, obtaining the expression level may also comprise amplifying the plurality of targets. In some embodiments, obtaining the expression level may also comprise quantifying the plurality of targets.

[0012] Disclosed herein in some embodiments is a method of prescribing a treatment regimen for a cancer to an individual in need thereof, comprising (a) obtaining an expression profile from a sample obtained from the individual, wherein the expression profile comprises more than one target targets selected from Tables 2, 4, 11 or 55; (b) comparing the expression profile from the sample to an expression profile of a control or standard; and (c) prescribing a treatment regimen based on (i) the deviation of the expression profile of the sample from a control or standard derived from a healthy individual or population of healthy individuals, or (ii) the similarity of the expression profiles of the sample and a control or standard derived from an individual or population of individuals who have or have had the cancer. In some embodiments, the plurality of targets comprises at least 5 targets selected from Tables 2, 4, 11

or 55. In some embodiments, the plurality of targets comprises at least 10 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 15 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 20 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 30 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 35 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 40 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 22 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 30 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 35 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 40 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 5 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets is selected from SEQ ID NOs:1-43. In some embodiments, the plurality of targets is selected from SEQ ID NOs:1-22. In certain embodiments, the plurality of targets is selected from the group consisting of: PBX1, MYBPC1, LASP1, CAMK2N1, RABGAP1, UBE2C, PCAT-32, NF1B, TNFRSF19, PCDH7, ANO7, GLYATL1P4/PCAT-80, C6orf10, IQGAP3, THBS2, EPPK1, NUSAP1, ZWILCH, S1P4, SENP7, ANLN, C10orf116, PPP6R3, PDS5B, TOP2A, IL1RAP, CENPE, GALNT8, KCNQ1, C6orf155, LUZP2, HEATR3, TMEM108, CFBXXbac-BPG116M5.17, ECHDC2, and ARNTL. In other embodiments the plurality of targets is selected from the group consisting of: PBX1, MYBPC1, LASP1, CAMK2N1, RABGAP1, UBE2C, PCAT-32, NF1B, TNFRSF19, PCDH7, ANO7, GLYATL1P4/PCAT-80, C6orf10, IQGAP3, THBS2, EPPK1, NUSAP1, ZWILCH, and S1P4. In some embodiments, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In some embodiments, the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas. In some embodiments, the cancer is a prostate cancer. In some embodiments, the cancer is a

pancreatic cancer. In some embodiments, the cancer is a breast cancer. In some embodiments, the cancer is a thyroid cancer. In some embodiments, the cancer is a lung cancer. In some embodiments, the method further comprises a software module executed by a computer-processing device to compare the expression profiles. In some embodiments, the deviation is the expression level of more than one target targets from the sample is greater than the expression level of more than one target from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of more than one target from the sample is at least about 30% greater than the expression level of more than one target from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of more than one target from the sample is less than the expression level of more than one target from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of more than one target from the sample is at least about 30% less than the expression level of more than one target from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the method further comprises using a machine to isolate the target or the probe from the sample. In some embodiments, the method further comprises contacting the sample with a label that specifically binds to the target, the probe, or a combination thereof. In some embodiments, the method further comprises contacting the sample with a label that specifically binds to a target selected from Tables 2, 4, 11 or 55, or a combination thereof. In some embodiments, the method further comprises amplifying the target, the probe, or any combination thereof. In some embodiments, the method further comprises sequencing the target, the probe, or any combination thereof. In some embodiments, the method further comprises converting the expression levels of the target sequences into a likelihood score that indicates the probability that a biological sample is from a patient who will exhibit no evidence of disease, who will exhibit systemic cancer, or who will exhibit biochemical recurrence. In some embodiments, the method further comprises quantifying the expression level of the plurality of targets. In some embodiments, the method further comprises labeling the plurality of targets. In some embodiments, the target sequences are differentially expressed the cancer. In some embodiments, the differential expression is dependent on aggressiveness. In some embodiments, the expression profile is determined by a method selected from the group consisting of RT-PCR, Northern blotting, ligase chain reaction, array hybridization, and a

combination thereof. In some embodiments, obtaining 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, obtaining the expression level may also comprise sequencing the plurality of targets. In some embodiments, obtaining the expression level may also comprise amplifying the plurality of targets. In some embodiments, obtaining the expression level may also comprise quantifying the plurality of targets.

[0013] Further disclosed herein is a classifier for analyzing a cancer, wherein the classifier has an AUC value of at least about 0.60. The AUC of the classifier may be at least about 0.60, 0.61, 0.62, 0.63, 0.64, 0.65, 0.66, 0.67, 0.68, 0.69, 0.70 or more. The AUC of the classifier may be at least about 0.71, 0.72, 0.73, 0.74, 0.75, 0.76, 0.77, 0.78, 0.79, 0.80 or more. The AUC of the classifier may be at least about 0.81, 0.82, 0.83, 0.84, 0.85, 0.86, 0.87, 0.88, 0.89, 0.90 or more. The AUC of the classifier may be at least about 0.91, 0.92, 0.93, 0.94, 0.95, 0.96, 0.97, 0.98, 0.99 or more. The 95% CI of a classifier or biomarker may be between about 1.10 to 1.70. In some instances, the difference in the range of the 95% CI for a biomarker or classifier is between about 0.25 to about 0.50, between about 0.27 to about 0.47, or between about 0.30 to about 0.45.

[0014] Further disclosed herein is a method for analyzing a cancer, comprising use of more than one classifier, wherein the significance of the of more than one classifier is based on one 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), 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 of more than one classifier 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 significance of the of more than one classifier may be based on three 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), 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).

[0015] The one or more metrics may comprise AUC. The one or more metrics may comprise AUC and AUC P-value. The one or more metrics may comprise AUC P-value and Wilcoxon Test P-value. The one or more metrics may comprise Wilcoxon Test P-value. The one or more metrics may comprise AUC and Univariable Analysis Odds Ratio P-value (uvaORPval). The one or more metrics may comprise multivariable analysis Odds Ratio P-value (mvaORPval) and Multivariable Analysis Hazard Ratio P-value (mvaHRPval). The one or more metrics may comprise AUC and Multivariable Analysis Hazard Ratio P-value (mvaHRPval). The one or more metrics may comprise Wilcoxon Test P-value and Multivariable Analysis Hazard Ratio P-value (mvaHRPval).

[0016] The clinical significance of the classifier may be based on the AUC value. The AUC of the classifier may be at least about 0.60, 0.61, 0.62, 0.63, 0.64, 0.65, 0.66, 0.67, 0.68, 0.69, 0.70 or more. The AUC of the classifier may be at least about 0.71, 0.72, 0.73, 0.74, 0.75, 0.76, 0.77, 0.78, 0.79, 0.80 or more. The AUC of the classifier may be at least about 0.81, 0.82, 0.83, 0.84, 0.85, 0.86, 0.87, 0.88, 0.89, 0.90 or more. The AUC of the classifier may be at least about 0.91, 0.92, 0.93, 0.94, 0.95, 0.96, 0.97, 0.98, 0.99 or more. The 95% CI of a classifier or biomarker may be between about 1.10 to 1.70. In some instances, the difference in the range of the 95% CI for a biomarker or classifier is between about 0.25 to about 0.50, between about 0.27 to about 0.47, or between about 0.30 to about 0.45.

[0017] The clinical significance of the classifier may be based on Univariable Analysis Odds Ratio P-value (uvaORPval). The Univariable Analysis Odds Ratio P-value (uvaORPval) of the classifier may be between about 0-0.4. The Univariable Analysis Odds Ratio P-value (uvaORPval) of the classifier may be between about 0-0.3. The Univariable Analysis Odds Ratio P-value (uvaORPval) of the classifier may be between about 0-0.2. The Univariable Analysis Odds Ratio P-value (uvaORPval) of the classifier may be less than or equal to 0.25, 0.22, 0.21, 0.20, 0.19, 0.18, 0.17, 0.16, 0.15, 0.14, 0.13, 0.12, 0.11. The Univariable Analysis Odds Ratio P-value (uvaORPval) of the classifier may be less than or equal to 0.10, 0.09, 0.08, 0.07, 0.06, 0.05, 0.04, 0.03, 0.02, 0.01. The Univariable Analysis Odds Ratio P-value (uvaORPval) of the classifier may be less than or equal to 0.009, 0.008, 0.007, 0.006, 0.005, 0.004, 0.003, 0.002, 0.001.

[0018] The clinical significance of the classifier may be based on multivariable analysis Odds Ratio P-value (mvaORPval). The multivariable analysis Odds Ratio P-value (mvaORPval) of the classifier may be between about 0-1. The multivariable analysis Odds Ratio P-value (mvaORPval) of the classifier may be between about 0-0.9. The multivariable analysis Odds Ratio P-value (mvaORPval) of the classifier may be between about 0-0.8. The multivariable analysis Odds Ratio P-value (mvaORPval) of the classifier may be less than or equal to 0.90, 0.88, 0.86, 0.84, 0.82, 0.80. The multivariable analysis Odds Ratio P-value (mvaORPval) of the classifier may be less than or equal to 0.78, 0.76, 0.74, 0.72, 0.70, 0.68, 0.66, 0.64, 0.62, 0.60, 0.58, 0.56, 0.54, 0.52, 0.50. The multivariable analysis Odds Ratio P-value (mvaORPval) of the classifier may be less than or equal to 0.48, 0.46, 0.44, 0.42, 0.40, 0.38, 0.36, 0.34, 0.32, 0.30, 0.28, 0.26, 0.25, 0.22, 0.21, 0.20, 0.19, 0.18, 0.17, 0.16, 0.15, 0.14, 0.13, 0.12, 0.11. The multivariable analysis Odds Ratio P-value (mvaORPval) of the classifier may be less than or equal to 0.10, 0.09, 0.08, 0.07, 0.06, 0.05, 0.04, 0.03, 0.02, 0.01. The multivariable analysis Odds Ratio P-value (mvaORPval) of the classifier may be less than or equal to 0.009, 0.008, 0.007, 0.006, 0.005, 0.004, 0.003, 0.002, 0.001.

[0019] The clinical significance of the classifier may be based on the Kaplan Meier P-value (KM P-value). The Kaplan Meier P-value (KM P-value) of the classifier may be between about 0-0.8. The Kaplan Meier P-value (KM P-value) of the classifier may be between about 0-0.7. The Kaplan Meier P-value (KM P-value) of the classifier may be less than or equal to 0.80, 0.78, 0.76, 0.74, 0.72, 0.70, 0.68, 0.66, 0.64, 0.62, 0.60, 0.58, 0.56, 0.54, 0.52, 0.50. The Kaplan Meier P-value (KM P-value) of the classifier may be less than or equal to 0.48, 0.46, 0.44, 0.42, 0.40, 0.38, 0.36, 0.34, 0.32, 0.30, 0.28, 0.26, 0.25, 0.22, 0.21, 0.20, 0.19, 0.18, 0.17, 0.16, 0.15, 0.14, 0.13, 0.12, 0.11. The Kaplan Meier P-value (KM P-value) of the classifier may be less than or equal to 0.10, 0.09, 0.08, 0.07, 0.06, 0.05, 0.04, 0.03, 0.02, 0.01. The Kaplan Meier P-value (KM P-value) of the classifier may be less than or equal to 0.009, 0.008, 0.007, 0.006, 0.005, 0.004, 0.003, 0.002, 0.001.

[0020] The clinical significance of the classifier may be based on the survival AUC value (survAUC). The survival AUC value (survAUC) of the classifier may be between about 0-1. The survival AUC value (survAUC) of the classifier may be between about 0-0.9. The survival AUC value (survAUC) of the classifier may be less than or equal to 1, 0.98, 0.96, 0.94, 0.92, 0.90, 0.88, 0.86, 0.84, 0.82, 0.80. The survival AUC value (survAUC) of the classifier may be less than or equal to 0.80, 0.78, 0.76, 0.74, 0.72, 0.70, 0.68, 0.66, 0.64, 0.62, 0.60, 0.58, 0.56, 0.54, 0.52, 0.50. The survival AUC value (survAUC) of the classifier may

be less than or equal to 0.48, 0.46, 0.44, 0.42, 0.40, 0.38, 0.36, 0.34, 0.32, 0.30, 0.28, 0.26, 0.25, 0.22, 0.21, 0.20, 0.19, 0.18, 0.17, 0.16, 0.15, 0.14, 0.13, 0.12, 0.11. The survival AUC value (survAUC) of the classifier may be less than or equal to 0.10, 0.09, 0.08, 0.07, 0.06, 0.05, 0.04, 0.03, 0.02, 0.01. The survival AUC value (survAUC) of the classifier may be less than or equal to 0.009, 0.008, 0.007, 0.006, 0.005, 0.004, 0.003, 0.002, 0.001.

[0021] The clinical significance of the classifier may be based on the Univariable Analysis Hazard Ratio P-value (uvaHRPval). The Univariable Analysis Hazard Ratio P-value (uvaHRPval) of the classifier may be between about 0-0.4. The Univariable Analysis Hazard Ratio P-value (uvaHRPval) of the classifier may be between about 0-0.3. The Univariable Analysis Hazard Ratio P-value (uvaHRPval) of the classifier may be less than or equal to 0.40, 0.38, 0.36, 0.34, 0.32. The Univariable Analysis Hazard Ratio P-value (uvaHRPval) of the classifier may be less than or equal to 0.30, 0.29, 0.28, 0.27, 0.26, 0.25, 0.24, 0.23, 0.22, 0.21, 0.20. The Univariable Analysis Hazard Ratio P-value (uvaHRPval) of the classifier may be less than or equal to 0.19, 0.18, 0.17, 0.16, 0.15, 0.14, 0.13, 0.12, 0.11. The Univariable Analysis Hazard Ratio P-value (uvaHRPval) of the classifier may be less than or equal to 0.10, 0.09, 0.08, 0.07, 0.06, 0.05, 0.04, 0.03, 0.02, 0.01. The Univariable Analysis Hazard Ratio P-value (uvaHRPval) of the classifier may be less than or equal to 0.009, 0.008, 0.007, 0.006, 0.005, 0.004, 0.003, 0.002, 0.001.

[0022] The clinical significance of the classifier may be based on the Multivariable Analysis Hazard Ratio P-value (mvaHRPval)mva HRPval. The Multivariable Analysis Hazard Ratio P-value (mvaHRPval)mva HRPval of the classifier may be between about 0-1. The Multivariable Analysis Hazard Ratio P-value (mvaHRPval)mva HRPval of the classifier may be between about 0-0.9. The Multivariable Analysis Hazard Ratio P-value (mvaHRPval)mva HRPval of the classifier may be less than or equal to 1, 0.98, 0.96, 0.94, 0.92, 0.90, 0.88, 0.86, 0.84, 0.82, 0.80. The Multivariable Analysis Hazard Ratio P-value (mvaHRPval)mva HRPval of the classifier may be less than or equal to 0.80, 0.78, 0.76, 0.74, 0.72, 0.70, 0.68, 0.66, 0.64, 0.62, 0.60, 0.58, 0.56, 0.54, 0.52, 0.50. The Multivariable Analysis Hazard Ratio P-value (mvaHRPval)mva HRPval of the classifier may be less than or equal to 0.48, 0.46, 0.44, 0.42, 0.40, 0.38, 0.36, 0.34, 0.32, 0.30, 0.28, 0.26, 0.25, 0.22, 0.21, 0.20, 0.19, 0.18, 0.17, 0.16, 0.15, 0.14, 0.13, 0.12, 0.11. The Multivariable Analysis Hazard Ratio P-value (mvaHRPval)mva HRPval of the classifier may be less than or equal to 0.10, 0.09, 0.08, 0.07, 0.06, 0.05, 0.04, 0.03, 0.02, 0.01. The Multivariable Analysis Hazard Ratio P-value

(mvaHRPval)mva HRPval of the classifier may be less than or equal to 0.009, 0.008, 0.007, 0.006, 0.005, 0.004, 0.003, 0.002, 0.001.

[0023] The clinical significance of the classifier may be based on the Multivariable Analysis Hazard Ratio P-value (mvaHRPval). The Multivariable Analysis Hazard Ratio P-value (mvaHRPval) of the classifier may be between about 0 to about 0.60. significance of the classifier may be based on the Multivariable Analysis Hazard Ratio P-value (mvaHRPval). The Multivariable Analysis Hazard Ratio P-value (mvaHRPval) of the classifier may be between about 0 to about 0.50. significance of the classifier may be based on the Multivariable Analysis Hazard Ratio P-value (mvaHRPval). The Multivariable Analysis Hazard Ratio P-value (mvaHRPval) of the classifier may be less than or equal to 0.50, 0.47, 0.45, 0.43, 0.40, 0.38, 0.35, 0.33, 0.30, 0.28, 0.25, 0.22, 0.20, 0.18, 0.16, 0.15, 0.14, 0.13, 0.12, 0.11, 0.10. The Multivariable Analysis Hazard Ratio P-value (mvaHRPval) of the classifier may be less than or equal to 0.10, 0.09, 0.08, 0.07, 0.06, 0.05, 0.04, 0.03, 0.02, 0.01. The Multivariable Analysis Hazard Ratio P-value (mvaHRPval) of the classifier may be less than or equal to 0.01, 0.009, 0.008, 0.007, 0.006, 0.005, 0.004, 0.003, 0.002, 0.001.

[0024] The method may further comprise determining an expression profile based on the more than one classifier. The method may further comprise providing a sample from a subject. The subject may be a healthy subject. The subject may be suffering from a cancer or suspected of suffering from a cancer. The method may further comprise diagnosing a cancer in a subject based on the expression profile or classifier. The method may further comprise treating a cancer in a subject in need thereof based on the expression profile or classifier. The method may further comprise determining a treatment regimen for a cancer in a subject in need thereof based on the expression profile or classifier. The method may further comprise prognosing a cancer in a subject based on the expression profile or classifier.

[0025] Further disclosed herein is a kit for analyzing a cancer, comprising (a) a probe set comprising a plurality of target sequences, wherein the plurality of target sequences comprises more than one target sequence listed in Table 11; and (b) 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 kit further comprises a computer model or algorithm for correlating the expression level or expression profile with disease state or outcome. In some embodiments, the kit further comprises a computer model or algorithm for designating a treatment modality for the individual. In some embodiments, the kit further comprises a computer model or algorithm for normalizing expression level or expression profile of the

target sequences. In some embodiments, the kit further comprises a computer model or algorithm comprising a robust multichip average (RMA), probe logarithmic intensity error estimation (PLIER), non-linear fit (NLFIT) quantile-based, nonlinear normalization, or a combination thereof. In some embodiments, the plurality of target sequences comprises at least 5 target sequences selected from Table 11. In some embodiments, the plurality of target sequences comprises at least 10 target sequences selected from Table 11. In some embodiments, the plurality of target sequences comprises at least 15 target sequences selected from Table 11. In some embodiments, the plurality of target sequences comprises at least 20 target sequences selected from Table 11. In some embodiments, the plurality of target sequences comprises at least 30 target sequences selected from Table 11. In some embodiments, the plurality of target sequences comprises at least 35 target sequences selected from Table 11. In some embodiments, the plurality of targets comprises at least 40 target sequences selected from Table 11. In some embodiments, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In some embodiments, the cancer is selected from the group consisting of skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas. In some embodiments, the cancer is a prostate cancer. In some embodiments, the cancer is a pancreatic cancer. In some embodiments, the cancer is a breast cancer. In some embodiments, the cancer is a thyroid cancer. In some embodiments, the cancer is a lung cancer.

[0026] Further disclosed herein is a kit for analyzing a cancer, comprising (a) a probe set comprising a plurality of target sequences, wherein the plurality of target sequences hybridizes to more than one target selected from Tables 2, 4, 11 or 55; and (b) 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 kit further comprises a computer model or algorithm for correlating the expression level or expression profile with disease state or outcome. In some embodiments, the kit further comprises a computer model or algorithm for designating a treatment modality for the individual. In some embodiments, the kit further comprises a computer model or algorithm for normalizing expression level or expression profile of the target sequences. In some embodiments, the kit further comprises a computer model or algorithm comprising a robust multichip average (RMA), probe logarithmic intensity error estimation (PLIER), non-linear fit (NLFIT) quantile-based, nonlinear

normalization, or a combination thereof. In some embodiments, the targets comprise at least 5 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the targets comprise at least 10 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the targets comprise at least 15 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the targets comprise at least 20 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the targets comprise at least 30 targets selected from Tables 2, 11 or 55. In some embodiments, the targets comprise at least 35 targets selected from Tables 2, 11 or 55. In some embodiments, the targets comprise at least 40 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 22 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 30 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 35 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 40 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of targets comprises at least 5 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets is selected from SEQ ID NOs:1-43. In some embodiments, the plurality of targets is selected from SEQ ID NOs:1-22. In some embodiments, the targets are selected from Table 2. In some embodiments, the targets are selected from Table 4. In some embodiments, the targets are selected from Table 11. In certain embodiments, the plurality of targets is selected from the group consisting of: PBX1, MYBPC1, LASP1, CAMK2N1, RABGAP1, UBE2C, PCAT-32, NF1B, TNFRSF19, PCDH7, ANO7, GLYATL1P4/PCAT-80, C6orf10, IQGAP3, THBS2, EPPK1, NUSAP1, ZWILCH, S1P4, SENP7, ANLN, C10orf116, PPP6R3, PDS5B, TOP2A, IL1RAP, CENPE, GALNT8, KCNQ1, C6orf155, LUZP2, HEATR3, TMEM108, CFBXXbac-BPG116M5.17, ECHDC2, and ARNTL. In other embodiments the plurality of targets is selected from the group consisting of: PBX1, MYBPC1, LASP1, CAMK2N1, RABGAP1, UBE2C, PCAT-32, NF1B, TNFRSF19, PCDH7, ANO7, GLYATL1P4/PCAT-80, C6orf10, IQGAP3, THBS2, EPPK1, NUSAP1, ZWILCH, and S1P4. In some embodiments, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In some embodiments, the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine

cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas. In some embodiments, the cancer is a prostate cancer. In some embodiments, the cancer is a pancreatic cancer. In some embodiments, the cancer is a breast cancer. In some embodiments, the cancer is a thyroid cancer. In some embodiments, the cancer is a lung cancer.

[0027] Disclosed herein in some embodiments is a system for analyzing cancer comprising a computer processing device for determining an expression profile for a probe set; 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 a cancer; and an output providing the analysis. In some embodiments, the probe set comprises a plurality of target sequences, wherein the plurality of target sequences hybridizes to more than one target sequence selected from Tables 2 or 4; or the plurality of target sequences comprises more than one target sequence selected from Table 11. In further embodiments the system further comprises an electronic memory device for capturing and storing an expression profile; a software module; a machine to isolate target or the probe from the sample; a machine to sequence the target or the probe; and/or a machine to amplify the target or the probe. In ceratin embodiments, the software module executed by the computer-processing device analyzes an expression profile. In an additional embodiment, the software compare executed by the computer-processing devices the expression profile to a standard or control. In one embodiment, the software module executed by the computer-processing device determines the expression level of the target. Inan embodiment, the software module executed by the computer-processing device transmits an analysis of the expression profile to the subject or a medical professional treating the subject. In a further embodiment, the system further comprises a label that specifically binds to the target, the probe, or a combination thereof. In some embodiments, the target sequences comprise at least 5 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the target sequences comprise at least 10 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the target sequences comprise at least 15 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the target sequences comprise at least 20 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the target sequences comprise at least 30 targets selected from Tables 2, 11 or 55. In some embodiments, the target sequences comprise at least 35 targets selected from Tables 2, 11 or 55. In some embodiments, the target sequences comprise comprises at least 40 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of target sequences

comprises at least 22 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of target sequences comprises at least 30 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of target sequences comprises at least 35 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of target sequences comprises at least 40 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of target sequences comprises 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of target sequences is selected from SEQ ID NOs:1-43. In some embodiments, the plurality of target sequences is selected from SEQ ID NOs:1-22. In certain embodiments, the plurality of targets is selected from the group consisting of: PBX1, MYBPC1, LASP1, CAMK2N1, RABGAP1, UBE2C, PCAT-32, NF1B, TNFRSF19, PCDH7, ANO7, GLYATL1P4/PCAT-80, C6orf10, IQGAP3, THBS2, EPPK1, NUSAP1, ZWILCH, S1P4, SENP7, ANLN, C10orf116, PPP6R3, PDS5B, TOP2A, IL1RAP, CENPE, GALNT8, KCNQ1, C6orf155, LUZP2, HEATR3, TMEM108, CFBXXbac-BPG116M5.17, ECHDC2, and ARNTL. In other embodiments the plurality of targets is selected from the group consisting of: PBX1, MYBPC1, LASP1, CAMK2N1, RABGAP1, UBE2C, PCAT-32, NF1B, TNFRSF19, PCDH7, ANO7, GLYATL1P4/PCAT-80, C6orf10, IQGAP3, THBS2, EPPK1, NUSAP1, ZWILCH, and S1P4. In an additional embodiment, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In a further embodiment, the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas.

[0028] Disclosed herein in some embodiments is a method for analyzing cancer comprising a computer processing device for determining an expression profile for a probe set; 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 a cancer; and an output providing the analysis. In some embodiments, the probe set comprises a plurality of target sequences, wherein the plurality of target sequences hybridizes to more than one target sequence selected from Tables 2 or 4; or the plurality of target sequences comprises more than one target sequence selected from Table 11. In further embodiments the method further comprises an electronic memory device for capturing and storing an expression profile; a

software module; a machine to isolate target or the probe from the sample; a machine to sequence the target or the probe; and/or a machine to amplify the target or the probe. In certain embodiments, the software module executed by the computer-processing device analyzes an expression profile. In an additional embodiment, the software compares executed by the computer-processing devices the expression profile to a standard or control. In one embodiment, the software module executed by the computer-processing device determines the expression level of the target. In an embodiment, the software module executed by the computer-processing device transmits an analysis of the expression profile to the subject or a medical professional treating the subject. In a further embodiment, the method further comprises a label that specifically binds to the target, the probe, or a combination thereof. In some embodiments, the target sequences comprise at least 5 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the target sequences comprise at least 10 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the target sequences comprise at least 15 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the target sequences comprise at least 20 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the target sequences comprise at least 30 targets selected from Tables 2, 11 or 55. In some embodiments, the target sequences comprise at least 35 targets selected from Tables 2, 11 or 55. In some embodiments, the target sequences comprise at least 40 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of target sequences comprises at least 22 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of target sequences comprises at least 30 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of target sequences comprises at least 35 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of target sequences comprises at least 40 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of target sequences comprises 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of target sequences is selected from SEQ ID NOs:1-43. In some embodiments, the plurality of target sequences is selected from SEQ ID NOs:1-22. In certain embodiments, the plurality of targets is selected from the group consisting of: PBX1, MYBPC1, LASP1, CAMK2N1, RABGAP1, UBE2C, PCAT-32, NF1B, TNFRSF19, PCDH7, ANO7, GLYATL1P4/PCAT-80, C6orf10, IQGAP3, THBS2, EPPK1, NUSAP1, ZWILCH, S1P4, SENP7, ANLN, C10orf116, PPP6R3, PDS5B, TOP2A, IL1RAP, CENPE, GALNT8, KCNQ1, C6orf155, LUZP2, HEATR3,

TMEM108, CFBXXbac-BPG116M5.17, ECHDC2, and ARNTL. In other embodiments the plurality of targets is selected from the group consisting of: PBX1, MYBPC1, LASP1, CAMK2N1, RABGAP1, UBE2C, PCAT-32, NF1B, TNFRSF19, PCDH7, ANO7, GLYATL1P4/PCAT-80, C6orf10, IQGAP3, THBS2, EPPK1, NUSAP1, ZWILCH, and S1P4. In an additional embodiment, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In a further embodiment, the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas.

BRIEF DESCRIPTION OF THE DRAWINGS

[0029] FIG. 1. Overview of the studies. CONSORT diagram illustrating the design for the training and independent validation studies.

[0030] FIG. 2. KM curves for BCR, METS, PCSM and Overall Survival events for NED, PSA and METs patients in the Discovery cohort. For each plot, probability of the event (BCR, METS, PCSM or OS) is shown in the Y-Axis. METS are also named SYS (for systemic event) or CR (for Clinical Recurrence).

[0031] FIG. 3. 43-Biomarker Set Methods

[0032] FIG. 4. PSR Annotation of the 43-Biomarker Set

[0033] FIG. 5. Biomarker variable mean squared error for selection of 22-biomarker signature

[0034] FIG. 6. Biomarker signature variable importance plot

[0035] FIG. 7. Development of Genomic Classifier (GC).

[0036] FIG. 8. Survival ROC to compare the accuracy of predicting metastatic disease (METS) at 5 years in different models. Survival ROC evaluates the ability of a marker measured at baseline (in this case RP) to discriminate between patients who develop CP from those who do not over a follow-up interval of 5 years. C discrimination index with 95% confidence intervals are shown for each prognostic classifier.

[0037] FIG. 9. Standard ROC and Discrimination plot for GC, CC and GCC.

[0038] FIG. 10. Calibration plots for probability of METS

[0039] FIG. 11. Discrimination plots for CC, GC, and GCC models (for METS)

[0040] **FIG. 12.** Survival decision curve analysis for the prognostic models at 5 years following radical prostatectomy. Performance of models is compared to extremes of classifying all patients as CP (thus potentially treating all patients, light gray line), against classifying no patients as CP (this treating none, horizontal dark gray line). A decision-to-treat threshold is a cutoff used to classify a patient as having CP or not. In decision curve analysis, this threshold varies from 0 to 1, and the sensitivity and specificity are calculated at each threshold, to determine the net-benefit. A model with a high net-benefit that does not overlap the “Treat All” line is optimal. The x-axis is the threshold probabilities while the y-axis is the net-benefit.

[0041] **FIG. 13.** Comparison of CC, GC and GCC cumulative Incidence (for METS)

[0042] **FIG. 14.** Cumulative incidence removing patients with adjuvant hormones: GPSM and GCC

[0043] **FIG. 15.** Cumulative incidence removing patients with adjuvant hormones: GPSM and GC.

[0044] **FIG. 16.** 5-year metastasis-free survival ROC in sampled validation study

[0045] **FIG. 17.** Cumulative Incidence: D’Amico and GC

[0046] **FIG. 18.** Cumulative incidence of GPSM and GC groups. A) Patients are segregated into low (<5), intermediate (5-9) and high risk (≥ 10) GPSM groups as suggested in Thompson et al. B) GC scores were segregated into low (<0.5) and high (≥ 0.5) for tentative risk groups. Irrespective of the method used, red lines indicated higher risk, orange intermediate risk and green lower risk. Number of patients (weighting controls by a factor of 5) at risk is shown below the x-axis, and the total number of events in each risk group is shown in boxes beside the lines.

[0047] **FIG. 19.** Discrimination plots showing segregation of Gleason 7 patients by CC (or CM, for Clinical Model) and GCC (n=382)

[0048] **FIG. 20.** CM and GCC Risk Groups of Gleason 7, 4+3 and 3+4 patients with CR endpoint (n=150)

[0049] **FIG. 21.** GCC stratification of Gleason 7, 4+3 and 3+4 patients with PCSM endpoint (n=150)

[0050] **FIG. 22.** Gleason 4+3 (n=50) and 3+4 (n=100) sub-stratification by GCC with METS (or CR, for Clinical Recurrence) endpoint

[0051] **FIG. 23.** Gleason 4+3 (n=50) and 3+4 (n=100) sub-stratification by GCC with PCSM endpoint

[0052] FIG. 24. Stratification of uniformly treated N+ patient by GCC and CC (or CM, for Clinical Model) (n=97 and n=96) with METS (or CR, for Clinical Recurrence) endpoint

[0053] FIG. 25. Stratification of uniformly treated N+ patient by GCC and and CC (or CM, for Clinical Model) (n=97 and n=96) with PCSM endpoint

[0054] FIG. 26. Multidimensional scaling plot of (A) the training and (B) the testing sets. Controls are indicated as '+' and cases are indicated as circles. In both the training and validation sets the controls tend to cluster on the left of the plot and the cases on the right of the plot. In this manner, most of the biological differences are expressed in the first dimension of the scaling. Random forest proximity [<http://www.stat.berkeley.edu/~breiman/>] was used to measure the 22 marker distance between samples.

[0055] FIG. 27. Performance of external signatures in training and testing sets. For each signature, the institution associated to it, year of publication, lead author, the AUC obtained in the training and testing sets, as well as the 95% Confidence Interval for this metric is shown.

[0056] FIG. 28. Performance of single genes in training and testing sets. For each gene, the AUC obtained in the training and testing sets, as well as the 95% Confidence Interval for this metric is shown.

[0057] FIG. 29. ROC curve and AUC with 95% confidence interval for classifiers and individual clinicopathologic variables in training and testing sets. CC: clinical-only classifier. GC: genomic classifier. GCC: combined genomic-clinical classifier.

[0058] FIG. 30. ROC curve of multivariable models and individual clinicopathologic variables. A) ROC curves in Training B) ROC curves in testing.

[0059] FIG. 31. Metastasis-Free 5-year Survival ROC of GC an individual clinicopathologic variables in the independent validation set.

[0060] FIG. 32. Metastasis-Free 5-year Decision Curve of GC an individual clinicopathologic variables in the independent validation set.

[0061] FIG. 33. Distribution of GC scores among pathologic GS categories in testing. GC scores are plotted with a jitter so as to more easily differentiate the patients among each Pathologic GS (x-axis) groups. Cases (black) and controls patients (gray) are shown for each category. The dashed black line indicates the GC cutoff of 0.5. Trends show the patients with high GC scores tend to have high Gleason Scores as well.

[0062] FIG. 34. Distribution of GC scores among pathologic GS categories in the independent validation set. METS = triangle, METS-free = circle

[0063] **FIG. 35A-C.** Prostate Cancer Specific Mortality Kaplan-Meier Plots on Training and Testing Sets. FIG 35A –Gleason Score = 7; FIG 35B –Gleason Score = 8; FIG 35C –Gleason Score $\geq$ 9.

[0064] **FIG. 36.** Kaplan Meier estimates for all PSA Controls with metastasis endpoint. PSA controls were separated into two groups based on high (>0.5) or low risk according to GC. Log-rank p-values are shown in the upper right corner.

[0065] **FIG. 37.** Survival decision curve analysis of GC and CAPRA-S.

[0066] **FIG. 38.** Distribution of GC scores among CAPRA-S score categories.

[0067] **FIG. 39.** The cumulative incidence plot for the CAPRA-S high risk group (A) and stratified by GC score (B).

[0068] **FIG. 40A-C.** Prediction Curve for GC, CAPRA-S and an integrated genomic-clinical model. (A) CAPRA-S; (B) GC; (C) Integrated Genomic-Clinical model.

[0069] **FIG. 41A-B.** Breakdown of treatment recommendations pre and post-GC for Low and High GC Risk groups in the Adjuvant setting. (A) pre-GC; (B) post-GC.

[0070] **FIG. 42.** Proportion of recommendations for treatment for the indicated values of clinical variables (eg: Presence / Absence) Pre-GC and the resulting proportion recommended for treatment post-GC in High and Low GC Risk groups in the Adjuvant setting.

[0071] **FIG. 43.** Breakdown of treatment recommendations pre and post-GC for Low and High GC Risk groups in the Salvage setting. (A) pre-GC; (B) post-GC.

[0072] **FIG. 44.** Proportion of recommendations for treatment for the indicated values of clinical variables (eg: Presence / Absence) Pre-GC and the resulting proportion recommended for treatment post-GC in High and Low GC Risk groups in the Salvage setting.

[0073] **FIG. 45.** Urologists confidence in treatment recommendations made post GC test results.

[0074] **FIG. 46.** GC Score distribution among METS (right -light grey circles) and No-METS patients (left -dark grey circles).

[0075] **FIG. 47.** 3-year Survival ROC comparing GC and clinicopathologic features. Values within legend indicate AUC and its corresponding 95% Confidence Interval.

[0076] **FIG. 48.** 3-year Survival ROC of clinical-only and genomic-based models. Values within legend indicate AUC and its corresponding 95% Confidence.

[0077] **FIG. 49.** 3-year Survival ROC of clinical-only and genomic-based models after excluding patients with Adjuvant therapy. Values within legend indicate AUC and its corresponding 95% Confidence Interval.

[0078] **FIG. 50.** Distribution of GC scores among pathological Gleason Score categories for patients with and without metastasis after Biochemical Recurrence. METS (triangle); No-METS (circle).

[0079] **FIG. 51.** Cumulative Incidence of metastasis after BCR with a GC cut-off of 0.4

[0080] **FIG. 52.** Cumulative Incidence of metastasis after BCR with a GC cut-off of 0.5

[0081] **FIG. 53.** Cumulative Incidence of metastasis after BCR after excluding patients with Adjuvant Treatment

[0082] **FIG. 54.** Reclassification of BCR patients by GC

[0083] **FIG. 55.** 3-year Decision Curve Analysis

[0084] **FIG 56. GC prediction of metastasis in in 962 patients from multiple cohorts in the meta-validation study.** All 5 cohorts with metastasis information show good separation in Met probability between no mets patients and met patients. 6% Met probability at 5 years is indicated by a dash line. Medians of each group indicated by black lines.

[0085] **FIG 57. Proportion of low, intermediate and high risk patients as determined by GC shows GC probabilities relationship to cohort risk in the meta-validation study.** In cohorts with high risk (right), there are a higher proportion of intermediate and high risk patients compared to cohorts with lower risk (left). Cohort risk were determined based on prevalence of biochemical recurrence, pT3 and Gleason 8+.

[0086] **FIG 58. GC probabilities and Gleason Score in 997 patients from 7 cohorts in the meta-validation study.** Patients with adverse outcome tend to have higher probabilities than patients with no Mets in each Gleason Score subset. Median lines of Mets vs no Mets patients are shown.

[0087] **FIG 59. GC probabilities in 414 no BCR patients in the meta-validation study.** Observe few high GC probabilities events in non-BCR patients of 8 cohorts. For the few events above 6%, they may either be due to short follow up time or are treatment responders. Patients with any treatment are denoted as Tx while patients with no treatment are denoted as no Tx. Patients with no treatment information are denoted as unknown.

[0088] **FIG 60. 5-year survival ROC for prediction of metastasis after RP comparing GC with standard clinicopathologic variables in the NCCN/AUA high risk cohort.** SVI: seminal vesicle invasion, ECE: Extra capsular extension, SM: surgical margin, PathGS: pathological Gleason score, Pre-op PSA: pre-operative prostate specific antigen.

[0089] **FIG 61. AUC values for previously reported prognostic biomarkers in prostate cancer based on 5-year ROC for prediction of metastasis after RP in the NCCN/AUA**

high risk cohort. Survival AUC (95% CI) for predicting clinical metastasis by RNA expression analysis for several genes previously reported to be prognostic in the literature. Expression of each gene was evaluated using high-density microarray analysis of primary tumor from 648 men treated at Mayo Clinic with radical prostatectomy for localized prostate cancer with pT3 or pT2/SM disease.

[0090] FIG 62. 5-year survival ROC for prediction of metastasis after RP comparing GC with clinical-only models and genomic-clinical models in the NCCN/AUA high risk cohort. CC: clinical-only classifier, GCC: genomic-clinical classifier, Stephenson: Stephenson nomogram, CAPRA-S: Cancer of the Prostate Risk Assessment-Surgical.

[0091] Figure 63. Decision curve analysis for GC in the NCCN/AUA high risk cohort. Net clinical benefit of GC was compared to (A) other clinicopathologic factors and (B) clinical-only nomograms.

[0092] FIG 64. Reclassification of patients classified as high risk by AUA/NCCN criteria based on GC scores. Patients were categorized to low risk ($GC < 0.4$) and high risk ($GC \geq 0.4$) groups based on their GC scores.

[0093] FIG 65. Reclassification of patients classified as high risk by AUA/NCCN criteria based on GC scores after excluding those who received adjuvant treatments. Patients were categorized to low risk ($GC < 0.4$) and high risk ($GC \geq 0.4$) groups based on their GC scores.

[0094] FIG 66. Cumulative incidence probability of metastasis after RP in the NCCN/AUA high risk cohort. Patients were categorized to low risk ($GC < 0.4$) and high risk ($GC \geq 0.4$) groups based on their GC scores.

[0095] FIG 67. ROC curves and AUC values for prediction of metastatic disease progression across both cohorts in the APF subset study.

[0096] FIG 68. ROC curves and AUC values for prediction of metastatic disease progression in the SVI APF subset.

[0097] FIG 69. ROC curves and AUC values for prediction of metastatic disease progression in the ECE APF subset.

[0098] FIG 70. ROC curves and AUC values for prediction of metastatic disease progression in the SM+ APF subset.

[0099] FIG 71. ROC curves and AUC values for prediction of metastatic disease progression in the GS APF subset.

- [0100] Table 1. Clinical characteristics of Discovery and Validation data set
- [0101] Table 2. 43-Biomarker Set. Chromosomal coordinates correspond to the hg19 version of the human genome.
- [0102] Table 3. Gene Ontology Terms Enriched in the 43-Biomarker Signature
- [0103] Table 4. 22-Biomarker Set. Chromosomal coordinates correspond to the hg19 version of the human genome.
- [0104] Table 5. Comparison of Discrimination ability of classifiers in different datasets
- [0105] Table 6. Reclassification of GPSM categories by GC.
- [0106] Table 7. Univariable Analysis for panel of prognostic classifiers and clinicopathologic variables (for METS)
- [0107] Table 8. Multivariable Cox regression analysis.
- [0108] Table 9. Multivariable Analysis for panel of prognostic classifiers and clinicopathologic variables Adjusted for Hormone Therapy (for METS)
- [0109] Table 10. Multivariable Analysis of GC compared to GPSM and CC (for METS)
- [0110] Table 11. List of Target Sequences
- [0111] Table 12. Univariable and Multivariable Logistic Regression Analysis in Testing Set
- [0112] Table 13. Multivariable Cox proportional hazards modeling comparing genomic classifier (GC) to clinicopathologic variables using different Gleason Score parameterization in the independent validation set.
- [0113] Table 14. Multivariable Cox proportional hazard models of GC with Stephenson Nomogram
- [0114] Table 15. Multivariable Cox proportional hazards modeling of decile risk groups of the genomic classifier (GC) after adjusting for treatment.
- [0115] Table 16. Survival analysis of GC score risk groups (<0.4 , $0.4-0.6$, >0.6).
- [0116] Table 17. Reclassification by GC of Gleason Risk categories among cases and controls in the testing set.
- [0117] Table 18. Number of metastasis and PCSM events for different GC score risk groups among pathologic GS categories in the independent validation set.
- [0118] Table 19. Number of patients at risk of developing PCSM at various time points after BCR
- [0119] Table 20. Number of patients at risk of metastasis at various time points after BCR
- [0120] Table 21. Clinical characteristics of the cohort in Example 9.

- [0121] Table 22. Survival ROC AUCs and associated 95% confidence intervals for GC, CAPRA-S and other individual clinical variables.
- [0122] Table 23. Reclassification of GC low risk (GC Score <0.4) and GC high risk (GC Score ≥ 0.4) for CAPRA-S low, intermediate and high risk scores.
- [0123] Table 24. Univariable and Multivariable Analysis for GC, CAPRA-S and individual clinical variables.
- [0124] Table 25. Characteristics of urologists participating in study.
- [0125] Table 26. Characteristics of patient cases.
- [0126] Table 27. Probability of Changing Treatment Recommendation from Pre to Post GC test
- [0127] Table 28. Change in treatment intensity by initial Perceived and GC risks.
- [0128] Table 29. Detailed Overview of Probability of Changing Treatment Recommendation from Pre to Post GC test.
- [0129] Table 30. Proportions of patients with treatment recommended.
- [0130] Table 31. Urologist reported confidence in and influence on treatment recommendations.
- [0131] Table 32. Breakdown of treatment recommendations pre and post-GC for Low and High GC Risk groups in the Adjuvant setting
- [0132] Table 33. Clinical and pathologic characteristics of patient cohort.
- [0133] Table 34. Number of patients at risk of developing metastasis at various time points after BCR .
- [0134] Table 35. Number of patients at risk of developing metastasis at various time points after BCR.
- [0135] Table 36. Number of patients at risk of developing metastasis at various time points after BCR.
- [0136] Table 37. Survival Analysis for GC and clinicopathologic factors. Multivariable analysis is adjusted for adjuvant treatment, GC reported for 10% unit increase.
- [0137] Table 38. Survival Analysis for GC, Stephenson and CAPRA-S. Multivariable analyses are adjusted for adjuvant treatment, GC and Stephenson reported for 10% unit increase.
- [0138] Table 39: biomarkers from the 43 biomarker panel with significance for Wilcoxon P-value (auc.pvalue) and other metrics for the BCR event endpoint.

- [0139] Table 40: biomarkers from the 43 biomarker panel with significance for Wilcoxon P-value (auc.pvalue) and other metrics for the ECE endpoint.
- [0140] Table 41: biomarkers from the 43 biomarker panel with significance for Wilcoxon P-value (auc.pvalue) and other metrics for the LCR event endpoint.
- [0141] Table 42: biomarkers from the 43 biomarker panel with significance for Wilcoxon P-value (auc.pvalue) and other metrics for the LNI endpoint.
- [0142] Table 43: biomarkers from the 43 biomarker panel with significance for Wilcoxon P-value (auc.pvalue) and other metrics for the MET event endpoint.
- [0143] Table 44: biomarkers from the 43 biomarker panel with significance for Wilcoxon P-value (auc.pvalue) and other metrics for the OS event endpoint.
- [0144] Table 45: biomarkers from the 43 biomarker panel with significance for Wilcoxon P-value (auc.pvalue) and other metrics for the pathological Gleason endpoint.
- [0145] Table 46: biomarkers from the 43 biomarker panel with significance for Wilcoxon P-value (auc.pvalue) and other metrics for the PCSM event endpoint.
- [0146] Table 47: biomarkers from the 43 biomarker panel with significance for Wilcoxon P-value (auc.pvalue) and other metrics for the psaDT endpoint.
- [0147] Table 48: biomarkers from the 43 biomarker panel with significance for Wilcoxon P-value (auc.pvalue) and other metrics for the SVI endpoint.
- [0148] Table 49: pairwise biomarkers from the 43 biomarker panel with significance for Wilcoxon P-value (auc.pvalue $\leq$ 0.05) and other metrics for the BCR event endpoint.
- [0149] Table 50: pairwise biomarkers from the 43 biomarker panel with significance for Wilcoxon P-value (auc.pvalue $\leq$ 0.001) and other metrics for the MET event endpoint.
- [0150] Table 51: pairwise biomarkers from the 43 biomarker panel with significance for Wilcoxon P-value (auc.pvalue $\leq$ 0.05) and other metrics for the PCSM event endpoint.
- [0151] Table 52: pairwise biomarkers from the 43 biomarker panel with significance for Wilcoxon P-value (auc.pvalue $\leq$ 0.05) and other metrics for the psaDT endpoint.
- [0152] Table 53: biomarkers from the 2,040 biomarker library with significance for Wilcoxon P-value (auc.pvalue $\leq$ 0.05) and other metrics for the BCR event endpoint.
- [0153] Table 54: biomarkers from the 2,040 biomarker library with significance for Wilcoxon P-value (auc.pvalue $\leq$ 0.05) and other metrics for the MET event endpoint.
- [0154] Table 55: 2,040 biomarker library. For each feature, genomic category, associated Affymetrix probeset ID, Associated Gene, Kolmogorov Smirnov Test P-value demonstrating

statistical significance at 0.05 level is shown, together with Mean Decrease in Gini and Mean Decrease in Accuracy.

[0155] Table 56. Study characteristics and GC performance in the meta-validation study. Study characteristics of 5 cohorts with Metastasis information available and GC performance in predicting Metastasis. Overall accuracy, sensitivity and specificity reflect 6% Metastatic probability cutoff. NCCN high risk as defined by either pathologic tumor stage pT3 or positive surgical margins (SM).

[0156] Table 57. Percentage of treated patients in each study in relation to the cutoff in the meta-validation Study.

[0157] Table 58. Clinical and pathological characteristics of the cohort in the NCCN/AUA high risk cohort. The set of patients on this cohort correspond to a subset of patients reported elsewhere (Example 1) that have pT3N0M0 or pT2N0M0 with positive margins.

[0158] Table 59. Hazard ratio for GC and clinicopathological features in the NCCN/AUA high risk cohort. (A) Univariable setting. (B) Multivariable setting, by Cox proportional hazards modeling. CI: confidence interval; GC: genomic classifier.

[0159] Table 60. Hazard ratio for GC and clinicopathological features considering primary and secondary pathological Gleason grade separately in the NCCN/AUA high risk cohort. (A) Univariable setting. (B) Multivariable setting, by Cox proportional hazards modeling. CI: confidence interval; GC: genomic classifier.

[0160] Table 61. Hazard ratio for GC and clinical-only nomograms in the NCCN/AUA high risk cohort. (A) Univariable setting. (B) Multivariable setting, by Cox proportional hazards modeling. CI: confidence interval; GC: genomic classifier.

[0161] Table 62. Clinical and Pathological Characteristics of the cohorts used for the assessment of GC within different APF sets of patients.

[0162] Table 63. Multivariable Analysis of GC and different clinical-pathological variables across the two cohorts in the APF subset study. Odds Ratios for GC were calculated for 10% unit increase in score. Pathological Gleason score was dichotomized : ≥ 8 . Log2 of pPSA was calculated.

[0163] Table 64. Multivariable analysis for metastatic disease progression endpoint within APF subsets. GC is the most significant predictor of metastatic disease in APF patients after adjusting for other variables.

[0164] Table 65. Reclassification of APF subsets with the Genomic Classifier. For each APF subset, most of the prostate cancer deaths occur in patients with high GC scores.

DETAILED DESCRIPTION OF THE INVENTION

[0165] The present invention discloses systems and methods for diagnosing, predicting, and/or monitoring the status or outcome of a 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 suffering from a cancer; (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 the cancer based on the expression level of the plurality of targets.

[0166] 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.

[0167] In some instances, the plurality of targets comprises more than one target selected from Tables 2, 4, 11 or 55. 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, or at least about 10 targets selected from Table 2, 4, and 11. In other instances, the plurality of targets comprises at least about 12, at least about 15, at least about 17, at least about 20, at least about 22, at least about 25, at least about 27, at least about 30, at least about 32, at least about 35, at least about 37, or at least about 40 targets selected from Tables 2, 4, 11 or 55. In some instances, the targets are selected from Table 2. In some instances, the plurality of targets comprises 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 targets selected from Tables 2, 4, 11 or 55. In some instances, the plurality of targets is selected from SEQ ID NOs:1-43. In some instances, the plurality of targets is selected from SEQ ID NOs:1-22. In some instances, the targets are selected from Table 4. In some instances, the targets are selected from Table 11. 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 sequence. In some instances, the non-exonic sequence comprises an untranslated region (e.g., UTR), intronic region, intergenic region, or any combination thereof. Alternatively, the plurality of targets comprises an anti-sense sequence. In other instances, the plurality of targets comprises a non-coding RNA transcript.

[0168] Further disclosed herein, is a probe set for diagnosing, predicting, and/or monitoring a cancer in a subject. In some instances, the probe set comprises a plurality of probes capable of detecting an expression level of more than one target selected from Tables 2, 4, 11 or 55, wherein the expression level determines the cancer status of the subject with at least about 45% specificity. In some instances, detecting an expression level comprise detecting gene expression, protein expression, or any combination thereof. In some instances, the plurality of targets comprises more than one target selected from Tables 2, 4, 11 or 55. 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, or at least about 10 targets selected from Table 2, 4, and 11. In other instances, the plurality of targets comprises at least about 12, at least about 15, at least about 17, at least about 20, at least about 22, at least about 25, at least about 27, at least about 30, at least about 32, at least about 35, at least about 37, or at least about 40 targets selected from Tables 2, 4, 11 or 55. In some instances, the targets are selected from Table 2. In some instances, the targets are selected from Table 4. In some instances, the targets are selected from Table 11. . In some instances, the plurality of targets comprises 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 targets selected from Tables 2, 4, 11 or 55. In some instances, the plurality of targets is selected from SEQ ID NOs:1-43. In some instances, the plurality of targets is selected from SEQ ID NOs:1-22. 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 sequence. In some instances, the non-exonic sequence comprises an untranslated region (e.g., UTR), intronic region, intergenic region, or any combination thereof. Alternatively, the plurality of targets comprises an anti-sense sequence. In other instances, the plurality of targets comprises a non-coding RNA transcript.

[0169] Further disclosed herein are methods for characterizing a patient population. Generally, the method comprises: (a) providing a sample from a subject; (b) assaying the expression level for a plurality of targets in the sample; and (c) characterizing the subject based on the expression level of the plurality of targets. In some instances, the plurality of targets comprises more than one target selected from Tables 2, 4, 11 or 55. 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, or at least about 10 targets selected from Tables 2, 4, 11 or 55. In other instances, the plurality of targets comprises at least about 12, at least about 15, at least about 17, at least about 20, at least about 22, at least about 25, at least about 27, at least about 30, at least about 32, at least about 35, at least about 37, or at least about 40 targets selected from Tables 2, 4, 11 or 55. In some instances, the targets are selected from Table 2. In some instances, the targets are selected from Table 4. In some instances, the targets are selected from Table 11. . In some instances, the plurality of targets comprises 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 targets selected from Tables 2, 4, 11 or 55. In some instances, the plurality of targets is selected from SEQ ID NOs:1-43. In some instances, the plurality of targets is selected from SEQ ID NOs:1-22. 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 sequence. In some instances, the non-exonic sequence comprises an untranslated region (e.g., UTR), intronic region, intergenic region, or any combination thereof. Alternatively, the plurality of targets comprises an anti-sense sequence. In other instances, the plurality of targets comprises a non-coding RNA transcript.

[0170] In some instances, characterizing the subject comprises determining whether the subject would respond to an anti-cancer therapy. Alternatively, characterizing the subject comprises identifying the subject as a non-responder to an anti-cancer therapy. Optionally, characterizing the subject comprises identifying the subject as a responder to an anti-cancer therapy.

[0171] 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.

Definitions

[0172] Unless defined otherwise or the context clearly dictates otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. In describing the present invention, the following terms may be employed, and are intended to be defined as indicated below.

[0173] The term "polynucleotide" as used herein refers to a polymer of greater than one nucleotide in length of ribonucleic acid (RNA), deoxyribonucleic acid (DNA), hybrid RNA/DNA, modified RNA or DNA, or RNA or DNA mimetics, including peptide nucleic acids (PNAs). The polynucleotides may be single- or double-stranded. The term includes polynucleotides composed of naturally-occurring nucleobases, sugars and covalent internucleoside (backbone) linkages as well as polynucleotides having non-naturally-occurring portions which function similarly. Such modified or substituted polynucleotides are well known in the art and for the purposes of the present invention, are referred to as "analogues."

[0174] "Complementary" or "substantially complementary" refers to the ability to hybridize or base pair between nucleotides or nucleic acids, such as, for instance, between a sensor peptide nucleic acid or polynucleotide and a target polynucleotide. Complementary nucleotides are, generally, A and T (or A and U), or C and G. Two single-stranded polynucleotides or PNAs are said to be substantially complementary when the bases of one strand, optimally aligned and compared and with appropriate insertions or deletions, pair with at least about 80% of the bases of the other strand, usually at least about 90% to 95%, and more preferably from about 98 to 100%.

[0175] Alternatively, substantial complementarity exists when a polynucleotide may hybridize under selective hybridization conditions to its complement. Typically, selective hybridization may occur when there is at least about 65% complementarity over a stretch of at least 14 to 25 bases, for example at least about 75%, or at least about 90% complementarity.

[0176] "Preferential binding" or "preferential hybridization" refers to the increased propensity of one polynucleotide to bind to its complement in a sample as compared to a noncomplementary polymer in the sample.

[0177] Hybridization conditions may typically include salt concentrations of less than about 1M, more usually less than about 500 mM, for example less than about 200 mM. In the case of hybridization between a peptide nucleic acid and a polynucleotide, the hybridization can be done in solutions containing little or no salt. Hybridization temperatures can be as low as 5° C, but are typically greater than 22° C, and more typically greater than about 30° C, for example in excess of about 37° C. Longer fragments may require higher hybridization temperatures for specific hybridization as is known in the art. Other factors may affect the stringency of hybridization, including base composition and length of the complementary strands, presence of organic solvents and extent of base mismatching, and the combination of parameters used is more important than the absolute measure of any one alone. Other hybridization conditions which may be controlled include buffer type and concentration, solution pH, presence and concentration of blocking reagents to decrease background binding such as repeat sequences or blocking protein solutions, detergent type(s) and concentrations, molecules such as polymers which increase the relative concentration of the polynucleotides, metal ion(s) and their concentration(s), chelator(s) and their concentrations, and other conditions known in the art.

[0178] "Multiplexing" herein refers to an assay or other analytical method in which multiple analytes are assayed. In some instances, the multiple analytes are from the same sample. In some instances, the multiple analytes are assayed simultaneously. Alternatively, the multiple analytes are assayed sequentially. In some instances, assaying the multiple analytes occurs in the same reaction volume. Alternatively, assaying the multiple analytes occurs in separate or multiple reaction volumes.

[0179] A "target sequence" as used herein (also occasionally referred to as a "PSR" or "probe selection region") refers to a region of the genome against which one or more probes can be designed. A "target sequence" may be a coding target or a non-coding target. A "target sequence" may comprise exonic and/or non-exonic sequences. Alternatively, a "target sequence" may comprise an ultraconserved region. An ultraconserved region is generally a sequence that is at least 200 base pairs and is conserved across multiple species. An ultraconserved region may be exonic or non-exonic. 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.

[0180] As used herein, a probe is any polynucleotide capable of selectively hybridizing to a target sequence or its complement, or to an RNA version of either. A probe may comprise ribonucleotides, deoxyribonucleotides, peptide nucleic acids, and combinations thereof. A probe may optionally comprise one or more labels. In some embodiments, a probe may be used to amplify one or both strands of a target sequence or an RNA form thereof, acting as a sole primer in an amplification reaction or as a member of a set of primers.

[0181] As used herein, a non-coding target may comprise a nucleotide sequence. The nucleotide sequence is a DNA or RNA sequence. A non-coding target may include a UTR sequence, an intronic sequence, or a non-coding RNA transcript. A non-coding target also includes sequences which partially overlap with a UTR sequence or an intronic sequence. A non-coding target also includes non-exonic transcripts.

[0182] As used herein, a coding target includes nucleotide sequences that encode for a protein and peptide sequences. The nucleotide sequence is a DNA or RNA sequence. The coding target includes protein-coding sequence. Protein-coding sequences include exon-coding sequences (e.g., exonic sequences).

[0183] As used herein, diagnosis of cancer may include the identification of cancer in a subject, determining the malignancy of the cancer, or determining the stage of the cancer.

[0184] As used herein, prognosis of cancer may include predicting the clinical outcome of the patient, assessing the risk of cancer recurrence, determining treatment modality, or determining treatment efficacy.

[0185] "Having" is an open-ended phrase like "comprising" and "including," and includes circumstances where additional elements are included and circumstances where they are not.

[0186] "Optional" or "optionally" means that the subsequently described event or circumstance may or may not occur, and that the description includes instances where the event or circumstance occurs and instances in which it does not.

[0187] As used herein 'NED' describes a clinically distinct disease state in which patients show no evidence of disease (NED') at least 5 years after surgery, 'PSA' describes a clinically distinct disease state in which patients show biochemical relapse only (two successive increases in prostate-specific antigen levels but no other symptoms of disease with at least 5 years follow up after surgery; 'PSA') and 'SYS' describes a clinically distinct disease state in

which patients develop biochemical relapse and present with systemic cancer disease or metastases ('SYS') within five years after the initial treatment with radical prostatectomy.

[0188] The terms "METS", "SYS", "systemic event", "Systemic progression", "CR" or "Clinical Recurrence" may be used interchangeably and generally refer to patients that experience BCR (biochemical recurrence) and that develop metastases (confirmed by bone or CT scan). The patients may experience BCR within 5 years of RP (radical prostatectomy). The patients may develop metastases within 5 years of BCR. In some cases, patients regarded as METS may experience BCR after 5 years of RP.

[0189] As used herein, the term "about" refers to approximately a $\pm 10\%$ variation from a given value. It is to be understood that such a variation is always included in any given value provided herein, whether or not it is specifically referred to.

[0190] Use of the singular forms "a," "an," and "the" include plural references unless the context clearly dictates otherwise. Thus, for example, reference to "a polynucleotide" includes a plurality of polynucleotides, reference to "a target" includes a plurality of such targets, reference to "a normalization method" includes a plurality of such methods, and the like. Additionally, use of specific plural references, such as "two," "three," etc., read on larger numbers of the same subject, unless the context clearly dictates otherwise.

[0191] Terms such as "connected," "attached," "linked" and "conjugated" are used interchangeably herein and encompass direct as well as indirect connection, attachment, linkage or conjugation unless the context clearly dictates otherwise.

[0192] Where a range of values is recited, it is to be understood that each intervening integer value, and each fraction thereof, between the recited upper and lower limits of that range is also specifically disclosed, along with each subrange between such values. The upper and lower limits of any range can independently be included in or excluded from the range, and each range where either, neither or both limits are included is also encompassed within the invention. Where a value being discussed has inherent limits, for example where a component can be present at a concentration of from 0 to 100%, or where the pH of an aqueous solution can range from 1 to 14, those inherent limits are specifically disclosed. Where a value is explicitly recited, it is to be understood that values, which are about the same quantity or amount as the recited value, are also within the scope of the invention, as are ranges based thereon. Where a combination is disclosed, each sub-combination of the elements of that combination is also specifically disclosed and is within the scope of the invention. Conversely, where different elements or groups of elements are disclosed,

combinations thereof are also disclosed. Where any element of an invention is disclosed as having a plurality of alternatives, examples of that invention in which each alternative is excluded singly or in any combination with the other alternatives are also hereby disclosed; more than one element of an invention can have such exclusions, and all combinations of elements having such exclusions are hereby disclosed.

Coding and Non-coding Targets

[0193] 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.

[0194] 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).

[0195] 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).

[0196] In some instances, the plurality of targets may be differentially expressed. In some instances, a plurality of probe selection regions (PSRs) is differentially expressed.

[0197] In some instances, the plurality of targets comprises more than one target selected from Tables 2, 4, 11 or 55. 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, or at least about 10 targets selected from Tables 2, 4, 11 or 55. In other instances, the plurality of targets comprises at least about 12, at least about 15, at least about 17, at least about 20, at least about 22, at least about 25, at least about 27, at least about 30, at least about 32, at least about 35, at least about 37, or at least about 40 targets selected from Tables 2, 4, 11 or 55. In some instances, the targets are selected from Table 2. In some

instances, the targets are selected from Table 4. In some instances, the targets are selected from Table 11. . In some instances, the plurality of targets comprises 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 targets selected from Tables 2, 4, 11 or 55. In some instances, the plurality of targets is selected from SEQ ID NOs:1-43. In some instances, the plurality of targets is selected from SEQ ID NOs:1-22. 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 sequence. Alternatively, a non-coding target comprises a UTR sequence, an intronic sequence, 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 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.

[0198] In some instances, the plurality of targets is at least about 70% identical to a sequence selected from SEQ ID NOs 1-43. Alternatively, the plurality of targets is at least about 80% identical to a sequence selected from SEQ ID NOs 1-43. In some instances, the plurality of targets is at least about 85% identical to a sequence selected from SEQ ID NOs 1-43. In some instances, the plurality of targets is at least about 90% identical to a sequence selected from SEQ ID NOs 1-43. Alternatively, the plurality of targets is at least about 95% identical to a sequence selected from SEQ ID NOs 1-43.

Probes/Primers

[0199] The present invention provides for a probe set for diagnosing, monitoring and/or predicting a status or outcome of a cancer in a subject comprising a plurality of probes, wherein (i) the probes in the set are capable of detecting an expression level of more than one non-coding target; and (ii) the expression level determines the cancer status of the subject with at least about 40% specificity.

[0200] The probe set may comprise more than one polynucleotide probe. 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.

[0201] 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.

[0202] 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. The 5,362,207 raw expression probes are summarized and normalized into 1,411,399 probe selection regions ("PSRs"). After removal (or filtration) of cross-hybridizing PSRs, highly variable PSRs (variance above the 90th percentile), and PSRs containing more than 4 probes, approximately 1.1 million PSRs remain. 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.

[0203] These remaining 1.1 million 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, 18,902 features remained in analysis for further selection. Feature selection was performed by regularized logistic regression using the elastic-net penalty. The regularized regression was 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 were tabulated. In some instances, features that were selected in at least 25% of the total runs were used for model building.

[0204] One skilled in the art understands that the nucleotide sequence of the polynucleotide probe need not be identical to its target sequence in order to specifically hybridize thereto. The polynucleotide probes of the present invention, therefore, comprise a nucleotide sequence that is at least about 65% identical to a region of the coding target or non-coding target selected from Tables 2, 4, 11 or 55. In another embodiment, the nucleotide sequence of the polynucleotide probe is at least about 70% identical a region of the coding target or non-coding target from Tables 2, 4, 11 or 55. In another embodiment, the nucleotide sequence of the polynucleotide probe is at least about 75% identical a region of the coding target or non-coding target from Tables 2, 4, 11 or 55. In another embodiment, the nucleotide sequence of the polynucleotide probe is at least about 80% identical a region of the coding target or non-coding target from Tables 2, 4, 11 or 55. In another embodiment, the nucleotide sequence of the polynucleotide probe is at least about 85% identical a region of the coding target or non-coding target from Tables 2, 4, 11 or 55. In another embodiment, the nucleotide sequence of the polynucleotide probe is at least about 90% identical a region of the coding target or non-coding target from Tables 2, 4, 11 or 55. In a further embodiment, the nucleotide sequence of the polynucleotide probe is at least about 95% identical to a region of the coding target or non-coding target from Tables 2, 4, 11 or 55. In some instances, the targets are selected from Table 2. In some instances, the targets are selected from Table 4. In some instances, the targets are selected from Table 11.

[0205] Methods of determining sequence identity are known in the art and can be determined, for example, by using the BLASTN program of the University of Wisconsin Computer Group (GCG) software or provided on the NCBI website. The nucleotide sequence of the polynucleotide probes of the present invention may exhibit variability by differing (*e.g.* by nucleotide substitution, including transition or transversion) at one, two, three, four or more nucleotides from the sequence of the coding target or non-coding target.

[0206] Other criteria known in the art may be employed in the design of the polynucleotide probes of the present invention. For example, the probes can be designed to have <50% G content and/or between about 25% and about 70% G+C content. Strategies to optimize probe hybridization to the target nucleic acid sequence can also be included in the process of probe selection.

[0207] Hybridization under particular pH, salt, and temperature conditions can be optimized by taking into account melting temperatures and by using empirical rules that

correlate with desired hybridization behaviors. Computer models may be used for predicting the intensity and concentration-dependence of probe hybridization.

[0208] 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.

[0209] 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.

[0210] 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 Tables 2, 4, 11 or 55. 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 Tables 2, 4, 11 or 55. 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 Tables 2, 4, 11 or 55. 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 Tables 2, 4, 11 or 55. 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 Tables 2, 4, 11 or 55. In some instances, the targets are selected from Table 2. In some instances, the targets are selected from Table 4. In some instances, the targets are selected from Table 11.

[0211] In some embodiments, the probe set comprises a plurality of target sequences that hybridize to a plurality of targets, wherein the at least about 20% of the plurality of targets are targets selected from Tables 2, 4, 11 or 55. In some embodiments, the probe set comprises a plurality of target sequences that hybridize to a plurality of targets, wherein the at least about 25% of the plurality of targets are targets selected from Tables 2, 4, 11 or 55. In some embodiments, the probe set comprise a plurality of target sequences that hybridize to a plurality of targets, wherein the at least about 30% of the plurality of targets are targets selected from Tables 2, 4, 11 or 55. In some embodiments, the probe set comprise a plurality of target sequences that hybridize to a plurality of targets, wherein the at least about 35% of the plurality of targets are targets selected from Tables 2, 4, 11 or 55. In some embodiments, the probe set comprise a plurality of target sequences that hybridize to a plurality of targets, wherein the at least about 40% of the plurality of targets are targets selected from Tables 2, 4, 11 or 55. In some embodiments, the probe set comprise a plurality of target sequences that hybridize to a plurality of targets, wherein the at least about 45% of the plurality of targets are targets selected from Tables 2, 4, 11 or 55. In some embodiments, the probe set comprise a plurality of target sequences that hybridize to a plurality of targets, wherein the at least about 50% of the plurality of targets are targets selected from Tables 2, 4, 11 or 55. In some embodiments, the probe set comprise a plurality of target sequences that hybridize to a plurality of targets, wherein the at least about 60% of the plurality of targets are targets selected from Tables 2, 4, 11 or 55. In some embodiments, the probe set comprise a plurality of target sequences that hybridize to a plurality of targets, wherein the at least about 70% of the plurality of targets are targets selected from Tables 2, 4, 11 or 55. In some instances, the targets are selected from Table 2. In some instances, the targets are selected from Table 4. In some instances, the targets are selected from Table 11.

[0212] 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.

[0213] 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.

[0214] 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 any of Tables 2, 4, 11 or 55 (or subgroups thereof as set forth herein), an RNA form thereof, or a complement to either thereof. In some instances, the targets are selected from Table 2. In some instances, the targets are selected from Table 4. In some instances, the targets are selected from Table 11.

[0215] As is known in the art, a nucleoside is a base-sugar combination and a nucleotide is a nucleoside that further includes a phosphate group covalently linked to the sugar portion of the nucleoside. In forming oligonucleotides, the phosphate groups covalently link adjacent nucleosides to one another to form a linear polymeric compound, with the normal linkage or backbone of RNA and DNA being a 3' to 5' phosphodiester linkage. Specific examples of polynucleotide probes or primers useful in this invention include oligonucleotides containing modified backbones or non-natural internucleoside linkages. As defined in this specification, oligonucleotides having modified backbones include both those that retain a phosphorus atom in the backbone and those that lack a phosphorus atom in the backbone. For the purposes of the present invention, and as sometimes referenced in the art, modified oligonucleotides that do not have a phosphorus atom in their internucleoside backbone can also be considered to be oligonucleotides.

[0216] Exemplary polynucleotide probes or primers having modified oligonucleotide backbones include, for example, those with one or more modified internucleotide linkages that are phosphorothioates, chiral phosphorothioates, phosphorodithioates, phosphotriesters, aminoalkylphosphotriesters, methyl and other alkyl phosphonates including 3'-alkylene phosphonates and chiral phosphonates, phosphinates, phosphoramidates including 3'-amino phosphoramidate and aminoalkylphosphoramidates, thionophosphoramidates, thionoalkylphosphonates, thionoalkylphosphotriesters, and boranophosphates having normal 3'-5' linkages, 2'-5' linked analogs of these, and those having inverted polarity wherein the adjacent pairs of nucleoside units are linked 3'-5' to 5'-3' or 2'-5' to 5'-2'. Various salts, mixed salts and free acid forms are also included.

[0217] Exemplary modified oligonucleotide backbones that do not include a phosphorus atom are formed by short chain alkyl or cycloalkyl internucleoside linkages, mixed heteroatom and alkyl or cycloalkyl internucleoside linkages, or one or more short chain heteroatomic or heterocyclic internucleoside linkages. Such backbones include morpholino linkages (formed in part from the sugar portion of a nucleoside); siloxane backbones; sulfide, sulfoxide and sulphone backbones; formacetyl and thioformacetyl backbones; methylene formacetyl and thioformacetyl backbones; alkene containing backbones; sulphamate backbones; methyleneimino and methylenehydrazino backbones; sulphonate and sulfonamide backbones; amide backbones; and others having mixed N, O, S and CH₂ component parts.

[0218] The present invention also contemplates oligonucleotide mimetics in which both the sugar and the internucleoside linkage of the nucleotide units are replaced with novel groups. The base units are maintained for hybridization with an appropriate nucleic acid target compound. An example of such an oligonucleotide mimetic, which has been shown to have excellent hybridization properties, is a peptide nucleic acid (PNA). In PNA compounds, the sugar-backbone of an oligonucleotide is replaced with an amide containing backbone, in particular an aminoethylglycine backbone. The nucleobases are retained and are bound directly or indirectly to aza-nitrogen atoms of the amide portion of the backbone.

[0219] The present invention also contemplates polynucleotide probes or primers comprising "locked nucleic acids" (LNAs), which may be novel conformationally restricted oligonucleotide analogues containing a methylene bridge that connects the 2'-O of ribose with the 4'-C. LNA and LNA analogues may display very high duplex thermal stabilities with complementary DNA and RNA, stability towards 3'-exonuclease degradation, and good solubility properties. Synthesis of the LNA analogues of adenine, cytosine, guanine, 5-

methylcytosine, thymine and uracil, their oligomerization, and nucleic acid recognition properties have been described. Studies of mismatched sequences show that LNA obey the Watson-Crick base pairing rules with generally improved selectivity compared to the corresponding unmodified reference strands.

[0220] LNAs may form duplexes with complementary DNA or RNA or with complementary LNA, with high thermal affinities. The universality of LNA-mediated hybridization has been emphasized by the formation of exceedingly stable LNA:LNA duplexes. LNA:LNA hybridization was shown to be the most thermally stable nucleic acid type duplex system, and the RNA-mimicking character of LNA was established at the duplex level. Introduction of three LNA monomers (T or A) resulted in significantly increased melting points toward DNA complements.

[0221] Synthesis of 2'-amino-LNA and 2'-methylamino-LNA has been described and thermal stability of their duplexes with complementary RNA and DNA strands reported. Preparation of phosphorothioate-LNA and 2'-thio-LNA have also been described.

[0222] Modified polynucleotide probes or primers may also contain one or more substituted sugar moieties. For example, oligonucleotides may comprise sugars with one of the following substituents at the 2' position: OH; F; O-, S-, or N-alkyl; O-, S-, or N-alkenyl; O-, S- or N-alkynyl; or O-alkyl-O-alkyl, wherein the alkyl, alkenyl and alkynyl may be substituted or unsubstituted C₁ to C₁₀ alkyl or C₂ to C₁₀ alkenyl and alkynyl. Examples of such groups are: O[(CH₂)_n O]_mCH₃, O(CH₂)_n OCH₃, O(CH₂)_n NH₂, O(CH₂)_n CH₃ ONH₂, and O(CH₂)_n ON[((CH₂)_n CH₃)₂], where n and m are from 1 to about 10. Alternatively, the oligonucleotides may comprise one of the following substituents at the 2' position: C₁ to C₁₀ lower alkyl, substituted lower alkyl, alkaryl, aralkyl, O-alkaryl or O-aralkyl, SH, SCH₃, OCN, Cl, Br, CN, CF₃, OCF₃, SOCH₃, SO₂ CH₃, ONO₂, NO₂, N₃, NH₂, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, an RNA cleaving group, a reporter group, an intercalator, a group for improving the pharmacokinetic properties of an oligonucleotide, or a group for improving the pharmacodynamic properties of an oligonucleotide, and other substituents having similar properties. Specific examples include 2'-methoxyethoxy (2'-O--CH₂ CH₂ OCH₃, also known as 2'-O-(2-methoxyethyl) or 2'-MOE), 2'-dimethylaminooxyethoxy (O(CH₂)₂ ON(CH₃)₂ group, also known as 2'-DMAOE), 2'-methoxy (2'-O--CH₃), 2'-aminopropoxy (2'-OCH₂ CH₂ CH₂ NH₂) and 2'-fluoro (2'-F).

[0223] Similar modifications may also be made at other positions on the polynucleotide probes or primers, particularly the 3' position of the sugar on the 3' terminal nucleotide or in

2'-5' linked oligonucleotides and the 5' position of 5' terminal nucleotide. Polynucleotide probes or primers may also have sugar mimetics such as cyclobutyl moieties in place of the pentofuranosyl sugar.

[0224] Polynucleotide probes or primers may also include modifications or substitutions to the nucleobase. As used herein, "unmodified" or "natural" nucleobases include the purine bases adenine (A) and guanine (G), and the pyrimidine bases thymine (T), cytosine (C) and uracil (U).

[0225] Modified nucleobases include other synthetic and natural nucleobases such as 5-methylcytosine (5-me-C), 5-hydroxymethyl cytosine, xanthine, hypoxanthine, 2-aminoadenine, 6-methyl and other alkyl derivatives of adenine and guanine, 2-propyl and other alkyl derivatives of adenine and guanine, 2-thiouracil, 2-thiothymine and 2-thiocytosine, 5-halouracil and cytosine, 5-propynyl uracil and cytosine, 6-azo uracil, cytosine and thymine, 5-uracil (pseudouracil), 4-thiouracil, 8-halo, 8-amino, 8-thiol, 8-thioalkyl, 8-hydroxyl and other 8-substituted adenines and guanines, 5-halo particularly 5-bromo, 5-trifluoromethyl and other 5-substituted uracils and cytosines, 7-methylguanine and 7-methyladenine, 8-azaguanine and 8-azaadenine, 7-deazaguanine and 7-deazaadenine and 3-deazaguanine and 3-deazaadenine. Further nucleobases include those disclosed in U.S. Pat. No. 3,687,808; The Concise Encyclopedia Of Polymer Science And Engineering, (1990) pp 858-859, Kroschwitz, J. I., ed. John Wiley & Sons; Englisch *et al.*, *Angewandte Chemie, Int. Ed.*, 30:613 (1991); and Sanghvi, Y. S., (1993) *Antisense Research and Applications*, pp 289-302, Crooke, S. T. and Lebleu, B., ed., CRC Press. Certain of these nucleobases are particularly useful for increasing the binding affinity of the polynucleotide probes of the invention. These include 5-substituted pyrimidines, 6-azapyrimidines and N-2, N-6 and O-6 substituted purines, including 2-aminopropyladenine, 5-propynyluracil and 5-propynylcytosine. 5-methylcytosine substitutions have been shown to increase nucleic acid duplex stability by 0.6-1.2°C.

[0226] One skilled in the art recognizes that it is not necessary for all positions in a given polynucleotide probe or primer to be uniformly modified. The present invention, therefore, contemplates the incorporation of more than one of the aforementioned modifications into a single polynucleotide probe or even at a single nucleoside within the probe or primer.

[0227] One skilled in the art also appreciates that the nucleotide sequence of the entire length of the polynucleotide probe or primer does not need to be derived from the target sequence. Thus, for example, the polynucleotide probe may comprise nucleotide sequences at

the 5' and/or 3' termini that are not derived from the target sequences. Nucleotide sequences which are not derived from the nucleotide sequence of the target sequence may provide additional functionality to the polynucleotide probe. For example, they may provide a restriction enzyme recognition sequence or a "tag" that facilitates detection, isolation, purification or immobilization onto a solid support. Alternatively, the additional nucleotides may provide a self-complementary sequence that allows the primer/probe to adopt a hairpin configuration. Such configurations are necessary for certain probes, for example, molecular beacon and Scorpion probes, which can be used in solution hybridization techniques.

[0228] The polynucleotide probes or primers can incorporate moieties useful in detection, isolation, purification, or immobilization, if desired. Such moieties are well-known in the art (see, for example, Ausubel *et al.*, (1997 & updates) *Current Protocols in Molecular Biology*, Wiley & Sons, New York) and are chosen such that the ability of the probe to hybridize with its target sequence is not affected.

[0229] Examples of suitable moieties are detectable labels, such as radioisotopes, fluorophores, chemiluminophores, enzymes, colloidal particles, and fluorescent microparticles, as well as antigens, antibodies, haptens, avidin/streptavidin, biotin, haptens, enzyme cofactors / substrates, enzymes, and the like.

[0230] 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.

[0231] 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.

[0232] 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.

[0233] 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.

[0234] Coding schemes may optionally be used, comprising encoded particles and/or encoded tags associated with different polynucleotides of the invention. A variety of different coding schemes are known in the art, including fluorophores, including SCNCs, deposited metals, and RF tags.

[0235] Polynucleotides from the described target sequences may be employed as probes for detecting target sequences expression, for ligation amplification schemes, or may be used as primers for amplification schemes of all or a portion of a target sequences. When amplified, either strand produced by amplification may be provided in purified and/or isolated form.

[0236] In one embodiment, polynucleotides of the invention include (a) a nucleic acid depicted in Tables 2, 4, 11 or 55; (b) an RNA form of any one of the nucleic acids depicted in Tables 2, 4, 11 or 55; (c) a peptide nucleic acid form of any of the nucleic acids depicted in

Tables 2, 4, 11 or 55; (d) a nucleic acid comprising at least 20 consecutive bases of any of (a-c); (e) a nucleic acid comprising at least 25 bases having at least 90% sequenced identity to any of (a-c); and (f) a complement to any of (a-e).

[0237] Complements may take any polymeric form capable of base pairing to the species recited in (a)-(e), including nucleic acid such as RNA or DNA, or may be a neutral polymer such as a peptide nucleic acid. Polynucleotides of the invention can be selected from the subsets of the recited nucleic acids described herein, as well as their complements.

[0238] In some embodiments, polynucleotides of the invention comprise at least 20 consecutive bases of the nucleic acid sequence of a target selected from any of Tables 2, 4, 11 or 55 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 any of Tables 2, 4, 11 or 55, as applicable. In some instances, the targets are selected from Table 2. In some instances, the targets are selected from Table 4. In some instances, the targets are selected from Table 11.

[0239] 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.

[0240] In one embodiment, solutions comprising polynucleotide and a solvent are also provided. In some embodiments, the solvent may be water or may be predominantly aqueous. In some embodiments, the solution may comprise at least two, three, four, five, six, seven, eight, nine, ten, twelve, fifteen, seventeen, twenty or more different polynucleotides, including primers and primer pairs, of the invention. Additional substances may be included in the solution, alone or in combination, including one or more labels, additional solvents, buffers, biomolecules, polynucleotides, and one or more enzymes useful for performing methods described herein, including polymerases and ligases. The solution may further comprise a primer or primer pair capable of amplifying a polynucleotide of the invention present in the solution.

[0241] 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.

[0242] Substrates can be planar crystalline substrates such as silica based substrates (e.g. glass, quartz, or the like), or crystalline substrates used in, e.g., the semiconductor and microprocessor industries, such as silicon, gallium arsenide, indium doped GaN and the like, and include semiconductor nanocrystals.

[0243] 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.

[0244] Silica aerogels can also be used as substrates, and can be prepared by methods known in the art. Aerogel substrates may be used as free standing substrates or as a surface coating for another substrate material.

[0245] The substrate can take any form and typically is a plate, slide, bead, pellet, disk, particle, microparticle, nanoparticle, strand, precipitate, optionally porous gel, sheets, tube, sphere, container, capillary, pad, slice, film, chip, multiwell plate or dish, optical fiber, etc. The substrate can be any form that is rigid or semi-rigid. The substrate may contain raised or depressed regions on which an assay component is located. The surface of the substrate can be etched using known techniques to provide for desired surface features, for example trenches, v-grooves, mesa structures, or the like.

[0246] Surfaces on the substrate can be composed of the same material as the substrate or can be made from a different material, and can be coupled to the substrate by chemical or physical means. Such coupled surfaces may be composed of any of a wide variety of materials, for example, polymers, plastics, resins, polysaccharides, silica or silica-based materials, carbon, metals, inorganic glasses, membranes, or any of the above-listed substrate materials. The surface can be optically transparent and can have surface Si-OH functionalities, such as those found on silica surfaces.

[0247] The substrate and/or its optional surface can be chosen to provide appropriate characteristics for the synthetic and/or detection methods used. The substrate and/or surface can be transparent to allow the exposure of the substrate by light applied from multiple

directions. The substrate and/or surface may be provided with reflective "mirror" structures to increase the recovery of light.

[0248] The substrate and/or its surface is generally resistant to, or is treated to resist, the conditions to which it is to be exposed in use, and can be optionally treated to remove any resistant material after exposure to such conditions.

[0249] The substrate or a region thereof may be encoded so that the identity of the sensor located in the substrate or region being queried may be determined. Any suitable coding scheme can be used, for example optical codes, RFID tags, magnetic codes, physical codes, fluorescent codes, and combinations of codes.

Preparation of Probes and Primers

[0250] The polynucleotide probes or primers of the present invention can be prepared by conventional techniques well-known to those skilled in the art. For example, the polynucleotide probes can be prepared using solid-phase synthesis using commercially available equipment. As is well-known in the art, modified oligonucleotides can also be readily prepared by similar methods. The polynucleotide probes can also be synthesized directly on a solid support according to methods standard in the art. This method of synthesizing polynucleotides is particularly useful when the polynucleotide probes are part of a nucleic acid array.

[0251] Polynucleotide probes or primers can be fabricated on or attached to the substrate by any suitable method, for example the methods described in U.S. Pat. No. 5,143,854, PCT Publ. No. WO 92/10092, U.S. Patent Application Ser. No. 07/624,120, filed Dec. 6, 1990 (now abandoned), Fodor et al., Science, 251: 767-777 (1991), and PCT Publ. No. WO 90/15070). Techniques for the synthesis of these arrays using mechanical synthesis strategies are described in, e.g., PCT Publication No. WO 93/09668 and U.S. Pat. No. 5,384,261. Still further techniques include bead based techniques such as those described in PCT Appl. No. PCT/US93/04145 and pin based methods such as those described in U.S. Pat. No. 5,288,514. Additional flow channel or spotting methods applicable to attachment of sensor polynucleotides to a substrate are described in U. S. Patent Application Ser. No. 07/980,523, filed Nov. 20, 1992, and U.S. Pat. No. 5,384,261.

[0252] Alternatively, the polynucleotide probes of the present invention can be prepared by enzymatic digestion of the naturally occurring target gene, or mRNA or cDNA derived therefrom, by methods known in the art.

Diagnostic Samples

[0253] 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 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.

[0254] 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.

[0255] 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.

[0256] 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).

[0257] 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.

[0258] 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.

[0259] 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.

[0260] 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.

[0261] 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.

[0262] 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.

[0263] 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

[0264] 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

[0265] 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.

[0266] In some embodiments, the kit comprises primers or primer pairs specific for those subsets and combinations of target sequences described herein. At least two, three, four or five primers or pairs of primers suitable for selectively amplifying the same number of target sequence-specific polynucleotides 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 same number of target sequence-representative polynucleotides of interest.

[0267] 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, or non-exonic target described herein, at least a portion of a nucleic acid sequence depicted in one of SEQ ID NOs: 1-43, a nucleic acid sequence corresponding to a target selected from Tables 2, 4, 11 or 55, 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, or non-exonic transcript described herein, nucleic acids depicted in one of SEQ ID NOs: 1-43, a nucleic acid sequence corresponding to a target selected from Tables 2, 4, 11 or 55, RNA forms thereof, or complements thereto. At least two, three, four or five primers or pairs of primers suitable for selectively amplifying the same number of target sequence-specific polynucleotides 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 same number of target sequence-representative polynucleotides of interest. In some instances, the targets are selected from Table 2. In some instances, the targets are selected from Table 4. In some instances, the targets are selected from Table 11.

[0268] 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.

[0269] 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.

[0270] 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.

Devices

[0271] Devices useful for performing methods of the invention are also provided. The devices can comprise means for characterizing the expression level of a target sequence of the invention, for example components for performing one or more methods of nucleic acid extraction, amplification, and/or detection. Such components may include one or more of an amplification chamber (for example a thermal cycler), a plate reader, a spectrophotometer, capillary electrophoresis apparatus, a chip reader, and or robotic sample handling components. These components ultimately can obtain data that reflects the expression level of the target sequences used in the assay being employed.

[0272] The devices may include an excitation and/or a detection means. Any instrument that provides a wavelength that can excite a species of interest and is shorter than the emission wavelength(s) to be detected can be used for excitation. Commercially available devices can provide suitable excitation wavelengths as well as suitable detection component.

[0273] Exemplary excitation sources include a broadband UV light source such as a deuterium lamp with an appropriate filter, the output of a white light source such as a xenon lamp or a deuterium lamp after passing through a monochromator to extract out the desired wavelength(s), a continuous wave (cw) gas laser, a solid state diode laser, or any of the pulsed lasers. Emitted light can be detected through any suitable device or technique; many suitable approaches are known in the art. For example, a fluorimeter or spectrophotometer may be used to detect whether the test sample emits light of a wavelength characteristic of a label used in an assay.

[0274] The devices typically comprise a means for identifying a given sample, and of linking the results obtained to that sample. Such means can include manual labels, barcodes, and other indicators which can be linked to a sample vessel, and/or may optionally be included in the sample itself, for example where an encoded particle is added to the sample. The results may be linked to the sample, for example in a computer memory that contains a sample designation and a record of expression levels obtained from the sample. Linkage of the results to the sample can also include a linkage to a particular sample receptacle in the device, which is also linked to the sample identity.

[0275] In some instances, the devices also comprise a means for correlating the expression levels of the target sequences being studied with a prognosis of disease outcome. In some instances, such means comprises one or more of a variety of correlative techniques, including lookup tables, algorithms, multivariate models, and linear or nonlinear combinations of expression models or algorithms. The expression levels may be converted to one or more likelihood scores, reflecting likelihood that the patient providing the sample may exhibit a particular disease outcome. The models and/or algorithms can be provided in machine readable format and can optionally further designate a treatment modality for a patient or class of patients.

[0276] The device also comprises output means for outputting the disease status, prognosis and/or a treatment modality. Such output means can take any form which transmits the results to a patient and/or a healthcare provider, and may include a monitor, a printed format, or both. The device may use a computer system for performing one or more of the steps provided.

[0277] In some embodiments, the method, systems, and kits disclosed herein further comprise the transmission of data/information. For example, data/information derived from the detection and/or quantification of the target may be transmitted to another device and/or

instrument. In some instances, the information obtained from an algorithm is transmitted to another device and/or instrument. Transmission of the data/information may comprise the transfer of data/information from a first source to a second source. The first and second sources may be in the same approximate location (e.g., within the same room, building, block, campus). Alternatively, first and second sources may be in multiple locations (e.g., multiple cities, states, countries, continents, etc).

[0278] In some instances, transmission of the data/information comprises digital transmission or analog transmission. Digital transmission may comprise the physical transfer of data (a digital bit stream) over a point-to-point or point-to-multipoint communication channel. Examples of such channels are copper wires, optical fibers, wireless communication channels, and storage media. In some embodiments, the data is represented as an electromagnetic signal, such as an electrical voltage, radiowave, microwave, or infrared signal.

[0279] Analog transmission may comprise the transfer of a continuously varying analog signal. The messages can either be represented by a sequence of pulses by means of a line code (baseband transmission), or by a limited set of continuously varying wave forms (passband transmission), using a digital modulation method. The passband modulation and corresponding demodulation (also known as detection) can be carried out by modem equipment. According to the most common definition of digital signal, both baseband and passband signals representing bit-streams are considered as digital transmission, while an alternative definition only considers the baseband signal as digital, and passband transmission of digital data as a form of digital-to-analog conversion.

Amplification and Hybridization

[0280] 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.

[0281] 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 lipase 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.

[0282] 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.

[0283] 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.

[0284] 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.

[0285] 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.

[0286] 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.

[0287] 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).

[0288] 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(R) 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

[0289] 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.

[0290] 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.

[0291] 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.

[0292] 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

[0293] 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

[0294] 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.

[0295] 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

[0296] 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 any of Tables 2, 4, 11 or 55 or a product derived thereof can be used.

Desirably, an array may be specific for 5, 10, 15, 20, 25, 30, 50, 75, 100, 150, 200 or more of transcripts of a target selected from any of Tables 2, 4, 11 or 55. In some instances, the target is selected from Table 2. In other instances, the target is selected from Table 4. In some embodiments, the target is selected from Table 11. 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.).

[0297] 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.

[0298] 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 Prognostic array is a chip.

Data Analysis

[0299] 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.

[0300] 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.

[0301] 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.

[0302] 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.

[0303] 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.

[0304] 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.

Additional Techniques and Tests

[0305] Factors known in the art for diagnosing and/or suggesting, selecting, designating, recommending or otherwise determining a course of treatment for a patient or class of patients suspected of having cancer can be employed in combination with measurements of the target sequence expression. The methods disclosed herein may include additional techniques such as cytology, histology, ultrasound analysis, MRI results, CT scan results, and measurements of PSA levels.

[0306] Certified tests for classifying disease status and/or designating treatment modalities may also be used in diagnosing, predicting, and/or monitoring the status or outcome of a cancer in a subject. A certified test may comprise a means for characterizing the expression

levels of one or more of the target sequences of interest, and a certification from a government regulatory agency endorsing use of the test for classifying the disease status of a biological sample.

[0307] In some embodiments, the certified test may comprise reagents for amplification reactions used to detect and/or quantitate expression of the target sequences to be characterized in the test. An array of probe nucleic acids can be used, with or without prior target amplification, for use in measuring target sequence expression.

[0308] The test is submitted to an agency having authority to certify the test for use in distinguishing disease status and/or outcome. Results of detection of expression levels of the target sequences used in the test and correlation with disease status and/or outcome are submitted to the agency. A certification authorizing the diagnostic and/or prognostic use of the test is obtained.

[0309] Also provided are portfolios of expression levels comprising a plurality of normalized expression levels of the target selected from any of Tables 2, 4, 11 or 55. In some instances, the target is selected from Table 2. In other instances, the target is selected from Table 4. In some embodiments, the target is selected from Table 11. Such portfolios may be provided by performing the methods described herein to obtain expression levels from an individual patient or from a group of patients. The expression levels can be normalized by any method known in the art; exemplary normalization methods that can be used in various embodiments include Robust Multichip Average (RMA), probe logarithmic intensity error estimation (PLIER), non-linear fit (NLFIT) quantile-based and nonlinear normalization, and combinations thereof. Background correction can also be performed on the expression data; exemplary techniques useful for background correction include mode of intensities, normalized using median polish probe modeling and sketch-normalization.

[0310] In some embodiments, portfolios are established such that the combination of genes in the portfolio exhibit improved sensitivity and specificity relative to known methods. In considering a group of genes for inclusion in a portfolio, a small standard deviation in expression measurements correlates with greater specificity. Other measurements of variation such as correlation coefficients can also be used in this capacity. The invention also encompasses the above methods where the expression level determines the status or outcome of a cancer in the subject with at least about 45% specificity. In some embodiments, the expression level determines the status or outcome of a cancer in the subject with at least about 50% specificity. In some embodiments, the expression level determines the status or

outcome of a cancer in the subject with at least about 55% specificity. In some embodiments, the expression level determines the status or outcome of a cancer in the subject with at least about 60% specificity. In some embodiments, the expression level determines the status or outcome of a cancer in the subject with at least about 65% specificity. In some embodiments, the expression level determines the status or outcome of a cancer in the subject with at least about 70% specificity. In some embodiments, the expression level determines the status or outcome of a cancer in the subject with at least about 75% specificity. In some embodiments, the expression level determines the status or outcome of a cancer in the subject with at least about 80% specificity. In some embodiments, the expression level determines the status or outcome of a cancer in the subject with at least about 85% specificity. In some embodiments, the expression level determines the status or outcome of a cancer in the subject with at least about 90% specificity. In some embodiments, the expression level determines the status or outcome of a cancer in the subject with at least about 95% specificity.

[0311] The invention also encompasses the any of the methods disclosed herein where the accuracy of diagnosing, monitoring, and/or predicting a status or outcome of a cancer is at least about 45%. In some embodiments, the accuracy of diagnosing, monitoring, and/or predicting a status or outcome of a cancer is at least about 50%. In some embodiments, the accuracy of diagnosing, monitoring, and/or predicting a status or outcome of a cancer is at least about 55%. In some embodiments, the accuracy of diagnosing, monitoring, and/or predicting a status or outcome of a cancer is at least about 60%. In some embodiments, the accuracy of diagnosing, monitoring, and/or predicting a status or outcome of a cancer is at least about 65%. In some embodiments, the accuracy of diagnosing, monitoring, and/or predicting a status or outcome of a cancer is at least about 70%. In some embodiments, the accuracy of diagnosing, monitoring, and/or predicting a status or outcome of a cancer is at least about 75%. In some embodiments, the accuracy of diagnosing, monitoring, and/or predicting a status or outcome of a cancer is at least about 80%. In some embodiments, the accuracy of diagnosing, monitoring, and/or predicting a status or outcome of a cancer is at least about 85%. In some embodiments, the accuracy of diagnosing, monitoring, and/or predicting a status or outcome of a cancer is at least about 90%. In some embodiments, the accuracy of diagnosing, monitoring, and/or predicting a status or outcome of a cancer is at least about 95%.

[0312] The accuracy of a classifier or biomarker may be determined by the 95% confidence interval (CI). Generally, a classifier or biomarker is considered to have good accuracy if the

95% CI does not overlap 1. In some instances, the 95% CI of a classifier or biomarker is at least about 1.08, 1.10, 1.12, 1.14, 1.15, 1.16, 1.17, 1.18, 1.19, 1.20, 1.21, 1.22, 1.23, 1.24, 1.25, 1.26, 1.27, 1.28, 1.29, 1.30, 1.31, 1.32, 1.33, 1.34, or 1.35 or more. The 95% CI of a classifier or biomarker may be at least about 1.14, 1.15, 1.16, 1.20, 1.21, 1.26, or 1.28. The 95% CI of a classifier or biomarker may be less than about 1.75, 1.74, 1.73, 1.72, 1.71, 1.70, 1.69, 1.68, 1.67, 1.66, 1.65, 1.64, 1.63, 1.62, 1.61, 1.60, 1.59, 1.58, 1.57, 1.56, 1.55, 1.54, 1.53, 1.52, 1.51, 1.50 or less. The 95% CI of a classifier or biomarker may be less than about 1.61, 1.60, 1.59, 1.58, 1.56, 1.55, or 1.53. The 95% CI of a classifier or biomarker may be between about 1.10 to 1.70, between about 1.12 to about 1.68, between about 1.14 to about 1.62, between about 1.15 to about 1.61, between about 1.15 to about 1.59, between about 1.16 to about 1.60, between about 1.19 to about 1.55, between about 1.20 to about 1.54, between about 1.21 to about 1.53, between about 1.26 to about 1.63, between about 1.27 to about 1.61, or between about 1.28 to about 1.60.

[0313] In some instances, the accuracy of a biomarker or classifier is dependent on the difference in range of the 95% CI (e.g., difference in the high value and low value of the 95% CI interval). Generally, biomarkers or classifiers with large differences in the range of the 95% CI interval have greater variability and are considered less accurate than biomarkers or classifiers with small differences in the range of the 95% CI intervals. In some instances, a biomarker or classifier is considered more accurate if the difference in the range of the 95% CI is less than about 0.60, 0.55, 0.50, 0.49, 0.48, 0.47, 0.46, 0.45, 0.44, 0.43, 0.42, 0.41, 0.40, 0.39, 0.38, 0.37, 0.36, 0.35, 0.34, 0.33, 0.32, 0.31, 0.30, 0.29, 0.28, 0.27, 0.26, 0.25 or less. The difference in the range of the 95% CI of a biomarker or classifier may be less than about 0.48, 0.45, 0.44, 0.42, 0.40, 0.37, 0.35, 0.33, or 0.32. In some instances, the difference in the range of the 95% CI for a biomarker or classifier is between about 0.25 to about 0.50, between about 0.27 to about 0.47, or between about 0.30 to about 0.45.

[0314] The invention also encompasses the any of the methods disclosed herein where the sensitivity is at least about 45%. In some embodiments, the sensitivity is at least about 50%. In some embodiments, the sensitivity is at least about 55%. In some embodiments, the sensitivity is at least about 60%. In some embodiments, the sensitivity is at least about 65%. In some embodiments, the sensitivity is at least about 70%. In some embodiments, the sensitivity is at least about 75%. In some embodiments, the sensitivity is at least about 80%. In some embodiments, the sensitivity is at least about 85%. In some embodiments, the sensitivity is at least about 90%. In some embodiments, the sensitivity is at least about 95%.

[0315] In some instances, the classifiers or biomarkers disclosed herein are clinically significant. In some instances, the clinical significance of the classifiers or biomarkers is determined by the AUC value. In order to be clinically significant, the AUC value is at least about 0.5, 0.55, 0.6, 0.65, 0.7, 0.75, 0.8, 0.85, 0.9, or 0.95. The clinical significance of the classifiers or biomarkers can be determined by the percent accuracy. For example, a classifier or biomarker is determined to be clinically significant if the accuracy of the classifier or biomarker is at least about 50%, 55%, 60%, 65%, 70%, 72%, 75%, 77%, 80%, 82%, 84%, 86%, 88%, 90%, 92%, 94%, 96%, or 98%.

[0316] In other instances, the clinical significance of the classifiers or biomarkers is determined by the median fold difference (MDF) value. In order to be clinically significant, the MDF value is at least about 0.8, 0.9, 1.0, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.9, or 2.0. In some instances, the MDF value is greater than or equal to 1.1. In other instances, the MDF value is greater than or equal to 1.2. Alternatively, or additionally, the clinical significance of the classifiers or biomarkers is determined by the t-test P-value. In some instances, in order to be clinically significant, the t-test P-value is less than about 0.070, 0.065, 0.060, 0.055, 0.050, 0.045, 0.040, 0.035, 0.030, 0.025, 0.020, 0.015, 0.010, 0.005, 0.004, or 0.003. The t-test P-value can be less than about 0.050. Alternatively, the t-test P-value is less than about 0.010.

[0317] In some instances, the clinical significance of the classifiers or biomarkers is determined by the clinical outcome. For example, different clinical outcomes can have different minimum or maximum thresholds for AUC values, MDF values, t-test P-values, and accuracy values that would determine whether the classifier or biomarker is clinically significant. In another example, a classifier or biomarker is considered clinically significant if the P-value of the t-test was less than about 0.08, 0.07, 0.06, 0.05, 0.04, 0.03, 0.02, 0.01, 0.005, 0.004, 0.003, 0.002, or 0.001. In some instances, the P-value may be based on any of the following comparisons: BCR vs non-BCR, CP vs non-CP, PCSM vs non-PCSM. For example, a classifier or biomarker is determined to be clinically significant if the P-values of the differences between the KM curves for BCR vs non-BCR, CP vs non-CP, PCSM vs non-PCSM is lower than about 0.08, 0.07, 0.06, 0.05, 0.04, 0.03, 0.02, 0.01, 0.005, 0.004, 0.003, 0.002, or 0.001.

[0318] In some instances, the performance of the classifier or biomarker is based on the odds ratio. A classifier or biomarker may be considered to have good performance if the odds ratio is at least about 1.30, 1.31, 1.32, 1.33, 1.34, 1.35, 1.36, 1.37, 1.38, 1.39, 1.40, 1.41, 1.42,

1.43, 1.44, 1.45, 1.46, 1.47, 1.48, 1.49, 1.50, 1.52, 1.55, 1.57, 1.60, 1.62, 1.65, 1.67, 1.70 or more. In some instances, the odds ratio of a classifier or biomarker is at least about 1.33.

[0319] The clinical significance of the classifiers and/or biomarkers may be based on Univariable Analysis Odds Ratio P-value (uvaORPval). The Univariable Analysis Odds Ratio P-value (uvaORPval) of the classifier and/or biomarker may be between about 0-0.4. The Univariable Analysis Odds Ratio P-value (uvaORPval) of the classifier and/or biomarker may be between about 0-0.3. The Univariable Analysis Odds Ratio P-value (uvaORPval) of the classifier and/or biomarker may be between about 0-0.2. The Univariable Analysis Odds Ratio P-value (uvaORPval) of the classifier and/or biomarker may be less than or equal to 0.25, 0.22, 0.21, 0.20, 0.19, 0.18, 0.17, 0.16, 0.15, 0.14, 0.13, 0.12, 0.11. The Univariable Analysis Odds Ratio P-value (uvaORPval) of the classifier and/or biomarker may be less than or equal to 0.10, 0.09, 0.08, 0.07, 0.06, 0.05, 0.04, 0.03, 0.02, 0.01. The Univariable Analysis Odds Ratio P-value (uvaORPval) of the classifier and/or biomarker may be less than or equal to 0.009, 0.008, 0.007, 0.006, 0.005, 0.004, 0.003, 0.002, 0.001.

[0320] The clinical significance of the classifiers and/or biomarkers may be based on multivariable analysis Odds Ratio P-value (mvaORPval). The multivariable analysis Odds Ratio P-value (mvaORPval) of the classifier and/or biomarker may be between about 0-1. The multivariable analysis Odds Ratio P-value (mvaORPval) of the classifier and/or biomarker may be between about 0-0.9. The multivariable analysis Odds Ratio P-value (mvaORPval) of the classifier and/or biomarker may be between about 0-0.8. The multivariable analysis Odds Ratio P-value (mvaORPval) of the classifier and/or biomarker may be less than or equal to 0.90, 0.88, 0.86, 0.84, 0.82, 0.80. The multivariable analysis Odds Ratio P-value (mvaORPval) of the classifier and/or biomarker may be less than or equal to 0.78, 0.76, 0.74, 0.72, 0.70, 0.68, 0.66, 0.64, 0.62, 0.60, 0.58, 0.56, 0.54, 0.52, 0.50. The multivariable analysis Odds Ratio P-value (mvaORPval) of the classifier and/or biomarker may be less than or equal to 0.48, 0.46, 0.44, 0.42, 0.40, 0.38, 0.36, 0.34, 0.32, 0.30, 0.28, 0.26, 0.25, 0.22, 0.21, 0.20, 0.19, 0.18, 0.17, 0.16, 0.15, 0.14, 0.13, 0.12, 0.11. The multivariable analysis Odds Ratio P-value (mvaORPval) of the classifier and/or biomarker may be less than or equal to 0.10, 0.09, 0.08, 0.07, 0.06, 0.05, 0.04, 0.03, 0.02, 0.01. The multivariable analysis Odds Ratio P-value (mvaORPval) of the classifier and/or biomarker may be less than or equal to 0.009, 0.008, 0.007, 0.006, 0.005, 0.004, 0.003, 0.002, 0.001.

[0321] The clinical significance of the classifiers and/or biomarkers may be based on the Kaplan Meier P-value (KM P-value). The Kaplan Meier P-value (KM P-value) of the classifier and/or biomarker may be between about 0-0.8. The Kaplan Meier P-value (KM P-value) of the classifier and/or biomarker may be between about 0-0.7. The Kaplan Meier P-value (KM P-value) of the classifier and/or biomarker may be less than or equal to 0.80, 0.78, 0.76, 0.74, 0.72, 0.70, 0.68, 0.66, 0.64, 0.62, 0.60, 0.58, 0.56, 0.54, 0.52, 0.50. The Kaplan Meier P-value (KM P-value) of the classifier and/or biomarker may be less than or equal to 0.48, 0.46, 0.44, 0.42, 0.40, 0.38, 0.36, 0.34, 0.32, 0.30, 0.28, 0.26, 0.25, 0.22, 0.21, 0.20, 0.19, 0.18, 0.17, 0.16, 0.15, 0.14, 0.13, 0.12, 0.11. The Kaplan Meier P-value (KM P-value) of the classifier and/or biomarker may be less than or equal to 0.10, 0.09, 0.08, 0.07, 0.06, 0.05, 0.04, 0.03, 0.02, 0.01. The Kaplan Meier P-value (KM P-value) of the classifier and/or biomarker may be less than or equal to 0.009, 0.008, 0.007, 0.006, 0.005, 0.004, 0.003, 0.002, 0.001.

[0322] The clinical significance of the classifiers and/or biomarkers may be based on the survival AUC value (survAUC). The survival AUC value (survAUC) of the classifier and/or biomarker may be between about 0-1. The survival AUC value (survAUC) of the classifier and/or biomarker may be between about 0-0.9. The survival AUC value (survAUC) of the classifier and/or biomarker may be less than or equal to 1, 0.98, 0.96, 0.94, 0.92, 0.90, 0.88, 0.86, 0.84, 0.82, 0.80. The survival AUC value (survAUC) of the classifier and/or biomarker may be less than or equal to 0.80, 0.78, 0.76, 0.74, 0.72, 0.70, 0.68, 0.66, 0.64, 0.62, 0.60, 0.58, 0.56, 0.54, 0.52, 0.50. The survival AUC value (survAUC) of the classifier and/or biomarker may be less than or equal to 0.48, 0.46, 0.44, 0.42, 0.40, 0.38, 0.36, 0.34, 0.32, 0.30, 0.28, 0.26, 0.25, 0.22, 0.21, 0.20, 0.19, 0.18, 0.17, 0.16, 0.15, 0.14, 0.13, 0.12, 0.11. The survival AUC value (survAUC) of the classifier and/or biomarker may be less than or equal to 0.10, 0.09, 0.08, 0.07, 0.06, 0.05, 0.04, 0.03, 0.02, 0.01. The survival AUC value (survAUC) of the classifier and/or biomarker may be less than or equal to 0.009, 0.008, 0.007, 0.006, 0.005, 0.004, 0.003, 0.002, 0.001.

[0323] The clinical significance of the classifiers and/or biomarkers may be based on the Univariable Analysis Hazard Ratio P-value (uvaHRPval). The Univariable Analysis Hazard Ratio P-value (uvaHRPval) of the classifier and/or biomarker may be between about 0-0.4. The Univariable Analysis Hazard Ratio P-value (uvaHRPval) of the classifier and/or biomarker may be between about 0-0.3. The Univariable Analysis Hazard Ratio P-value (uvaHRPval) of the classifier and/or biomarker may be less than or equal to 0.40, 0.38, 0.36,

0.34, 0.32. The Univariable Analysis Hazard Ratio P-value (uvaHRPval) of the classifier and/or biomarker may be less than or equal to 0.30, 0.29, 0.28, 0.27, 0.26, 0.25, 0.24, 0.23, 0.22, 0.21, 0.20. The Univariable Analysis Hazard Ratio P-value (uvaHRPval) of the classifier and/or biomarker may be less than or equal to 0.19, 0.18, 0.17, 0.16, 0.15, 0.14, 0.13, 0.12, 0.11. The Univariable Analysis Hazard Ratio P-value (uvaHRPval) of the classifier and/or biomarker may be less than or equal to 0.10, 0.09, 0.08, 0.07, 0.06, 0.05, 0.04, 0.03, 0.02, 0.01. The Univariable Analysis Hazard Ratio P-value (uvaHRPval) of the classifier and/or biomarker may be less than or equal to 0.009, 0.008, 0.007, 0.006, 0.005, 0.004, 0.003, 0.002, 0.001.

[0324] The clinical significance of the classifiers and/or biomarkers may be based on the Multivariable Analysis Hazard Ratio P-value (mvaHRPval)mva HRPval. The Multivariable Analysis Hazard Ratio P-value (mvaHRPval)mva HRPval of the classifier and/or biomarker may be between about 0-1. The Multivariable Analysis Hazard Ratio P-value (mvaHRPval)mva HRPval of the classifier and/or biomarker may be between about 0-0.9. The Multivariable Analysis Hazard Ratio P-value (mvaHRPval)mva HRPval of the classifier and/or biomarker may be less than or equal to 1, 0.98, 0.96, 0.94, 0.92, 0.90, 0.88, 0.86, 0.84, 0.82, 0.80. The Multivariable Analysis Hazard Ratio P-value (mvaHRPval)mva HRPval of the classifier and/or biomarker may be less than or equal to 0.80, 0.78, 0.76, 0.74, 0.72, 0.70, 0.68, 0.66, 0.64, 0.62, 0.60, 0.58, 0.56, 0.54, 0.52, 0.50. The Multivariable Analysis Hazard Ratio P-value (mvaHRPval)mva HRPval of the classifier and/or biomarker may be less than or equal to 0.48, 0.46, 0.44, 0.42, 0.40, 0.38, 0.36, 0.34, 0.32, 0.30, 0.28, 0.26, 0.25, 0.22, 0.21, 0.20, 0.19, 0.18, 0.17, 0.16, 0.15, 0.14, 0.13, 0.12, 0.11. The Multivariable Analysis Hazard Ratio P-value (mvaHRPval)mva HRPval of the classifier and/or biomarker may be less than or equal to 0.10, 0.09, 0.08, 0.07, 0.06, 0.05, 0.04, 0.03, 0.02, 0.01. The Multivariable Analysis Hazard Ratio P-value (mvaHRPval)mva HRPval of the classifier and/or biomarker may be less than or equal to 0.009, 0.008, 0.007, 0.006, 0.005, 0.004, 0.003, 0.002, 0.001.

[0325] The clinical significance of the classifiers and/or biomarkers may be based on the Multivariable Analysis Hazard Ratio P-value (mvaHRPval). The Multivariable Analysis Hazard Ratio P-value (mvaHRPval) of the classifier and/or biomarker may be between about 0 to about 0.60. significance of the classifier and/or biomarker may be based on the Multivariable Analysis Hazard Ratio P-value (mvaHRPval). The Multivariable Analysis Hazard Ratio P-value (mvaHRPval) of the classifier and/or biomarker may be between about

0 to about 0.50. significance of the classifier and/or biomarker may be based on the Multivariable Analysis Hazard Ratio P-value (mvaHRPval). The Multivariable Analysis Hazard Ratio P-value (mvaHRPval) of the classifier and/or biomarker may be less than or equal to 0.50, 0.47, 0.45, 0.43, 0.40, 0.38, 0.35, 0.33, 0.30, 0.28, 0.25, 0.22, 0.20, 0.18, 0.16, 0.15, 0.14, 0.13, 0.12, 0.11, 0.10. The Multivariable Analysis Hazard Ratio P-value (mvaHRPval) of the classifier and/or biomarker may be less than or equal to 0.10, 0.09, 0.08, 0.07, 0.06, 0.05, 0.04, 0.03, 0.02, 0.01. The Multivariable Analysis Hazard Ratio P-value (mvaHRPval) of the classifier and/or biomarker may be less than or equal to 0.01, 0.009, 0.008, 0.007, 0.006, 0.005, 0.004, 0.003, 0.002, 0.001.

[0326] The classifiers and/or biomarkers disclosed herein may outperform current classifiers or clinical variables in providing clinically relevant analysis of a sample from a subject. In some instances, the classifiers or biomarkers may more accurately predict a clinical outcome or status as compared to current classifiers or clinical variables. For example, a classifier or biomarker may more accurately predict metastatic disease. Alternatively, a classifier or biomarker may more accurately predict no evidence of disease. In some instances, the classifier or biomarker may more accurately predict death from a disease. The performance of a classifier or biomarker disclosed herein may be based on the AUC value, odds ratio, 95% CI, difference in range of the 95% CI, p-value or any combination thereof.

[0327] The performance of the classifiers and/or biomarkers disclosed herein may be determined by AUC values and an improvement in performance may be determined by the difference in the AUC value of the classifier or biomarker disclosed herein and the AUC value of current classifiers or clinical variables. In some instances, a classifier and/or biomarker disclosed herein outperforms current classifiers or clinical variables when the AUC value of the classifier and/or or biomarker disclosed herein is greater than the AUC value of the current classifiers or clinical variables by at least about 0.05, 0.06, 0.07, 0.08, 0.09, 0.10, 0.11, 0.12, 0.13, 0.14, 0.15, 0.16, 0.17, 0.18, 0.19, 0.20, 0.22, 0.25, 0.27, 0.30, 0.32, 0.35, 0.37, 0.40, 0.42, 0.45, 0.47, 0.50 or more. In some instances, the AUC value of the classifier and/or or biomarker disclosed herein is greater than the AUC value of the current classifiers or clinical variables by at least about 0.10. In some instances, the AUC value of the classifier and/or or biomarker disclosed herein is greater than the AUC value of the current classifiers or clinical variables by at least about 0.13. In some instances, the AUC value of the

classifier and/or or biomarker disclosed herein is greater than the AUC value of the current classifiers or clinical variables by at least about 0.18.

[0328] The performance of the classifiers and/or biomarkers disclosed herein may be determined by the odds ratios and an improvement in performance may be determined by comparing the odds ratio of the classifier or biomarker disclosed herein and the odds ratio of current classifiers or clinical variables. Comparison of the performance of two or more classifiers, biomarkers, and/or clinical variables can be generally be based on the comparison of the absolute value of (1-odds ratio) of a first classifier, biomarker or clinical variable to the absolute value of (1-odds ratio) of a second classifier, biomarker or clinical variable.

Generally, the classifier, biomarker or clinical variable with the greater absolute value of (1-odds ratio) can be considered to have better performance as compared to the classifier, biomarker or clinical variable with a smaller absolute value of (1-odds ratio).

[0329] In some instances, the performance of a classifier, biomarker or clinical variable is based on the comparison of the odds ratio and the 95% confidence interval (CI). For example, a first classifier, biomarker or clinical variable may have a greater absolute value of (1-odds ratio) than a second classifier, biomarker or clinical variable, however, the 95% CI of the first classifier, biomarker or clinical variable may overlap 1 (e.g., poor accuracy), whereas the 95% CI of the second classifier, biomarker or clinical variable does not overlap 1. In this instance, the second classifier, biomarker or clinical variable is considered to outperform the first classifier, biomarker or clinical variable because the accuracy of the first classifier, biomarker or clinical variable is less than the accuracy of the second classifier, biomarker or clinical variable. In another example, a first classifier, biomarker or clinical variable may outperform a second classifier, biomarker or clinical variable based on a comparison of the odds ratio; however, the difference in the 95% CI of the first classifier, biomarker or clinical variable is at least about 2 times greater than the 95% CI of the second classifier, biomarker or clinical variable. In this instance, the second classifier, biomarker or clinical variable is considered to outperform the first classifier.

[0330] In some instances, a classifier or biomarker disclosed herein more accurate than a current classifier or clinical variable. The classifier or biomarker disclosed herein is more accurate than a current classifier or clinical variable if the range of 95% CI of the classifier or biomarker disclosed herein does not span or overlap 1 and the range of the 95% CI of the current classifier or clinical variable spans or overlaps 1.

[0331] In some instances, a classifier or biomarker disclosed herein more accurate than a current classifier or clinical variable. The classifier or biomarker disclosed herein is more accurate than a current classifier or clinical variable when difference in range of the 95% CI of the classifier or biomarker disclosed herein is about 0.70, 0.60, 0.50, 0.40, 0.30, 0.20, 0.15, 0.14, 0.13, 0.12, 0.10, 0.09, 0.08, 0.07, 0.06, 0.05, 0.04, 0.03, 0.02 times less than the difference in range of the 95% CI of the current classifier or clinical variable. The classifier or biomarker disclosed herein is more accurate than a current classifier or clinical variable when difference in range of the 95% CI of the classifier or biomarker disclosed herein between about 0.20 to about 0.04 times less than the difference in range of the 95% CI of the current classifier or clinical variable.

[0332] In some instances, the methods disclosed herein may comprise the use of a genomic classifier (GC) model. A general method for developing a GC model may comprise (a) providing a sample from a subject suffering from a cancer; (b) assaying the expression level for a plurality of targets; (c) generating a model by using a machine learning algorithm. In some instances, the machine learning algorithm comprises Random Forests. In another example, a GC model may developed by using a machine learning algorithm to analyze and rank genomic features. Analyzing the genomic features may comprise classifying one or more genomic features. The method may further comprise validating the classifier and/or refining the classifier by using a machine learning algorithm.

[0333] The methods disclosed herein may comprise generating one or more clinical classifiers (CC). The clinical classifier can be developed using one or more clinicopathologic variables. The clinicopathologic variables may be selected from the group comprising Lymph node invasion status (LNI); Surgical Margin Status (SMS); Seminal Vesicle Invasion (SVI); Extra Capsular Extension (ECE); Pathological Gleason Score; and the pre-operative PSA. The method may comprise using one or more of the clinicopathologic variables as binary variables. Alternatively, or additionally, the one or more clinicopathologic variables may be converted to a logarithmic value (e.g., log10). The method may further comprise assembling the variables in a logistic regression. In some instances, the CC is combined with the GC to produce a genomic clinical classifier (GCC).

[0334] In some instances, the methods disclosed herein may comprise the use of a genomic-clinical classifier (GCC) model. A general method for developing a GCC model may comprise (a) providing a sample from a subject suffering from a cancer; (b) assaying the

expression level for a plurality of targets; (c) generating a model by using a machine learning algorithm. In some instances, the machine learning algorithm comprises Random Forests.

Cancer

[0335] 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. 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, breast cancer, lung cancer, colon cancer, prostate cancer, pancreatic cancer, thyroid cancer). Cancer is not confined to humans; animals and other living organisms can get cancer.

[0336] 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.

[0337] 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).

[0338] 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.

[0339] 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.

[0340] 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 astocytoma 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 oligodendriogliomas. Nongliomas include meningiomas, pituitary adenomas, primary CNS lymphomas, and medulloblastomas. In some instances, the cancer is a meningioma.

[0341] 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.

[0342] 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

[0343] 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.

[0344] 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).

[0345] 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.

[0346] 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.

[0347] 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.

[0348] 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).

Cancer Grade

[0349] In pathology, grading is a measure of the cell appearance in tumors and other neoplasms. Some pathology grading systems apply only to malignant neoplasms (cancer); others apply also to benign neoplasms. The neoplastic grading is a measure of cell anaplasia

(reversion of differentiation) in the sampled tumor and is based on the resemblance of the tumor to the tissue of origin.^[1] Grading in cancer is distinguished from staging, which is a measure of the extent to which the cancer has spread.

[0350] Pathology grading systems classify the microscopic cell appearance abnormality and deviations in their rate of growth with the goal of predicting developments at tissue level (see also the 4 major histological changes in dysplasia).

[0351] Cancer is a disorder of cell life cycle alteration that leads (non-trivially) to excessive cell proliferation rates, typically longer cell lifespans and poor differentiation. The grade score (numerical: G1 up to G4) increases with the lack of cellular differentiation - it reflects how much the tumor cells differ from the cells of the normal tissue they have originated from (see 'Categories' below). Tumors may be graded on four-tier, three-tier, or two-tier scales, depending on the institution and the tumor type.

[0352] The histologic tumor grade score along with the metastatic (whole-body-level cancer-spread) staging are used to evaluate each specific cancer patient, develop their individual treatment strategy and to predict their prognosis. The most commonly used system of grading is as per the guidelines of the American Joint Commission on Cancer. As per their standards, the following are the grading categories: GX Grade cannot be assessed; G1 Well differentiated (Low grade); G2 Moderately differentiated (Intermediate grade); G3 Poorly differentiated (High grade) and G4 Undifferentiated (High grade).

[0353] The Gleason system is used to grade the adenocarcinoma cells in prostate cancer. This system uses a grading score ranging from 2 to 10. A Gleason score is given to prostate cancer based upon its microscopic appearance. Cancers with a higher Gleason score are more aggressive and have a worse prognosis. The Gleason score is based on the sum of two numbers: the first number is the grade of the most common tumor pattern, the second number is the grade of the second most common pattern. If there are three patterns the first number is the most common and the second is the one with the highest grade. Gleason patterns are associated with the following features: Pattern 1 - The cancerous prostate closely resembles normal prostate tissue. The glands are small, well-formed, and closely packed; Pattern 2 - The tissue still has well-formed glands, but they are larger and have more tissue between them; Pattern 3 - The tissue still has recognizable glands, but the cells are darker. At high magnification, some of these cells have left the glands and are beginning to invade the surrounding tissue; Pattern 4 - The tissue has few recognizable glands. Many cells are invading the surrounding tissue; Pattern 5 - The tissue does not have recognizable glands.

There are often just sheets of cells throughout the surrounding tissue. A pathologist examines the biopsy specimen and attempts to give a score to the two patterns. First called the primary grade, represents the majority of tumor (has to be greater than 50% of the total pattern seen). Second - a secondary grade - relates to the minority of the tumor (has to be less than 50%, but at least 5%, of the pattern of the total cancer observed). These grades are then added to obtain the final Gleason score.

Therapeutic regimens

[0354] 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.

[0355] 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).

[0356] 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.

[0357] 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 into 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.

[0358] Alkaloids may be derived from plants and block cell division may also be used for the treatment of cancer. Alkaloids 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.

[0359] 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).

[0360] 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.

[0361] 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.

[0362] 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.

[0363] 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.

[0364] 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.

[0365] 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.

[0366] 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.

[0367] 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.

[0368] 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®.

[0369] 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.

[0370] 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.

[0371] 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.

[0372] 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.

[0373] 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.

[0374] 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 (¹³¹I) 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 ¹³¹I 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 ¹³¹I.

[0375] 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.

[0376] 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.

[0377] 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.

[0378] 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.

[0379] 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.

[0380] 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.

[0381] 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.

[0382] 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.

[0383] 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.

[0384] 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.

[0385] 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.

[0386] 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.

[0387] 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.

[0388] 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.

[0389] 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.

[0390] 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.

[0391] 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.

[0392] 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.

[0393] 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.

[0394] 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.

[0395] 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.

[0396] 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.

[0397] 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.

[0398] 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.

[0399] 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.

[0400] 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, fifty or more of the target sequences corresponding to a target selected from any of Tables 2, 4, 11 or 55, or of the subsets described herein, or of a combination thereof. In some instances, the target is selected from Table 2. In other instances, the target is selected from Table 4. In some embodiments, the target is selected from Table 11. 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.

[0401] 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.

Exemplary embodiments

[0402] Disclosed herein, in some embodiments, is a method for diagnosing, predicting, and/or monitoring a status or outcome of a cancer a subject, comprising: (a) assaying an expression level of a plurality of targets in a sample from the subject, wherein more than one target of the plurality of targets is selected from the group consisting of targets identified in Tables 2, 4, 11 or 55; and (b) for diagnosing, predicting, and/or monitoring a status or outcome of a cancer based on the expression levels of the plurality of targets. In some embodiments, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In some embodiments, the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas. In some embodiments, the cancer is a prostate cancer. In some embodiments, the cancer is a pancreatic cancer. In some embodiments, the cancer is a thyroid cancer. In some embodiments, the cancer is a bladder cancer. In some embodiments, the cancer is a lung cancer. In some embodiments, the method further comprises assaying an expression level of a coding target. In some instances, the coding target is selected from the group consisting of targets identified in Tables 2, 4, 11 or 55. In some embodiments, the coding target is an exon-coding transcript. In some embodiments, the exon-coding transcript is an exonic sequence. In some embodiments, the method further comprises assaying an expression level of a non-coding target. In some instances, the non-coding target is selected from the group consisting of targets identified in Tables 2, 4, 11 or 55. In some instances, the non-coding target is a non-coding transcript. In other instances, the non-coding target is an intronic sequence. In other instances, the non-coding target is an intergenic sequence. In some instances, the non-coding target is a UTR sequence. In other instances, the non-coding target is a non-coding RNA transcript. In some embodiments, the target comprises a nucleic acid sequence. In some embodiments, the nucleic acid sequence is a DNA sequence. In some embodiments, the nucleic acid sequence is an RNA sequence. In other instances, the target comprises a polypeptide sequence. In some instances, the plurality of targets comprises 2 or more targets selected from the group of targets identified in Tables 2, 4, 11 or 55. In some instances, the

plurality of targets comprises 5 or more targets selected from the group of targets identified in Tables 2, 4, 11 or 55. In some instances, the plurality of targets comprises 10 or more targets selected from the group of targets identified in Tables 2, 4, 11 or 55. In some instances, the plurality of targets comprises 15 or more targets selected from the group of targets identified in Tables 2, 4, 11 or 55. In some instances, the plurality of targets comprises 20 or more targets selected from the group of targets identified in Tables 2, 4, 11 or 55. In some instances, the plurality of targets comprises 25 or more targets selected from the group of targets identified in Tables 2, 4, 11 or 55. In some instances, the plurality of targets comprises 30 or more targets selected from the group of targets identified in Tables 2, 4, 11 or 55. In some instances, the plurality of targets comprises 35 or more targets selected from the group of targets identified in Tables 2, 4, 11 or 55. In some instances, the plurality of targets comprises 40 or more targets selected from the group of targets identified in Tables 2, 4, 11 or 55. In some instances, the target is selected from Table 2. In other instances, the target is selected from Table 4. In some embodiments, the target is selected from Table 11. In some embodiments, assaying the expression level comprises detecting and/or quantifying a nucleotide sequence of the plurality of targets. Alternatively, assaying the expression level comprises detecting and/or quantifying a polypeptide sequence of the plurality of targets. In some embodiments, assaying the expression level comprises detecting and/or quantifying the DNA levels of the plurality of targets. In some embodiments, assaying the expression level comprises detecting and/or quantifying the RNA or mRNA levels of the plurality of targets. In some embodiments, assaying the expression level comprises detecting and/or quantifying the protein level of the plurality of targets. In some embodiments, the diagnosing, predicting, and/or monitoring the status or outcome of a cancer comprises determining the malignancy of the cancer. In some embodiments, the diagnosing, predicting, and/or monitoring the status or outcome of a cancer includes determining the stage of the cancer. In some embodiments, the diagnosing, predicting, and/or monitoring the status or outcome of a cancer includes assessing the risk of cancer recurrence. In some embodiments, diagnosing, predicting, and/or monitoring the status or outcome of a cancer may comprise determining the efficacy of treatment. In some embodiments, diagnosing, predicting, and/or monitoring the status or outcome of a cancer may comprise determining a therapeutic regimen. Determining a therapeutic regimen may comprise administering an anti-cancer therapeutic. Alternatively, determining the treatment for the cancer may comprise modifying a therapeutic regimen.

Modifying a therapeutic regimen may comprise increasing, decreasing, or terminating a therapeutic regimen.

[0403] Further disclosed, in some embodiments, is method for determining a treatment for a cancer in a subject, comprising: a) assaying an expression level of a plurality of targets in a sample from the subject, wherein more than one target of the plurality of targets is selected from the group consisting of targets identified in Tables 2, 4, 11 or 55; and b) determining the treatment for a cancer based on the expression levels of the plurality of targets. In some embodiments, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In some embodiments, the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas. In some embodiments, the cancer is a prostate cancer. In some embodiments, the cancer is a pancreatic cancer. In some embodiments, the cancer is a bladder cancer. In some embodiments, the cancer is a thyroid cancer. In some embodiments, the cancer is a lung cancer. In some embodiments, the coding target is selected from a sequence listed in Tables 2, 4, 11 or 55. In some embodiments, the method further comprises assaying an expression level of a coding target. In some instances, the coding target is selected from the group consisting of targets identified in Tables 2, 4, 11 or 55. In some embodiments, the coding target is an exon-coding transcript. In some embodiments, the exon-coding transcript is an exonic sequence. In some embodiments, the method further comprises assaying an expression level of a non-coding target. In some instances, the non-coding target is selected from the group consisting of targets identified in Tables 2, 4, 11 or 55. In some instances, the non-coding target is a non-coding transcript. In other instances, the non-coding target is an intronic sequence. In other instances, the non-coding target is an intergenic sequence. In some instances, the non-coding target is a UTR sequence. In other instances, the non-coding target is a non-coding RNA transcript. In some embodiments, the target comprises a nucleic acid sequence. In some embodiments, the nucleic acid sequence is a DNA sequence. In some embodiments, the nucleic acid sequence is an RNA sequence. In other instances, the target comprises a polypeptide sequence. In some instances, the plurality of targets comprises 2 or more targets selected from the group of targets identified in Tables 2, 4, 11 or 55. In some instances, the plurality of targets comprises 5 or more targets selected from the group of

targets identified in Tables 2, 4, 11 or 55. In some instances, the plurality of targets comprises 10 or more targets selected from the group of targets identified in Tables 2, 4, 11 or 55. In some instances, the plurality of targets comprises 15 or more targets selected from the group of targets identified in Tables 2, 4, 11 or 55. In some instances, the plurality of targets comprises 20 or more targets selected from the group of targets identified in Tables 2, 4, 11 or 55. In some instances, the plurality of targets comprises 25 or more targets selected from the group of targets identified in Tables 2, 4, 11 or 55. In some instances, the plurality of targets comprises 30 or more targets selected from the group of targets identified in Tables 2, 4, 11 or 55. In some instances, the plurality of targets comprises 35 or more targets selected from the group of targets identified in Tables 2, 4, 11 or 55. In some instances, the plurality of targets comprises 40 or more targets selected from the group of targets identified in Tables 2, 4, 11 or 55. In some instances, the target is selected from Table 2. In other instances, the target is selected from Table 4. In some embodiments, the target is selected from Table 11. In some embodiments, the plurality of targets comprises 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets is selected from SEQ ID NOs:1-43. In some embodiments, the plurality of targets is selected from SEQ ID NOs:1-22. In some embodiments, assaying the expression level comprises detecting and/or quantifying a nucleotide sequence of the plurality of targets. In some embodiments, determining the treatment for the cancer includes determining the efficacy of treatment. Determining the treatment for the cancer may comprise administering an anti-cancer therapeutic. Alternatively, determining the treatment for the cancer may comprise modifying a therapeutic regimen. Modifying a therapeutic regimen may comprise increasing, decreasing, or terminating a therapeutic regimen.

[0404] The methods use the probe sets, probes and primers described herein to provide expression signatures or profiles from a test sample derived from a subject having or suspected of having cancer. In some embodiments, such methods involve contacting a test sample with a probe set comprising a plurality of probes under conditions that permit hybridization of the probe(s) to any target nucleic acid(s) present in the test sample and then detecting any probe:target duplexes formed as an indication of the presence of the target nucleic acid in the sample. Expression patterns thus determined are then compared to one or more reference profiles or signatures. Optionally, the expression pattern can be normalized.

The methods use the probe sets, probes and primers described herein to provide expression signatures or profiles from a test sample derived from a subject to classify the cancer as recurrent or non-recurrent.

[0405] In some embodiments, such methods involve the specific amplification of target sequences nucleic acid(s) present in the test sample using methods known in the art to generate an expression profile or signature which is then compared to a reference profile or signature.

[0406] In some embodiments, the invention further provides for prognosing patient outcome, predicting likelihood of recurrence after prostatectomy and/or for designating treatment modalities.

[0407] In one embodiment, the methods generate expression profiles or signatures detailing the expression of the target sequences having altered relative expression with different cancer outcomes.

[0408] In some embodiments, the methods detect combinations of expression levels of sequences exhibiting positive and negative correlation with a disease status. In one embodiment, the methods detect a minimal expression signature.

[0409] The gene expression profiles of each of the target sequences comprising the portfolio can be fixed in a medium such as a computer readable medium. This can take a number of forms. For example, a table can be established into which the range of signals (e.g., intensity measurements) indicative of disease or outcome is input. Actual patient data can then be compared to the values in the table to determine the patient samples diagnosis or prognosis. In a more sophisticated embodiment, patterns of the expression signals (e.g., fluorescent intensity) are recorded digitally or graphically.

[0410] The expression profiles of the samples can be compared to a control portfolio. The expression profiles can be used to diagnose, predict, or monitor a status or outcome of a cancer. For example, diagnosing, predicting, or monitoring a status or outcome of a cancer may comprise diagnosing or detecting a cancer, cancer metastasis, or stage of a cancer. In other instances, diagnosing, predicting, or monitoring a status or outcome of a cancer may comprise predicting the risk of cancer recurrence. Alternatively, diagnosing, predicting, or monitoring a status or outcome of a cancer may comprise predicting mortality or morbidity.

[0411] Further disclosed herein are methods for characterizing a patient population. Generally, the method comprises: (a) providing a sample from a subject; (b) assaying the expression level for a plurality of targets in the sample; and (c) characterizing the subject

based on the expression level of the plurality of targets. In some embodiments, the method further comprises assaying an expression level of a coding target. In some instances, the coding target is selected from the group consisting of targets identified in Tables 2, 4, 11 or 55. In some embodiments, the coding target is an exon-coding transcript. In some embodiments, the exon-coding transcript is an exonic sequence. In some embodiments, the method further comprises assaying an expression level of a non-coding target. In some instances, the non-coding target is selected from the group consisting of targets identified in Tables 2, 4, 11 or 55. In some instances, the non-coding target is a non-coding transcript. In other instances, the non-coding target is an intronic sequence. In other instances, the non-coding target is an intergenic sequence. In some instances, the non-coding target is a UTR sequence. In other instances, the non-coding target is a non-coding RNA transcript. In some embodiments, the target comprises a nucleic acid sequence. In some embodiments, the nucleic acid sequence is a DNA sequence. In some embodiments, the nucleic acid sequence is an RNA sequence. In other instances, the target comprises a polypeptide sequence. In some instances, the plurality of targets comprises 2 or more targets selected from the group of targets identified in Tables 2, 4, 11 or 55. In some instances, the plurality of targets comprises 5 or more targets selected from the group of targets identified in Tables 2, 4, 11 or 55. In some instances, the plurality of targets comprises 10 or more targets selected from the group of targets identified in Tables 2, 4, 11 or 55. In some instances, the plurality of targets comprises 15 or more targets selected from the group of targets identified in Tables 2, 4, 11 or 55. In some instances, the plurality of targets comprises 20 or more targets selected from the group of targets identified in Tables 2, 4, 11 or 55. In some instances, the plurality of targets comprises 25 or more targets selected from the group of targets identified in Tables 2, 4, 11 or 55. In some instances, the plurality of targets comprises 30 or more targets selected from the group of targets identified in Tables 2, 4, 11 or 55. In some instances, the plurality of targets comprises 35 or more targets selected from the group of targets identified in Tables 2, 4, 11 or 55. In some instances, the plurality of targets comprises 40 or more targets selected from the group of targets identified in Tables 2, 4, 11 or 55. In some instances, the target is selected from Table 2. In other instances, the target is selected from Table 4. In some embodiments, the target is selected from Table 11. In some embodiments, the plurality of targets comprises 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of

targets is selected from SEQ ID NOs:1-43. In some embodiments, the plurality of targets is selected from SEQ ID NOs:1-22. In some embodiments, assaying the expression level comprises detecting and/or quantifying a nucleotide sequence of the plurality of targets. In some instances, the method may further comprise diagnosing a cancer in the subject. In some embodiments, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In some embodiments, the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas. In some embodiments, the cancer is a prostate cancer. In some embodiments, the cancer is a pancreatic cancer. In some embodiments, the cancer is a bladder cancer. In some embodiments, the cancer is a thyroid cancer. In some embodiments, the cancer is a lung cancer. In some instances, characterizing the subject comprises determining whether the subject would respond to an anti-cancer therapy. Alternatively, characterizing the subject comprises identifying the subject as a non-responder to an anti-cancer therapy. Optionally, characterizing the subject comprises identifying the subject as a responder to an anti-cancer therapy.

[0412] Further disclosed herein are methods for selecting a subject suffering from a cancer for enrollment into a clinical trial. Generally, the method comprises: (a) providing a sample from a subject; (b) assaying the expression level for a plurality of targets in the sample; and (c) characterizing the subject based on the expression level of the plurality of targets. In some embodiments, the method further comprises assaying an expression level of a coding target. In some instances, the coding target is selected from the group consisting of targets identified in Tables 2, 4, 11 or 55. In some embodiments, the coding target is an exon-coding transcript. In some embodiments, the exon-coding transcript is an exonic sequence. In some embodiments, the method further comprises assaying an expression level of a non-coding target. In some instances, the non-coding target is selected from the group consisting of targets identified in Tables 2, 4, 11 or 55. In some instances, the non-coding target is a non-coding transcript. In other instances, the non-coding target is an intronic sequence. In other instances, the non-coding target is an intergenic sequence. In some instances, the non-coding target is a UTR sequence. In other instances, the non-coding target is a non-coding RNA transcript. In some embodiments, the target comprises a nucleic acid sequence. In some

embodiments, the nucleic acid sequence is a DNA sequence. In some embodiments, the nucleic acid sequence is an RNA sequence. In other instances, the target comprises a polypeptide sequence. In some instances, the plurality of targets comprises 2 or more targets selected from the group of targets identified in Tables 2, 4, 11 or 55. In some instances, the plurality of targets comprises 5 or more targets selected from the group of targets identified in Tables 2, 4, 11 or 55. In some instances, the plurality of targets comprises 10 or more targets selected from the group of targets identified in Tables 2, 4, 11 or 55. In some instances, the plurality of targets comprises 15 or more targets selected from the group of targets identified in Tables 2, 4, 11 or 55. In some instances, the plurality of targets comprises 20 or more targets selected from the group of targets identified in Tables 2, 4, 11 or 55. In some instances, the plurality of targets comprises 25 or more targets selected from the group of targets identified in Tables 2, 4, 11 or 55. In some instances, the plurality of targets comprises 30 or more targets selected from the group of targets identified in Tables 2, 4, 11 or 55. In some instances, the plurality of targets comprises 35 or more targets selected from the group of targets identified in Tables 2, 4, 11 or 55. In some instances, the plurality of targets comprises 40 or more targets selected from the group of targets identified in Tables 2, 4, 11 or 55. In some instances, the target is selected from Table 2. In other instances, the target is selected from Table 4. In some embodiments, the target is selected from Table 11. In some embodiments, the plurality of targets comprises 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets is selected from SEQ ID NOs:1-43. In some embodiments, the plurality of targets is selected from SEQ ID NOs:1-22. In some embodiments, assaying the expression level comprises detecting and/or quantifying a nucleotide sequence of the plurality of targets. In some instances, the method may further comprise diagnosing a cancer in the subject. In some embodiments, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In some embodiments, the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas. In some embodiments, the cancer is a prostate cancer. In some embodiments, the cancer is a pancreatic cancer. In some embodiments, the cancer is a bladder

cancer. In some embodiments, the cancer is a thyroid cancer. In some embodiments, the cancer is a lung cancer. In some instances, characterizing the subject comprises determining whether the subject would respond to an anti-cancer therapy. Alternatively, characterizing the subject comprises identifying the subject as a non-responder to an anti-cancer therapy. Optionally, characterizing the subject comprises identifying the subject as a responder to an anti-cancer therapy.

[0413] Further disclosed herein is a method of analyzing a cancer in an individual in need thereof, comprising (a) obtaining an expression profile from a sample obtained from the individual, wherein the expression profile comprises more than one target selected from Tables 2, 4, 11 or 55; and (b) comparing the expression profile from the sample to an expression profile of a control or standard. In some embodiments, the plurality of targets comprises at least 5 targets selected from Tables 2, 4, 11 or 55. In some embodiments, wherein the plurality of targets comprises at least 10 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 15 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 20 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets is selected from SEQ ID NOs:1-43. In some embodiments, the plurality of targets is selected from SEQ ID NOs:1-22. In some embodiments, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In some embodiments, the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas. In some embodiments, the method further comprises a software module executed by a computer-processing device to compare the expression profiles. In some embodiments, the method further comprises providing diagnostic or prognostic information to the individual about the cardiovascular disorder based on the comparison. In some embodiments, the method further comprises diagnosing the individual with a cancer if the expression profile of the sample (a) deviates from the control or standard from a healthy individual or population of healthy individuals, or (b) matches the control or standard from an individual or population

of individuals who have or have had the cancer. In some embodiments, the method further comprises predicting the susceptibility of the individual for developing a cancer based on (a) the deviation of the expression profile of the sample from a control or standard derived from a healthy individual or population of healthy individuals, or (b) the similarity of the expression profiles of the sample and a control or standard derived from an individual or population of individuals who have or have had the cancer. In some embodiments, the method further comprises prescribing a treatment regimen based on (a) the deviation of the expression profile of the sample from a control or standard derived from a healthy individual or population of healthy individuals, or (b) the similarity of the expression profiles of the sample and a control or standard derived from an individual or population of individuals who have or have had the cancer. In some embodiments, the method further comprises altering a treatment regimen prescribed or administered to the individual based on (a) the deviation of the expression profile of the sample from a control or standard derived from a healthy individual or population of healthy individuals, or (b) the similarity of the expression profiles of the sample and a control or standard derived from an individual or population of individuals who have or have had the cancer. In some embodiments, the method further comprises predicting the individual's response to a treatment regimen based on (a) the deviation of the expression profile of the sample from a control or standard derived from a healthy individual or population of healthy individuals, or (b) the similarity of the expression profiles of the sample and a control or standard derived from an individual or population of individuals who have or have had the cancer. In some embodiments, the deviation is the expression level of more than one target from the sample is greater than the expression level of more than one target from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of more than one target from the sample is at least about 30% greater than the expression level of more than one target from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of more than one target from the sample is less than the expression level of more than one target from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of more than one target from the sample is at least about 30% less than the expression level of more than one target from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the method further comprises using a machine to isolate

the target or the probe from the sample. In some embodiments, the method further comprises contacting the sample with a label that specifically binds to the target, the probe, or a combination thereof. In some embodiments, the method further comprises contacting the sample with a label that specifically binds to a target selected from Tables 2, 4, 11 or 55 or a combination thereof. In some instances, the target is selected from Table 2. In other instances, the target is selected from Table 4. In some embodiments, the target is selected from Table 11. In some embodiments, the method further comprises amplifying the target, the probe, or any combination thereof. In some embodiments, the method further comprises sequencing the target, the probe, or any combination thereof. In some embodiments, the method further comprises converting the expression levels of the target sequences into a likelihood score that indicates the probability that a biological sample is from a patient who will exhibit no evidence of disease, who will exhibit systemic cancer, or who will exhibit biochemical recurrence. In some embodiments, the target sequences are differentially expressed the cancer. In some embodiments, the differential expression is dependent on aggressiveness. In some embodiments, the expression profile is determined by a method selected from the group consisting of RT-PCR, Northern blotting, ligase chain reaction, array hybridization, and a combination thereof.

[0414] Also disclosed herein is a method of diagnosing cancer in an individual in need thereof, comprising (a) obtaining an expression profile from a sample obtained from the individual, wherein the expression profile comprises more than one target selected from Tables 2, 4, 11 or 55; (b) comparing the expression profile from the sample to an expression profile of a control or standard; and (c) diagnosing a cancer in the individual if the expression profile of the sample (i) deviates from the control or standard from a healthy individual or population of healthy individuals, or (ii) matches the control or standard from an individual or population of individuals who have or have had the cancer. In some embodiments, the plurality of targets comprises at least 5 targets selected from Tables 2, 4, 11 or 55. In some embodiments, wherein the plurality of targets comprises at least 10 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 15 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 20 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the

plurality of targets is selected from SEQ ID NOs:1-43. In some embodiments, the plurality of targets is selected from SEQ ID NOs:1-22. In some embodiments, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In some embodiments, the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas. In some embodiments, the method further comprises a software module executed by a computer-processing device to compare the expression profiles. In some embodiments, the deviation is the expression level of more than one target from the sample is at least about 30% greater than the expression level of more than one target from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of more than one target from the sample is less than the expression level of more than one target from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of more than one target from the sample is at least about 30% less than the expression level of more than one target from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the method further comprises using a machine to isolate the target or the probe from the sample. In some embodiments, the method further comprises contacting the sample with a label that specifically binds to the target, the probe, or a combination thereof. In some embodiments, the method further comprises contacting the sample with a label that specifically binds to a target selected from Tables 2, 4, 11 or 55, or a combination thereof. In some embodiments, the method further comprises amplifying the target, the probe, or any combination thereof. In some embodiments, the method further comprises sequencing the target, the probe, or any combination thereof. In some embodiments, the method further comprises converting the expression levels of the target sequences into a likelihood score that indicates the probability that a biological sample is from a patient who will exhibit no evidence of disease, who will exhibit systemic cancer, or who will exhibit biochemical recurrence. In some embodiments, the target sequences are differentially expressed the cancer. In some embodiments, the differential expression is dependent on aggressiveness. In some embodiments, the expression profile is determined by a method selected from the group consisting of RT-PCR, Northern blotting, ligase chain reaction, array hybridization, and a combination thereof.

[0415] In some embodiments is a method of predicting whether an individual is susceptible to developing a cancer, comprising (a) obtaining an expression profile from a sample obtained from the individual, wherein the expression profile comprises more than one target selected from Tables 2, 4, 11 or 55; (b) comparing the expression profile from the sample to an expression profile of a control or standard; and (c) predicting the susceptibility of the individual for developing a cancer based on (i) the deviation of the expression profile of the sample from a control or standard derived from a healthy individual or population of healthy individuals, or (ii) the similarity of the expression profiles of the sample and a control or standard derived from an individual or population of individuals who have or have had the cancer. In some embodiments, the plurality of targets comprises at least 5 targets selected from Tables 2, 4, 11 or 55. In some embodiments, wherein the plurality of targets comprises at least 10 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 15 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 20 targets selected from Tables 2, 4, 11 or 55. In some instances, the target is selected from Table 2. In other instances, the target is selected from Table 4. In some embodiments, the target is selected from Table 11. In some embodiments, the plurality of targets comprises 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets is selected from SEQ ID NOs:1-43. In some embodiments, the plurality of targets is selected from SEQ ID NOs:1-22. In some embodiments, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In some embodiments, the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas. In some embodiments, the method further comprises a software module executed by a computer-processing device to compare the expression profiles. In some embodiments, the deviation is the expression level of more than one target from the sample is at least about 30% greater than the expression level of more than one target from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of more than one target from the sample is less than the expression

level of more than one target from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of more than one target from the sample is at least about 30% less than the expression level of more than one target from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the method further comprises using a machine to isolate the target or the probe from the sample. In some embodiments, the method further comprises contacting the sample with a label that specifically binds to the target, the probe, or a combination thereof. In some embodiments, the method further comprises contacting the sample with a label that specifically binds to a target selected from Tables 2, 4, 11 or 55, or a combination thereof. In some embodiments, the method further comprises amplifying the target, the probe, or any combination thereof. In some embodiments, the method further comprises sequencing the target, the probe, or any combination thereof. In some embodiments, the method further comprises converting the expression levels of the target sequences into a likelihood score that indicates the probability that a biological sample is from a patient who will exhibit no evidence of disease, who will exhibit systemic cancer, or who will exhibit biochemical recurrence. In some embodiments, the target sequences are differentially expressed the cancer. In some embodiments, the differential expression is dependent on aggressiveness. In some embodiments, the expression profile is determined by a method selected from the group consisting of RT-PCR, Northern blotting, ligase chain reaction, array hybridization, and a combination thereof.

[0416] In some embodiments is a method of predicting an individual's response to a treatment regimen for a cancer, comprising: (a) obtaining an expression profile from a sample obtained from the individual, wherein the expression profile comprises more than one target selected from Tables 2, 4, 11 or 55; (b) comparing the expression profile from the sample to an expression profile of a control or standard; and (c) predicting the individual's response to a treatment regimen based on (i) the deviation of the expression profile of the sample from a control or standard derived from a healthy individual or population of healthy individuals, or (ii) the similarity of the expression profiles of the sample and a control or standard derived from an individual or population of individuals who have or have had the cancer. In some embodiments, the plurality of targets comprises at least 5 targets selected from Tables 2, 4, 11 or 55. In some embodiments, wherein the plurality of targets comprises at least 10 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 15 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of

targets comprises at least 20 targets selected from Tables 2, 4, 11 or 55. In some instances, the target is selected from Table 2. In other instances, the target is selected from Table 4. In some embodiments, the target is selected from Table 11. In some embodiments, the plurality of targets comprises 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets is selected from SEQ ID NOs:1-43. In some embodiments, the plurality of targets is selected from SEQ ID NOs:1-22. In some embodiments, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In some embodiments, the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas. In some embodiments, the method further comprises a software module executed by a computer-processing device to compare the expression profiles. In some embodiments, the deviation is the expression level of more than one target from the sample is at least about 30% greater than the expression level of more than one target from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of more than one target from the sample is less than the expression level of more than one target from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of more than one target from the sample is at least about 30% less than the expression level of more than one target from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the method further comprises using a machine to isolate the target or the probe from the sample. In some embodiments, the method further comprises contacting the sample with a label that specifically binds to the target, the probe, or a combination thereof. In some embodiments, the method further comprises contacting the sample with a label that specifically binds to a target selected from Tables 2, 4, 11 or 55, or a combination thereof. In some embodiments, the method further comprises amplifying the target, the probe, or any combination thereof. In some embodiments, the method further comprises sequencing the target, the probe, or any combination thereof. In some embodiments, the method further comprises converting the expression levels of the target sequences into a likelihood score that indicates the probability

that a biological sample is from a patient who will exhibit no evidence of disease, who will exhibit systemic cancer, or who will exhibit biochemical recurrence. In some embodiments, the target sequences are differentially expressed the cancer. In some embodiments, the differential expression is dependent on aggressiveness. In some embodiments, the expression profile is determined by a method selected from the group consisting of RT-PCR, Northern blotting, ligase chain reaction, array hybridization, and a combination thereof.

[0417] A method of prescribing a treatment regimen for a cancer to an individual in need thereof, comprising (a) obtaining an expression profile from a sample obtained from the individual, wherein the expression profile comprises more than one target selected from Tables 2, 4, 11 or 55; (b) comparing the expression profile from the sample to an expression profile of a control or standard; and (c) prescribing a treatment regimen based on (i) the deviation of the expression profile of the sample from a control or standard derived from a healthy individual or population of healthy individuals, or (ii) the similarity of the expression profiles of the sample and a control or standard derived from an individual or population of individuals who have or have had the cancer. In some embodiments, the plurality of targets comprises at least 5 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 10 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 15 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 20 targets selected from Tables 2, 4, 11 or 55. In some instances, the target is selected from Table 2. In other instances, the target is selected from Table 4. In some embodiments, the target is selected from Table 11. In some embodiments, the plurality of targets comprises 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets is selected from SEQ ID NOs:1-43. In some embodiments, the plurality of targets is selected from SEQ ID NOs:1-22. In some embodiments, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In some embodiments, the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas. In some embodiments, the method further comprises a software module executed by a computer-

processing device to compare the expression profiles. In some embodiments, the deviation is the expression level of more than one target from the sample is at least about 30% greater than the expression level of more than one target from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of more than one target from the sample is less than the expression level of more than one target from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the deviation is the expression level of more than one target from the sample is at least about 30% less than the expression level of more than one target from a control or standard derived from a healthy individual or population of healthy individuals. In some embodiments, the method further comprises using a machine to isolate the target or the probe from the sample. In some embodiments, the method further comprises contacting the sample with a label that specifically binds to the target, the probe, or a combination thereof. In some embodiments, the method further comprises contacting the sample with a label that specifically binds to a target selected from Tables 2, 4, 11 or 55, or a combination thereof. In some embodiments, the method further comprises amplifying the target, the probe, or any combination thereof. In some embodiments, the method further comprises sequencing the target, the probe, or any combination thereof. In some embodiments, the method further comprises converting the expression levels of the target sequences into a likelihood score that indicates the probability that a biological sample is from a patient who will exhibit no evidence of disease, who will exhibit systemic cancer, or who will exhibit biochemical recurrence. In some embodiments, the target sequences are differentially expressed the cancer. In some embodiments, the differential expression is dependent on aggressiveness. In some embodiments, the expression profile is determined by a method selected from the group consisting of RT-PCR, Northern blotting, ligase chain reaction, array hybridization, and a combination thereof.

[0418] Further disclosed herein is a kit for analyzing a cancer, comprising (a) a probe set comprising a plurality of target sequences, wherein the plurality of target sequences comprises more than one target sequence listed in Table 11; and (b) 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 kit further comprises a computer model or algorithm for correlating the expression level or expression profile with disease state or outcome. In some embodiments, the kit further comprises a computer model or algorithm for designating a treatment modality for the individual. In some embodiments, the kit further comprises a

computer model or algorithm for normalizing expression level or expression profile of the target sequences. In some embodiments, the kit further comprises a computer model or algorithm comprising a robust multichip average (RMA), probe logarithmic intensity error estimation (PLIER), non-linear fit (NLFIT) quantile-based, nonlinear normalization, or a combination thereof. In some embodiments, the plurality of targets comprises at least 10 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 15 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 20 targets selected from Tables 2, 4, 11 or 55. In some instances, the target is selected from Table 2. In other instances, the target is selected from Table 4. In some embodiments, the target is selected from Table 11. In some embodiments, the plurality of targets comprises 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets is selected from SEQ ID NOs:1-43. In some embodiments, the plurality of targets is selected from SEQ ID NOs:1-22. In some embodiments, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In some embodiments, the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas.

[0419] Further disclosed herein is a system for analyzing a cancer, comprising (a) a probe set comprising a plurality of target sequences, wherein (i) the plurality of target sequences hybridizes to more than one target selected from Tables 2 or 4; or (ii) the plurality of target sequences comprises more than one target sequences selected from Table 11; and (b) 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 a cancer. In some embodiments, the system further comprises electronic memory for capturing and storing an expression profile. In some embodiments, the system further comprises a computer-processing device, optionally connected to a computer network. In some embodiments, the system further comprises a software module executed by the computer-processing device to analyze an expression profile. In some embodiments, the system further comprises a software module executed by the computer-processing device to compare the expression profile to a

standard or control. In some embodiments, the system further comprises a software module executed by the computer-processing device to determine the expression level of the target. In some embodiments, the system further comprises a machine to isolate the target or the probe from the sample. In some embodiments, the system further comprises a machine to sequence the target or the probe. In some embodiments, the system further comprises a machine to amplify the target or the probe. In some embodiments, the system further comprises a label that specifically binds to the target, the probe, or a combination thereof. In some embodiments, the system further comprises a software module executed by the computer-processing device to transmit an analysis of the expression profile to the individual or a medical professional treating the individual. In some embodiments, the system further comprises a software module executed by the computer-processing device to transmit a diagnosis or prognosis to the individual or a medical professional treating the individual. In some embodiments, the plurality of targets comprises at least 5 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 10 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 15 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets comprises at least 20 targets selected from Tables 2, 4, 11 or 55. In some instances, the target is selected from Table 2. In other instances, the target is selected from Table 4. In some embodiments, the target is selected from Table 11. In some embodiments, the plurality of targets comprises 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the plurality of targets is selected from SEQ ID NOs:1-43. In some embodiments, the plurality of targets is selected from SEQ ID NOs:1-22. In some embodiments, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In some embodiments, the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas.

[0420] Disclosed herein in some embodiments is a method for analyzing cancer comprising a computer processing device for determining an expression profile for a probe set; 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 a cancer; and an output providing the analysis. In some embodiments, the probe set comprises a plurality of target sequences, wherein the plurality of target sequences hybridizes to more than one target sequence selected from Tables 2 or 4; or the plurality of target sequences comprises more than one target sequence selected from Table 11. In further embodiments the method further comprises an electronic memory device for capturing and storing an expression profile; a software module; a machine to isolate target or the probe from the sample; a machine to sequence the target or the probe; and/or a machine to amplify the target or the probe. In certain embodiments, the software module executed by the computer-processing device analyzes an expression profile. In an additional embodiment, the software compare executed by the computer-processing devices the expression profile to a standard or control. In one embodiment, the software module executed by the computer-processing device determines the expression level of the target. In an embodiment, the software module executed by the computer-processing device transmits an analysis of the expression profile to the subject or a medical professional treating the subject. In a further embodiment, the method further comprises a label that specifically binds to the target, the probe, or a combination thereof. In some embodiments, the target sequences comprise at least 5 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the target sequences comprise at least 10 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the target sequences comprise at least 15 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the target sequences comprise at least 20 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the target sequences comprise at least 30 targets selected from Tables 2, 11 or 55. In some embodiments, the target sequences comprise at least 35 targets selected from Tables 2, 11 or 55. In some embodiments, the target sequences comprise at least 40 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of target sequences comprises at least 22 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of target sequences comprises at least 30 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of target sequences comprises at least 35 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of target sequences comprises at least 40 targets selected from Tables 2, 11 or 55. In some embodiments, the plurality of target sequences comprises 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 targets selected from Tables 2, 4, 11 or 55. In some embodiments, the

plurality of target sequences is selected from SEQ ID NOs:1-43. In some embodiments, the plurality of target sequences is selected from SEQ ID NOs:1-22. In an additional embodiment, the cancer is selected from the group consisting of a carcinoma, sarcoma, leukemia, lymphoma, myeloma, and a CNS tumor. In a further embodiment, the cancer is selected from the group consisting of bladder cancer, skin cancer, lung cancer, colon cancer, pancreatic cancer, prostate cancer, liver cancer, thyroid cancer, ovarian cancer, uterine cancer, breast cancer, cervical cancer, kidney cancer, epithelial carcinoma, squamous carcinoma, basal cell carcinoma, melanoma, papilloma, and adenomas.

EXAMPLES

Example 1. Validation Studies in Subjects with Prostate Cancer

Study Design

[0421] This study used a previously described case-control study for biomarker discovery and a case-cohort for independent validation. A STROBE flow diagram providing an overview of the case-control study is available in (FIG. 1).

[0422] The discovery study was a nested case-control described in detail in Nakagawa et al 2008. Archived formalin-fixed paraffin embedded (FFPE) blocks of tumors were selected from 621 patients that had undergone a radical prostatectomy (RP) at the Mayo Clinic Comprehensive Cancer Centre between the years 1987-2001 providing a median of 18.16 years of follow-up. The patients were randomly split into a training and test sets; the training set was used for biomarker discovery and classifier development and the testing set was used to measure performance and with model selection.

[0423] Patients were retrospectively classified into one of three outcomes: NED: No evidence of disease for those patients with no biochemical or other clinical signs of disease progression (at least 10 years follow-up); PSA: prostate-specific antigen biochemical recurrence for those patients with two successive increases in PSA measurements above an established cut-point of >0.2 ng/ (with the subsequent measure 0.05 ng/mL above the first measurement) within 5 years of RP and no detectable metastases up to 10 years after RP; METS: for those patients experience BCR within 5 years of RP and that developed metastases (confirmed by bone or CT scan) within 5 years of BCR. Patient selection for nested case-control design is outlined in Nakagawa.

[0424] On average, METS patients were diagnosed within 3.22 years following BCR and 5.79 years following RP, implying that this METS group experienced rapid onset of

metastatic disease. Some PSA patients do experience metastatic disease (n=18, or 9.9% of all PSA patients in the discovery study), however, these patients have the event 10 years beyond RP and thus are outside the MET definition. Due to the condition that both PSA and MET groups had to experience BCR event within 5 years of RP, there is no statistically significant difference for the time to BCR between PSA (median: 1.70 years [IQR:0.65-3.44]) and MET (median: 2.26 years [IQR:0.78-3.94]) groups. Patients in this study did not receive a consistent treatment regimen, and may be highly treated with adjuvant interventions compared to other cohorts. Where possible we account for adjuvant interventions in analysis to mitigate its impact as a confounding factor (See Statistical Analysis).

[0425] We conducted a study that investigated the differences between NED, PSA and METS outcome groups and found there to be no statistically significant differences between the NED and PSA groups, with the largest difference in genomic and clinicopathologic variables to be found when comparing METS against NED or PSA groups. We have evidence to believe that NED and PSA groups may represent a less aggressive type of prostate cancer, and that these patients will likely not experience metastatic progression in their life-time, conversely METS patients represent rapid disease onset and more aggressive prostate cancer. To maximize discovery of biomarkers that identified oncogenic drivers of aggressive disease, we combined the NED and PSA groups into a unified Non-METS group to compare against the METS.

[0426] The discovery study included 621 patients who underwent RP at the Mayo Clinic between 1987-2001. Patients who received neo-adjuvant interventions were excluded. After chip quality control (<http://www.affymetrix.com>), 545 unique patients (209 with mets after RP and 336 with BCR only or NED) were available for the biomarker discovery study (median follow-up, 18.2 years). The study patients were further subdivided by random draw into training (n=359) and testing (n=186) subsets, balancing for the distribution of clinicopathologic variables (Table 1) as previously described.

Table 1. Clinical characteristics of Discovery and Validation data set

Clinical variable	Values	Discovery				Independent Validation	
		Training		Testing			
		No mets	mets	No mets	mets	No mets	mets
# patients	-	218	141	118	68	150	69
Pathological Tumour Stage	T2	105	40	56	18	71	14
	T3/4	101	67	48	37	62	40
	TxN+	12	34	14	13	17	15
Pre-Op PSA	<10 ng/ml	124	66	58	34	86	33
	≥10 ≤20	53	31	22	11	39	20
	>20 ng/ml	38	43	33	17	25	16
	NA	3	1	5	6	0	0
Pathological Gleason score	≤6	41	4	16	2	15	0
	7	125	49	70	27	82	29
	≥8	52	88	32	39	53	40
Path features	SM+	98	81	54	33	64	39
	ECE+	96	86	50	41	54	44
	SVI+	47	63	34	32	45	36
Biochemical recurrence (BCR)	Censored	99	0	58	0	109	0
	Event	119	141	60	68	41	69
Prostate-specific mortality (PCSM)	Censored	216	47	117	33	150	41
	Event	2	94	1	35	0	28
Adjuvant Radiation	No	203	120	112	56	135	60
	Yes	15	21	8	12	15	9
Adjuvant ADT	No	187	95	89	50	108	37
	Yes	31	46	29	18	42	32

[0427] The initial Clinical characteristics of these samples related to biochemical recurrence (BCR), METS (or clinical recurrence (CR)), prostate cancer specific mortality (PCSM) and overall survival are shown in FIG. 2.

[0428] Subjects for independent validation were identified from a population of 1,010 men prospectively enrolled in the Mayo Clinic tumor registry who underwent RP for prostatic adenocarcinoma from 2000-2006 and were at high risk for disease recurrence. High-risk for recurrence was defined by pre-operative PSA >20ng/mL, or pathological Gleason score ≥8, or seminal vesicle invasion (SVI) or GPSM (Gleason, PSA, seminal vesicle and margin status) score ≥10. Data was collected using a case-cohort design over the follow-up period (median, 8.06 years), 71 patients developed metastatic disease (*mets*) as evidenced by positive bone and/or CT scans. Data was collected using a case-cohort design, which involved selection of all 73 cases combined with a random sample of 202 patients (~20%) from the entire cohort. After exclusion for tissue unavailability and samples that failed microarray quality control, the independent validation cohort consisted of 219 (69 cases) unique patients.

RNA Extraction and Microarray Hybridization

[0429] Following pathological review of FFPE primary prostatic adenocarcinoma specimens from patients in the discovery and validation cohorts, tumor was macrodissected from surrounding stroma from 3-4 10µm tissue sections. Total RNA was extracted, amplified

using the Ovation FFPE kit (NuGEN, San Carlos, CA), and hybridized to Human Exon 1.0 ST GeneChips (Affymetrix, Santa Clara, CA) that profiles coding and non-coding regions of the transcriptome using approximately 1.4 million probe selection regions, hereinafter referred to as features.

[0430] For the discovery study, total RNA was prepared as described herein. For the independent validation study, total RNA was extracted and purified using a modified protocol for the commercially available RNeasy FFPE nucleic acid extraction kit (Qiagen Inc., Valencia, CA). RNA concentrations were determined using a Nanodrop ND-1000 spectrophotometer (Nanodrop Technologies, Rockland, DE). Purified total RNA was subjected to whole-transcriptome amplification using the WT-Ovation FFPE system according to the manufacturer's recommendation with minor modifications (NuGen, San Carlos, CA). For the discovery study the WT-Ovation FFPE V2 kit was used together with the Exon Module while for the validation only the Ovation® FFPE WTA System was used. Amplified products were fragmented and labeled using the Encore™ Biotin Module (NuGen, San Carlos, CA) and hybridized to Affymetrix Human Exon (HuEx) 1.0 ST GeneChips following manufacturer's recommendations (Affymetrix, Santa Clara, CA). Only 604 out of a total 621 patients had specimens available for hybridization.

Microarray Processing

Microarray Quality Control

[0431] The Affymetrix Power Tools packages provide an index characterizing the quality of each chip, independently, named "pos_vs_neg_AUC". This index compares signal values for positive and negative control probesets defined by the manufacturer. Values for the AUC are in [0, 1], arrays that fall under 0.6 were removed from analysis.

[0432] Only 545 unique samples, out of the total 604 with available specimens (inter- and intra-batch duplicates were run), were of sufficient quality for further analysis; 359 and 187 samples were available from the training and testing sets respectively. We re-evaluated the variable balance between the training and testing sets and found there to be no statistically significant difference for any of the variables.

Microarray Normalization, Probeset filtering, and Batch Effect Correction

[0433] Probeset summarization and normalization was performed by fRMA, which is available through Bioconductor. The fRMA algorithm relates to RMA with the exception that it specifically attempts to consider batch effect during probeset summarization and is capable of storing the model parameters in so called 'frozen vectors'. We generated a custom set of

frozen vectors by randomly selecting 15 arrays from each of the 19 batches in the discovery study. The frozen vectors can be applied to novel data without having to renormalize the entire dataset. We furthermore filtered out unreliable PSRs by removing cross-hybridizing probes as well as high PSRs variability of expression values in a prostate cancer cell line and those with fewer than 4 probes. Following fRMA and filtration the data was decomposed into its principal components and an analysis of variance model was used to determine the extent to which a batch effect remains present in the first 10 principal components. We chose to remove the first two principal components, as they were highly correlated with the batch processing date.

Non-coding RNA analysis

[0434] Sequence information from each probe in a PSR can be aligned and annotated against the human reference genome by xmapcore (Yates, et al., X:Map: Annotation and visualization of genome structure for Affymetrix exon array analysis, *Nucleic Acids Res.* (2008), Epub.) Using annotation data from the human genome version hg19/GRCh37 (Ensembl annotation release 62), we categorize the PSRs into coding, non-coding (UTR) and non-coding (intronic) as defined by xmapcore.

[0435] The PSRs that cannot be categorized in the groups above are further categorized as follows:

[0436] Non-coding (Non-unique): one or more probes don't align perfectly to the genome, or one or more probes align perfectly to multiple regions of the genome.

[0437] Non-coding (ncTranscript): PSR correspond to the exon of a non-coding transcript.

[0438] Non-coding (CDS_Antisense): PSR corresponds to a segment in the opposite strand of the coding sequence of a protein-coding transcript.

[0439] Non-coding (UTR_Antisense): PSR corresponds to a segment in the opposite strand of the UTR sequence (5' or 3') of a transcript.

[0440] Non-coding (Intronic_Antisense): PSR correspond to a segment in the opposite strand of the intronic sequence of a protein-coding transcript.

[0441] Non-coding (ncTranscript_Antisense): PSR correspond to the exon of a non-coding transcript in the opposite strand.

[0442] Non-coding (Intergenic): if the probes were not categorized under any of the groups above and it is annotated as 'intergenic' by xmapcore.

[0443] We additionally used xmapcore to annotate the gene symbol, gene synonym, Ensembl gene ID and biological description for any PSRs that overlapped with a transcript

when necessary; this excludes alignments to non-coding (non-unique) and non-coding (intergenic) sequences.

Example 2: A 43-Biomarker Set for Prostate Cancer

[0444] Overview of the entire microarray analysis pipeline is provided in FIG. 3.

Feature Selection

[0445] The remaining features following the analysis in Example 1 were subjected to filtration by a t-test between the METS and non-METS samples in the training set (n=359). Using a p-value cut-off of 0.01, 18,902 features remain in analysis for further selection. Feature selection was performed by regularized logistic regression using the elastic-net penalty through the glmnet v1.7 package available in R with an alpha-value of 0.5 with three-fold cross validation. The regularized regression, with cross validation, was bootstrapped over 1000 times using all training data (n=359); with each iteration of bootstrapping we tabulated features that had a non-zero co-efficient. Features that were selected in at least 25% of the total runs were used for model building.

Non-coding RNA Analysis

[0446] We annotated the 43-biomarker set with labels described in Example 1 to identify the extent of non-coding features. We show the various labels within the 43-biomarker set in FIG. 4. Table 2 shows that most of the PSRs are found within the boundaries of a gene, with only one probe set (3802328) being intergenic. Assessment of the ontology term enrichment for the genes in Table 3 using DAVID tools shows that the set of genes is enriched, as expected in the case of cancer, for the biological processes of sister chromatid segregation, cell division and chromosome segregation (after Bonferroni correction, significance level of 0.08, Table 3).

Table 2. 43-Biomarker Set. Chromosomal coordinates correspond to the hg19 version of the human genome. (Markers in the 43-biomarker set are annotated as RF43. Markers in the 22-biomarker set are annotated as RF22.)

SEQ ID NO:	Biomarker Panel	Chromosome	Start	End	Category	Strand	Symbol	ENSEMBL ID
1.	RF22, RF43	1	164790778	164790861	CODING	1	PBX1	ENSG00000185630
2.	RF22, RF43	12	102043061	102043198	CODING	1	MYBPC1	ENSG00000196091

3.	RF22, RF43	17	370546 99	370547 47	CODING	1	LASP1	ENSG0000 0002834
4.	RF22, RF43	1	208090 88	208101 89	NON_CODING (CDS_ANTISENSE)	1	CAMK2 N1	ENSG0000 0162545
5.	RF22, RF43	9	125827 478	125827 705	NON_CODING (CDS_ANTISENSE)	-1	RABGA P1	ENSG0000 0011454
6.	RF22, RF43	20	444453 47	444455 62	NON_CODING (CDS_ANTISENSE)	-1	UBE2C	ENSG0000 0175063
7.	RF22, RF43	5	140018 62	140020 03	NON_CODING (ncTRANSCRIPT)	1	PCAT- 32	
8.	RF22, RF43	9	140891 54	140891 87	NON_CODING (INTRONIC)	-1	NFIB	ENSG0000 0147862
9.	RF22, RF43	12	102021 374	102021 490	NON_CODING (INTRONIC)	1	MYBPC 1	ENSG0000 0196091
10.	RF22, RF43	13	241576 11	241580 03	NON_CODING (INTRONIC)	1	TNFRS F19	ENSG0000 0127863
11.	RF22, RF43	4	309752 79	309754 41	NON_CODING (INTRONIC)	1	PCDH7	ENSG0000 0169851
12.	RF22, RF43	2	242138 538	242138 661	NON_CODING (ncTRANSCRIPT)	1	ANO7	ENSG0000 0146205
13.	RF22, RF43	11	588110 43	588110 70	NON_CODING (ncTRANSCRIPT)	1	GLYAT L1P4	ENSG0000 0254399
14.	RF22, RF43	6	323307 51	323310 82	NON_CODING (INTRONIC)	-1	C6orf10	ENSG0000 0206310
15.	RF22, RF43	1	156495 410	156496 002	NON_CODING (UTR)	-1	IQGAP3	ENSG0000 0183856
16.	RF22, RF43	2	242163 962	242164 581	NON_CODING (UTR)	1	ANO7	ENSG0000 0146205
17.	RF22, RF43	6	169616 207	169616 770	NON_CODING (UTR)	-1	THBS2	ENSG0000 0186340
18.	RF22, RF43	8	144939 574	144939 986	NON_CODING (UTR)	-1	EPPK1	ENSG0000 0227184
19.	RF22, RF43	15	416724 63	416729 32	NON_CODING (UTR)	1	NUSAP 1	ENSG0000 0137804
20.	RF22, RF43	15	668412 41	668418 00	NON_CODING (UTR)	1	ZWILC H	ENSG0000 0174442
21.	RF22, RF43	19	318009 5	318032 8	NON_CODING (UTR)	1	S1PR4	ENSG0000 0125910
22.	RF22, RF43	20	444454 72	444455 07	NON_CODING (UTR)	1	UBE2C	ENSG0000 0175063

23.	RF43	3	101212 717	101212 786	CODING	-1	SENP7	ENSG0000 0138468
24.	RF43	7	364506 79	364507 50	CODING	1	ANLN	ENSG0000 0011426
25.	RF43	10	887302 50	887302 88	CODING	1	C10orf1 16	ENSG0000 0148671
26.	RF43	11	683825 13	683826 88	CODING	1	PPP6R3	ENSG0000 0110075
27.	RF43	13	333275 27	333276 56	CODING	1	PDS5B	ENSG0000 0083642
28.	RF43	17	385525 72	385526 98	CODING	-1	TOP2A	ENSG0000 0131747
29.	RF43	3	190366 433	190366 480	CODING	1	IL1RAP	ENSG0000 0196083
30.	RF43	4	104057 451	104057 507	CODING	-1	CENPE	ENSG0000 0138778
31.	RF43	12	485460 0	485475 5	CODING	1	GALNT 8	ENSG0000 0130035
32.	RF43	17	385553 14	385553 64	CODING	-1	TOP2A	ENSG0000 0131747
33.	RF43	11	277226 6	277259 2	NON_CODING (CDS_ANTISENSE)	-1	KCNQ1	ENSG0000 0053918
34.	RF43	18	242373 26	242374 36	NON_CODING (INTERGENIC)	-1		
35.	RF43	6	721197 21	721197 51	NON_CODING (INTRONIC)	-1	C6orf15 5	ENSG0000 0233237
36.	RF43	11	249974 29	249977 06	NON_CODING (INTRONIC)	1	LUZP2	ENSG0000 0187398
37.	RF43	12	102030 525	102030 872	NON_CODING (INTRONIC)	1	MYBPC 1	ENSG0000 0196091
38.	RF43	16	501040 59	501040 87	NON_CODING (INTRONIC)	1	HEATR 3	ENSG0000 0155393
39.	RF43	3	132829 328	132829 491	NON_CODING (INTRONIC_ANTI SENSE)	-1	TMEM1 08	ENSG0000 0144868
40.	RF43	6	319144 55	319145 76	NON_CODING (ncTRANSCRIPT)	1	CFB XXbac- BPG116 M5.17	ENSG0000 0243649 ENSG0000 0244255
41.	RF43	7	596768 9	596771 6	NON_CODING (NON_UNIQUE)	1		
42.	RF43	1	533795 70	533797 55	NON_CODING (UTR)	-1	ECHDC 2	ENSG0000 0121310
43.	RF43	11	133767 93	133768 32	NON_CODING (UTR)	1	ARNTL	ENSG0000 0133794

Table 3. Gene Ontology Terms Enriched in the 43-Biomarker Signature

GO Term	Biological Process	Genes Involved	P-value	Adjusted P-value
GO:0000819	Sister Chromatid Segregation	CENPE, NUSAP1, PDS5B, TOP2A	6.99E-05	0.0736
GO:0051301	Cell Division	ANLN, CENPE, NUSAP1, PDS5B, UBE2C, ZWILCH	7.04E-05	0.074
GO:0007059	Chromosome Segregation	CENPE, NUSAP1, PDS5B, TOP2A	7.27E-05	0.0765

[0447] The set of probe sets reported here is rich in novel information for prostate cancer prognosis, as most of the probe sets fall in non-coding regions suggesting that non-coding RNAs may constitute a set of highly informative markers for prostate cancer.

Example 3: A 22-Biomarker Signature for Prostate Cancer and comparison to clinical and integrated models.

[0448] To further ensure robustness of the features in the signature, we applied a final filtration method that would establish the minimal number of features required to minimize the mean squared error (MSE) of the model. To do this we used the rfcv function from the randomForest package, using 10-fold cross validation and a step value of 0.9. This method will order the features in accordance to their variable importance and iteratively remove 10% of lowest ranking features and measure the MSE at each step. We selected the number of features that were at the knee of the curve, shown in FIG. 5. At all features to the left of this knee have a highly variable MSE, which becomes more stable to the right of the knee of the curve. The knee of the curve occurs at approximately 22 features. FIG. 6 calculated the variable importance by ranking the features according to their mean decrease in accuracy (MDA) and mean decrease in gini (MDG). Some features have low MDA and MDG, which may warrant their removal from the marker set, however FIG. 5 shows that the inclusion of even some of the less differentiating features still contributed to a lower MSE. . An overview of the feature selection and microarray methods is shown in FIG. 7.

Classifier Development

[0449] We developed three classifiers using the aforementioned 22 features, clinicopathologic variables, and a combination of both. We referred to the classifiers as the genomic classifier (GC), clinical classifier (CC) and integrated genomic clinical classifier (GCC); they are described in detail below. The primary endpoint for classifier development was the METS event. Although it is typical to report probabilities of progression at 2, 5, 7 or 10 years after METS, the design of the discovery study prevents us from reporting probabilities that are meaningful outside of study. For this reason, the scores for all of the aforementioned models prognosticate whether a given individual will experience metastatic

disease progression, as this endpoint is not subject to modeling disease prevalence or time to an event but rather the presence or absence of features that indicate disease aggression.

Genomic classifier (GC)

[0450] A total of 22 features were used for model building. As a further method of standardization, the expression values for the 22 features were percentile ranked for each patient. We used a random forest from the randomForest package available in R for model building and used the tune function, from the e1071 package, to identify the optimal model parameters; the optimal parameters were established to be: nodesize = 80, ntree = 700, mtry = 15. The tuning parameters were selected to optimize classification accuracy in the training set. The model built from the training data is frozen and stored for future application to novel data. The model for classification built from the 22-biomarker feature set is henceforth referred to as the genomic classifier (GC) when applied to novel data. Notable, the final feature set (Table 4) is such that most of the 22 features in GC were ncRNA and only three were from protein-encoding mRNA (Table 4).

[0451] The GC outputs a score between [0,1], where 1 indicates higher metastatic potential. The score is derived as an output of the random forest, and rather than representing a probability it represents the total percentage of the trees in the forest that classified a new case as METS. Alternatively, it may also be said that each decision tree within the random forest decides whether the expression levels of the 22 features in a given tumor sample is more representative of MET disease or not. We used a 0.5 cutoff to classify patients as having METS or not because it is objective and used the simple Majority rule logic.

Clinical Classifier (CC)

[0452] A clinical classifier (CC) for predicting the METS end point was developed using the following clinicopathologic variables: Lymph node invasion status (LNI); Surgical Margin Status (SMS); Seminal Vesicle Invasion (SVI); Extra Capsular Extension (ECE); Pathological Gleason Score; and the pre-operative PSA. The first four clinical variables (LNI, SMS, SVI and ECE) are used as binary variables, indicating present or not; the pre-operative PSA values are taken to log10. The clinical variables were assembled in a logistic regression and the trained model was used to predict METS in the testing set and validation study. CC produces a probability between 0 and 1, where 0 indicates low metastatic potential and 1 indicates a high metastatic potential.

Table 4. 22-Biomarker Set. Chromosomal coordinates correspond to the hg19 version of the human genome.

Gene	Cyt. Band	# Markers	Annotation of Markers	Biology	Differential Expression mets vs Non-mets
CAMK2N1	1p36.12	1	CODING AS	Cell Cycle Progression / Control Of Signaling Pathway	Upregulated
IQGAP3	1q23.1	1	3' UTR	Cell Proliferation / Control Of Signaling Pathway	Upregulated
PBX1	1q23.3	1	CODING	Proto-Oncogene / Transcription Factor / Immune Response	Downregulated
ANO7	2q37.3	2	3' UTR/ncTRANSCRIPT**	Cell Adhesion	Downregulated
PCDH7	4p15.1	1	INTRONIC	Cell Adhesion	Downregulated
PCAT-32	5p15.2	1	ncTRANSCRIPT	ncRNA DIFFERENTIALLY EXPRESSED IN PROSTATE CANCER	Downregulated
TSBP	6p21.32	1	INTRONIC	Testis-Specific Basic Protein / Immune Response	Downregulated
THBS2	6q27	1	3' UTR	Cell-Cell, Cell-Matrix Interaction / Modulator Of Angiogenesis	Upregulated
EPPK1	8q24.3	1	3' UTR	Cytoskeleton Maintanance In Epithelial Cells	Upregulated
NFIB	9p23	1	INTRONIC	Cell Proliferation / Transcription Factor	Downregulated
RABGAP1	9q33.2	1	CODING AS	Cell Cycle Progression / Microtubule Nucleation	Upregulated
GLYATL1P4	11q12.1	1	ncTRANSCRIPT	Pseudogene	Downregulated
MYBPC1	12q23.2	2	CODING/INTRONIC	Epithelial Cell Protein	Downregulated
TNFRSF19	13q12.12	1	INTRONIC	Type I Cell Surface Receptor / Control Of Signaling Pathway	Downregulated
NUSAP1	15q15.1	1	3' UTR	Cell Cycle Progression / Microtubule	Upregulated

				Stabilization	
ZWILCH	15q22.31	1	3' UTR	Cell Cycle Progression / Chromosome Segregation	Upregulated
LASP1	17q12	1	CODING	Cell Proliferation / Cytoskeletal-Associated Protein	Upregulated
S1PR4	19p13.3	1	3' UTR	Cell Differentiation	Upregulated
UBE2C	20q13.12	2	3'UTR/CODING AS	Cell Cycle Progression	Upregulated

[0453] The motivation for developing the CC was to compare the GC and GCC (described below) against a prognostic model that was developed for a similar endpoint. As the majority of post-operative nomograms prognosticate BCR in an “all-comers” population, we felt it was necessary to compare GC and GCC against a nomogram based on a high-risk population with the METS endpoint. The CC served as an intermediate benchmark between the GC and GCC and made it possible to quantify the difference additional genomic information provided in risk prediction.

Genomic Clinical Classifier (GCC)

[0454] The GC scores were assembled along with clinicopathologic variables used for CC using a logistic linear regression model fitted to the training data. The combined GC and CC model is referred to as Genomic Clinical Classifier (GCC).

Comparison to Nakagawa 17-gene signature

[0455] This discovery cohort was previously profiled using the Illumina DASL expression microarray (Cancer Panel v1) containing 502 oncogenes, tumor suppressors genes and genes in their associate pathways. Nakagawa (2008) describes the development of a 17 gene signature to predict METS (referred to as systemic progression in that text). We translated the 17 gene signature from the DASL platform to the HuEx platform and re-modeled those genes in the training set using logistic regression. We compare the performance of the 17-gene signature against GC, CC and GCC.

[0456] We found that in both training and testing, GC, CC and GCC outperformed the 17-gene signature (and also the GPSM nomogram); the AUC results are summarized in Table 5.

Table 5. Comparison of Discrimination ability of classifiers in different datasets

Model	Training	Testing	Validation*
GC	0.90	0.76	0.79
GCC	0.90	0.75	0.82
CC	0.76	0.70	0.70
GPSM	0.71	0.62	0.59
DASL17	0.73	0.60	0.64

*Survival ROC analysis was used for case-cohort validation study

Statistical Analysis

[0457] The CC, GC and GCC prediction models were evaluated in the independent validation cohort and compared to the GPSM scores for predicting the primary endpoint of mets. Researchers at GenomeDx were blinded to the outcomes and the initial analysis was conducted by Mayo Clinic statisticians (RC and EJB). C discrimination index (c-index), an extension of the area under the ROC curve for the case of censored survival data was used to initially compare the performance of each model to predict mets. The 95% confidence intervals for the c-index were approximated through bootstrapping.

[0458] Following de-blinding, several additional analyses were performed. Calibration plots, survival ROC, and decision curves were used to assess overall discrimination. Decision curve analysis was used to compare the net benefit (e.g., the gain in sensitivity weighted by a loss in specificity) over a range of 'decision-to-treat' threshold probabilities using the clinical-only vs. genomic models. Survival ROC and decision curves were evaluated for prediction of mets within 5 years after RP. Graphical diagnostic, ROC-based, and Censored data methods were used to determine a tentative cut-off for GC on the discovery set.

[0459] Cox proportional hazards regression analysis was used to test for associations between models and the mets endpoint. Proportional hazards assumptions of the Cox model were confirmed by evaluating the scaled Schoenfeld residuals. Due to the case-cohort design of the validation study, survival analysis utilized the Lin-Ying method, weighting the controls to reflect mets incidence in the cohort at large. Cumulative incidence curves were constructed using competing risks analysis to accommodate censoring due to death, and other events, which bias Kaplan-Meier estimates of incidence. CC, GC and GCC models were subdivided into tertiles as an objective demarcation of low, intermediate and high risk groups. The GPSM score risk groups were defined previously.

[0460] Analyses were performed using R v 2.14.1 (www.R-project.org). All tests were two-sided and a Type I error probability of 5%. The study was approved by the Mayo Clinic Institutional Review Board.

Biomarker Evaluation

Independent validation of prognostic classifiers

[0461] In a blinded-independent validation study, 5-year survival ROC curves for metastasis-free end point showed a c-index of 0.70 and 0.59 for CC and GPSM, respectively (FIG. 8). GC outperformed these clinicopathologic prediction models with a c-index of 0.79, which increased to 0.82 in the integrated GCC model. In addition, the 95% confidence intervals (CIs) of the genomic models overlapped extensively, indicating comparable predictive performances (FIG. 8).

[0462] Moreover, discrimination box-plots and calibration curves show the improved performance for classifiers that used the genomic variables over clinicopathologic models (CC and GPSM) (FIG.s 9-11).

[0463] A decision curve comparing the models is shown in FIG. 12. At 'decision-to-treat' threshold probabilities (e.g., probability of metastatic disease at 5 years after RP), ranging from 5-25%, the net benefit of the genomic-based models exceeded that of both clinical-only models. Collectively, these data imply that the genomic panel significantly improves predictive ability.

[0464] Cumulative incidence plots compared the incidence of mets events in the risk groups for each model (FIG. 3). Difference in cumulative incidence between risk groups defined by GC tentative cut-off was highly significant for GC ($p < 0.001$), with the group below the 0.5 potential cut-off having an incidence of $< 2.5\%$ at 5-years post RP, and the group equal or above the cut-off had 5-year post RP cumulative incidence of $\sim 18\%$. However, after using a prior cut-off for GPSM, the risk groups were not significantly different ($p = 0.35$). We also compared cumulative incidence plots of mets events between tertiles for each model (FIG. 13, 14, 15). In order to assess the performance of the models in a different categorization of risk groups, we used the D'Amico definition of low, intermediate and high risk patients (FIG.s 16, 17). Based on this, $\sim 60\%$ of our high-risk cohort falls under the definitions of low and intermediate risk patients as defined by D'Amico as low or intermediate.

[0465] Difference in cumulative incidence between tertiles was highly significant for GCC ($p < 0.001$), with the 1st tertile group having an incidence of $< 1\%$ at 5-years post RP and only

three cases of mets (which all occurred > 5 years post RP). The 2nd tertile had 5-year post RP cumulative incidence of 5% (less than the 7.5% rate in the full cohort) and the 3rd tertile GCC group had 44 mets events, with 5-year incidence of ~15%. In addition, the majority of patients in the 3rd GCC tertile experienced mets within 3 years of RP. The cumulative incidence differences between tertiles were also significant for both GC and CC models (FIG. 13). The GPSM, and GC groups defined by their pre-determined cut-offs, and GPSM and GCC groups defined by tertiles were also compared when patients who received adjuvant androgen deprivation therapy were excluded from the analysis, and GC and GCC groups were significantly different (FIG.s 14-15).

[0466] Table 6 shows the comparison of GPSM and GC categorization of subjects to risk groups. The study consists of mainly high-risk patients; as such there are no GPSM low risk patients. Here we show that GC can adequately identify those patients that are truly high-risk from those that are not, we confirm this using a McNemar's test. Considering this is a high-risk cohort of adverse pathology, most patients were GPSM high-risk (n=196) with a smaller number of GPSM intermediate-risk (n=23). GPSM and GC gave consistent results in 88 (40%) of subjects, but GC reclassified 124 out of 196 (63%) GPSM high-risk (GPSM >10) patients into lower risk groups. With additional genomic information, the GC systematically downgraded GPSM high-risk subjects to lower risk categories ($p < 0.0001$ McNemar's test). Given, the low cumulative incidences of metastatic disease (FIG. 18), even patients with 'high-risk' adverse pathology or GPSM scores who have low GC scores, have a very low probability of mets.

[0467] Univariable analysis is detailed in Table 7 and shows that in this high-risk cohort, the majority of the clinicopathologic variables, with the exception of margin status and pre-operative PSA, were significant prognostic factors. GC has a high precision in estimating increasing risk of 56% of developing mets for every 0.1 unit increment in GC score (HR=1.56, CI: 1.35-1.80, $p < 0.001$). However, with multivariable Cox regression modeling of the individual clinical and genomic components of the GCC model, while GC remained a significant variable with an HR of 1.48 (CI: 1.27-1.73, $p < 0.001$) for every 0.1 unit increment in GC score, no clinical variables remained significant for predicting mets (Tables 8-9). In Table 8, GC is adjusted for clinicopathologic components of GCC (seminal vesicle invasion, pathological Gleason sum, pre-operative PSA, extra-capsular extension, lymph node involvement and positive margin as well as administration of adjuvant hormones. The Lin-

Ying method was used to account for the case-cohort design when determining the hazard ratios. The GC hazard ratio is for a 0.1 unit change in the GC risk score.

[0468] GC was also adjusted for CC and GPSM in separate multivariable regression analyses and yet remained the only significant risk factor (Table 10).

Table 6. Reclassification of GPSM categories by GC.

# patients (% mets by 5 years)	GC<0.5	GC>=0.5	GPSM Totals
GPSM Intermediate	16(4%)	7(4%)	23(8%)
GPSM High	124(29%)	72(63%)	196(92%)
GC Totals	140(33%)	79(67%)	

Table 7. Univariable Analysis for panel of prognostic classifiers and clinicopathologic variables (for mets)

	Hazard ratio (95% CI)	p-value
GC	1.56 (1.35-1.80)	< 0.001
GCC	1.40 (1.24-1.58)	< 0.001
CC	1.31 (1.15-1.49)	< 0.001
Pathologic Gleason Sum	2.45 (1.38-4.36)	= 0.002
GPSM	1.32 (1.12-1.56)	< 0.001
Extra Capsular Extension	2.68 (1.49-4.83)	= 0.001
Seminal Vesicle Invasion	2.18 (1.22-3.87)	= 0.007
Lymph Node Invasion	2.18 (1.04-4.56)	0.04
Pre-operative PSA	1.21 (0.94-1.57)	0.15
Positive Margins	0.96 (0.54-1.69)	0.88

Table 8. Multivariable Cox regression analysis.

	Hazard ratio (95% CI)	p-value
GC	1.48 (1.27-1.75)	<0.001
Seminal Vesicle Invasion	1.83 (0.83-4.09)	0.14
Gleason Sum	1.47 (0.70-3.08)	0.30
Extra Capsular Extension	1.37 (0.63-3.01)	0.43
Pre-operative PSA	1.13 (0.79-1.63)	0.51
Positive Margins	1.10 (0.53-2.25)	0.80
Lymph Node Invasion	0.94 (0.28-3.15)	0.92

*adjusted for adjuvant hormone therapy

Table 9. Multivariable Analysis for panel of prognostic classifiers and clinicopathologic variables Adjusted for Hormone Therapy (for mets)

	Hazard ratio (95% CI)	p-value
GC	1.49 (1.27-1.75)	<0.001
Seminal Vesicle Invasion	1.75 (0.80-3.85)	0.16
Gleason Sum	1.43 (0.70-2.90)	0.33
Extra Capsular Extension	1.32 (0.61-2.86)	0.49
Pre-operative PSA	1.15 (0.81-1.62)	0.44
Positive Margins	1.09 (0.53-2.25)	0.81
Lymph Node Invasion	0.85 (0.30-2.45)	0.77
Hormone Therapy*	0.92 (0.44-1.93)	0.84

*Adjusted for salvage or adjuvant hormone therapy

Table 10. Multivariable Analysis of GC compared to GPSM and CC (for mets)

MVA with GC and GPSM		
	Hazard ratio (95% CI)	p-value
GC	1.51 (1.31-1.75)	<0.001
GPSM	1.16 (0.96-1.39)	0.17
MVA with GC and CC		
	Hazard ratio (95% CI)	p-value
GC	1.51 (1.29-1.75)	<0.001
GPSM	1.12 (0.96-1.30)	0.16

Discussion

[0469] This study describes the development and independent validation of a novel prognostic biomarker signature, a genomic classifier (GC) identified by analyzing 764 high-risk radical prostatectomy patients (545 in discovery set and 219 in an independent validation set) with long-term follow-up. The GC was designed to predict rapid metastatic disease progression, an endpoint based on radiographic imaging that is clinically much more relevant for aggressive prostate cancer than most previous biomarker reports using the BCR endpoint. All tumor specimens were profiled using high-density microarray analysis of RNA from archived patient FFPE specimens. The transcriptome-wide approach allowed interrogation of a much richer genomic dataset, including many thousands of ncRNAs, compared to previous efforts which were primarily protein-coding 'gene-centric'. The GC model was validated in an independent blinded study of a contemporary cohort (2000-2006) of prostatectomy patients with adverse pathology, reflecting the population where clinical variables and nomogram models fail to decipher the small percentage of men who will develop lethal prostate cancer.

[0470] In the high-risk validation cohort of 1,010 men treated at the Mayo Clinic, only 7.5% developed metastatic disease. Even after accounting for use of adjuvant therapy, risk stratification based on pathology alone failed to accurately predict metastatic disease and supporting the notion that even high risk prostate cancer is a molecularly heterogeneous disease. The improved calibration of genomic models over clinical-only models may be due to incorporation of true molecular drivers of aggressive disease in the GC models, so that even in a clinicopathologic homogeneous 'high-risk' patient population, GC can better segregate 'true high-risk' patients from the majority who will not progress. Decision curve analysis also showed that the prognostic classifiers using genomic information had a broader range of clinical benefit, based on "decision-to-treat" thresholds, compared to clinical-only models. Again, the limited range of benefit shown by the CC and GPSM models may be a further reflection of their limited discriminative ability in high risk men. Lastly, even after adjusting for adjuvant therapy multivariable analysis showed GC remained the only significant predictor, suggesting that the genomic signature captures most of the prognostic information as it relates to metastatic disease development in the high-risk cohort.

[0471] To our knowledge, this is the first study to extensively validate a biomarker signature based primarily on ncRNA. This may be an important reason why the GC model (only 3 features selected from protein-encoding mRNA; see Table 4) showed significantly improved performance over previous gene-based models. Supporting this notion, we recently reported our reanalysis of the MSKCC Prostate Oncogenome Project expression data and demonstrated that ncRNA expression was more prognostic than protein-coding genes and in multivariable analysis provided predictive information independent of the Kattan nomogram. The importance of ncRNA in aggressive prostate cancer is further highlighted by several recent studies that have demonstrated their involvement in tumor cell invasion and metastasis.

[0472] The vast majority of patients with aggressive disease have adverse pathology. However, the fact remains that most patients with adverse pathology will not die from prostate cancer. The question remains for most urologists and their patients, of when, and how, to intervene for patients with adverse pathology. Up to 20% of RP patients with adverse pathology in contemporary practice will inevitably require additional intervention with radiation, hormones or chemotherapy as durable cancer control will not be achieved using radical surgery alone. Three large, randomized clinical trials (SWOG 8794, EORTC 22911 and ARO 96-02) have shown improved biochemical recurrence-free and/or metastasis-free

survival for men with adverse pathology when treated with immediate adjuvant radiation therapy versus initial observation. Initial reports from the RTOG 96-01 trial, which randomized early salvage radiation patients to anti-androgen therapy or observation, indicated that intensification with multimodal therapy post RP reduces the incidence of metastatic disease. Despite this evidence, urologists have not widely adopted adjuvant intervention after RP and favor instead treatment upon PSA relapse or biochemical recurrence (BCR).

[0473] This practice, however, may lead to under-treatment of some patients in the adjuvant setting, where radiation has a proven benefit and over-treatment of many patients in the salvage setting, since BCR is a poor surrogate for metastatic disease.

[0474] As management strategies evolve, a 'reverse stage-shift' has occurred in the last decade, whereby more low-risk patients opt for active surveillance and more high-risk patients undergo RP. As a result, urologists are seeing a higher proportion of patients with adverse pathology after RP. In a contemporary cohort of men with adverse pathology we show that adding genomic variables to established clinical risk factors significantly improves prediction models for metastatic disease. Furthermore, we found that most of the prognostic information for predicting metastatic disease is captured by the genomic variables, which are measured in the primary tumor. This data supports the notion that genomic alterations in lethal prostate cancer manifest early on, many years before metastatic disease can be radiographically imaged. Improved identification of patients most at risk for developing disease may better serve those most in need for adjuvant therapy. It is in these patients that we are further testing the performance of this classifier, its usefulness in guiding risk stratification and decision-making after RP in additional validation studies. More accurate prediction of lethal prostate cancer within this high risk population of surgical prostate cancer patients may lead ultimately to improved outcomes.

Gleason 7 Sub Cohort Analysis

[0475] Patients with pathological Gleason stage 7 represent a difficult to classify intermediate category in prostate-cancer clinical decision making. It has been suggested that patients with a primary Gleason 4 and secondary Gleason 3 (4+3) have a worse outcome than 3+4 patients. We demonstrated that GCC was better able to segregate Gleason 7 patients with improved outcome compared to the current 4+3 vs. 3+4 method. First, we compared the capacity of the CC (also referred to as the Clinical Model, or CM) and GCC to segregate Gleason 7 patients (FIG. 19), the discrimination plots in this analysis showed that CC does

not segregate these patients at all. Departing from CC model, we compared the survival outcome for the Gleason 7 patients based on the aforementioned clinical practice and GCC. FIG. 20 clearly shows the superiority of the GCC in segregating these patients with a mets endpoint (also referred to as Clinical Recurrence, or CR). Importantly, the GCC is also able to segregate patients when the endpoint was changed to PCSM; the conventional 4+3 vs. 3+4 methods has a limited capacity to separate patients as shown in FIG. 21. We further separate samples into their respective 4+3 and 3+4 categories and assessed the performance of the GCC within these groups and found that for both mets and PCSM end points the GCC was capable of significantly segregating patients into high ($GCC \geq 0.5$) and low risk ($GCC < 0.5$) groups (FIG.s 22-23).

Application to Adjuvant Hormones Lymph Node Positive Patients

[0476] We assessed the capacity of GCC to segregate a set of Lymph Node positive (N+) patients uniformly treated with adjuvant hormone therapy. We compared its performance against CC and used both the mets and PCSM endpoint (FIG.s 24-25). Since GCC and CC contain LNI status as a variable in model training and prediction, the LNI status might augment the results when the analysis is focused solely on N+ patients. Overall however either model is intended to be applied to broad range of patients with varying pathological characteristics and so it is practical to consider CC and GCC with LNI status even when focusing on the N+ group. Furthermore, N+ patients are uniformly treated in clinical settings with Adjuvant Hormones (ADTHx+) as standard of care; the ability of the GCC to further segregate the N+ patients into good and poor outcomes even after ADT might indicate an important clinical utility that could warrant the treatment of high risk ($GCC > 0.5$) patients with additional therapies. Currently, there are no existing clinical instruments that further differentiate N+ patients.

Example 4: Method of Diagnosing a Leukemia in a Subject

[0477] A subject arrives at a doctor's office and complains of symptoms including bone and joint pain, easy bruising, and fatigue. The doctor examines the subject and also notices that the subject's lymph nodes are also swollen. Bone marrow and blood samples are obtained from the subject. Microarray analysis of the samples obtained from the subject reveal aberrant expression of one or more transcripts selected from Tables 2, 4, 11 or 55 and the subject is diagnosed with acute lymphoblastic leukemia.

Example 5: Method of Determining a Treatment for Breast Cancer in a Subject

[0478] A subject is diagnosed with breast cancer. A tissue sample is obtained from the subject. Nucleic acids are isolated from the tissue sample and a probe set comprising at least ten probes capable of detecting the expression of at least one non-coding RNA transcript and at least one protein-coding transcript. Analysis of the expression level of one or more transcripts selected from Tables 2, 4, 11 or 55 reveals the subject has a tamoxifen-resistant breast cancer and gefitinib is recommended as an alternative therapy.

Example 6: Method of Determining the Prognosis a Pancreatic Cancer in a Subject

[0479] A subject is diagnosed with pancreatic cancer. A tissue sample is obtained from the subject. The tissue sample is assayed for the expression level of biomarkers comprising one or more transcripts selected from Tables 2, 4, 11 or 55. Based on the expression level of the one or more transcripts selected from Tables 2, 4, 11 or 55, it is determined that the pancreatic cancer has a high risk of recurrence.

Example 7: A 22-marker genomic classifier (GC) outperformed previously reported genomic signatures and individual gene biomarkers

[0480] As described in Example 3, a final set of 22 markers was selected for building a random forest classifier. The high-density array used in this study permits measurement of the expression patterns of RNAs associated with multiple biological processes in prostate cancer progression. Also, this transcriptome-wide approach allowed interrogation of a much richer genomic dataset, including thousands of ncRNA. Furthermore, the genomic markers measure the biological potential of the tumor to metastasize. The biological processes represented in the 22 markers include cell cycle progression, cell adhesion, tumor cell motility, migration and immune system modulation. Multidimensional scaling analysis depicts clustering of cases and controls based on the expression of these 22 markers (**FIG. 26**). Controls correspond to pooled NED and PSA patients since, at a fold-change threshold of 1.5 (after correcting for false-discovery), only 2 (out of ~1.4 million) features were found to be differentially expressed between these two groups, compared to 1187 and 887 in metastasis outcomes compared to NED and PSA groups. A random forest machine-learning algorithm was used to generate GC scores on the training and testing set after assembling the 22 markers with forest parameters to optimize for highest accuracy in the training set. The performance of GC was compared to that of previously published gene signatures: Agell et al 2012, Bibikova et al 2007, Bismar et al 2006, Cuzick et al 2011, Glinsky et al 2005, LaPointe et al 2004, Larkin et al 2012, Nakagawa et al 2008, Olmos et al 2012, Penney et al 2011,

Ramaswamy et al 2003, Ross et al 2012, Talantov et al 2010, Varambally et al 2005 and Yu et al 2007 and individual genomic markers associated with prostate cancer progression including CHGA, DAB2IP, GOLPH2, PAP, ETV1 and ERG, KI-67, PSA, PSCA, PSMA, AMACR, GSTP1, PCA3, B7-H3, TOP2A and CAV1. Each genomic marker and gene in the signatures were mapped to its associated Affymetrix *core* transcript cluster (<http://www.affymetrix.com/analysis/index.affx>) where available, otherwise the *extended* transcript cluster was used. Based on the fRMA summarized expression values for the individual genes, the signatures were modeled in the training set using a random forest and tuned with the *tune.randomForest* function from the e1071 R package. Tuning involved performing a 20 by 20 grid search to find the optimal “mtry” and “nodesize” model parameters evaluated via 5-fold cross validation in order to maximize accuracy.

[0481] The performance of the classifiers and the individual genes was subsequently assessed in both training and testing sets (**FIG. 27** and **FIG. 28**). As expected, we observed high AUCs in training for nearly all the external signatures, similar to what was observed with GC. When applied to testing, the AUC for each model decreased. Among the 17 external signatures that were modeled, 12 were statistically significant predictors of metastasis (e.g., their 95% confidence intervals did not drop below a threshold random chance AUC of 0.5) (**FIG. 27**). The AUC of GC was 0.08 points higher than the top performing external signature, the 16-gene signature reported by Bibikova et al, which had an AUC of 0.68 (95% CI : 0.60 – 0.76,). In contrast to the expression signature models, the performance of the 16 single genes tested were expected to be similar in the training and testing sets. These genomic markers showed an overall agreement in performance, with differences in significance possibly explained by the smaller sample size of the testing set compared to the training set (**FIG. 28**). Of the 16 genomic markers, only B7-H3 (CD276), GSTP1 and PCA3 were statistically significant in both the training and testing sets (**FIG. 28**). Again, none of the individual genomic markers outperformed GC or the top performing clinical predictor, GS (AUCs $\leq$ 0.64).

Example 8: A 22-marker genomic classifier (GC) outperformed individual clinicopathologic variables and was prognostic within different Gleason Scores groups

[0482] Clinical variables were calculated, categorized or transformed as follows. Pathological Gleason Score (GS, or pathGS) was dichotomized into groups with the threshold of ≥ 8 ; although convention is to segregate GS into three groups (≤ 6 , 7, ≥ 8) the relative lack of patients with $GS \leq 6$ prompted the dichotomization of GS. The pre-operative PSA (pPSA),

measured immediately prior to RP, was log₂-transformed. The following variables were binary: Extra-capsular Extension (ECE); Seminal Vesicle Invasion (SVI); Surgical Margins (SM+, or SMS) and Lymph Node Involvement (N+, or LNI). Hormone and radiation therapy were included as separate binary covariates if administered in an adjuvant (<90 days post RP) or salvage (following PSA rise) setting. Treatments administered subsequent to clinical metastasis were not included.

[0483] In the training set (see Example 1), ROC area-under the curve (AUC) values for GC, CC and GCC were 0.90, 0.76 and 0.91 respectively, outperforming all individual clinical variables: GS, N+, ECE, SVI, SM+, N+, pPSA and Tumor Volume (**FIG. 29**). In the testing set, GC and GCC had the highest AUC of 0.75, and 0.74, respectively for predicting cases. The clinical-only CC had an AUC of 0.69, which was only marginally better than pathological Gleason score alone (0.65). The shape of the ROC curves for GC and GCC showed that these models had the highest specificity and sensitivity compared to clinical models above a threshold of ~50% specificity (**FIG. 30**).

[0484] A blinded study independently validated GC for prediction of clinical metastasis (metastasis) following radical prostatectomy. The results showed that the GC model had improved performance over any individual clinicopathologic variable or multivariable prediction model. In this independent validation set, the AUC of 5-year survival ROC curves demonstrated that GC had higher discriminatory ability than individual clinicopathologic variables (**FIG. 31**). The GC model had an AUC of 0.79 for predicting clinical metastasis at 5 years post RP with median follow up of 6.7 years. Furthermore, 5-year survival decision curve analysis on the independent validation set showed that GC had a higher net benefit over a wider range of ‘decision-to-treat’ probabilities than clinicopathologic factors (**FIG. 32**).

[0485] In order to test for the effect size of individual variables as well as dependencies among these variables, we performed univariable and multivariable analyses using logistic regression on the testing set (Table 12). In univariable analysis, we found GC, CC, GCC, GS, SVI and ECE to be statistically significant predictors of cases ($p < 0.05$). The odds ratio for GC was 1.42 for every 10% increase in GC score. When dichotomized into low and high GC risk groups, as described above, the odds ratio was 6.79 (95% CI: 3.46 – 13.29), more than twice the odds ratio of Gleason score (OR: 3.02 (95% CI: 1.61 – 5.68)) for predicting cases. In multivariable analysis, after adjustment for post RP treatment, GC remained the only significant prognostic variable ($p < 0.001$) with an OR of 1.36 for every 10% increase in GC score. The independent significance of GC suggested that a more direct measure of tumor

biology (e.g., 22-marker expression signature) added significant prognostic information for prediction of early metastasis after rising PSA, which was not captured by the clinical variables available from pathological analysis.

[0486] In univariable analysis (UVA) on the independent validation set, GC had the highest significant hazard ratio (HR) among classifiers (Table 7). In multivariable analysis (MVA) on the independent validation set, only GC retained a significant HR when adjusted for clinical variables and postoperative adjuvant therapy (Table 8; $P < 0.001$). Gleason score was alternatively parameterized (e.g., 3+4, 4+3, 8, 9-10) but this did not change the significance of GC (Table 13). Three additional MVA models were performed to model GC with CC, GPSM and the Stephenson nomogram. Only the Stephenson nomogram retained a significant HR ($p < 0.04$) with GC as the dominant variable in the model (Table 10, Table 14).

Table 12.

	Univariable		Multivariable	
	Odds Ratio (95% CI)	P	Odds Ratio (95% CI)	P
GC	1.42 (1.28 – 1.60)	$p < 0.001$	1.36 (1.16 – 1.60)	$p < 0.001$
GCC	1.36 (1.21 – 1.53)	$p < 0.001$	n.a	n.a
CC	1.35 (1.15 – 1.59)	$p < 0.001$	n.a	n.a
pPSA	0.99 (0.77 – 1.26)	0.92	0.75 (0.52 – 1.07)	0.11
Pathologic GS ≥ 8	3.02 (1.61 – 5.68)	$p < 0.001$	1.91 (0.85 – 4.33)	0.12
SVI	2.44 (1.30 – 4.58)	0.01	1.93 (0.79 – 4.73)	0.15
Tumor Volume	1.02 (0.97 – 1.06)	0.44	0.97 (0.92 – 1.04)	0.42
N+	1.69 (0.74 – 3.88)	0.21	1.42 (0.41 – 4.96)	0.58
SM+	1.05 (0.57 – 1.93)	0.87	0.93 (0.40 – 2.17)	0.87
ECE	2.01 (1.18 – 3.73)	0.03	1.00 (0.45 – 2.20)	0.99
* MVA adjusted for adjuvant and salvage treatment interventions				

Table 13.

	Hazard Ratio (95% CI)	P
GC ¹	1.47 (1.26-1.73)	< 0.001
Pathological Gleason Score*		
6+7(3+4)	ref	
7(4+3)	3.30 (1.21-9.04)	0.02
8	3.99 (1.48-10.77)	0.01
9-10	2.21 (0.78-6.25)	0.14
Pre-operative Prostate-specific Antigen ²	1.23 (0.81-1.85)	0.34
Seminal Vesicle Invasion	2.05 (0.85-4.98)	0.11

Positive Surgical Margin	1.21 (0.55-2.67)	0.64
Extra-capsular Extension	1.29 (0.55-3.01)	0.56
Lymph Node Involvement	0.75 (0.21-2.70)	0.66
Adjuvant Radiation	0.87 (0.23-3.32)	0.83
Adjuvant Hormone	0.88 (0.35-2.24)	0.79
*Reference Gleason score combined 6 and 3+4 as model did not converge with using Gleason 6 only as reference		
¹ Hazard ratio reported for 10% increase of GC score.		
² Hazard ratio reported for 1.0 unit increments of log-transformed level.		
Abbreviations – CI: confidence interval; GC: genomic classifier.		

Table 14.

		Hazard Ratio (95% CI)	P
Model	GC ¹	1.49 (1.27-1.73)	< 0.001
	Stephenson ¹	1.15 (1.01-1.31)	0.04
¹ Hazard ratio reported for 10% increase of GC score. Abbreviations – CI: confidence interval; GC: genomic classifier			

[0487] To investigate the magnitude of the hazards ratio for incremental increases in GC score we evaluated the effect size of each 10% increase in GC score for predicting clinical metastasis after adjusting for postoperative treatment (Table 15). We observed a general trend of increasing HR, and decreasing probability of metastasis-free survival with increasing deciles. However, this was not statistically significant because of the small number of patients, in the higher GC deciles. GC score deciles were then incrementally collapsed to create three GC risk groups (GC scores <0.4, 0.4-0.6, ≥0.6) and these showed significant differences in HR (and survival) in comparison to the reference group as well as to the prior level (Table 16).

Table 15.

		ref= first GC decile		ref= prior GC decile		Clinical Metastasis-free Probability		
GC Deciles	% of Patients	HR (95% CI)	P	HR (95% CI)	P	3- year	5- year	8- year
0.00000- 0.1	10	NA	NA			100%	98%	98%
0.10001- 0.2	17%	0.60 (0.04- 10.20)	0.72	0.60 (0.04- 10.20)	0.72	100%	100%	99%

0.20001-0.3	19%	5.56 (0.66-47.14)	0.12	9.28 (1.13-76.08)	0.04	100%	97%	92%
0.30001-0.4	13%	5.86 (0.64-53.68)	0.12	1.05 (0.33-3.32)	0.93	96%	95%	92%
0.40001-0.5	12%	6.06 (0.68-53.89)	0.11	1.04 (0.29-3.74)	0.96	96%	95%	90%
0.50001-0.6	9%	11.12 (1.25-99.33)	0.03	1.83 (0.52-6.49)	0.35	96%	92%	80%
0.60001-0.7	12%	17.35 (2.06-146.25)	0.009	1.56 (0.52-4.71)	0.43	89%	86%	77%
0.70001-0.8	4%	16.68 (1.62-171.63)	0.02	0.96 (0.24-3.84)	0.96	87%	78%	NA*
0.80001-0.9	2%	95.51 (8.82-1034.17)	< 0.001	5.73 (0.97-33.63)	0.05	65%	NA*	NA*
0.90001-1.0	1%	106.63 (11.20-1014.70)	< 0.001	1.12 (0.21-5.83)	0.9	80%	NA*	NA*
* Model adjusted for adjuvant treatment								
** No patients left due to censoring or experiencing clinical metastasis events								

Table 16.

		reference = GC<0.4		reference= prior GC group		Clinical Metastasis-free Probability		
GC risk categories	% of Patients	Hazard Ratio (95% CI)	P	Hazard Ratio (95% CI)	P	3- year	5- year	8- year
< 0.4	60%	NA	NA			99%	98%	95%
0.4-0.6	21%	2.39 (1.10-5.17)	0.03	2.39 (1.10-5.17)	0.03	96%	94%	87%
> 0.6	19%	7.30 (3.51-15.14)	< 0.001	3.06 (1.40-6.72)	0.005	86%	78%	73%
Model adjusted for adjuvant treatments								

[0488] The distribution of cases and controls in the testing set by both GC and Gleason score risk groups was illustrated in **FIG. 33** and summarized in Table 17. Among GS ≤ 6 tumors (n=18) none had high GC scores, while among GS 7 tumors (n=97), nearly a third (29%) had high GC scores and half of these were cases that developed early metastasis after rising PSA. While most patients with high Gleason scores (≥ 8) had high GC scores, among the 29 (40%) with low GC scores there were only 7 cases with 3 deaths from prostate cancer. Overall, 116 out of 186 (62%) testing set patients had low GC scores of which only 21 were cases resulting in 7 deaths from prostate cancer. Among the 70 (38%) patients with high GC scores, there were 42 cases and 25 of these men died of prostate cancer. In the independent

validation set, GC distribution in Gleason score groups showed high concordance (**FIG. 34**, Table 18); still GC identified significant number of clinically high risk patients who did not experience adverse outcomes in this set. Among patients with low Gleason score (GS 5 to 6), none had high GC scores (≥ 0.6) or had clinical metastasis on study follow up. As expected, 40% of patients with GS ≥ 8 had high GC scores (≥ 0.6), of whom 62% experienced metastasis and 41% died of their disease. However, more than a third of patients with GS ≥ 8 (36%) had low GC scores (< 0.4), and the majority of these men did not have metastasis (77%) or die of prostate cancer (85%) at follow up. Among patients with GS 7 tumors, 41% had high GC scores (≥ 0.4) and 44% of these men had clinical metastasis but for GS 7 with low GC scores (< 0.4), 86% of them did not metastasize and only 3% died of their disease. This reclassification demonstrated that while GC scores trend higher with higher Gleason score, GC may be used to further identify a considerable number of men with 'high risk' Gleason ≥ 8 tumors that may never develop clinical metastasis and conversely from among 'intermediate risk' Gleason 7 tumors a subset enriched for clinical metastasis events.

Table 17.

Gleason Category	GC ≤ 0.5			GC > 0.5		
	n	n METs (%*)	n PCSM (%)	n	n METs (%)	n PCSM (%)
GS ≤ 6	18	2 (11)	0	0	0	0
GS 7	69	12 (17)	4 (5.7)	28	14 (50)	4 (14)
GS 8	12	4 (33)	1 (8.3)	11	6 (54)	5 (45)
GS ≥ 9	17	3 (17)	2 (12)	31	22 (70)	16 (51)

Table 18.

Path GS Categories	GC Score < 0.4			$0.4 \leq$ GC Score ≤ 0.6			GC Score > 0.6			TOTAL
	Total N (%)	Mets	PCSM	Total N (%)	Mets	PCSM	Total N (%)	Mets	PCSM	
5-6	13 (87)	0	0	2 (13)	0	0	0 (0)	0	0	15
7	66 (59)	9	2	24 (22)	10	1	21 (19)	10	3	111
8	16 (42)	6	2	9 (24)	3	1	13 (34)	7	6	38
9-10	17 (31)	4	3	14 (25)	4	1	24 (44)	16	9	55
TOTAL N	112 (51)	19	7	49 (22)	17	3	58 (27)	33	18	219

[0489] The clinical significance of GC was further evidenced by the statistically significant differences of low and high-risk GC groups for the Prostate Cancer Specific Mortality Endpoint (PCSM) found within different Gleason Score Risk Groups (**FIG. 35A-C** and Table 19). Also, GC was able to significantly ($p < 0.05$) separate those PSA patients that would go on to experience later clinical metastasis (**FIG. 36**). As the KM method not only takes into consideration the number of patients at risk but also censored data (e.g., patients for which there was a loss of follow up at some point in time) to compute the proportions, the number of patients at risk for each time point in FIG. 35-36 are shown in Tables 19-20, respectively. These results suggested that GC can accurately predict metastasis long before it can be detected radiographically, may better guide post-surgical treatment decisions, and may help prevent over-treatment, toxicity, and morbidity.

Table 19.

		Time to PCSM after BCR (years)					
		0	5	10	15	20	
Gleason Score = 7	GC $\leq$ 0.5	217	118	85	24	1	# Patients at risk
	GC $>$ 0.5	54	39	14	2	--	
Gleason Score = 8	GC $\leq$ 0.5	38	22	16	4	--	
	GC $>$ 0.5	30	26	14	4	1	
Gleason Score = 9	GC $\leq$ 0.5	55	37	20	1	--	
	GC $>$ 0.5	88	40	16	4	1	

Table 20.

		Time to PCSM after BCR (years)					
		0	5	10	15	20	
GC $\leq$ 0.5		158	158	118	38	4	# Patients at risk
GC $>$ 0.5		26	26	16	5	--	

Example 9: Combined value of genomic biomarkers and CAPRA-S in predicting prostate cancer death in a high-risk surgical cohort

[0490] Most men with lethal prostate cancer present initially with localized disease, and develop biochemical recurrence (BCR) following local treatment. Biomarkers potentially improve prediction of progression risk after radical prostatectomy (RP). We compared two validated post-RP classifiers: a genomic classifier (GC) and CAPRA-S (based on standard clinicopathologic parameters), to predict cancer-specific mortality (CSM) in a contemporary cohort of RP patients.

Materials and Methods

Patient Population

[0491] Subjects were identified from a population of 1,010 men prospectively enrolled in the Mayo Clinic tumor registry who underwent RP for prostatic adenocarcinoma from 2000-2006 (see Example 1). This population was clinically high-risk for metastasis, as defined by pre-operative prostate-specific antigen (PSA) levels $>20\text{ng/mL}$, pathological Gleason score ≥ 8 , Seminal Vesicle Invasion (SVI), or GPSM (Gleason score; pre-operative PSA; SVI; surgical margin status, SMS) score ≥ 10 . Data was collected using a case-cohort design; of the 1,010 men, 73 (7.2%) patients developed metastatic disease as evidenced by bone and/or CT scans. These 73 men were defined as cases. A 20% random sample of the entire cohort was selected for analysis (202 patients), which included 19 cases. The remaining 54 cases not selected by random sampling were also included for analysis, resulting in a total of 256 patients. After exclusion for tissue unavailability and quality control, the independent validation cohort consisted of 219 patients (69 cases and 150 controls; median follow-up, 6.69 years).

Tissue Processing

[0492] Following histopathological review, total RNA was extracted and amplified from macrodissected FFPE primary prostatic adenocarcinoma specimens, and hybridized to Human Exon 1.0 ST GeneChips (Affymetrix, Santa Clara, CA) that profile coding and non-coding regions of the transcriptome using approximately 1.4 million probe selection regions, hereafter referred to as features.

Classifier Development

[0493] We compared and integrated two validated post-RP classifiers: GC and CAPRA-S. The GC was developed using a nested-case control study and contains the 22 biomarker set as disclosed in Example 3. The primary endpoint of GC was metastatic disease progression, defined as a positive bone or CT scan. Patients with GC scores ≥ 0.4 were considered at high risk of progression to metastases. GC was independently validated in follow-up blinded study, of the patient population presented here. CAPRA-S is a nomogram that is based on standard clinical parameters, developed using the CAPSURE registry and biochemical recurrence (BCR) as the primary endpoint (Cooperberg, M. R., et al, The CAPRA-S score: A straightforward tool for improved prediction of outcomes after radical prostatectomy. Cancer, 117(22), 5039-46.). CAPRA-S scores ≥ 6 were considered at higher risk of BCR. Out of the

219 patients, 212 had sufficient data with which to calculate the CAPRA-S score. Of these, 28 had CSM events.

[0494] GC and CAPRA-S were integrated using a cox-proportional hazard model with prostate cancer specific mortality (CSM) as the primary endpoint. Although GC and CAPRA-S classifiers were developed for different endpoints (metastases and BCR, respectively), high scores in these models could translate to greater risk of CSM. Neither GC nor CAPRA-S were trained or further refined on this patient population and the raw classifier scores were used for an integrated genomic and clinical classifier. This integrated genomic-clinical classifier, characterized by the equation $0.20 * \text{CAPRA-S} + 5.68 * \text{GC}$, was validated using the optimism estimate of the c-index (calculated by bootstrapped validation), and its performance was further evaluated in an independent low risk patient population.

Statistical Analysis

[0495] The area under the receiver operating characteristic (ROC) curve was used to initially compare classifier performance to predict metastasis. Calibration plots, ROC curves and decision curves were used to assess overall discrimination. Survival decision curve analysis was used to compare the net benefit (e.g., gain in sensitivity weighted by loss in specificity) over a range of “decision-to-treat” threshold probabilities using the GC and CAPRA-S classifiers. The decision curve was evaluated for prediction of CSM within 5 years post-RP.

[0496] Cox proportional hazards analysis was used to test for associations between classifiers and adverse pathologic features (APFs) for the CSM endpoint. The proportional hazard analysis used a Barlow weighting scheme to account for the case-cohort design of the study, the Lin-Ying method was used to refine estimates of the variance. Cumulative incidence curves were constructed using Fine-Gray competing risks analysis to accommodate censoring due to death. Analyses were performed using R v2.14.1.

Results

[0497] Table 21 shows the clinical characteristics of the cohort used for this study. The high number of metastasis and CSM events demonstrated the high risk of this cohort. CAPRA-S and GC were the most prognostic indicators of CSM by survival ROC analysis (Table 22). GC had a survival AUC of 0.78 (0.65-0.89 95% CI) whereas CAPRA-S had a survival AUC of 0.76 (0.65-0.88 95% CI). Survival decision curve analysis (FIG. 37) showed that GC had a higher Net Benefit over a range of “decision-to-treat” threshold probabilities.

Table 21.

	Total n (%)
Pre-operative Prostate-specific Antigen	
<10 ng/mL	119 (54)
10-20 ng/mL	59 (27)
>20 ng/mL	41 (19)
Pathological Gleason Score	
≤6	15 (7)
7	111 (51)
≥8	93 (42)
Pathological Stage	
pT2N0M0	85 (39)
pT3/4N0M0	102 (47)
pTanyN+M0	32 (15)
Adverse Pathologic Features	
Positive surgical margins	123 (56)
Extra-capsular extension	95 (43)
Seminal vesicle invasion	81 (37)
Post-Operative Treatment	
Adjuvant radiation	24 (11)
Adjuvant androgen deprivation therapy	74 (34)
Salvage radiation	68 (31)
Salvage androgen deprivation therapy	86 (39)
Clinical Outcomes	
Biochemical recurrence	110 (50)
Clinical metastasis	69 (31)
Prostate cancer-specific mortality	28 (13)

Table 22

Survival AUC (95%CI)	
GC	0.78 (0.65 - 0.89)
CAPRA-S	0.76 (0.65 - 0.88)
Pathologic Gleason Score	0.73 (0.63 - 0.84)
Pre-operative PSA	0.48 (0.33 - 0.56)
Positive Margins	0.51 (0.35 - 0.65)
Lymph Nodes	0.62 (0.46 - 0.72)
Seminal Vesicle Invasion	0.60 (0.42 - 0.70)
Extra Capsular Extension	0.48 (0.33 - 0.56)

[0498] When GC and CAPRA-S scores were compared, while trends suggest that both GC and CAPRA-S had high agreement with respect to patients that are truly at risk of lethal prostate cancer (FIG. 38), there was also substantial reclassification of CAPRA-S risk categories by GC. Namely GC was more specific as it reclassified 108 patients to lower risk without significantly impacting sensitivity (Table 23).

Table 23.

	GC Score <0.4		GC Score ≥ 0.4		
CAPRA-S risk	Total Patients	Total CSM	Total Patients	Total CSM	Total
	n	n (csm total %)	n	n (csm total %)	
≤ 2	1	n.a	n.a	n.a	1
3 to 5	68	6 (8.8)	40	2 (5.0)	108
≥ 6	39	1 (2.5)	64	19 (30)	103
Total	108	7	104	21	212

[0499] The cumulative incidence plot (accounting for other causes of death as a competing risk) for the CAPRA-S high risk group was shown (CAPRA-S ≥ 6 ; FIG. 39A). When this group was stratified by GC (FIG. 39B), patients with both high CAPRA-S scores and GC scores were at considerably higher risk than those with low GC scores.

[0500] Univariable (UVA) and Multivariable analysis (MVA) was used to further assess the statistical significance of the classifiers and clinical variables individually (UVA) and in presence of other variables (MVA). As shown in Table 24, GC, CAPRA-S and pathological Gleason Score were highly statistically significant in UVA (p-value < 0.001), whereas Lymph Node Involvement and Extra capsular Extension were significant (p-value = 0.01). In MVA, while CAPRA-S was not included in multivariable analysis as the clinicopathologic factors in this analysis comprise CAPRA-S, only GC and pathological Gleason Score remained statistically significant (Table 24).

Table 24.

	Univariable Analysis	Multivariable Analysis

	Hazard Ratio (95% CI)	p-value	Hazard Ratio (95% CI)	p-value
GC*	1.83 (1.42 – 2.36)	p<0.001	1.61 (1.24 – 2.10)	p<0.001
CAPRA-S**	1.42 (1.19 – 1.70)	p<0.001	n.a	n.a
Path Gleason Score	7.84 (2.80 – 21.97)	p<0.001	4.80 (1.38 – 16.71)	0.01
Pre-operative PSA	1.11 (0.79 – 1.56)	0.54	1.01 (0.60 – 1.70)	0.96
Positive Margins	0.66 (0.29 – 1.52)	0.33	0.50 (0.18 – 1.38)	0.18
Lymph Nodes	3.53 (1.36 – 9.16)	0.01	1.45 (0.43 – 4.91)	0.55
Seminal Vesicle Invasion	2.11 (0.92 – 4.86)	0.08	1.79 (0.60 – 5.29)	0.29
Extra Capsular Extension	3.52 (1.40 – 8.81)	0.01	2.11 (0.69 – 6.42)	0.19
* GC hazard ratio is adjusted for a step size of 0.1				
** CAPRA-S is not included in multivariable analysis as the clinicopathologic factors in this analysis comprise CAPRA-S				

[0501] A second MVA between GC and CAPRA-S suggested both GC (HR :1.62 , p <0.001) and CAPRA-S (HR:1.22, p = 0.01) offered independent and statistically significant prognostic information. An integrated model improved risk stratification over either model alone (FIG. 40).

[0502] In summary, among men treated with RP at high risk of recurrence based on clinicopathologic variables, both GC and CAPRA-S were significant predictors of CSM. GC was able to effectively 'down-risk' men stratified to high risk based on CAPRA-S alone. GC provided independent prognostic information, and a model integrating GC and CAPRA-S may further improve prediction of lethal prostate cancer.

Example 10: Clinical Utility of a genomic-based prognostic test for metastasis in high-risk post-prostatectomy patients.

[0503] Prostate cancer presents a significant population health burden in the United States. As the most frequently diagnosed cancer among men, almost 240,000 new cases are projected for 2013 (ACS, 2013). About half of these men will be treated with radical prostatectomy (RP) (Marciscano et al., 2012) and while many will achieve a durable cure, up to 50% will present with one or more adverse pathology features such as, seminal vesicle invasion (SVI), extracapsular extension (ECE) or positive surgical margins (Swanson et al., 2007, NCCN, 2013). Although these patients are considered by guidelines to be at an increased risk for disease progression, only a minority will develop metastatic disease and ultimately die of prostate cancer (Pound et al.). Further, while close monitoring with postoperative PSA testing can identify men at risk, the time to biochemical recurrence (BCR)

after RP is not predictive for metastatic disease (Boorjian et al., 2011). And, while PSA doubling time (PSAdt) is a good surrogate, its accurate determination may not be possible in all patients as it requires precious time that the patient might not have (Freedland et al., 2007).

[0504] Treatment recommendations from National Comprehensive Cancer Network (NCCN) guidelines include radiation and/or hormone therapy or active surveillance (observation). These guidelines are based in part on results from three independent phase III randomized clinical trials that have demonstrated improvements in biochemical-free, metastasis-free and cancer-specific survival in high-risk post-RP men treated with radiation therapy (RT) (Bolla et al., 2005; Thompson et al., 2009; Wiegel et al., 2009). Despite this, deciding on appropriate use of radiation therapy post RP remains a challenging task. Knowledge that most clinically high-risk post-RP patients will never develop metastasis may be resulting in concern over inappropriate or over-utilization of secondary therapy in this population. Recognizing these factors, guidelines state that “predicting prognosis is essential for patient decision-making, treatment selection, and adjuvant therapy” (NCCN, 2013). Therefore, a need persists to more accurately characterize a patient’s risk of metastasis following RP to guide treatment decisions.

[0505] Current assessment of risk used when considering postoperative secondary therapy is conducted based on individual clinicopathologic variables and/or through use of nomograms (Lughezzani et al, 2010). However, the ability to identify patients at substantially higher risk of metastasis and lethal prostate cancer on the basis of clinicopathologic features alone is limited. Therefore, the need is evident for novel risk prediction tools such as genomic information that reflect the true biological potential for tumor recurrence and spread. One such tool is a postoperative genomic classifier (GC) test as described in Example 3 that uses a whole-transcriptome microarray assay with formalin-fixed paraffin embedded prostate cancer specimens. Developed in collaboration with the Mayo Clinic, it was designed to predict early clinical metastasis following RP (Erho 2013). In a blinded clinical validation study of a contemporary high-risk population of post RP men with adverse pathology, the GC test was found to more accurately predict metastasis post-RP than clinical risk models (Davicioni, E. et al 2013).

[0506] In assessing a novel molecular test, experts have recommended that evidence be collected not only on the clinical validity of the test, but also on how use of the test influenced clinical practice management, a well-established measure of the test’s clinical

utility (Hornberger et al. Mole Gen, 2012, CDC, 2007). The primary objective of the study herein, was to determine how urologists' knowledge of results of the GC test influenced adjuvant and salvage treatment recommendations following RP.

MATERIALS AND METHODS

[0507] This clinical utility study used a prospective, pre-post design, consisting of two independent sub-studies to assess patient cases at different points in patient management; both are collectively referred to herein as the DECIDE study (DECision-Impact DEcipher). In one study, urologist treatment recommendations were assessed in the adjuvant setting, following RP without any evidence of PSA rise or BCR. In the other, treatment recommendations were assessed for a different cohort of cases in the salvage setting, following RP with evidence of PSA rise or BCR. Urologists were invited to review a set of twelve cases and provide treatment recommendations for cases at each of the adjuvant and salvage time points. Urologists were presented de-identified clinical results from real patients involved in a previously conducted clinical validation study (Davicioni et al. 2013) and asked to provide treatment recommendations based solely on the clinical information provided (pre-GC). Then, results of the GC test were assessed for the same de-identified cases and urologists were asked again to provide treatment recommendations (post-GC). Twenty urologists participated in the adjuvant setting study and 15 in the salvage setting study.

[0508] The study was conducted in accordance with the Declaration of Helsinki and the Belmont report and was reviewed and approved by an independent IRB (Quorum Review Inc., Seattle, WA).

[0509] The primary objective of this study was to assess the effect of the GC test on urologists' adjuvant and salvage treatment recommendations for clinically and pathologically high-risk post-RP cases. Secondary objectives were to investigate specific changes in recommendation, proclivity of the GC result to result in more or less intensification of treatment, the relative importance of the GC to clinical variables and impact of the GC on urologist confidence with treatment recommendations. Protocol-defined eligibility criteria for participation in the study required US board certified urologists practicing for at least 3 years and performing a high volume of RPs annually (Table 25). All urologists participating in the study were fellowship trained, urologic oncologists. Potential participants were identified through conference delegate lists and through established networks of key opinion leaders and were assessed for eligibility using an available database. Email invites were sent to 50 urologists meeting the inclusion criteria. Enrollment packages were sent to eligible urologists

interested in participating in the study and included a cover letter, an educational primer on the GC test, a confidentiality agreement and a web link to the study's informed consent form (ICF) and electronic case report questionnaires (eCRQ).

Table 25.

	Total	Adjuvant Evaluation	Salvage Evaluation
	n=21	n=20	n=15
	No. (%)	No. (%)	No. (%)
Practice setting			
Tertiary Care	13 (62%)	12 (60%)	9 (60%)
Community (hospital or private)	8 (38%)	8 (40%)	6 (40%)
No. of years in practice			
Mean	8.1	8.3	7.8
Range	3-25	3-25	3-25
No. Radical Prostatectomy per year			
Mean	184	179	200
Range	30-300	30-300	30-300
Geographic region			
West/South Central	4 (20%)	4 (20%)	3 (20%)
South East	4 (20%)	4 (20%)	3 (20%)
Mid Atlantic	4 (20%)	3 (15%)	2 (13%)
North East	5 (25%)	5 (25%)	5 (33%)
North Central	4 (20%)	4 (20%)	2 (13%)

[0510] Twenty-four high-risk post-RP patient cases (12 adjuvant and 12 salvage) were selected for urologist review from the previously conducted clinical validation study. The number of patient cases was selected to provide enough cases to sufficiently evaluate urologist decision making across a range of high-risk patient types and was limited to twelve cases in each treatment setting so as to minimize study participant fatigue in reviewing patient cases. All cases were high-risk post-RP as defined by the presence of one or more adverse pathological features including (1) pathological Gleason score 8+ or Gleason score 7 with primary pattern 4; (2) pathological stage T3a (extracapsular extension) or T3b (seminal vesicle invasion); (3) positive surgical margins; or (4) Gleason grade upgrade from biopsy to surgery. Cases that did not experience a PSA nadir after RP were excluded from the study.

[0511] Cases were selected on the basis of their clinical risk factors and the GC predicted probability of developing metastatic disease at 5 and 3 years post-RP for the adjuvant and salvage treatment settings, respectively. In the adjuvant setting, six cases with concordant clinical risk features and GC risk and six cases with discordant predicted risk were selected. In the salvage setting, these numbers were 5 and 7, respectively. Clinical risk was determined based on the following clinicopathological variables: age at surgery, pre-operative PSA levels, pathologic stage, biopsy and pathologic Gleason score, presence or absence of SVI, presence or absence of ECE, surgical margin status and lymph node involvement (Table 26). Additionally, PSA doubling time (PSAdt) and time to BCR were provided for cases evaluated in the salvage setting. High (low) GC risk was defined as a 5- or 3-year predicted probability of metastasis greater (less) than 6% for the adjuvant setting and greater (less) than 18% for the salvage setting. The predicted probability was obtained from a prediction curve that uses Cox regression modeling to convert the oligonucleotide microarray 22-marker GC score into a patient probability of clinical metastasis at 5 years post RP. A function was created that translated GC scores into 5-year clinical metastasis event probabilities, and the resulting line of best fit was used for future predictions for novel patients. The curve allowed for the translation of a GC score (x-axis) into a patient's probability of clinical metastasis (y-axis) by visual inspection or by simple calculation. The threshold cut-off for the GC test of $\geq 6\%$ was used to identify a patient at elevated risk for clinical metastasis above the average risk for other similar high-risk (e.g., patients with one or more adverse pathology features) or conversely at lower risk than the average risk of such patients for patients with Decipher test results $< 6\%$.

Table 26.

	Adjuvant	Salvage
	No. (N=12) (%)	No. (N=12) (%)
Age (Years at RP or at BCR)		
Median (Min, Max)	60 (48, 70)	66 (57, 74)
Pre-operative Prostate-specific Antigen		
<10 ng/mL	10 (83.3)	9 (75)
10-20 ng/mL	1 (8.3)	2 (16.7)
>20 ng/mL	1 (8.3)	0
NA	0	1 (8.3)
D'Amico risk groups		
Low	2 (16.7)	1 (8.3)

Intermediate	4 (33.3)	7 (58.3)
High	6 (50)	4 (33.3)
Pathological Stage		
pT2N0M0	6 (50)	8 (66.7)
pT3N0M0	6 (50)	4 (33.3)
Extra-capsular Extension		
Present	5 (41.7)	3 (25)
Seminal Vesicle Invasion		
Present	4 (33.3)	2 (16.7)
Surgical Margin Status		
Positive	8 (66.7)	6 (50)
Pathological Gleason Score		
6	3 (25)	0
7 (3+4)	4 (33.3)	2 (16.7)
7 (4+3)	1 (8.3)	4 (33.3)
8	1 (8.3)	5 (41.7)
9	2 (16.7)	1 (8.3)
10	1 (8.3)	0
Time to BCR (months)		
Median (Min, Max)	NA	16 (1, 112)
≤36 months	NA	9 (75)
>36 months	NA	3 (25)
PSAdT		
<6 months	NA	5 (41.7)
≥6 months	NA	6 (50)
<9 months	NA	9 (75)
≥9 months	NA	2 (16.7)
NA	NA	1 (8.3)

[0512] All cases were de-identified and presented in a randomized fashion to eliminate bias toward the urologist's pre- and post-GC treatment recommendations. Cases were randomized both from urologist to urologist and from pre to post-GC. Clinical variables and GC test results information were provided to urologists through a secure online platform, and all treatment recommendations were collected using the eCRQ. Treatment recommendations included referral to a radiation oncologist for radiation and/or initiation of hormones, close observation, or any other recommendation not listed on the eCRQ.

[0513] Confidence intervals for probability of recommendation change from pre- to post-GC were constructed using a normal approximation, a significance level of 5%, and all recommendations were considered as independent. Chi-squared tests were used for univariate assessment of treatment predictors and multivariable analyses were performed using logistic

regression. All statistical analyses were performed using SAS 9.2 (Cary, NC). All tests were 2-sided with a Type I error probability of 5%.

RESULTS

[0514] Participating physicians were all practicing, ‘high-volume’ urologists performing an average of 184 RPs per year (Table 25). Twenty-one urologists from 18 different institutions across the US participated: 20 in the adjuvant, and 15 in the salvage settings. Fourteen of these urologists completed assessment of cases in both sub-studies. Of the 21 urologists, 38% (n = 8) practiced in a community-based hospital or private practice setting and 62% (n = 13) practiced in tertiary care centers, the majority (85%) of which are National Cancer Institute (NCI) designated comprehensive cancer centers. Urologists had been practicing and performing surgery for 3 to 25 years (mean 8.1 years) and all had extensive experience managing and treating patients with prostate cancer both before and after RP.

[0515] Twelve patient cases were retrospectively selected for urologist review in each of the adjuvant and salvage settings (Table 26). Half of the adjuvant patient cases were pre-operatively deemed low to intermediate risk according to D’Amico risk groups but were all subsequently up-graded/staged postoperatively. Furthermore, 75% of these cases presented with a pathologic Gleason score ≥ 7 , and 36% were ≥ 65 years of age at the time of surgery. For cases reviewed in the salvage setting, half had a time to BCR ≤ 24 months, and 75% presented with a rapid PSA_{dt} (< 9 months). The majority (58%) of these cases were ≥ 65 years of age at the time of BCR.

[0516] In the adjuvant treatment setting, 43% (95% CI: 37-49%) of recommendations changed following review of the GC test results (Table 27). Specifically, among case evaluations with a pre-GC recommendation involving treatment, 27% (95% CI: 19-35%) of recommendations were changed to observation post-GC. Notably, for case evaluations with a pre-GC recommendation of radiation alone (n=100), 31% (95% CI: 22-41%) changed to observation post-GC (Table 27). Among the case evaluations where observation was initially chosen (n=114), treatment was recommended for 37% of case evaluations post-GC, primarily in favor of radiation therapy (37/42). This can be visualized in FIG. 41, which shows how in comparison to pre-GC, post-GC urologist recommendations for observation or treatment (radiation and/or hormones) aligned to a high degree with the risk assigned by the GC test.

Table 27.

		Adjuvant	Salvage

Treatment Recommendation					Treatment Recommendation		
Pre-GC	Post-GC	N Pre-GC	Change N (%)	95% CI	N Pre-GC	Change N (%)	95% CI
Overall	Any Change	240	103 (43%)	37-49%	180	95 (53%)	45-60%
Observation	Any Treatment	114	42 (37%)	28-46%	31	19 (61%)	42-78%
	Radiation	114	37 (32%)	24-42%	31	12 (39%)	22-58%
	Hormone therapy	114	4 (4%)	1-9%	31	0 (0%)	
	Radiation + Hormone therapy	114	1 (0.9%)	0-5%	31	7 (23%)	10-41%
	Other*	114	1 (1%)	0-5%	31	2 (7%)	0.8-21%
Any Treatment	Observation	125	34 (27%)	19-35%	143	23 (16%)	11-23%
Radiation	Observation	100	31 (31%)	22-41%	82	11 (13%)	7-23%
Hormone therapy	Observation	1	1 (100%)	3-100%	6	1 (17%)	0.4-64%
Radiation + Hormone therapy	Observation	24	2 (8%)	1-27%	55	11 (20%)	10-33%
Other*	Observation	1	1 (100%)	3-100%	6	0 (0%)	
*In the adjuvant setting, 'other' treatment recommendations included: "recheck path" and "medical oncologist and radiation oncologist consult" *In the salvage setting 'other' treatment recommendations included: "DRE, imaging" x3, "DRE, imaging, possible referral to radiation oncologist" x2, and "referral to medical oncologist"							

[0517] In the salvage setting, treatment recommendations changed 53% (95% CI: 45-60%) of the time (Table 27). Among case evaluations with a pre-GC recommendation involving treatment (n=143), 16% (95% CI: 11-23%) changed to observation post-GC. Expectedly, there were fewer pre-GC recommendations of observation (n=31) for case evaluations with BCR, 61% were recommended to change from observation to any treatment post-GC with radiation alone (n=12) or in combination with hormonal therapy (n=7) (Table 27). Similar to the analysis of the adjuvant setting above, we observed a trend that showed alignment of observation versus treatment recommendations with the GC score, even though treatment recommendation rates were higher overall in the salvage setting (FIG. 43). When accounting

for intra-observer correlation, urologists' probability of changing recommendation was approximately normally distributed, with estimated probabilities of recommendation change of 43% (95% CI 36-50%) in the adjuvant setting and 53% (95% CI 39-67%) in the salvage setting. This indicated that no urologist is always changing or failing to change their recommendation from pre- to post-GC in either setting.

[0518] To further examine the impact of the relationships between clinicopathologic variables and the GC test results in urologist treatment recommendations, we evaluated the proportion of urologists recommending treatment pre- and post-GC over the complete set of case evaluations as well as within individual clinicopathologic variables for high and low GC risk patients (Table 29A-B). GC risk was established based on whether the predicted probability of developing metastasis was above (high GC risk) or below (low GC risk) the average risk for the original study population (see methods). Overall, in the adjuvant setting, treatment was recommended 52% of the time pre-GC. Upon reviewing the GC test results, those with a low GC risk were recommended treatment only 21% of the time compared to those with a high GC risk who were recommended treatment 90% of the time ($p < 0.0001$). Similarly, in the salvage setting, the overall proportion of treatment recommendation was 79% pre-GC, but post-GC fell to 75% in the low GC risk group and rose to 85% in the high-risk GC group ($p = 0.031$).

Table 29A.

Table 29A. Adjuvant Setting								
		Post-GC Recommendation						
		N (row %) [95% CI]						
		Observe	Any Treatment	Radiation therapy	Radiation + Hormone therapy	Hormone therapy	Other	
Pre-GC Recommendation	Observe	71 (62%)	42 (37%)	37 (32%)	1 (0.9%)	4 (4%)	1 (1%)	114
		[52-71%]	[28-46%]	[24-42%]	[0-5%]	[1-9%]	[0-5%]	
	Any Treatment	34 (27%)	91 (73%)	NA	NA	0	0	125
		[19-35%]	[64-806%]					
	Radiation therapy	31 (31%)	NA	51 (51%)	18 (18%)	0	0	100
		[22-41%]		[41-61%]	[11-27%]			
	Radiation + Hormone Therapy	2 (8%)	NA	6 (25%)	16 (67%)	0	0	24
		[1-27%]		[10-47%]	[45-84%]			
	Hormone	1 (100%)	NA	0	0	0	0	1

	Therapy	[3-100%]						
	Other*	1 (100%) [3-100%]	0	0	0	0	0	1
	Totals	106	133	94	35	4	1	240

Shaded region breaks out "Any Treatment" into the three available treatment options and are not included in row and column totals

*In the adjuvant setting, 'other' treatment recommendations included: "recheck path" and "medical oncologist and radiation oncologist consult"

Table 29B.

Table 29B. Salvage Setting								
		Post-GC Recommendation						Totals
		N (row %) [95% CI]						
		Observe	Any Treatment	Radiation therapy	Radiation + Hormone therapy	Hormone therapy	Other	
Pre-GC Recommendation	Observe	10 (32%) [17-51%]	19 (61%)	12 (39%) [22-58%]	7 (23%)	0	2 (7%) [0.8-21%]	31
			[42-78%]		[10-41%]			
	Any Treatment	23 (16%)	118 (86%)	78 (55%)	37 (26%)	3 (2%)	2 (2%) [0.3-9%]	143
		[11-23%]	[79-91%]	[46-63%]	[19-34%]	[0.4-6%]		
	Radiation	11 (13)	69 (84%)	53 (65%) [53-75%]	16 (20%) [12-30%]	0	2 (2%) [0.3-9%]	82
		[7-23%]	[74-91%]					
	Radiation + Hormone Therapy	11 (20%) [10-33%]	44 (80%)	23 (42%) [29-56%]	20 (36%) [24-50%]	1 (2%) [0-10%]	0	55
		[67-90%]						
	Hormone Therapy	1 (17%) [0.4-64%]	5 (83%) [36-100%]	2 (33%) [4-78%]	1 (17%) [0.4-64%]	2 (33%) [4.3-78%]	0	6
		[54-100%]						
	Other*	0	6 (100%)	1 (17%) [0.4-64%]	5 (83%)	0	0	6
			[54-100%]		[36-100%]			
Totals		33	143	91	49	3	4	180

Shaded region breaks out "Any Treatment" into the three available treatment options and are not included in row and column totals

*In the salvage setting 'other' treatment recommendations included: "DRE, imaging" x3, "DRE, imaging, possible referral to radiation oncologist" x2, and "referral to medical oncologist"

[0519] When evaluating individual clinical variables in the adjuvant setting (Table 30), patients with ECE represented the subgroup with the highest proportion of treatment recommendations pre-GC (77%); this fell to 28% for low GC risk case evaluations and rose to 97% for high GC risk case evaluations post-GC ($p < 0.0001$) (FIG. 42). Similarly, in cases with positive surgical margins, 54% were recommended treatment pre-GC. Treatment

recommendation dropped to 18% for cases with low GC risk and rose to 93% in high GC risk cases ($p < 0.0001$). For cases with pathological Gleason score ≥ 7 disease, 50% were recommended treatment pre-GC, among those with low GC risk only 25% were recommended treatment versus 88% of those cases with high GC risk ($p < 0.01$). The largest magnitude in change was observed in cases with SVI. Pre-GC, 70% of SVI cases were recommended treatment, but this dropped to 42% of cases post-GC. Among those cases with low GC risk, only 23% were recommended treatment in the presence of SVI. Cases with high GC risk apparently were perceived by urologists to reinforce the high-risk SVI pathology and 95% were recommended for treatment ($p < 0.0001$). These results reinforced the impact of the GC test and indicated that the proportion of treatment recommendation was more strongly associated with the GC risk (or probability of developing metastasis) than any of the clinical variables (Table 30). Evaluation of individual clinical variables in the salvage setting (Table 30), showed that differences in adverse pathology within ECE, SVI and margin status did not appear to influence treatment recommendations post-GC (FIG. 44). The main driver for treatment recommendations was PSA_{dt}. As expected, cases with a rapid PSA_{dt} of < 6 months were recommended for treatment by 93% of urologists pre-GC. However, the proportion dropped to 73% within low GC risk patients post-GC. For cases with longer PSA_{dt} (and hence a presumed better prognosis), only 14 recommendations for treatment were made pre-GC, but this increased to 25 post-GC and all of these cases had high GC risk. As observed for the adjuvant setting, within the salvage setting study, GC risk had a stronger impact on the recommendation to treat than most clinical variables (other than margin status).

Table 30.

				Treatment Recommended Post-GC		P-Value for Effect of Clinical Variable Pre-GC	P-values for Post-GC Treatment	
Time point	Variable		Treatment Recommended Pre-GC	Low GC Risk	High GC Risk		Effect of GC risk	Effect of clinical Variable
Adjuvant	Overall		125 (52.1%)	25 (20.8%)	108 (90%)		< 0.0001	NA
	ECE	Absent	48 (34.3%)	14 (17.5%)	50 (83.3%)	< 0.0001	< 0.0001	0.16
		Present	77 (77%)	11 (27.5%)	58 (96.7%)			
	SVI	Absent	69 (43.1%)	11 (18.3%)	89 (89%)	< 0.0001	< 0.0001	0.36
		Present	56 (70%)	14 (23.3%)	19 (95%)			
	Positive Margins	Absent	39 (48.8%)	14 (23.3%)	15 (75%)	0.49	< 0.0001	0.24

		Present	86 (53.8%)	11 (18.3%)	93 (93%)			
	Gleason Upgrading	Downgrade	40 (66.7%)	9 (22.5%)	20 (100%)	<0.0001		
		No Change	45 (37.5%)	13 (21.7%)	49 (81.7%)		< 0.0001	0.97
		Upgrade	40 (66.7%)	3 (15%)	39 (97.5%)			
	Pathological Gleason	<7	36 (45%)	10 (16.7%)	20 (100%)	0.046		
		7	50 (50%)	15 (25%)	35 (87.5%)		0.011	0.5
		>7	39 (65%)		53 (88.3%)			
Salvage	Overall		143 (79.4%)	79 (75.2%)	64 (85.3%)		0.031	NA
	ECE	Absent	98 (72.6%)	42 (70%)	64 (85.3%)	0.0003	0.009	0.1
		Present	45 (100%)	37 (82.2%)				
	SVI	Absent	113 (75.3%)	56 (74.7%)	64 (85.3%)	0.0051	0.03	0.62
		Present	30 (100%)	23 (76.7%)				
	Positive Margins	Absent	53 (58.9%)	7 (46.7%)	64 (85.3%)	<0.0001	0.0005	0.007
		Present	90 (100%)	72 (80%)				
	Gleason Upgrading	No Change	101 (74.8%)	48 (80%)	64 (85.3%)	0.008	0.23	0.14
		Upgrade	42 (93.3%)	31 (68.9%)				
	Pathological Gleason	7	75 (83.3%)	48 (80%)	26 (86.7%)	0.29	0.03	0.37
		>7	68 (75.6%)	31 (68.9%)	38 (84.4%)			
	BCR Time	< 36 months	123 (91.1%)	79 (79.2%)	27 (90.0%)	<0.0001	0.8	0.11
		≥ 36 months	20 (44.4%)		37 (82.2%)			
	PSAdt	< 6 months	70 (93.3%)	44 (73.3%)	14 (93.3%)	0.007	0.058	0.72
		≥ 6 months	67 (74.4%)	35 (77.8%)	38 (84.4%)			
		< 9 months	123 (91.1%)	79 (75.2%)	27 (90%)	<0.0001	0.11	0.93
		≥ 9 months	14 (46.7%)		25 (83.3%)			

Low (High) GC Risk at Adjuvant timepoint = 5 year predicted probability < 6% (> 6%)
 Low (High) GC Risk at Salvage timepoint = 3 year predicted probability < 18% (> 18%)

[0520] To measure recommended changes in treatment intensity, we established a baseline clinical perception of risk (hereafter referred to as perceived risk). Cases were considered low perceived risk if less than half of urologists recommended treatment and high perceived risk if more than half recommended treatment in the absence of the GC test results. In the adjuvant and salvage settings we observed that if perceived risk was high but GC risk was low, then, respectively, 50% and 46% of recommendations reduced treatment intensity post-GC (e.g., radiation to observation or radiation/hormone combination to radiation only) (Table 28). Very few recommendations were made that increased treatment intensity, (only 5% and 3.8%, respectively for adjuvant and salvage treatment recommendations). Conversely, for cases with an initial low perceived risk but high GC risk, we observed a 55% and 58% increase in treatment intensity in both the adjuvant and salvage settings, respectively. Influence of GC risk on change in intensity for all clinical risk categories and treatment settings were highly statistically significant (< 0.0001). Furthermore, a multivariable model adjusting for the pre-GC clinical risk showed that GC risk influenced change in treatment recommendation intensity ($p < 0.0001$). To understand the extent to which the GC test result impacts confidence in making a treatment recommendation, urologists were asked to report on the degree to which they felt confident in the treatment recommendation made for case evaluations both pre- and post-GC, as well as the extent to which they felt the GC test result influenced those treatment recommendations. Results showed that for case evaluations where a treatment recommendation was made, urologist confidence in treatment recommendations increased by 25% and 23% in the adjuvant and salvage settings, respectively. Additionally, urologists reported that the GC test result influenced their treatment recommendation in 83.5% (adjuvant) and 87.4% (salvage) of case evaluations (Table 31). As shown in FIG. 45, urologists report increased confidence in treatment recommendations made post GC test results. Table 32 shows five de-identified patients from the cohort used in this study, their clinical characteristics, the predicted probability at five years based on GC test and the actual clinical outcome observed. As seen there, Low predicted probabilities by GC test correspond with no evidence of disease, whereas high predicted probability corresponds with metastatic disease.

Table 28.

Timepoint	Perceived Risk	GC Risk	Decrease	No Change	Increase
Adjuvant	high	low	20 (50%)	18 (45%)	2 (5%)
		high	3 (5%)	35 (58.3%)	22 (36.7%)
	low	low	15 (18.8%)	60 (75%)	5 (6.3%)
Salvage	high	high	3 (5%)	24 (40%)	33 (55%)
		low	48 (45.7%)	53 (50.5%)	4 (3.8%)
	low	high	1 (3.3%)	17 (56.7%)	12 (40%)
		high	4 (8.9%)	15 (33.3%)	26 (57.8%)
Low (High) Perceived Risk = < half (> half) of clinicians initially recommend treatment Low (High) GC Risk at Adjuvant timepoint = 5 year predicted probability < 6% (> 6%) Low (High) GC Risk at Salvage timepoint = 3 year predicted probability < 18% (> 18%)					

Table 31.

	All		Recommendation Changed	
Adjuvant	Pre-GC Test	Post-GC Test	Pre-GC Test	Post-GC Test
Confidence in treatment recommendation				
Agree	72.9%	81.7%	70.9%	88.3%
Disagree	3.8%	5.8%	4.9%	2.9%
Neutral	23.3%	12.5%	24.3%	8.7%
GC test influenced treatment recommendation				
Agree	NA	62.5%	NA	83.5%
Disagree	NA	8.3%	NA	2.9%
Neutral	NA	29.2%	NA	13.6%
Salvage	Pre-GC Test	Post-GC Test	Pre-GC Test	Post-GC Test
Confidence in treatment recommendation				
Agree	72.8%	82.2%	68.4%	84.2%
Disagree	4.4%	2.8%	5.3%	2.1%
Neutral	22.8%	15.0%	26.3%	13.7%
GC test influenced treatment recommendation				
Agree	NA	68.3%	NA	87.4%
Disagree	NA	11.1%	NA	4.2%
Neutral	NA	20.6%	NA	8.4%
Agreement with confidence in treatment recommendation was assessed on a 5 point Likert scale				

where 3 was considered neutral

Table 32.

	Age	pPSA	ECE	SVI	SM	Gleason	Nomogram*	Predicted prob of mets at 5 years	Actual outcome**
A	58	194	+	+	+	3+4	High	Low (5%)	NED
B	60	22	+	-	+	4+3	High	Low (4%)	NED
C	46	11	-	-	+	3+4	Int	Low (2%)	NED
D	54	10	+	-	+	3+4	Int	High (44%)	MET
E	61	5	-	-	-	4+4	Low	High (55%)	MET
Note: All of these patients were conservatively managed and did not receive any treatment post-RP *UCSF CAPRA-S **NED = No evidence of disease; MET = metastatic disease									

DISCUSSION

[0521] This clinical utility study was designed to prospectively assess the effect of a genomic classifier (GC) test that predicts metastasis following RP on urologists' adjuvant and salvage treatment recommendations. The performance of the GC test was previously reported in a blinded, independent validation study of a population of 1,010 men at high risk of recurrence (based on adverse pathology) post RP. That study revealed that 60% of clinically high-risk patients would be reclassified as low risk with a cumulative incidence of metastasis of only 2.4% at 5 years post RP. Conversely, patients with the highest GC scores (19% of the population) had nearly 10 times higher cumulative incidence of metastasis by 5 years. Findings from this current study demonstrated that knowledge of the GC test result frequently impacted urologists' treatment recommendations in both the adjuvant (43%) and salvage settings (53%). Furthermore, we were able to show that for patients with low GC risk, while pre-GC urologists recommended treatment 43% of the time, post-GC they were recommended to observation 79% of the time. Taken together, the clinical validation and utility results implied that among the population of prostate cancer patients at high-risk of recurrence following RP, the majority of patients tested post GC will be recommended to close observation.

[0522] Guidelines on evidence development for molecular tests drafted in the past 3-5 years have urged going beyond obtaining evidence on assay analytical and clinical validity, encouraging additional research on how a test influences clinical practice management. To date in this nascent field, the number of published studies is fairly limited, but growing. In a clinical study of a molecular assay for stage II colon cancer, Srivastava et al. found that physicians changed chemotherapy decisions in 45% of patients, which fully validated predictions from a simulation of changes in NCCN guideline-directed treatment. One of the most studied areas of practice management change in molecular medicine has been risk prediction in breast cancer. In a comprehensive and systematic review of clinical validity and changes in clinical practice patterns, Hornberger et al. found 15 studies reporting on 5 different tests. They found chemotherapy recommendation changed between <1%-13% as reported in 4 studies of an online clinical decision support tool, compared with a median change across all studies of less than 35% in recommendations for a multi-gene assay. In comparison with these examples of accepted oncology tests, the finding in our study of a 43-53% change in recommendation upon receipt of the test results is supportive evidence that the GC test provides additional useful clinical information to guide therapy selection.

[0523] This study revealed relevant findings relating to current practice patterns for high-risk patients post-RP and confirmed urologist proclivity for not only increased salvage treatment at the point of BCR but also increased intensification of treatment when compared to the adjuvant setting. Overall, urologists' recommended treatment over 1.5 times as often in the salvage versus the adjuvant setting; treatment recommendations were made for 79% of case evaluations pre-GC in the salvage setting, 39% of which involved a recommendation for multi-modal (e.g., radiation and hormone) therapy. This compares to a recommendation for multi-modal therapy in only 19% of case evaluations pre-GC in the adjuvant setting. In addition, the findings imply a potential to over-treat in the salvage setting as evidence suggested that even in patients presenting with BCR, less than one-third will go on to develop metastasis. This is not without consequences for the patient as both postoperative radiation and hormone therapy incur with considerable morbidities including urinary incontinence and impotence, which can affect long-term patient quality of life.

[0524] Results from this study also confirmed that urologist decision-making in the adjuvant setting was mainly focused on whether or not to recommend postoperative radiation therapy. Prior to presentation of the GC test results, urologists recommended treatment in 52% of case evaluations with 99% of those recommendations including radiation therapy and

only 20% of recommendations including hormone therapy. Accurate direction of radiation therapy to patients who are at highest biological risk for developing metastasis is critical as the morbidities and costs associated with treating patients with radiation modalities such as IMRT run high. Furthermore, we observed that the GC risk significantly influenced the treatment recommendations irrespective of the presence or absence of specific clinicopathologic features. Additionally, these findings suggested that in the salvage setting, the sensitivity of PSA rise may motivate urologists to recommend treatment despite its poor specificity. This hinted towards a role for the GC test to improve urologist decision-making in this setting. Similar results were found relating to the intensification of treatment, where changes in intensity were driven primarily by GC risk rather than the perceived risk. This suggested that given the information from the GC test, presumably measuring the true biological potential of a patient's tumor, urologists are more willing to commit to the intensification of therapy than if this recommendation were solely based on rising PSA and clinicopathologic variables (e.g., pre-GC).

[0525] Treatment recommendations changed in 43% of adjuvant setting case evaluations and 53% of salvage setting case evaluations. These findings demonstrated that knowledge of the genomic biomarker information in this GC test frequently influences these urologists' judgments about appropriate treatment in both the adjuvant and salvage settings.

Conclusion:

[0526] The DECIDE study assessed the effect of the GC test on urologist treatment recommendations for high-risk case evaluations in the adjuvant and salvage treatment settings. Findings demonstrated that knowledge of the GC test result frequently impacted urologists' treatment recommendations in both the adjuvant and salvage settings. Furthermore, the GC test appeared to better direct urologist treatment recommendations irrespective of the presence or absence of conventional pathology and clinical variables that are currently used to assess risk in these patients.

[0527] In conclusion, this study suggested that when implemented into routine clinical practice, the GC test had the potential to change treatment recommendations after radical prostatectomy and better identify patients that may benefit from intensive multimodal therapy, while sparing those who can be closely observed without initiating aggressive secondary therapy.

Example 11: Validation of a genomic classifier that predicts metastatic disease progression in men with biochemical recurrence post radical prostatectomy

[0528] Roughly 50,000 men per year will present with biochemical recurrence (BCR) following local treatment for prostate cancer. These men, with rising PSAs as the lone indicator of recurrence, present a management dilemma due to their varied outcomes. While the post-radical prostatectomy (RP) recurrence group of patients is highly enriched for those who will develop lethal disease, many of these patients will experience BCR without developing subsequent metastases. Thus, there is a clear need to improve patient risk stratification in this context. Here, we evaluated a genomic classifier (GC, see Example 3) in men with BCR for its ability to predict clinical metastasis (e.g. positive bone or CT scans).

Methods

Patient Cohort

[0529] The aim of this study was to determine whether molecular features of primary prostate tumor specimens could aid in the prediction of outcomes at the time of BCR. Accordingly, we selected 110 Caucasian patients from a high risk cohort of over 1,000 men who experienced BCR following radical prostatectomy and for whom tissue was available (see Example 1). Only men with adenocarcinoma at the time of radical prostatectomy were included. Following prostatectomy, men were typically followed by a PSA measurement every 3 months for the first year, every 6 months for the second year and then annually thereafter. Biochemical recurrence was defined as a PSA > 0.2 ng/ml with a subsequent confirmatory value. At the time of biochemical recurrence, men were restaged with a CT or MRI as well as a bone scan which were then performed on a yearly basis. Time to biochemical recurrence was defined as the time from radical prostatectomy to first detectable PSA > 0.2 ng/ml. Metastasis was defined as a positive bone scan or visceral or extra-pelvic nodal metastasis seen on CT scan. Men who experienced BCR less than 6 months or had missing clinicopathologic variables were excluded from the analyses (n=85). Men who experienced metastasis following biochemical recurrence were designated as "Mets" and men without metastasis after biochemical recurrence were designated as "No-Mets". Adjuvant setting was defined as any treatment within 90 days after surgery. Salvage therapy was defined as any treatment after 90 days. Patient tumor and treatment characteristics are detailed in Table 33.

Table 33.

Patients	Total	Mets	Mets-Free	P-value*

Characteristics				
n	n (row %)	n (row %)	n (row %)	
Study Cohort	85	51(60)	34(40)	
Age				0.822
46-60	35	21(60)	14(40)	
61-74	50	30(60)	20(40)	
Pathological Stage				0.026
pT2N0M0	22	8(36)	14(64)	
pT3/4N0M0	46	30(65)	16(35)	
pTanyN+M0	17	13(76)	4(24)	
Pathological Gleason Score (path GS)				0.034
≤6	4	0 (0.0)	4(100.0)	
7	44	23(52)	21(48)	
≥8	27	18(67)	9(33)	
Pre-operative Prostate-specific Antigen (pre-op PSA)				0.362
<10 ng/mL	38	22(58)	16(42)	
10-20 ng/mL	28	15(54)	13(46)	
>20 ng/mL	19	14(74)	5(26)	
Seminal Vesicle Invasion (SVI)	38	29(76)	9(24)	0.011
Positive Surgical Margin (SM+)	50	29(58)	21(42)	0.822
Extra-capsular Extension (ECE)	50	36(72)	14(28)	0.013
Prostate Cancer-specific Mortality	22	22(100)	0(0)	---
Adjuvant Radiation Therapy	11	8(72)	3(27)	0.552
Adjuvant Androgen Deprivation Therapy	37	29(78)	8(22)	0.005
Salvage Radiation Therapy	41	25(61)	16(39)	0.965
Salvage Androgen Deprivation Therapy	57	44(77)	13(23)	< 0.001
Time to BCR				0.19
≤ 2 years	51	34(67)	17(33)	
> 2 years	34	17(50)	17(50)	
PSAdT (NA=12)				0.006
≤ 9 months	48	33(68)	15(31)	
> 9 months	25	8(32)	17(68)	

*Pearson's chi-squared or Fisher Exact Test

Specimen Selection and Processing

[0530] Following histopathological review, formalin-fixed paraffin embedded (FFPE) prostatic adenocarcinoma tissues from the primary tumor at the time of prostatectomy were macrodissected. Total RNA was then extracted and purified using RNeasy FFPE nucleic acid extraction kit (Qiagen Inc., Valencia, CA), and subjected to whole-transcriptome amplification using the WT-Ovation FFPE system (NuGen, San Carlos, CA). Amplified products were fragmented, labeled, and hybridized to Human Exon 1.0 ST GeneChips (Affymetrix, Santa Clara, CA) that profile coding and non-coding regions of the transcriptome using approximately 1.4 million probe selection regions, each representing a genomic biomarker or feature. Following microarray quality control using the Affymetrix Power Tools packages, probeset summarization and normalization was performed by frozen robust multi-array analysis, which is available through Bioconductor. Human Exon GeneChip files corresponding to these cases are available from the National Center for Biotechnology Information's Gene Expression Omnibus database.

Calculation of GC scores, PSADT and nomogram scores

[0531] Previously we described a validated 22-marker genomic classifier (GC) (see Example 3). Here we employed the same GC, with GC scores outputted as a value between 0 and 1. Depending on the analysis, GC score were treated as a categorical or continuous variable. Graphical diagnostic, receiver operating characteristic (ROC)-based methods on the training dataset was used to estimate an optimal cut-off for GC score. PSADT a measure of how fast the PSA levels doubles was calculated by natural log of 2 divided by slope of linear regression line of log 2 of PSA measures over time. CAPRA-S scores were calculated as described in Cooperberg et al. (Cooperberg Cancer 2011), and Stephenson 5 year probability of survival were calculated using nomogram described in Stephenson et al.

Statistical Analyses

[0532] All statistical analyses were performed in R v2.14.1. All tests were two-sided with a type I error probability of 5%. GC was compared to standard clinicopathologic variables, PSADT, time to BCR, clinical-only classifiers (CC, CAPRA-S scores and Stephenson's nomogram) and the integrated clinical and genomic classifier (GCC) for predicting metastatic disease. The concordance summary index (extension of c-index), an extension of area under

the ROC curve (AUC) for censored data was used to compare classifier performance to predict metastasis. For the survival ROC function, the nearest-neighbour estimator was used with $\lambda=0.002$ to approximate survival function density. Calibration plots were used to assess the agreement between observed and predicted outcomes. Decision curve analysis was used to assess the net increase/decrease in the proportion of necessary/unnecessary treated patients. Survival ROC and decision curves were evaluated for prediction of metastasis within 3 years post-BCR.

[0533] Cox Proportional Hazard Regression model for case-cohort design was used to evaluate the prognostic value and significance of GC and clinicopathologic risk factors in predicting the development of metastasis after BCR. Proportional hazards assumptions of the Cox model were confirmed by evaluating the scaled Schoenfeld residuals. GC was used as a continuous variable (step size=0.1); pathological Gleason score was dichotomized into <8 and ≥ 8 considering the small number of patients who had the score of 6 and below; pre-operative PSA values were log transformed due to their skewed distribution; SVI, SM, extra-capsular extension (ECE) were used as binary variables. In the Cox model, the estimated risks were adjusted for the administration of adjuvant hormone therapy. Cumulative incidence curves were constructed using Fine-Gray competing risks analysis to estimate the risk of failure due to prostate cancer only, after removing other type of failures (e.g. other reason for death). Time-dependent analyses were performed by weighting patients without the event as suggested by Barlow.

Results

[0534] Characteristics of men in our cohort who experienced BCR following RP are detailed in Table 33. Median time to BCR was 14.60 months (range 1.1-85.33). Men experiencing metastasis following BCR ("mets") did so with a median time of 37.16 months (range 3.15-111.54). These men had higher pathological grade and stage at prostatectomy, higher pre-operative PSAs, a more rapid time to BCR and more rapid PSA_dTs (Table 33). They were also more likely to receive adjuvant and salvage therapies (Table 33).

[0535] Discrimination plots of the GC scores for mets (right –light grey circles) and no-mets (left –dark grey circles) patients is shown in FIG. 46. Non-overlap of the notches demonstrates that the difference in GC score distribution between mets and no-mets is statistically significant. Based on the AUC of 3-year survival ROC analysis, GC shows better performance (sens/spec) than clinical measures as it outperforms clinicopathologic factors (FIG. 47) and clinical-only classifiers (FIG. 48). GC was not improved when integrating it

with clinicopathologic features (GCC, FIG. 48). As this represented a high risk population, a sizable fraction of men in the study received adjuvant therapy and this could potentially confound the results. When excluding patients with adjuvant therapy, the AUC of 3-year survival ROC remained statistically significant (FIG. 49). GC score distribution among pathological Gleason Score groups showed that, while there is an overall direct correlation between both scores, GC was able to reassess the risk of many patients based on the biology of the primary tumor (FIG. 50 –Mets = triangle, No-Mets = circle).

The cumulative incidence of GC high risk patients were statistically higher than GC low risk patients at any point in time following BCR using an optimal ROC-based cut-off of ≥ 0.4 , encompassing 73% of men who would develop metastasis (FIG. 51). As shown in FIG. 51, at 3 years from BCR, the GC low group has a 0.08 incidence rate and the GC high group has a 0.4 incidence rate. At 5 years from BCR, the GC low group has an incidence rate of 0.1 and the GC high group has an incidence rate of 0.54 (FIG. 51). Statistical significance was also achieved when partitioning the set of patients into low and high risk when using a cut off of 0.5 (majority-based criteria) (FIG. 52). As the KM method not only takes into consideration the number of patients at risk but also censored data (e.g., patients for which there was a loss of follow up at some point in time) to compute the proportions, the number of patients at risk for each time point in FIG. 51-52 are shown in Tables 34-35, respectively.

Table 34.

	Time to PCSM after BCR (years)					# Patients at risk
	0	2	4	6	8	
GC Low	139	106	76	41	10	# Patients at risk
GC High	82	39	19	10	5	

Table 35.

	Time to PCSM after BCR (years)						# Patients at risk
	0	2	4	6	8	10	
GC ≤ 0.5	183	177	139	92	61	15	# Patients at risk
GC > 0.5	91	72	51	20	11	--	

[0536] As shown in FIG. 53, at 3 years, the GC low group has a 0.08 incidence rate and the GC high group has a 0.17 incidence rate; and at 5 years, the GC low group has a 0.11 incidence rate and the GC high group has a 0.26 incidence rate. Since treatment was confounded with the patient's diagnosis or disease status, we observed that by excluding

treated patients we lost a group of cases, thus having a lower incidence rate for GC ≥ 0.4 patients (FIG. 53). Still, the difference in cumulative incidence between GC high risk and GC low risk patients remained statistically significant. As the KM method not only takes into consideration the number of patients at risk but also censored data (e.g., patients for which there was a loss of follow up at some point in time) to compute the proportions, the number of patients at risk for each time point in FIG. 53 is shown in Table 36.

Table 36.

	Time to PCSM after BCR (years)					# Patients at risk
	0	2	4	6	8	
GC Low	104	79	50	25	10	
GC High	30	27	18	10	5	

[0537] Majority of patients with GC < 0.4 (64%) did not develop metastatic disease by the end of study follow-up time (FIG. 54).

[0538] Hypothetically, if a decision to treat is made when a classifier implies a risk of 25% or higher, using the estimated net benefit, it can be shown that the reduction in unnecessary treatments among 100 patients using the GC model was 31 patients in comparison to maximum 10 patients for clinical-only models (FIG. 55).

[0539] Univariable (UVA) and Multivariable analysis (MVA) based on Cox Proportional Hazard was used to further assess the statistical significance of the classifiers and clinical variables individually (UVA) and in presence of other variables (MVA). These analyses show that GC accurately predicts metastasis following BCR. In univariable analysis, GC score predicted metastasis following BCR, as did clinicopathologic variables and clinical-only models (Table 37 and Table 38). GC score and pathological Gleason Score remained the only significant predictors of metastatic disease in a multivariable model after adjusting for clinicopathologic information (Table 37). In multivariable models involving GC and clinical-only classifiers, GC remained significant while the clinical-only classifiers were not significant (Table 38).

[0540] In summary, when compared to clinicopathologic variables, GC better predicted metastatic progression among our cohort of men with BCR following RP. These results suggested that use of GC allowed for better selection of men requiring additional treatment at the time of BCR.

Table 37.

	Univariable Cox Proportional Hazard			Multivariable Cox Proportional Hazard		
	Hazard Ratio	95% CI	<i>P</i>	Hazard Ratio	95% CI	<i>P</i>
GC	1.62	1.33-1.96	< 0.001	1.36	1.09-1.68	0.01
Path GS $\geq$ 8	2.55	1.14-5.70	0.02	2.7	1.02-7.16	0.05
Pre-op PSA (log2)	1.15	0.74-1.77	0.53	1.06	0.75-1.51	0.73
SVI	3.05	1.36-6.85	0.01	1.61	0.62-4.21	0.33
SM	0.55	0.25-1.25	0.16	0.63	0.27-1.52	0.31
ECE	3.02	1.31-6.96	0.01	1.47	0.62-3.48	0.38
LNI	5.22	1.93-14.13	0	0.62	0.18-2.15	0.46

Table 38.

	Univariable Cox Proportional Hazard			Multivariable Cox Proportional Hazard		
	Hazard			Hazard		
	Hazard Ratio	95% CI	<i>P</i>	Hazard Ratio	95% CI	<i>P</i>
GC	1.62	1.33-1.96	< 0.001	1.4	1.12-1.75	0
Stephenson	1.51	1.33-1.72	< 0.001	1.13	0.92-1.37	0.25
GC	1.62	1.33-1.96	< 0.001	1.44	1.16-1.78	< 0.001
CAPRA-S	1.58	1.35-1.85	< 0.001	1.11	0.89-1.39	0.34

Example 12: Prognostic value of univariable and pairwise combination of prognostic features from a 43 Biomarker Panel for Prostate Cancer Progression across different endpoints

[0541] The 43 biomarkers discovered in Example 2 (Table 2) were assessed for their performance across a range of different metrics and endpoints.

[0542] In tables 39 to 48, those biomarkers that were found as univariable classifiers to be statistically significant in the training and testing sets (see Example 1) based on a Wilcoxon test (p -value ≤ 0.05) for the Area under the ROC curve (AUC) metric, are shown for a number of relevant clinical endpoints: Extra Capsular Extension (ECE), Seminal Vesicle Invasion (SVI), Surgical Margin Status (SMS), Lymph Node Involvement (LNI), Biochemical Recurrence Event (BCR), Local Recurrence Event (LCR), Metastasis Event

(Mets Event), Prostate Cancer Specific Mortality Event (PCSM), Overall Survival (OS), pathological Gleason (pathGS) and Prostate Specific Antigen Doubling Time (PSADT). Endpoints associated to a time-to-event present also metrics that allow to consider this component in the performance assessment. Whereas results are shown for the testing set (as defined in Example 1), these biomarkers were significant also in the training set of the discovery study.

[0543] Further significance of the selected features was evidenced by multiple metrics and are also listed in tables 39 to 48 (either in their raw values or as their associated P-value for assessment of statistical significance) including:

- Sensitivity: proportion of the actual number of patients with the event that are correctly identified as such. Higher values indicate better performance.
- Specificity: proportion of the actual number of patients without the event that are correctly identified as such. Higher values indicate better performance.
- Area under the ROC curve (AUC). Corresponds to the area under the receiver operating characteristic curve, which plots the performance of a feature or classifier for all thresholds of sensitivity and specificity. Higher values indicate better performance.
- Accuracy: Proportion of patients correctly predicted. Higher values indicate better performance.
- Positive Predictive Value: proportion of predicted events that are true events. Higher values indicate better performance.
- Negative Predictive Value: proportion of predicted non-events that are true non-events. Higher values indicate better performance.
- Detection Rate: The portion of true positives from the whole population. Higher values indicate better performance.
- Detection Prevalence: The portion of predicted events from the whole population. Higher values indicate better performance.
- Median Fold Difference: the ratio of the median expression value for each group. Values away from 1 indicate better performance.
- Survival AUC: assesses the discriminatory power of the classifier across all thresholds of sensitivity and specificity taking into account the time to event. Higher values indicate better performance.
- KM P-value: Kaplan Meier curves are obtained by partitioning the expression values into low and high risk groups using the PAM clustering method. A Kaplan Meier curve for one of these groups shows the probability over time of being free of the event, given the number of patients

at risk and the censored data. The p-value is computed and measures the significance of the differences between both groups over time. P-values ≤ 0.05 are considered significant. Lower values indicate better performance.

- Univariable Analysis (UVA) odds ratio: measures the effect size of the feature or classifier when partitioning the scores into low and high risk groups. For this metric, these groups are obtained by partitioning the set of samples into low and high risk values using the PAM clustering method. Values away from 1 indicate better performance.
- Multivariable Analysis (MVA) odds ratio: measures the independent prognostic ability of the feature or classifier when partitioning the values into low and high risk groups. For this metric, these groups are obtained by partitioning the set of samples into low and high risk using the PAM clustering method. Values away from 1 indicate better performance.
- UVA hazard ratio: measures the ratio of the hazard rates when partitioning the values into low and high risk groups and incorporates the time to event through Cox proportionate hazard modeling. For this metric, these groups are obtained by partitioning the scores into low and high risk using the PAM clustering method. Values away from 1 indicate better performance.
- MVA hazard ratio: measures the independent prognostic ability relative to other variables when partitioning the values into low and high risk groups and incorporates the time to event through Cox proportionate hazard modeling. For this metric, these groups are obtained by partitioning the scores into low and high risk using the PAM clustering method. Values away from 1 indicate better performance.

[0544] The associated p-value provided for the metrics gives a measure of the statistical significance of the corresponding metric. The threshold of P-value ≤ 0.05 is used as a way of defining those features that are statistically significant for the given metric and endpoint. The AUC lower and AUC upper, as well as the Accuracy lower and Accuracy upper, represent the lower and upper bound of the 95% Confidence Interval for those metrics.

Table 39: biomarkers from the 43 biomarker panel with significance for Wilcoxon P-value (auc.pvalue) and other metrics for the BCR event endpoint. Auc.pvalue : Wilcoxon Test P-value. MFD: Median Fold Difference. KM: Kaplan Meier curves. survAUC: survival AUC. uvaORPval: Univariable Analysis Odds Ratio P-value. mvaORPval: multivariable analysis Odds Ratio P-value. uvaHRPval: Univariable Analysis Hazard Ratio P-value. mvaHRPval: Multivariable Analysis Hazard Ratio P-value.

SEQ ID NO.	auc	auc.pvalue	Accuracy	Sensitivity	Specificity	Pos.Pred .Value	Neg.Pred . Value
SEQ ID NO. 6	0.62	0.01	0.61	0.62	0.59	0.77	0.41
SEQ	0.60	0.03	0.59	0.63	0.52	0.74	0.38

ID NO. 22							
SEQ ID NO. 19	0.59	0.04	0.60	0.63	0.53	0.75	0.39
SEQ ID NO. 28	0.59	0.04	0.59	0.64	0.48	0.73	0.38
SEQ ID NO. 16	0.61	0.02	0.42	0.45	0.34	0.60	0.22
SEQ ID NO. 5	0.60	0.03	0.61	0.66	0.50	0.75	0.40
SEQ ID NO. 4	0.60	0.02	0.48	0.30	0.86	0.83	0.36
SEQ ID NO.	mfd	uvaOR Pval	mvaORPv al	KM P- value	survAUC	uvaHRP val	mvaHRP val
SEQ ID NO. 6	1.09	0.02	0.06	0.00	0.64	0.00	0.08
SEQ ID NO. 22	1.15	0.03	0.09	0.03	0.64	0.00	0.01
SEQ ID NO. 19	1.06	0.13	0.02	0.00	0.65	0.02	0.01
SEQ ID NO. 28	1.09	0.06	0.02	0.08	0.63	0.01	0.01
SEQ ID NO. 16	0.97	0.12	0.58	0.01	0.39	0.11	0.86
SEQ ID NO. 5	1.08	0.05	0.05	0.16	0.54	0.19	0.52
SEQ ID NO. 4	1.03	0.02	0.06	0.00	0.65	0.00	0.00

Table 40: biomarkers from the 43 biomarker panel with significance for Wilcoxon P-value (auc.pvalue) and other metrics for the ECE endpoint. Auc.pvalue : Wilcoxon Test P-value. MFD: Median Fold Difference. KM: Kaplan Meier curves. uvaORPval: Univariable Analysis Odds Ratio P-value. mvaORPval: multivariable analysis Odds Ratio P-value.

SEQ ID NO.	auc	auc.pvalue	Accuracy	Sensitivity	Specificity
SEQ ID NO. 6	0.62	0.01	0.57	0.63	0.52
SEQ ID NO. 22	0.65	0.00	0.59	0.67	0.51
SEQ ID NO. 15	0.59	0.04	0.53	0.68	0.39
SEQ ID NO. 19	0.60	0.02	0.55	0.63	0.47
SEQ ID NO. 28	0.59	0.03	0.58	0.68	0.47
SEQ ID NO. 16	0.59	0.03	0.45	0.46	0.43
SEQ ID NO. 17	0.62	0.00	0.61	0.74	0.49
SEQ ID NO. 10	0.59	0.04	0.41	0.32	0.49
SEQ ID NO. 37	0.60	0.02	0.45	0.31	0.58
SEQ ID NO.	Pos.Pred.Value	Neg.Pred.Value	mfd	uvaORPval	mvaORPval
SEQ ID NO. 6	0.55	0.59	1.08	0.01	0.12
SEQ ID NO. 22	0.56	0.62	1.20	0.00	0.06
SEQ ID NO. 15	0.52	0.56	1.04	0.04	0.10
SEQ ID NO. 19	0.53	0.57	1.07	0.03	0.64
SEQ ID NO. 28	0.55	0.61	1.10	0.02	0.66
SEQ ID NO. 16	0.44	0.46	0.97	0.02	0.49
SEQ ID NO. 17	0.58	0.66	1.06	0.01	0.28
SEQ ID NO. 10	0.38	0.43	0.90	0.10	0.66
SEQ ID NO. 37	0.41	0.47	0.94	0.02	0.11

Table 41: biomarkers from the 43 biomarker panel with significance for Wilcoxon P-value (auc.pvalue) and other metrics for the LCR event endpoint. Auc.pvalue : Wilcoxon Test P-value. MFD: Median Fold Difference. KM: Kaplan Meier curves. Surv AUC: survival AUC. uvaORPval:

Univariable Analysis Odds Ratio P-value. mvaORPval: multivariable analysis Odds Ratio P-value. uvaHRPval: Univariable Analysis Hazard Ratio P-value. mvaHRPval: Multivariable Analysis Hazard Ratio P-value.

SEQ ID NO.	auc	auc.pvalue	Accuracy	Sensitivity	Specificity	Pos.Pred.Value	Neg.Pred.Value
SEQ ID NO. 4	0.76	0.00	0.78	0.67	0.80	0.30	0.95
SEQ ID NO. 36	0.65	0.02	0.42	0.86	0.37	0.15	0.95
SEQ ID NO. 26	0.64	0.03	0.54	0.71	0.52	0.16	0.93
SEQ ID NO.	mfd	uvaPval	mvaPval	KM P-value	survAUC	uvaHRPval	mvaHRPval
SEQ ID NO. 4	1.19	0.00	0.02	0.00	0.93	0.00	0.00
SEQ ID NO. 36	1.03	0.14	0.09	0.04	0.77	0.12	0.05
SEQ ID NO. 26	1.06	0.04	0.03	0.02	0.78	0.02	0.01

Table 42: biomarkers from the 43 biomarker panel with significance for Wilcoxon P-value (auc.pvalue) and other metrics for the LNI endpoint. Auc.pvalue : Wilcoxon Test P-value. MFD: Median Fold Difference. KM: Kaplan Meier curves. uvaORPval: Univariable Analysis Odds Ratio P-value. mvaORPval: multivariable analysis Odds Ratio P-value.

SEQ ID NO.	auc	auc.pvalue	Accuracy	Sensitivity	Specificity
SEQ ID NO. 28	0.66	0.01	0.49	0.81	0.43
SEQ ID NO. 32	0.72	0.00	0.59	0.81	0.55
SEQ ID NO. 17	0.65	0.01	0.47	0.81	0.42
SEQ ID NO. 37	0.63	0.04	0.54	0.19	0.60
SEQ ID NO. 42	0.62	0.04	0.31	0.56	0.27
SEQ ID NO.	Pos.Pred.Value	Neg.Pred.Value	mfd	uvaORPval	mvaORPval
SEQ ID NO. 28	0.20	0.93	1.15	0.01	0.72
SEQ ID NO. 32	0.23	0.95	1.18	0.00	0.21
SEQ ID NO. 17	0.19	0.93	1.05	0.02	0.70
SEQ ID NO. 37	0.07	0.81	0.92	0.07	0.97
SEQ ID NO. 42	0.11	0.78	0.96	0.03	0.12

Table 43: biomarkers from the 43 biomarker panel with significance for Wilcoxon P-value (auc.pvalue) and other metrics for the MET event endpoint. Auc.pvalue : Wilcoxon Test P-value. MFD: Median Fold Difference. KM: Kaplan Meier curves. survAUC: survival AUC. uvaORPval: Univariable Analysis Odds Ratio P-value. mvaORPval: multivariable analysis Odds Ratio P-value. uvaHRPval: Univariable Analysis Hazard Ratio P-value. mvaHRPval: Multivariable Analysis Hazard Ratio P-value.

SEQ ID NO.	auc	auc.pvalue	Accuracy	Sensitivity	Specificity	Pos.Pred. Value	Neg.Pred. Value
SEQ ID NO. 6	0.67	0.00	0.61	0.72	0.54	0.48	0.77
SEQ ID NO. 22	0.66	0.00	0.59	0.74	0.51	0.46	0.77
SEQ ID NO. 20	0.65	0.00	0.60	0.72	0.53	0.47	0.77
SEQ ID NO. 15	0.70	0.00	0.59	0.82	0.46	0.47	0.82
SEQ ID NO. 19	0.67	0.00	0.60	0.74	0.52	0.47	0.77
SEQ ID NO. 12	0.60	0.03	0.44	0.41	0.45	0.30	0.57
SEQ ID NO. 28	0.66	0.00	0.58	0.75	0.48	0.46	0.77
SEQ ID NO. 32	0.61	0.01	0.59	0.63	0.57	0.46	0.73
SEQ ID NO. 16	0.66	0.00	0.37	0.34	0.38	0.24	0.50
SEQ ID NO. 17	0.61	0.02	0.55	0.74	0.45	0.43	0.75
SEQ ID NO. 18	0.61	0.01	0.58	0.47	0.64	0.43	0.68
SEQ ID NO. 4	0.67	0.00	0.73	0.47	0.87	0.68	0.74
SEQ ID NO. 2	0.59	0.04	0.40	0.46	0.37	0.30	0.54
SEQ ID NO. 24	0.64	0.00	0.63	0.56	0.67	0.49	0.72
SEQ ID NO. 26	0.59	0.03	0.56	0.99	0.59	0.54	0.43
SEQ ID NO.	mfd	uva ORPval	mva ORPval	KM P-value	surv AUC	uva HRPval	mva HRPval
SEQ ID NO. 6	1.10	0.00	0.02	0.00	0.75	0.00	0.01
SEQ ID NO. 22	1.24	0.00	0.04	0.00	0.69	0.00	0.00
SEQ ID NO. 20	1.07	0.00	0.01	0.00	0.73	0.00	0.00

SEQ ID NO. 15	1.10	0.00	0.05	0.00	0.74	0.00	0.03
SEQ ID NO. 19	1.14	0.00	0.01	0.00	0.75	0.00	0.00
SEQ ID NO. 12	0.96	0.03	0.20	0.03	0.31	0.01	0.01
SEQ ID NO. 28	1.18	0.00	0.05	0.00	0.67	0.00	0.01
SEQ ID NO. 32	1.14	0.01	0.15	0.01	0.64	0.00	0.02
SEQ ID NO. 16	0.95	0.00	0.21	0.00	0.34	0.00	0.06
SEQ ID NO. 17	1.04	0.01	0.23	0.01	0.67	0.01	0.09
SEQ ID NO. 18	1.05	0.00	0.06	0.08	0.62	0.00	0.07
SEQ ID NO. 4	1.09	0.00	0.01	0.00	0.71	0.00	0.00
SEQ ID NO. 2	0.92	0.04	0.55	0.03	0.39	0.05	0.76
SEQ ID NO. 24	1.12	0.00	0.00	0.00	0.72	0.00	0.00
SEQ ID NO. 26	1.02	0.03	0.02	0.04	0.64	0.02	0.02

Table 44: biomarkers from the 43 biomarker panel with significance for Wilcoxon P-value (auc.pvalue) and other metrics for the OS event endpoint. Auc.pvalue : Wilcoxon Test P-value. MFD: Median Fold Difference. KM: Kaplan Meier curves. survAUC: survival AUC. uvaORPval: Univariable Analysis Odds Ratio P-value. mvaORPval: multivariable analysis Odds Ratio P-value. uvaHRPval: Univariable Analysis Hazard Ratio P-value. mvaHRPval: Multivariable Analysis Hazard Ratio P-value.

SEQ ID NO.	auc	auc.pvalue	Accuracy	Sensitivity	Specificity	Pos.Pred. Value	Neg.Pred. Value
SEQ ID NO. 22	0.60	0.02	0.58	0.65	0.50	0.59	0.56
SEQ ID NO. 19	0.60	0.02	0.54	0.61	0.47	0.56	0.52
SEQ ID NO. 9	0.59	0.04	0.46	0.59	0.32	0.49	0.41
SEQ ID NO. 17	0.62	0.00	0.58	0.68	0.45	0.58	0.56
SEQ ID NO. 18	0.59	0.04	0.54	0.44	0.65	0.58	0.51
SEQ ID NO. 4	0.65	0.00	0.63	0.39	0.90	0.81	0.57
SEQ ID	0.61	0.01	0.42	0.49	0.35	0.46	0.38

NO. 2							
SEQ ID NO.	mfd	uva ORPval	mva ORPval	KM P-value	surv AUC	uva HRPval	mva HRPval
SEQ ID NO. 22	1.18	0.02	0.12	0.00	0.61	0.00	0.03
SEQ ID NO. 19	1.06	0.06	0.40	0.00	0.82	0.00	0.03
SEQ ID NO. 9	0.96	0.03	0.34	0.66	0.46	0.20	0.32
SEQ ID NO. 17	1.04	0.01	0.45	0.01	0.63	0.00	0.18
SEQ ID NO. 18	1.03	0.02	0.23	0.06	0.62	0.01	0.44
SEQ ID NO. 4	1.04	0.00	0.03	0.00	0.64	0.00	0.05
SEQ ID NO. 2	0.92	0.01	0.81	0.13	0.47	0.20	0.93

Table 45: biomarkers from the 43 biomarker panel with significance for Wilcoxon P-value (auc.pvalue) and other metrics for the pathological Gleason endpoint. Auc.pvalue :
 Wilcoxon Test P-value. MFD: Median Fold Difference. uvaORPval: Univariable Analysis Odds Ratio P-value.

SEQ ID NO.	auc	auc.pvalue	Accuracy	Sensitivity
SEQ ID NO. 6	0.74	0.00	0.52	0.41
SEQ ID NO. 22	0.67	0.02	0.62	0.63
SEQ ID NO. 20	0.81	0.00	0.71	0.66
SEQ ID NO. 15	0.79	0.00	0.70	0.65
SEQ ID NO. 19	0.80	0.00	0.70	0.63
SEQ ID NO. 12	0.69	0.01	0.34	0.34
SEQ ID NO. 28	0.83	0.00	0.70	0.66
SEQ ID NO. 16	0.77	0.00	0.39	0.46
SEQ ID NO. 9	0.65	0.05	0.58	0.66
SEQ ID NO. 17	0.74	0.00	0.73	0.73
SEQ ID NO. 18	0.72	0.00	0.60	0.54
SEQ ID NO. 4	0.69	0.01	0.44	0.30

SEQ ID NO. 24	0.68	0.02	0.53	0.45	
SEQ ID NO. 40	0.69	0.01	0.55	0.68	
SEQ ID NO. 26	0.69	0.01	0.66	0.66	
SEQ ID NO.	Specificity	Pos.Pred. Value	Neg.Pred. Value	mfd	uvaORPval
SEQ ID NO. 6	0.94	0.97	0.29	1.21	0.00
SEQ ID NO. 22	0.56	0.85	0.28	1.29	0.03
SEQ ID NO. 20	0.89	0.96	0.40	1.13	0.00
SEQ ID NO. 15	0.89	0.96	0.39	1.18	0.00
SEQ ID NO. 19	0.94	0.98	0.40	1.25	0.00
SEQ ID NO. 12	0.33	0.67	0.11	0.89	0.01
SEQ ID NO. 28	0.83	0.94	0.38	1.62	0.00
SEQ ID NO. 16	0.11	0.67	0.05	0.91	0.00
SEQ ID NO. 9	0.28	0.78	0.17	0.92	0.05
SEQ ID NO. 17	0.72	0.91	0.41	1.17	0.00
SEQ ID NO. 18	0.83	0.93	0.31	1.17	0.02
SEQ ID NO. 4	1.00	1.00	0.26	1.05	0.01
SEQ ID NO. 24	0.83	0.91	0.28	1.20	0.04
SEQ ID NO. 40	0.06	0.74	0.04	0.97	0.02
SEQ ID NO. 26	0.67	0.89	0.33	1.08	0.03

Table 46: biomarkers from the 43 biomarker panel with significance for Wilcoxon P-value (auc.pvalue) and other metrics for the PCSM event endpoint. Auc.pvalue : Wilcoxon Test P-value. MFD: Median Fold Difference. KM: Kaplan Meier curves. survAUC: survival AUC. uvaORPval: Univariable Analysis Odds Ratio P-value. mvaORPval: multivariable analysis Odds Ratio P-value. uvaHRPval: Univariable Analysis Hazard Ratio P-value. mvaHRPval: Multivariable Analysis Hazard Ratio P-value.

SEQ ID NO.	auc	auc.pvalue	Accuracy	Sensitivity	Specificity	Pos.Pred. Value	Neg.Pred. Value
SEQ ID	0.72	0.00	0.56	0.81	0.51	0.28	0.92

NO. 6							
SEQ ID NO. 22	0.71	0.00	0.55	0.83	0.48	0.28	0.92
SEQ ID NO. 20	0.71	0.00	0.54	0.78	0.49	0.27	0.90
SEQ ID NO. 15	0.67	0.00	0.49	0.86	0.41	0.26	0.92
SEQ ID NO. 19	0.73	0.00	0.54	0.81	0.48	0.27	0.91
SEQ ID NO. 12	0.68	0.00	0.40	0.25	0.44	0.10	0.71
SEQ ID NO. 28	0.74	0.00	0.57	0.94	0.48	0.30	0.97
SEQ ID NO. 43	0.61	0.03	0.52	0.69	0.47	0.24	0.87
SEQ ID NO. 32	0.66	0.00	0.58	0.72	0.55	0.28	0.89
SEQ ID NO. 16	0.70	0.00	0.39	0.25	0.42	0.09	0.70
SEQ ID NO. 17	0.61	0.05	0.48	0.75	0.41	0.23	0.87
SEQ ID NO. 18	0.66	0.00	0.65	0.61	0.65	0.30	0.88
SEQ ID NO. 4	0.72	0.00	0.78	0.58	0.83	0.45	0.89
SEQ ID NO. 24	0.70	0.00	0.63	0.61	0.63	0.29	0.87
SEQ ID NO. 40	0.61	0.03	0.35	0.53	0.31	0.16	0.73
SEQ ID NO. 26	0.66	0.00	0.59	0.75	0.55	0.29	0.90
SEQ ID NO.	mfd	uva OR Pval	mva OR Pval	KM P-value	surv AUC	uva HRPval	mva HRPval
SEQ ID NO. 6	1.16	0.00	0.04	0.00	0.79	0.00	0.02
SEQ ID NO. 22	1.26	0.00	0.05	0.00	0.73	0.00	0.05
SEQ ID NO. 20	1.12	0.00	0.01	0.00	0.82	0.00	0.00
SEQ ID NO. 15	1.07	0.00	0.23	0.00	0.63	0.00	0.33
SEQ ID NO. 19	1.18	0.00	0.03	0.00	0.87	0.00	0.01
SEQ ID NO. 12	0.92	0.00	0.19	0.00	0.29	0.00	0.01
SEQ ID NO. 28	1.21	0.00	0.01	0.00	0.76	0.00	0.00

SEQ ID NO. 43	1.01	0.02	0.01	0.11	0.44	0.03	0.07
SEQ ID NO. 32	1.14	0.00	0.29	0.00	0.75	0.00	0.21
SEQ ID NO. 16	0.93	0.00	0.24	0.00	0.40	0.00	0.04
SEQ ID NO. 17	1.05	0.06	0.80	0.04	0.58	0.03	0.46
SEQ ID NO. 18	1.11	0.00	0.05	0.00	0.73	0.00	0.18
SEQ ID NO. 4	1.17	0.00	0.02	0.00	0.77	0.00	0.03
SEQ ID NO. 24	1.20	0.00	0.01	0.00	0.87	0.00	0.00
SEQ ID NO. 40	0.98	0.03	0.71	0.11	0.47	0.04	0.89
SEQ ID NO. 26	1.05	0.01	0.06	0.00	0.71	0.00	0.12

Table 47: biomarkers from the 43 biomarker panel with significance for Wilcoxon P-value (auc.pvalue) and other metrics for the psaDT endpoint. Auc.pvalue : Wilcoxon Test P-value. MFD: Median Fold Difference. uvaORPval: Univariable Analysis Odds Ratio P-value. mvaORPval: multivariable analysis Odds Ratio P-value.

SEQ ID NO.	auc	auc.pvalue	Accuracy	Sensitivity	Specificity	Pos. Pred. Value	Neg. Pred. Value	mfd	uva OR Pval	mva OR Pval
SEQ ID NO. 6	0.62	0.02	0.43	0.52	0.38	0.32	0.58	0.97	0.01	0.07
SEQ ID NO. 28	0.62	0.03	0.40	0.43	0.38	0.28	0.54	0.83	0.01	0.30
SEQ ID NO. 16	0.62	0.02	0.56	0.57	0.56	0.42	0.70	1.04	0.04	0.02

Table 48: biomarkers from the 43 biomarker panel with significance for Wilcoxon P-value (auc.pvalue) and other metrics for the SVI endpoint. Auc.pvalue : Wilcoxon Test P-value. MFD: Median Fold Difference. uvaORPval: Univariable Analysis Odds Ratio P-value. mvaORPval: multivariable analysis Odds Ratio P-value.

SEQ ID NO.	auc	auc.pvalue	Accuracy	Sensitivity	Specificity	Pos. Pred. Value	Neg. Pred. Value	mfd	uva OR Pval	mva OR Pval
SEQ ID NO. 6	0.63	0.00	0.56	0.67	0.51	0.43	0.73	1.08	0.00	0.08
SEQ ID NO. 22	0.60	0.03	0.53	0.65	0.46	0.40	0.71	1.08	0.02	0.15
SEQ ID NO. 19	0.64	0.00	0.56	0.70	0.49	0.43	0.75	1.09	0.00	0.04

SEQ ID NO. 17	0.67	0.00	0.58	0.77	0.47	0.44	0.79	1.06	0.00	0.02
SEQ ID NO. 18	0.61	0.01	0.63	0.55	0.68	0.49	0.73	1.10	0.04	0.08
SEQ ID NO. 4	0.69	0.00	0.68	0.41	0.83	0.57	0.72	1.09	0.00	0.02
SEQ ID NO. 26	0.61	0.01	0.59	0.64	0.57	0.45	0.74	1.04	0.07	0.09

[0545] In addition to the good performance of these variables as univariable predictors, the combination of them in pairs (pairwise classifiers) through a machine learning algorithm results in enhanced performance. As shown in Tables 49 to 52, pairwise classifiers can result in an improved performance for a given endpoint compared to their univariable counterparts, with all the classifiers listed presenting statistical significance based on, at least, Wilcoxon P-value. In those tables, each classifier name is described by the machine learning algorithm that combines the biomarkers as well as the SEQ ID NO of the corresponding biomarkers (Table 2, Table 11). The machine learning algorithms included in this analysis are Naïve Bayes (NB), recursive Partitioning (Rpart), Support Vector Machines (SVMs), Random Forest (RF) and K Nearest Neighbors (KNN). These machine learning algorithms were executed with default parameters using packages rpart 4.1-0, HDclassif 1.2.2, randomForest 4.6-7, caret 5.15-61, cluster 1.14.3, e1071 1.6-1, class 7.3-5 in R. Tables 49 to 52 contain metrics and endpoints described above for tables 39 to 48.

Table 49: pairwise biomarkers from the 43 biomarker panel with significance for Wilcoxon P-value (auc.pvalue≤0.05) and other metrics for the BCR event endpoint.
Auc.pvalue : Wilcoxon Test P-value. MFD: Median Fold Difference. KM: Kaplan Meier curves. mvaHRPval: Multivariable Analysis Hazard Ratio P-value.

Classifier	auc	auc. pvalue	Sensitivity	Specificity	Pos. Pred. Value	Neg. Pred. Value	KM P- value	Mva HRPval
svm~5+6	0.68	0.00	0.42	0.78	0.81	0.38	0.01	0.03
knn~5+19	0.67	0.00	0.59	0.69	0.81	0.43	0.00	0.00
rpart~4+39	0.66	0.00	0.42	0.81	0.83	0.39	0.00	0.00
nb~13+6	0.67	0.00	0.50	0.84	0.88	0.43	0.00	0.03
rpart~40+19	0.66	0.00	0.76	0.38	0.73	0.42	0.03	0.12
svm~16+5	0.65	0.00	0.58	0.71	0.81	0.43	0.00	0.50
rf~4+39	0.65	0.00	0.57	0.67	0.79	0.41	0.00	0.00
rpart~4+1	0.64	0.00	0.60	0.62	0.78	0.41	0.00	0.03
rpart~13+6	0.64	0.00	0.50	0.79	0.84	0.42	0.00	0.07
svm~16+6	0.65	0.00	0.48	0.72	0.79	0.39	0.00	0.05
nb~4+16	0.65	0.00	0.30	0.88	0.84	0.36	0.00	0.01
nb~4+13	0.65	0.00	0.26	0.91	0.87	0.36	0.00	0.00

svm~4+39	0.65	0.00	0.45	0.81	0.84	0.40	0.00	0.00
knn~18+28	0.64	0.00	0.68	0.50	0.75	0.41	0.01	0.11
nb~9+6	0.65	0.00	0.54	0.66	0.78	0.39	0.00	0.15
nb~4+1	0.64	0.00	0.35	0.86	0.85	0.38	0.00	0.00
rpart~18+13	0.64	0.00	0.52	0.67	0.78	0.39	0.01	0.89
svm~4+16	0.64	0.00	0.40	0.76	0.78	0.36	0.01	0.02
nb~18+13	0.64	0.00	0.57	0.64	0.78	0.40	0.01	0.21
rf~13+6	0.64	0.00	0.56	0.66	0.78	0.40	0.00	0.25
svm~4+24	0.64	0.00	0.29	0.86	0.82	0.35	0.00	0.00
svm~4+6	0.64	0.00	0.40	0.79	0.81	0.37	0.00	0.05
rpart~13+26	0.64	0.00	0.38	0.83	0.83	0.38	0.00	0.01
nb~1+6	0.64	0.00	0.37	0.78	0.78	0.36	0.04	0.03
knn~18+10	0.64	0.00	0.69	0.45	0.73	0.39	0.05	0.52
nb~4+32	0.64	0.00	0.32	0.86	0.84	0.36	0.00	0.00
rf~19+3	0.64	0.00	0.54	0.71	0.80	0.41	0.00	0.00
knn~13+22	0.64	0.00	0.73	0.43	0.74	0.42	0.01	0.10
nb~13+19	0.64	0.00	0.63	0.62	0.79	0.43	0.00	0.00
rpart~5+28	0.63	0.00	0.57	0.62	0.77	0.40	0.01	0.23
rpart~24+22	0.63	0.00	0.41	0.81	0.83	0.38	0.00	0.00
svm~5+28	0.64	0.00	0.49	0.72	0.80	0.39	0.01	0.29
svm~15+5	0.64	0.00	0.31	0.84	0.82	0.36	0.03	0.22
nb~5+6	0.64	0.00	0.36	0.81	0.81	0.36	0.01	0.05
rpart~13+20	0.64	0.00	0.54	0.62	0.76	0.38	0.06	0.01
svm~5+19	0.64	0.00	0.57	0.64	0.78	0.40	0.01	0.04
knn~5+22	0.63	0.00	0.54	0.71	0.80	0.41	0.00	0.03
knn~18+13	0.63	0.00	0.71	0.43	0.73	0.40	0.06	0.27
svm~13+6	0.64	0.00	0.47	0.79	0.83	0.40	0.00	0.10
rf~4+19	0.64	0.00	0.50	0.74	0.81	0.40	0.00	0.00
nb~16+5	0.64	0.00	0.61	0.62	0.78	0.42	0.02	0.33
knn~4+19	0.63	0.00	0.51	0.76	0.82	0.41	0.00	0.02
nb~16+6	0.64	0.00	0.44	0.78	0.81	0.38	0.00	0.07
nb~4+6	0.64	0.00	0.36	0.83	0.82	0.37	0.00	0.01
svm~4+5	0.64	0.00	0.55	0.67	0.79	0.40	0.01	0.27
rf~13+22	0.63	0.00	0.60	0.66	0.79	0.43	0.00	0.08
rpart~4+32	0.63	0.00	0.41	0.76	0.79	0.37	0.01	0.00
knn~4+39	0.63	0.00	0.70	0.47	0.74	0.42	0.01	0.00
rf~18+8	0.63	0.00	0.55	0.67	0.79	0.41	0.01	0.36
knn~4+22	0.63	0.00	0.67	0.55	0.77	0.43	0.00	0.02
rpart~11+5	0.63	0.00	0.41	0.78	0.80	0.37	0.07	0.09
rpart~9+6	0.63	0.00	0.50	0.74	0.81	0.40	0.00	0.27
knn~17+5	0.63	0.00	0.53	0.69	0.79	0.40	0.01	0.06
rpart~29+22	0.63	0.00	0.54	0.64	0.77	0.39	0.01	0.02
svm~16+18	0.63	0.00	0.41	0.72	0.76	0.36	0.06	0.22
knn~8+22	0.63	0.00	0.48	0.72	0.79	0.39	0.00	0.07
nb~4+28	0.63	0.00	0.34	0.83	0.81	0.36	0.00	0.00
svm~15+19	0.63	0.00	0.30	0.86	0.83	0.36	0.01	0.08
nb~13+22	0.63	0.00	0.48	0.72	0.79	0.39	0.01	0.01

rf~7+19	0.63	0.00	0.63	0.62	0.79	0.43	0.00	0.98
knn~4+9	0.63	0.00	0.44	0.76	0.80	0.38	0.00	0.01
rf~4+38	0.63	0.00	0.44	0.76	0.80	0.38	0.00	0.33
svm~9+6	0.63	0.00	0.44	0.72	0.78	0.37	0.01	0.40
rf~16+18	0.63	0.00	0.51	0.72	0.80	0.40	0.01	0.12
rf~42+19	0.63	0.00	0.57	0.66	0.78	0.41	0.00	0.00
rpart~18+32	0.63	0.00	0.49	0.67	0.77	0.38	0.02	0.07
knn~29+18	0.63	0.00	0.45	0.76	0.81	0.39	0.01	0.57
rf~12+38	0.63	0.01	0.45	0.74	0.79	0.38	0.02	0.36
rf~4+8	0.63	0.01	0.65	0.55	0.76	0.42	0.00	0.02
knn~11+5	0.62	0.01	0.72	0.45	0.74	0.42	0.05	0.42
rf~4+1	0.63	0.01	0.52	0.67	0.78	0.39	0.01	0.07
rf~16+39	0.63	0.01	0.49	0.69	0.78	0.38	0.01	0.74
nb~33+6	0.63	0.01	0.41	0.79	0.82	0.38	0.01	0.21
nb~32+6	0.63	0.01	0.31	0.90	0.87	0.37	0.00	0.04
svm~13+28	0.63	0.01	0.47	0.72	0.79	0.38	0.01	0.00
svm~1+6	0.63	0.01	0.41	0.72	0.76	0.36	0.03	0.07
svm~9+19	0.63	0.01	0.54	0.64	0.77	0.39	0.01	0.05
knn~5+6	0.62	0.01	0.51	0.76	0.82	0.41	0.00	0.20
nb~28+6	0.63	0.01	0.46	0.76	0.81	0.39	0.00	0.01
rpart~4+31	0.62	0.01	0.49	0.74	0.81	0.40	0.00	0.00
knn~16+39	0.62	0.01	0.71	0.38	0.72	0.37	0.23	0.62
svm~5+32	0.63	0.01	0.42	0.78	0.81	0.38	0.05	0.29
rpart~4+18	0.62	0.01	0.44	0.71	0.77	0.36	0.01	0.33
rpart~16+20	0.62	0.01	0.60	0.60	0.77	0.41	0.00	0.04
knn~32+6	0.62	0.01	0.46	0.72	0.79	0.38	0.01	0.02
svm~4+15	0.63	0.01	0.26	0.84	0.79	0.34	0.01	0.01
nb~7+6	0.62	0.01	0.45	0.78	0.82	0.39	0.00	0.54
knn~18+6	0.62	0.01	0.41	0.79	0.82	0.38	0.01	0.58
knn~39+22	0.62	0.01	0.53	0.67	0.78	0.39	0.00	0.06
rf~18+13	0.62	0.01	0.55	0.64	0.77	0.39	0.02	0.30
rpart~20+6	0.62	0.01	0.49	0.66	0.76	0.37	0.02	0.04
svm~19+28	0.62	0.01	0.43	0.76	0.80	0.38	0.01	0.01
svm~19+6	0.62	0.01	0.44	0.74	0.79	0.37	0.00	0.01
knn~12+22	0.62	0.01	0.45	0.76	0.81	0.39	0.00	0.00
knn~20+6	0.62	0.01	0.59	0.55	0.75	0.38	0.03	0.03
nb~1+22	0.62	0.01	0.49	0.59	0.72	0.34	0.31	0.01
nb~15+13	0.62	0.01	0.45	0.72	0.78	0.37	0.03	0.42
nb~16+18	0.62	0.01	0.50	0.67	0.77	0.38	0.02	0.27
nb~4+9	0.62	0.01	0.37	0.86	0.85	0.38	0.00	0.04
nb~9+22	0.62	0.01	0.41	0.74	0.78	0.36	0.03	0.12
svm~18+6	0.62	0.01	0.38	0.78	0.79	0.36	0.01	0.09
knn~4+16	0.62	0.01	0.54	0.66	0.78	0.39	0.01	0.01
rf~18+9	0.62	0.01	0.48	0.69	0.77	0.37	0.05	0.27
nb~5+19	0.62	0.01	0.61	0.53	0.74	0.38	0.09	0.05
svm~4+41	0.62	0.01	0.27	0.88	0.83	0.35	0.00	0.03
nb~4+36	0.62	0.01	0.22	0.88	0.80	0.34	0.01	0.01

nb~4+5	0.62	0.01	0.36	0.84	0.84	0.37	0.00	0.02
svm~24+6	0.62	0.01	0.34	0.83	0.81	0.36	0.00	0.09
nb~36+6	0.62	0.01	0.40	0.81	0.82	0.38	0.00	0.05
rpart~4+28	0.62	0.01	0.39	0.79	0.81	0.37	0.00	0.04
svm~5+22	0.62	0.01	0.48	0.71	0.78	0.38	0.03	0.01
rpart~39+18	0.61	0.01	0.45	0.71	0.77	0.37	0.02	0.52
rf~4+31	0.62	0.01	0.47	0.72	0.79	0.38	0.01	0.02
svm~28+6	0.62	0.01	0.41	0.74	0.78	0.36	0.01	0.01
rpart~18+22	0.61	0.01	0.37	0.84	0.84	0.38	0.00	0.32
nb~4+22	0.62	0.01	0.38	0.84	0.84	0.38	0.00	0.00
nb~4+24	0.62	0.01	0.26	0.90	0.85	0.35	0.00	0.00
nb~8+6	0.62	0.01	0.41	0.81	0.83	0.38	0.01	0.24
nb~13+32	0.62	0.01	0.50	0.67	0.77	0.38	0.06	0.02
rpart~13+22	0.62	0.01	0.59	0.59	0.76	0.40	0.01	0.11
rpart~16+28	0.62	0.01	0.45	0.71	0.77	0.37	0.05	0.06
rf~29+22	0.62	0.01	0.56	0.67	0.79	0.41	0.00	0.06
rpart~4+16	0.62	0.01	0.46	0.74	0.80	0.38	0.00	0.00
rf~1+22	0.62	0.01	0.54	0.66	0.78	0.39	0.01	0.16
svm~4+19	0.62	0.01	0.49	0.76	0.82	0.40	0.00	0.00
nb~18+6	0.62	0.01	0.44	0.74	0.79	0.37	0.00	0.04
nb~5+22	0.62	0.01	0.52	0.66	0.77	0.38	0.02	0.02
knn~10+22	0.62	0.01	0.73	0.45	0.75	0.43	0.01	0.61
rpart~4+8	0.62	0.01	0.50	0.69	0.78	0.38	0.01	0.14
nb~16+13	0.62	0.01	0.42	0.69	0.75	0.35	0.21	0.64
nb~4+33	0.62	0.01	0.29	0.91	0.88	0.37	0.00	0.05
rf~13+26	0.62	0.01	0.45	0.67	0.75	0.36	0.03	0.46
svm~18+8	0.62	0.01	0.48	0.69	0.78	0.38	0.03	0.44
rf~7+18	0.62	0.01	0.55	0.55	0.73	0.36	0.20	0.52
svm~38+6	0.62	0.01	0.46	0.76	0.81	0.39	0.00	0.18
nb~25+6	0.62	0.01	0.41	0.84	0.85	0.39	0.00	0.03
svm~32+6	0.62	0.01	0.36	0.81	0.81	0.36	0.00	0.02
svm~16+13	0.62	0.01	0.40	0.69	0.74	0.34	0.36	0.81
svm~4+9	0.62	0.01	0.39	0.79	0.81	0.37	0.00	0.15
svm~7+6	0.62	0.01	0.52	0.71	0.80	0.40	0.00	0.42
knn~15+41	0.61	0.01	0.56	0.64	0.77	0.40	0.02	0.46
rf~18+28	0.62	0.01	0.56	0.64	0.77	0.40	0.00	0.06
rpart~18+19	0.61	0.01	0.59	0.60	0.77	0.40	0.00	0.03
nb~4+7	0.62	0.01	0.36	0.79	0.79	0.36	0.02	0.25
svm~18+13	0.62	0.01	0.47	0.69	0.77	0.37	0.01	0.08
rpart~21+22	0.61	0.01	0.46	0.66	0.75	0.36	0.08	0.52
nb~37+6	0.62	0.01	0.48	0.72	0.79	0.39	0.00	0.21
rf~18+38	0.62	0.01	0.45	0.79	0.83	0.39	0.00	0.72
rf~8+22	0.62	0.01	0.54	0.64	0.77	0.39	0.01	0.21
nb~4+2	0.62	0.01	0.40	0.74	0.77	0.36	0.04	0.53
svm~39+32	0.62	0.01	0.32	0.86	0.84	0.36	0.02	0.01
knn~16+38	0.61	0.01	0.77	0.45	0.75	0.46	0.00	0.97
nb~2+6	0.62	0.01	0.46	0.74	0.80	0.38	0.01	0.99

rf~4+12	0.62	0.01	0.52	0.60	0.74	0.36	0.07	0.03
svm~4+13	0.62	0.01	0.33	0.90	0.88	0.38	0.00	0.00
nb~5+32	0.62	0.01	0.58	0.62	0.77	0.40	0.07	0.08
knn~12+16	0.61	0.01	0.43	0.78	0.81	0.38	0.00	0.04
knn~4+6	0.61	0.01	0.42	0.76	0.79	0.37	0.01	0.01
rf~9+19	0.62	0.01	0.58	0.64	0.78	0.41	0.00	0.00
rf~18+6	0.62	0.01	0.49	0.64	0.75	0.36	0.09	0.48
nb~4+8	0.62	0.01	0.25	0.90	0.84	0.35	0.00	0.02
svm~12+6	0.62	0.01	0.45	0.76	0.81	0.39	0.00	0.02
rpart~1+18	0.61	0.01	0.31	0.84	0.82	0.36	0.05	0.62
rpart~18+28	0.61	0.01	0.41	0.79	0.82	0.38	0.00	0.25
nb~19+6	0.62	0.01	0.38	0.79	0.80	0.37	0.01	0.01
nb~13+28	0.62	0.01	0.43	0.74	0.79	0.37	0.02	0.00
rpart~41+18	0.61	0.01	0.45	0.74	0.79	0.38	0.00	0.55
rpart~18+21	0.61	0.01	0.55	0.60	0.76	0.38	0.03	0.89
rf~4+34	0.61	0.01	0.68	0.47	0.74	0.40	0.04	0.03
nb~22+6	0.61	0.01	0.46	0.74	0.80	0.38	0.00	0.02
rf~12+31	0.61	0.01	0.53	0.57	0.73	0.35	0.03	0.05
knn~4+12	0.61	0.01	0.27	0.79	0.74	0.33	0.12	0.06
knn~4+5	0.61	0.01	0.72	0.43	0.74	0.41	0.07	0.34
rpart~4+42	0.61	0.01	0.55	0.66	0.78	0.40	0.01	0.62
svm~13+19	0.61	0.01	0.62	0.55	0.75	0.40	0.02	0.06
nb~16+38	0.61	0.01	0.36	0.69	0.72	0.33	0.58	0.41
nb~24+6	0.61	0.01	0.27	0.84	0.79	0.34	0.04	0.02
knn~16+6	0.61	0.01	0.45	0.71	0.77	0.37	0.04	0.49
nb~15+6	0.61	0.01	0.30	0.86	0.83	0.36	0.00	0.07
nb~15+5	0.61	0.01	0.55	0.71	0.81	0.42	0.00	0.43
svm~31+6	0.61	0.01	0.46	0.69	0.77	0.37	0.05	0.07
nb~5+28	0.61	0.01	0.49	0.72	0.80	0.39	0.01	0.05
rpart~39+22	0.61	0.01	0.53	0.62	0.76	0.38	0.03	0.01
nb~4+19	0.61	0.01	0.36	0.84	0.84	0.37	0.00	0.00
rf~4+16	0.61	0.01	0.55	0.60	0.76	0.38	0.05	0.00
nb~7+22	0.61	0.01	0.51	0.67	0.77	0.38	0.02	0.57
rpart~1+28	0.61	0.01	0.45	0.69	0.76	0.36	0.03	0.22
rpart~15+33	0.61	0.01	0.27	0.93	0.89	0.36	0.00	0.03
rf~35+5	0.61	0.01	0.58	0.59	0.76	0.39	0.09	0.83
rpart~8+6	0.61	0.01	0.45	0.78	0.82	0.39	0.00	0.25
rpart~18+26	0.61	0.01	0.26	0.83	0.77	0.34	0.08	0.38
svm~8+6	0.61	0.01	0.46	0.76	0.81	0.39	0.00	0.54
knn~9+22	0.61	0.01	0.45	0.71	0.77	0.37	0.02	0.15
rf~5+19	0.61	0.01	0.55	0.62	0.76	0.38	0.03	0.03
rpart~2+19	0.61	0.01	0.71	0.36	0.71	0.36	0.30	0.34
nb~16+22	0.61	0.01	0.45	0.69	0.76	0.36	0.05	0.02
nb~35+6	0.61	0.01	0.38	0.78	0.79	0.36	0.02	0.17
svm~4+7	0.61	0.01	0.44	0.78	0.81	0.38	0.00	0.38
svm~15+6	0.61	0.01	0.37	0.81	0.81	0.37	0.00	0.08
knn~9+19	0.61	0.01	0.59	0.62	0.77	0.40	0.01	0.06

rf~18+22	0.61	0.01	0.50	0.64	0.75	0.37	0.06	0.03
nb~1+28	0.61	0.01	0.41	0.74	0.78	0.36	0.03	0.00
nb~18+9	0.61	0.01	0.52	0.64	0.76	0.37	0.02	0.81
knn~16+28	0.61	0.01	0.77	0.41	0.74	0.44	0.00	0.03
nb~11+6	0.61	0.01	0.31	0.90	0.87	0.37	0.00	0.07
svm~21+6	0.61	0.01	0.45	0.71	0.77	0.37	0.02	0.58
nb~4+18	0.61	0.02	0.37	0.78	0.78	0.36	0.01	0.01
rf~4+7	0.61	0.02	0.51	0.64	0.76	0.37	0.05	0.45
svm~13+22	0.61	0.02	0.49	0.71	0.79	0.39	0.00	0.16
nb~4+38	0.61	0.02	0.38	0.74	0.76	0.35	0.07	0.67
rf~26+22	0.61	0.02	0.49	0.69	0.78	0.38	0.00	0.04
svm~41+6	0.61	0.02	0.49	0.71	0.79	0.39	0.01	0.07
rf~39+32	0.61	0.02	0.59	0.60	0.77	0.40	0.01	0.00
knn~29+6	0.61	0.02	0.44	0.72	0.78	0.37	0.02	0.04
rpart~33+19	0.59	0.02	0.45	0.74	0.79	0.38	0.00	0.01
svm~19+38	0.61	0.02	0.49	0.69	0.78	0.38	0.01	0.09
rf~7+6	0.61	0.02	0.58	0.62	0.77	0.40	0.02	0.92
svm~4+1	0.61	0.02	0.31	0.84	0.82	0.36	0.02	0.01
svm~26+19	0.61	0.02	0.37	0.79	0.80	0.36	0.01	0.03
nb~13+20	0.61	0.02	0.52	0.62	0.75	0.37	0.03	0.03
nb~41+6	0.61	0.02	0.33	0.83	0.81	0.36	0.01	0.11
rf~1+18	0.61	0.02	0.64	0.53	0.75	0.40	0.09	0.72
rpart~15+13	0.61	0.02	0.34	0.76	0.75	0.34	0.27	0.10
svm~4+28	0.61	0.02	0.38	0.78	0.79	0.36	0.01	0.00
nb~34+6	0.61	0.02	0.43	0.76	0.80	0.38	0.01	0.19
nb~32+22	0.61	0.02	0.48	0.64	0.74	0.36	0.09	0.01
nb~4+41	0.61	0.02	0.31	0.83	0.80	0.35	0.01	0.03
rf~5+22	0.61	0.02	0.59	0.59	0.76	0.39	0.07	0.05
nb~10+6	0.61	0.02	0.30	0.86	0.83	0.36	0.01	0.23
svm~3+28	0.61	0.02	0.26	0.84	0.79	0.34	0.04	0.01
knn~40+28	0.61	0.02	0.37	0.86	0.85	0.38	0.00	0.25
nb~1+18	0.61	0.02	0.34	0.74	0.75	0.34	0.25	0.17
nb~18+22	0.61	0.02	0.55	0.66	0.78	0.40	0.00	0.01
knn~37+6	0.61	0.02	0.65	0.43	0.72	0.36	0.22	0.63
svm~9+22	0.61	0.02	0.38	0.78	0.79	0.36	0.01	0.29
svm~16+38	0.61	0.02	0.36	0.74	0.75	0.34	0.18	0.40
nb~13+26	0.61	0.02	0.61	0.52	0.74	0.38	0.12	0.10
knn~13+6	0.61	0.02	0.67	0.50	0.75	0.41	0.02	0.31
svm~7+22	0.61	0.02	0.52	0.67	0.78	0.39	0.01	0.66
nb~4+20	0.61	0.02	0.41	0.76	0.79	0.37	0.00	0.01
svm~34+6	0.61	0.02	0.51	0.64	0.76	0.37	0.02	0.16
nb~1+16	0.61	0.02	0.37	0.72	0.75	0.34	0.44	0.51
rf~4+9	0.61	0.02	0.48	0.66	0.75	0.36	0.02	0.03
rpart~12+5	0.60	0.02	0.49	0.71	0.79	0.39	0.02	0.50
rpart~18+8	0.60	0.02	0.48	0.74	0.81	0.39	0.00	0.86
svm~2+6	0.61	0.02	0.52	0.64	0.76	0.38	0.02	0.98
rpart~9+19	0.60	0.02	0.59	0.59	0.76	0.39	0.01	0.02

svm~4+8	0.61	0.02	0.31	0.81	0.78	0.35	0.03	0.04
rpart~31+22	0.60	0.02	0.45	0.72	0.78	0.38	0.01	0.03
nb~4+15	0.61	0.02	0.32	0.83	0.80	0.36	0.00	0.01
svm~10+6	0.61	0.02	0.36	0.81	0.81	0.36	0.00	0.18
nb~18+32	0.61	0.02	0.41	0.72	0.77	0.36	0.02	0.02
svm~4+38	0.61	0.02	0.35	0.78	0.78	0.35	0.02	0.16
nb~4+25	0.61	0.02	0.38	0.83	0.83	0.38	0.00	0.00
knn~30+6	0.60	0.02	0.50	0.62	0.74	0.36	0.12	0.14
nb~15+16	0.61	0.02	0.33	0.71	0.71	0.32	0.56	0.59
svm~2+28	0.61	0.02	0.52	0.59	0.74	0.36	0.07	0.21
rpart~4+5	0.60	0.02	0.48	0.66	0.76	0.37	0.13	0.91
nb~16+28	0.61	0.02	0.52	0.66	0.77	0.38	0.02	0.02
svm~26+6	0.61	0.02	0.38	0.76	0.77	0.35	0.02	0.09
svm~16+34	0.61	0.02	0.37	0.74	0.76	0.35	0.16	0.43
rf~15+28	0.61	0.02	0.52	0.59	0.74	0.36	0.17	0.52
nb~18+5	0.61	0.02	0.63	0.48	0.73	0.37	0.48	0.39
rf~26+19	0.61	0.02	0.56	0.69	0.80	0.42	0.00	0.01
rpart~28+22	0.60	0.02	0.48	0.67	0.77	0.37	0.01	0.00
knn~12+6	0.60	0.02	0.46	0.76	0.81	0.39	0.00	0.02
knn~28+21	0.60	0.02	0.70	0.41	0.73	0.39	0.11	0.11
knn~36+6	0.60	0.02	0.48	0.67	0.76	0.37	0.04	0.01
rf~19+22	0.60	0.02	0.35	0.72	0.74	0.34	0.19	0.00
knn~13+21	0.60	0.02	0.73	0.45	0.75	0.43	0.05	0.21
rpart~1+29	0.60	0.02	0.30	0.83	0.80	0.35	0.23	0.68
rpart~26+22	0.60	0.02	0.38	0.79	0.80	0.37	0.00	0.01
nb~1+15	0.60	0.02	0.37	0.71	0.73	0.34	0.54	0.37
rpart~5+32	0.60	0.02	0.42	0.71	0.76	0.36	0.24	0.16
rf~9+28	0.60	0.02	0.48	0.69	0.77	0.37	0.01	0.02
svm~18+19	0.60	0.02	0.50	0.72	0.80	0.40	0.00	0.01
nb~14+6	0.60	0.02	0.40	0.81	0.82	0.38	0.00	0.03
knn~17+37	0.60	0.02	0.71	0.50	0.76	0.44	0.00	0.22
nb~9+19	0.60	0.02	0.56	0.60	0.76	0.38	0.00	0.07
rpart~20+28	0.60	0.02	0.63	0.50	0.73	0.38	0.03	0.00
svm~15+13	0.60	0.02	0.40	0.76	0.78	0.36	0.01	0.15
nb~17+6	0.60	0.02	0.48	0.67	0.76	0.37	0.02	0.01
rf~38+28	0.60	0.02	0.52	0.62	0.75	0.37	0.07	0.05
nb~16+32	0.60	0.02	0.39	0.71	0.75	0.34	0.19	0.12
rf~4+22	0.60	0.02	0.59	0.60	0.77	0.40	0.00	0.00
svm~16+22	0.60	0.02	0.47	0.60	0.72	0.34	0.23	0.09
nb~28+22	0.60	0.02	0.46	0.67	0.76	0.36	0.02	0.00
svm~41+38	0.60	0.02	0.34	0.76	0.75	0.34	0.33	0.78
knn~19+22	0.60	0.02	0.70	0.38	0.71	0.37	0.31	0.01
rpart~4+9	0.60	0.02	0.43	0.69	0.75	0.35	0.05	0.23
nb~28+32	0.60	0.02	0.45	0.64	0.73	0.35	0.10	0.00
svm~16+31	0.60	0.02	0.32	0.71	0.71	0.32	0.84	0.82
knn~15+24	0.60	0.02	0.57	0.59	0.75	0.38	0.05	0.13
rpart~4+34	0.60	0.02	0.53	0.64	0.76	0.38	0.01	0.10

svm~7+19	0.60	0.02	0.59	0.59	0.76	0.40	0.01	0.47
nb~1+19	0.60	0.02	0.70	0.45	0.74	0.41	0.05	0.00
rpart~26+19	0.60	0.02	0.62	0.53	0.75	0.39	0.04	0.01
rf~4+13	0.60	0.02	0.38	0.81	0.81	0.37	0.00	0.02
rpart~16+18	0.58	0.02	0.30	0.90	0.86	0.37	0.00	0.37
nb~18+28	0.60	0.02	0.42	0.64	0.72	0.33	0.21	0.01
svm~4+29	0.60	0.03	0.28	0.84	0.80	0.35	0.00	0.03
svm~1+18	0.60	0.03	0.35	0.81	0.80	0.36	0.02	0.90
rf~25+28	0.60	0.03	0.45	0.59	0.70	0.32	0.85	0.01
nb~24+22	0.60	0.03	0.51	0.62	0.75	0.36	0.05	0.00
svm~1+19	0.60	0.03	0.49	0.64	0.75	0.36	0.04	0.05
rf~8+19	0.60	0.03	0.35	0.72	0.74	0.34	0.25	0.04
nb~2+22	0.60	0.03	0.46	0.64	0.74	0.35	0.16	0.73
nb~12+6	0.60	0.03	0.51	0.67	0.77	0.38	0.01	0.02
svm~39+6	0.60	0.03	0.40	0.81	0.82	0.38	0.00	0.11
rpart~4+13	0.60	0.03	0.44	0.72	0.78	0.37	0.01	0.00
rpart~5+20	0.60	0.03	0.57	0.55	0.74	0.37	0.05	0.16
svm~4+22	0.60	0.03	0.42	0.83	0.84	0.39	0.00	0.00
svm~25+6	0.60	0.03	0.54	0.62	0.76	0.38	0.02	0.11
rpart~22+6	0.60	0.03	0.41	0.74	0.78	0.36	0.04	0.02
knn~4+1	0.60	0.03	0.70	0.41	0.73	0.39	0.19	0.04
rpart~7+20	0.60	0.03	0.65	0.50	0.74	0.39	0.03	0.88
nb~18+2	0.60	0.03	0.41	0.69	0.74	0.34	0.19	0.23
knn~17+22	0.60	0.03	0.45	0.66	0.74	0.35	0.03	0.01
knn~19+28	0.60	0.03	0.52	0.59	0.74	0.36	0.07	0.03
rpart~20+22	0.60	0.03	0.42	0.72	0.77	0.36	0.02	0.01
svm~39+22	0.60	0.03	0.52	0.62	0.75	0.37	0.04	0.02
knn~22+6	0.60	0.03	0.66	0.50	0.75	0.40	0.03	0.06
rpart~14+22	0.60	0.03	0.38	0.83	0.83	0.38	0.00	0.02
rpart~24+5	0.60	0.03	0.38	0.76	0.78	0.36	0.08	0.02
rf~16+38	0.60	0.03	0.52	0.66	0.77	0.38	0.01	0.69
svm~8+28	0.60	0.03	0.45	0.66	0.74	0.35	0.07	0.01
svm~4+32	0.60	0.03	0.38	0.76	0.78	0.36	0.01	0.00
nb~20+6	0.60	0.03	0.44	0.67	0.75	0.35	0.05	0.03
rpart~1+20	0.60	0.03	0.66	0.50	0.75	0.40	0.03	0.01
knn~24+13	0.60	0.03	0.58	0.53	0.73	0.36	0.07	0.03
rpart~41+28	0.60	0.03	0.38	0.78	0.79	0.36	0.00	0.00
svm~8+22	0.60	0.03	0.41	0.76	0.79	0.37	0.01	0.14
rf~16+28	0.60	0.03	0.47	0.67	0.76	0.36	0.08	0.12
nb~4+37	0.60	0.03	0.34	0.83	0.81	0.36	0.00	0.05
svm~28+21	0.60	0.03	0.40	0.76	0.78	0.36	0.00	0.06
nb~1+32	0.60	0.03	0.40	0.66	0.72	0.33	0.58	0.01
rpart~32+22	0.60	0.03	0.39	0.78	0.79	0.37	0.00	0.02
knn~42+19	0.60	0.03	0.61	0.59	0.76	0.40	0.01	0.02
knn~15+13	0.60	0.03	0.61	0.50	0.73	0.37	0.16	0.20
svm~13+26	0.60	0.03	0.27	0.90	0.85	0.36	0.00	0.05
rf~16+3	0.60	0.03	0.32	0.81	0.79	0.35	0.07	0.00

svm~16+28	0.60	0.03	0.43	0.84	0.86	0.40	0.00	0.01
nb~36+22	0.60	0.03	0.53	0.57	0.73	0.35	0.08	0.02
svm~24+5	0.60	0.03	0.30	0.84	0.81	0.36	0.04	0.02
nb~15+22	0.60	0.03	0.36	0.81	0.81	0.36	0.00	0.03
svm~4+18	0.60	0.03	0.32	0.78	0.76	0.34	0.05	0.03
svm~19+22	0.60	0.03	0.40	0.74	0.77	0.36	0.03	0.01
nb~15+28	0.60	0.03	0.34	0.81	0.80	0.36	0.00	0.01
nb~37+22	0.60	0.03	0.48	0.60	0.73	0.35	0.10	0.10
svm~33+6	0.60	0.03	0.41	0.69	0.75	0.35	0.20	0.27
svm~16+41	0.60	0.03	0.30	0.72	0.71	0.32	0.77	0.87
nb~21+6	0.60	0.03	0.42	0.76	0.79	0.37	0.01	0.34
nb~24+5	0.60	0.03	0.59	0.60	0.77	0.40	0.06	0.06
knn~1+18	0.60	0.03	0.70	0.43	0.73	0.40	0.09	0.61
nb~4+29	0.60	0.03	0.36	0.74	0.75	0.34	0.06	0.13
svm~16+10	0.60	0.03	0.53	0.62	0.76	0.38	0.08	0.67
nb~23+6	0.60	0.03	0.39	0.78	0.79	0.37	0.03	0.82
svm~16+19	0.60	0.03	0.47	0.62	0.73	0.35	0.26	0.18
rpart~4+41	0.60	0.03	0.33	0.84	0.82	0.36	0.00	0.20
rf~12+22	0.60	0.03	0.45	0.71	0.77	0.37	0.00	0.00
rf~20+6	0.60	0.03	0.51	0.62	0.75	0.36	0.11	0.25
nb~4+17	0.60	0.03	0.33	0.83	0.81	0.36	0.00	0.00
svm~4+27	0.60	0.03	0.38	0.74	0.77	0.35	0.00	0.01
knn~26+22	0.59	0.03	0.64	0.52	0.75	0.39	0.03	0.02
nb~16+2	0.60	0.03	0.49	0.69	0.78	0.38	0.03	0.14
svm~1+22	0.60	0.03	0.38	0.79	0.80	0.37	0.01	0.05
rf~9+6	0.60	0.03	0.45	0.66	0.74	0.35	0.07	0.20
rpart~24+19	0.59	0.03	0.52	0.62	0.75	0.37	0.04	0.00
nb~16+20	0.60	0.03	0.57	0.53	0.73	0.36	0.05	0.06
rpart~1+21	0.60	0.03	0.36	0.76	0.77	0.35	0.20	0.27
nb~38+6	0.60	0.03	0.39	0.76	0.78	0.36	0.04	0.99
nb~16+41	0.60	0.03	0.32	0.72	0.72	0.33	0.56	0.74
nb~4+14	0.60	0.03	0.26	0.88	0.83	0.35	0.00	0.01
rpart~42+22	0.59	0.03	0.49	0.60	0.73	0.35	0.07	0.09
nb~2+28	0.60	0.03	0.44	0.67	0.75	0.35	0.05	0.51
nb~4+11	0.60	0.03	0.23	0.93	0.88	0.35	0.00	0.01
nb~4+35	0.60	0.03	0.30	0.88	0.84	0.36	0.00	0.05
rpart~19+3	0.59	0.04	0.47	0.72	0.79	0.38	0.00	0.01
nb~5+2	0.60	0.04	0.38	0.86	0.86	0.38	0.00	0.31
svm~12+5	0.60	0.04	0.52	0.62	0.75	0.37	0.07	0.28
nb~35+5	0.60	0.04	0.64	0.53	0.75	0.40	0.09	0.77
rpart~20+34	0.59	0.04	0.59	0.53	0.74	0.37	0.10	0.03
knn~1+28	0.59	0.04	0.73	0.40	0.73	0.40	0.08	0.23
rf~41+20	0.60	0.04	0.52	0.66	0.77	0.38	0.02	0.03
nb~19+22	0.60	0.04	0.59	0.59	0.76	0.39	0.01	0.00
rpart~18+9	0.58	0.04	0.38	0.81	0.82	0.37	0.00	0.86
rpart~15+3	0.59	0.04	0.20	0.88	0.78	0.33	0.13	0.18
nb~8+22	0.60	0.04	0.55	0.60	0.75	0.38	0.06	0.10

nb~19+32	0.60	0.04	0.41	0.72	0.76	0.36	0.04	0.00
svm~17+6	0.60	0.04	0.39	0.72	0.76	0.35	0.05	0.04
rpart~16+22	0.59	0.04	0.49	0.67	0.77	0.38	0.02	0.18
svm~31+19	0.60	0.04	0.52	0.66	0.77	0.38	0.01	0.00
rpart~5+19	0.59	0.04	0.66	0.53	0.76	0.42	0.00	0.01
knn~41+19	0.59	0.04	0.73	0.40	0.73	0.40	0.02	0.00
nb~41+28	0.60	0.04	0.48	0.60	0.73	0.35	0.13	0.01
svm~15+22	0.60	0.04	0.34	0.84	0.83	0.37	0.00	0.05
rf~35+6	0.60	0.04	0.52	0.57	0.73	0.35	0.28	0.89
rpart~1+6	0.59	0.04	0.47	0.66	0.75	0.36	0.07	0.79
rf~17+9	0.60	0.04	0.49	0.67	0.77	0.38	0.04	0.17
nb~15+9	0.60	0.04	0.46	0.67	0.76	0.36	0.03	0.90
nb~26+6	0.60	0.04	0.45	0.72	0.78	0.37	0.01	0.05
rpart~15+20	0.59	0.04	0.52	0.66	0.77	0.38	0.00	0.13
rpart~1+19	0.59	0.04	0.54	0.64	0.77	0.39	0.03	0.00
knn~35+6	0.59	0.04	0.58	0.57	0.75	0.38	0.10	0.36
knn~35+5	0.59	0.04	0.45	0.72	0.78	0.37	0.09	0.81
rf~9+22	0.60	0.04	0.42	0.71	0.76	0.36	0.05	0.08
rpart~39+28	0.59	0.04	0.50	0.69	0.78	0.38	0.00	0.00
knn~24+8	0.59	0.04	0.52	0.62	0.75	0.37	0.06	0.13
rf~38+22	0.59	0.04	0.48	0.69	0.78	0.38	0.00	0.14
nb~16+11	0.59	0.04	0.42	0.64	0.72	0.33	0.44	0.80
svm~29+28	0.59	0.04	0.32	0.76	0.75	0.34	0.12	0.02
knn~39+32	0.59	0.04	0.67	0.48	0.74	0.40	0.10	0.00
knn~24+22	0.59	0.04	0.37	0.78	0.78	0.36	0.02	0.06
knn~4+36	0.59	0.04	0.69	0.40	0.72	0.37	0.09	0.07
knn~16+22	0.59	0.04	0.51	0.69	0.78	0.39	0.00	0.18
knn~16+3	0.59	0.04	0.62	0.57	0.76	0.40	0.04	0.02
rpart~18+38	0.59	0.04	0.55	0.60	0.75	0.38	0.05	0.22
nb~36+19	0.59	0.04	0.63	0.62	0.78	0.43	0.00	0.01
svm~16+32	0.59	0.04	0.30	0.79	0.76	0.34	0.10	0.13
knn~24+6	0.59	0.04	0.63	0.48	0.73	0.37	0.17	0.07
rpart~4+7	0.59	0.04	0.48	0.67	0.77	0.37	0.05	0.92
nb~25+22	0.59	0.04	0.48	0.72	0.79	0.39	0.00	0.01
knn~40+13	0.59	0.04	0.62	0.55	0.75	0.40	0.03	0.23
svm~39+19	0.59	0.04	0.54	0.64	0.77	0.39	0.00	0.00
nb~3+6	0.59	0.04	0.27	0.86	0.81	0.35	0.02	0.05
rpart~4+14	0.59	0.04	0.37	0.76	0.77	0.35	0.02	0.19
nb~18+8	0.59	0.04	0.41	0.72	0.77	0.36	0.06	0.86
svm~33+28	0.59	0.04	0.52	0.57	0.73	0.35	0.27	0.02
rf~20+22	0.59	0.04	0.43	0.69	0.75	0.35	0.07	0.04
nb~41+22	0.59	0.04	0.49	0.64	0.75	0.36	0.04	0.06
knn~37+20	0.59	0.04	0.36	0.81	0.81	0.36	0.00	0.15
knn~15+39	0.59	0.04	0.55	0.60	0.75	0.38	0.07	0.85
svm~2+22	0.59	0.04	0.57	0.52	0.72	0.35	0.16	0.41
nb~29+6	0.59	0.04	0.38	0.78	0.79	0.36	0.01	0.27
rf~31+19	0.59	0.04	0.56	0.52	0.72	0.35	0.20	0.02

nb~9+28	0.59	0.04	0.41	0.74	0.78	0.36	0.01	0.05
rf~29+19	0.59	0.04	0.54	0.59	0.74	0.37	0.02	0.00
svm~41+22	0.59	0.04	0.45	0.67	0.75	0.35	0.07	0.12
knn~15+3	0.59	0.04	0.46	0.64	0.74	0.35	0.25	0.11
nb~18+36	0.59	0.04	0.48	0.59	0.72	0.34	0.23	0.43
knn~4+42	0.59	0.04	0.76	0.29	0.70	0.35	0.27	0.04
svm~29+19	0.59	0.04	0.45	0.74	0.79	0.38	0.01	0.02
knn~39+19	0.59	0.04	0.54	0.66	0.78	0.39	0.01	0.00
nb~15+18	0.59	0.04	0.39	0.74	0.77	0.36	0.01	0.28
nb~7+28	0.59	0.04	0.45	0.71	0.77	0.37	0.01	0.41
rpart~1+22	0.59	0.04	0.30	0.86	0.83	0.36	0.01	0.09
rpart~25+22	0.59	0.04	0.56	0.50	0.71	0.34	0.34	0.13
rf~24+6	0.59	0.04	0.56	0.55	0.73	0.36	0.15	0.10
svm~4+34	0.59	0.04	0.36	0.74	0.75	0.34	0.05	0.01
rf~38+6	0.59	0.04	0.52	0.66	0.77	0.38	0.02	0.08
knn~5+32	0.59	0.05	0.70	0.45	0.74	0.40	0.04	0.08
svm~28+22	0.59	0.05	0.39	0.78	0.79	0.37	0.01	0.00
rpart~16+6	0.59	0.05	0.40	0.71	0.75	0.35	0.06	0.44
knn~4+20	0.59	0.05	0.56	0.57	0.74	0.37	0.01	0.03
nb~4+12	0.59	0.05	0.34	0.79	0.78	0.35	0.02	0.00
svm~4+42	0.59	0.05	0.49	0.72	0.80	0.39	0.00	0.01
rf~12+18	0.59	0.05	0.42	0.72	0.77	0.36	0.04	0.26
rpart~10+22	0.59	0.05	0.44	0.72	0.78	0.37	0.01	0.03
svm~35+19	0.59	0.05	0.42	0.74	0.78	0.37	0.03	0.05
knn~18+32	0.59	0.05	0.72	0.45	0.74	0.42	0.02	0.07
rpart~17+22	0.59	0.05	0.44	0.69	0.76	0.36	0.04	0.27
rpart~15+9	0.58	0.05	0.31	0.79	0.77	0.34	0.05	0.74
knn~4+34	0.59	0.05	0.67	0.40	0.71	0.35	0.22	0.01
knn~14+32	0.59	0.05	0.63	0.52	0.74	0.39	0.01	0.01
rpart~35+31	0.58	0.05	0.32	0.83	0.80	0.36	0.05	0.72
rf~1+28	0.59	0.05	0.52	0.62	0.75	0.37	0.09	0.39
svm~36+19	0.59	0.05	0.45	0.67	0.75	0.36	0.03	0.02
rpart~9+20	0.59	0.05	0.62	0.50	0.73	0.37	0.06	0.18
rf~26+28	0.59	0.05	0.54	0.57	0.73	0.36	0.02	0.01
knn~16+10	0.59	0.05	0.70	0.43	0.73	0.40	0.07	0.49
knn~42+18	0.59	0.05	0.52	0.59	0.73	0.35	0.24	0.68
rpart~9+22	0.58	0.05	0.39	0.79	0.81	0.37	0.00	0.17
rpart~4+6	0.59	0.05	0.43	0.67	0.74	0.35	0.14	0.13
rf~41+18	0.59	0.05	0.41	0.74	0.78	0.36	0.04	0.53
rf~18+37	0.59	0.05	0.38	0.78	0.79	0.36	0.03	0.91
svm~4+31	0.59	0.05	0.41	0.66	0.73	0.34	0.19	0.00
rpart~39+6	0.59	0.05	0.45	0.76	0.80	0.38	0.00	0.10
knn~18+8	0.59	0.05	0.46	0.69	0.77	0.37	0.02	0.84
svm~39+28	0.59	0.05	0.45	0.71	0.77	0.37	0.01	0.00
nb~11+22	0.59	0.05	0.59	0.55	0.75	0.38	0.03	0.03
rf~3+28	0.59	0.05	0.44	0.71	0.77	0.36	0.02	0.00
nb~39+6	0.59	0.05	0.39	0.71	0.75	0.34	0.10	0.10

nb~5+20	0.59	0.05	0.60	0.55	0.75	0.39	0.07	0.23

Table 50: pairwise biomarkers from the 43 biomarker panel with significance for Wilcoxon P-value (auc.pvalue<=0.001*) and other metrics for the MET event endpoint.
Auc.pvalue : Wilcoxon Test P-value. MFD: Median Fold Difference. KM: Kaplan Meier curves. mvaHRPval: Multivariable Analysis Hazard Ratio P-value. * Multiple classifiers with p-values between 0.001 and 0.05 not included.

Classifier	auc	auc. pvalue	Sensitivity	Specificity	Pos. Pred. Value	Neg. Pred. Value	KM P- value	Mva HRPval
nb~4+16	0.747	0.000	0.471	0.890	0.711	0.745	0.000	0.000
svm~4+16	0.741	0.000	0.544	0.763	0.569	0.744	0.000	0.001
nb~4+35	0.726	0.000	0.471	0.890	0.711	0.745	0.000	0.002
nb~16+6	0.725	0.000	0.574	0.746	0.565	0.752	0.000	0.001
nb~4+15	0.725	0.000	0.471	0.839	0.627	0.733	0.000	0.000
rpart~4+16	0.719	0.000	0.588	0.712	0.541	0.750	0.000	0.002
nb~15+16	0.724	0.000	0.471	0.771	0.542	0.717	0.000	0.005
nb~4+8	0.721	0.000	0.397	0.907	0.711	0.723	0.000	0.000
svm~4+8	0.718	0.000	0.441	0.822	0.588	0.719	0.000	0.000
nb~4+13	0.718	0.000	0.397	0.907	0.711	0.723	0.000	0.000
svm~35+19	0.717	0.000	0.544	0.729	0.536	0.735	0.000	0.001
nb~35+6	0.716	0.000	0.515	0.780	0.574	0.736	0.000	0.006
knn~4+16	0.711	0.000	0.735	0.669	0.562	0.814	0.000	0.000
nb~16+22	0.714	0.000	0.588	0.695	0.526	0.745	0.000	0.000
nb~15+24	0.714	0.000	0.500	0.763	0.548	0.726	0.000	0.001
svm~16+18	0.714	0.000	0.574	0.754	0.574	0.754	0.000	0.001
nb~16+19	0.713	0.000	0.662	0.678	0.542	0.777	0.000	0.000
nb~4+24	0.713	0.000	0.412	0.907	0.718	0.728	0.000	0.000
nb~16+18	0.712	0.000	0.647	0.669	0.530	0.767	0.000	0.001
svm~15+13	0.711	0.000	0.529	0.754	0.554	0.736	0.000	0.021
svm~16+19	0.711	0.000	0.618	0.661	0.512	0.750	0.000	0.001
nb~16+20	0.710	0.000	0.706	0.559	0.480	0.767	0.000	0.000
nb~15+28	0.710	0.000	0.471	0.805	0.582	0.725	0.000	0.002
svm~16+22	0.710	0.000	0.574	0.627	0.470	0.718	0.003	0.003
nb~35+19	0.710	0.000	0.765	0.602	0.525	0.816	0.000	0.001
nb~15+8	0.709	0.000	0.441	0.822	0.588	0.719	0.000	0.046
svm~19+28	0.708	0.000	0.559	0.737	0.551	0.744	0.000	0.001
svm~4+29	0.707	0.000	0.426	0.864	0.644	0.723	0.000	0.000
svm~13+22	0.706	0.000	0.618	0.678	0.525	0.755	0.000	0.003
rpart~15+33	0.697	0.000	0.338	0.873	0.605	0.696	0.000	0.121
nb~15+13	0.705	0.000	0.574	0.712	0.534	0.743	0.000	0.034
svm~31+19	0.705	0.000	0.662	0.653	0.523	0.770	0.000	0.000
svm~15+8	0.704	0.000	0.397	0.831	0.574	0.705	0.000	0.065
nb~35+22	0.704	0.000	0.750	0.525	0.477	0.785	0.000	0.007
svm~16+6	0.703	0.000	0.603	0.695	0.532	0.752	0.000	0.001
nb~4+1	0.703	0.000	0.500	0.839	0.642	0.744	0.000	0.000
svm~4+41	0.703	0.000	0.353	0.847	0.571	0.694	0.001	0.001

rpart~4+1	0.697	0.000	0.691	0.559	0.475	0.759	0.001	0.004
svm~4+31	0.702	0.000	0.574	0.712	0.534	0.743	0.000	0.000
nb~13+6	0.702	0.000	0.603	0.729	0.562	0.761	0.000	0.001
nb~4+12	0.702	0.000	0.500	0.822	0.618	0.740	0.000	0.000
nb~15+35	0.702	0.000	0.574	0.746	0.565	0.752	0.000	0.183
nb~4+2	0.701	0.000	0.559	0.763	0.576	0.750	0.000	0.056
svm~15+16	0.701	0.000	0.426	0.805	0.558	0.709	0.000	0.039
rpart~4+31	0.698	0.000	0.632	0.703	0.551	0.769	0.000	0.005
nb~4+28	0.700	0.000	0.471	0.822	0.604	0.729	0.000	0.000
nb~4+9	0.699	0.000	0.529	0.839	0.655	0.756	0.000	0.002
nb~35+20	0.699	0.000	0.824	0.449	0.463	0.815	0.000	0.001
nb~4+33	0.698	0.000	0.441	0.898	0.714	0.736	0.000	0.005
rpart~4+42	0.694	0.000	0.676	0.627	0.511	0.771	0.000	0.028
nb~4+19	0.697	0.000	0.500	0.822	0.618	0.740	0.000	0.000
nb~4+20	0.697	0.000	0.559	0.754	0.567	0.748	0.000	0.000
svm~4+19	0.696	0.000	0.691	0.746	0.610	0.807	0.000	0.000
svm~4+28	0.696	0.000	0.485	0.763	0.541	0.720	0.000	0.001
svm~8+22	0.695	0.000	0.529	0.737	0.537	0.731	0.000	0.004
rpart~4+13	0.692	0.000	0.544	0.703	0.514	0.728	0.000	0.000
nb~15+19	0.695	0.000	0.441	0.805	0.566	0.714	0.000	0.002
nb~15+6	0.695	0.000	0.397	0.839	0.587	0.707	0.000	0.006
nb~13+22	0.695	0.000	0.603	0.695	0.532	0.752	0.000	0.002
svm~29+19	0.695	0.000	0.603	0.729	0.562	0.761	0.000	0.000
rpart~4+18	0.690	0.000	0.559	0.703	0.521	0.735	0.000	0.005
svm~4+1	0.694	0.000	0.471	0.856	0.653	0.737	0.000	0.001
nb~16+28	0.694	0.000	0.632	0.627	0.494	0.747	0.000	0.001
svm~8+19	0.693	0.000	0.603	0.644	0.494	0.738	0.000	0.000
nb~8+22	0.692	0.000	0.706	0.619	0.516	0.785	0.000	0.003
nb~4+40	0.692	0.000	0.441	0.915	0.750	0.740	0.000	0.007
svm~13+28	0.692	0.000	0.588	0.695	0.526	0.745	0.000	0.000
rpart~15+13	0.688	0.000	0.456	0.780	0.544	0.713	0.000	0.151
nb~16+17	0.691	0.000	0.485	0.780	0.559	0.724	0.000	0.001
svm~19+38	0.691	0.000	0.632	0.678	0.531	0.762	0.000	0.003
rpart~15+20	0.674	0.000	0.691	0.661	0.540	0.788	0.000	0.000
svm~15+2	0.690	0.000	0.559	0.754	0.567	0.748	0.000	0.472
svm~15+28	0.690	0.000	0.441	0.805	0.566	0.714	0.000	0.002
nb~4+37	0.690	0.000	0.456	0.814	0.585	0.722	0.000	0.004
svm~40+6	0.690	0.000	0.691	0.576	0.485	0.764	0.000	0.050
nb~8+19	0.690	0.000	0.618	0.686	0.532	0.757	0.000	0.000
svm~8+6	0.690	0.000	0.588	0.720	0.548	0.752	0.000	0.005
nb~4+6	0.689	0.000	0.500	0.814	0.607	0.738	0.000	0.002
nb~15+22	0.689	0.000	0.471	0.788	0.561	0.721	0.000	0.004
svm~4+40	0.689	0.000	0.632	0.610	0.483	0.742	0.001	0.139
rpart~4+8	0.685	0.000	0.647	0.678	0.537	0.769	0.000	0.000
svm~15+19	0.689	0.000	0.412	0.847	0.609	0.714	0.000	0.010
svm~40+19	0.689	0.000	0.618	0.585	0.462	0.726	0.005	0.017
nb~15+9	0.688	0.000	0.574	0.669	0.500	0.731	0.001	0.069

nb~9+22	0.688	0.000	0.529	0.737	0.537	0.731	0.000	0.007
nb~4+32	0.688	0.000	0.500	0.873	0.694	0.752	0.000	0.000
nb~9+19	0.688	0.000	0.691	0.593	0.495	0.769	0.000	0.000
nb~40+6	0.687	0.000	0.515	0.780	0.574	0.736	0.000	0.033
rf~9+19	0.687	0.000	0.721	0.610	0.516	0.791	0.000	0.000
knn~4+12	0.684	0.000	0.382	0.831	0.565	0.700	0.000	0.002
nb~16+26	0.687	0.000	0.500	0.771	0.557	0.728	0.000	0.000
nb~4+31	0.687	0.000	0.485	0.839	0.635	0.739	0.000	0.001
nb~4+22	0.687	0.000	0.515	0.814	0.614	0.744	0.000	0.001
knn~4+19	0.683	0.000	0.647	0.703	0.557	0.776	0.000	0.000
nb~15+18	0.687	0.000	0.515	0.746	0.538	0.727	0.000	0.032
rpart~18+32	0.684	0.000	0.632	0.669	0.524	0.760	0.000	0.004
nb~4+42	0.686	0.000	0.397	0.856	0.614	0.711	0.000	0.005
nb~40+22	0.686	0.000	0.662	0.602	0.489	0.755	0.001	0.025
knn~4+42	0.681	0.000	0.838	0.314	0.413	0.771	0.021	0.001
nb~4+17	0.686	0.000	0.471	0.831	0.615	0.731	0.000	0.001
nb~13+19	0.685	0.000	0.779	0.576	0.515	0.819	0.000	0.000
nb~16+24	0.685	0.000	0.515	0.712	0.507	0.718	0.001	0.000
svm~24+2	0.685	0.000	0.456	0.771	0.534	0.711	0.000	0.008
rpart~16+20	0.678	0.000	0.721	0.568	0.490	0.779	0.000	0.001
rpart~35+6	0.681	0.000	0.529	0.737	0.537	0.731	0.000	0.007
rpart~13+6	0.680	0.000	0.647	0.729	0.579	0.782	0.000	0.001
nb~8+6	0.685	0.000	0.515	0.763	0.556	0.732	0.000	0.005
rf~4+12	0.684	0.000	0.647	0.610	0.489	0.750	0.000	0.002
svm~8+28	0.684	0.000	0.588	0.678	0.513	0.741	0.000	0.008
rpart~20+28	0.671	0.000	0.750	0.508	0.468	0.779	0.000	0.000
svm~4+13	0.684	0.000	0.456	0.856	0.646	0.732	0.000	0.000
svm~29+22	0.684	0.000	0.618	0.610	0.477	0.735	0.001	0.004
svm~4+27	0.684	0.000	0.515	0.754	0.547	0.730	0.000	0.006
nb~4+41	0.683	0.000	0.441	0.831	0.600	0.721	0.000	0.003
rpart~13+22	0.680	0.000	0.706	0.559	0.480	0.767	0.000	0.009
nb~28+6	0.683	0.000	0.588	0.720	0.548	0.752	0.000	0.002
rpart~2+19	0.674	0.000	0.809	0.381	0.430	0.776	0.005	0.060
svm~4+15	0.682	0.000	0.397	0.873	0.643	0.715	0.000	0.000
svm~4+38	0.682	0.000	0.515	0.805	0.603	0.742	0.000	0.001
rpart~4+32	0.679	0.000	0.500	0.729	0.515	0.717	0.001	0.001
svm~13+19	0.681	0.000	0.735	0.534	0.476	0.778	0.000	0.000
nb~8+28	0.681	0.000	0.647	0.686	0.543	0.771	0.000	0.002
knn~40+28	0.677	0.000	0.485	0.814	0.600	0.733	0.000	0.005
nb~15+20	0.680	0.000	0.662	0.610	0.495	0.758	0.000	0.003
rpart~35+19	0.677	0.000	0.618	0.686	0.532	0.757	0.000	0.008
nb~4+27	0.680	0.000	0.574	0.695	0.520	0.739	0.000	0.001
nb~15+17	0.680	0.000	0.471	0.729	0.500	0.705	0.001	0.011
nb~24+28	0.680	0.000	0.485	0.754	0.532	0.718	0.000	0.000
nb~9+6	0.680	0.000	0.632	0.610	0.483	0.742	0.001	0.011
svm~4+12	0.680	0.000	0.485	0.814	0.600	0.733	0.000	0.003
nb~37+22	0.679	0.000	0.603	0.627	0.482	0.733	0.001	0.010

svm~26+19	0.679	0.000	0.529	0.805	0.610	0.748	0.000	0.001
svm~4+9	0.679	0.000	0.529	0.780	0.581	0.742	0.000	0.006
nb~15+32	0.679	0.000	0.309	0.873	0.583	0.687	0.000	0.008
rf~4+31	0.679	0.000	0.559	0.678	0.500	0.727	0.001	0.003
svm~9+19	0.679	0.000	0.676	0.627	0.511	0.771	0.000	0.000
svm~15+35	0.679	0.000	0.426	0.847	0.617	0.719	0.000	0.229
nb~28+22	0.679	0.000	0.559	0.661	0.487	0.722	0.001	0.001
nb~35+28	0.678	0.000	0.603	0.712	0.547	0.757	0.000	0.025
svm~35+6	0.678	0.000	0.485	0.771	0.550	0.722	0.000	0.007
knn~4+43	0.674	0.000	0.515	0.720	0.515	0.720	0.001	0.018
nb~2+22	0.678	0.000	0.559	0.644	0.475	0.717	0.005	0.129
rpart~15+2	0.671	0.000	0.647	0.627	0.500	0.755	0.000	0.587
svm~9+22	0.678	0.000	0.500	0.763	0.548	0.726	0.000	0.014
svm~16+28	0.677	0.000	0.544	0.771	0.578	0.746	0.000	0.002
svm~19+22	0.677	0.000	0.500	0.729	0.515	0.717	0.000	0.001
nb~24+6	0.677	0.000	0.353	0.839	0.558	0.692	0.000	0.001
rpart~15+26	0.670	0.000	0.338	0.864	0.590	0.694	0.000	0.061
svm~16+38	0.677	0.000	0.471	0.754	0.525	0.712	0.001	0.054
rpart~4+28	0.673	0.000	0.515	0.771	0.565	0.734	0.000	0.002
svm~15+31	0.677	0.000	0.353	0.814	0.522	0.686	0.003	0.170
nb~40+19	0.677	0.000	0.706	0.534	0.466	0.759	0.001	0.008
nb~15+2	0.676	0.000	0.529	0.763	0.563	0.738	0.000	0.474
nb~40+20	0.676	0.000	0.691	0.559	0.475	0.759	0.001	0.007
svm~41+6	0.676	0.000	0.588	0.661	0.500	0.736	0.000	0.005
nb~4+23	0.676	0.000	0.500	0.805	0.596	0.736	0.000	0.052
svm~4+6	0.676	0.000	0.544	0.780	0.587	0.748	0.000	0.016
nb~4+29	0.676	0.000	0.485	0.763	0.541	0.720	0.000	0.010
knn~4+39	0.672	0.000	0.794	0.432	0.446	0.785	0.001	0.000
rf~13+26	0.675	0.000	0.588	0.686	0.519	0.743	0.000	0.001
rpart~9+19	0.662	0.000	0.706	0.568	0.485	0.770	0.000	0.001
nb~4+38	0.675	0.000	0.544	0.780	0.587	0.748	0.000	0.013
rf~4+19	0.675	0.000	0.574	0.661	0.494	0.729	0.000	0.000
nb~4+34	0.675	0.000	0.441	0.839	0.612	0.723	0.000	0.002
rf~4+1	0.675	0.000	0.632	0.644	0.506	0.752	0.000	0.023
nb~13+28	0.675	0.000	0.544	0.720	0.529	0.733	0.000	0.001
rpart~4+11	0.644	0.000	0.441	0.797	0.556	0.712	0.000	0.008
svm~37+19	0.675	0.000	0.647	0.585	0.473	0.742	0.001	0.000
nb~20+28	0.675	0.000	0.618	0.602	0.472	0.732	0.001	0.000
nb~42+6	0.674	0.000	0.500	0.788	0.576	0.732	0.000	0.018
rpart~33+19	0.647	0.000	0.574	0.720	0.542	0.746	0.000	0.001
rf~4+16	0.674	0.000	0.691	0.602	0.500	0.772	0.000	0.002
rpart~4+39	0.663	0.000	0.529	0.754	0.554	0.736	0.000	0.000
nb~4+36	0.674	0.000	0.368	0.915	0.714	0.715	0.000	0.001
nb~8+20	0.674	0.000	0.691	0.500	0.443	0.738	0.009	0.000
nb~24+22	0.674	0.000	0.618	0.619	0.483	0.737	0.001	0.000
svm~4+32	0.673	0.000	0.500	0.754	0.540	0.724	0.000	0.003
svm~13+6	0.673	0.000	0.559	0.712	0.528	0.737	0.000	0.001

rpart~4+29	0.669	0.000	0.559	0.678	0.500	0.727	0.001	0.000
svm~39+19	0.673	0.000	0.632	0.602	0.478	0.740	0.000	0.000
nb~15+40	0.672	0.000	0.382	0.856	0.605	0.706	0.000	0.258
nb~15+26	0.672	0.000	0.471	0.771	0.542	0.717	0.000	0.012
nb~17+28	0.672	0.000	0.529	0.686	0.493	0.717	0.001	0.001
nb~9+20	0.672	0.000	0.544	0.610	0.446	0.699	0.021	0.001
nb~13+20	0.672	0.000	0.603	0.593	0.461	0.722	0.004	0.000
nb~2+6	0.672	0.000	0.588	0.712	0.541	0.750	0.000	0.175
rpart~16+18	0.634	0.000	0.412	0.864	0.636	0.718	0.000	0.001
svm~4+35	0.672	0.000	0.471	0.797	0.571	0.723	0.000	0.007
svm~15+10	0.672	0.000	0.441	0.856	0.638	0.727	0.000	0.099
knn~15+8	0.668	0.000	0.735	0.542	0.481	0.780	0.000	0.113
knn~4+20	0.669	0.000	0.691	0.576	0.485	0.764	0.000	0.003
nb~15+37	0.671	0.000	0.426	0.771	0.518	0.700	0.001	0.150
svm~18+8	0.671	0.000	0.588	0.661	0.500	0.736	0.001	0.014
nb~2+19	0.671	0.000	0.544	0.695	0.507	0.726	0.001	0.033
nb~19+28	0.671	0.000	0.647	0.653	0.518	0.762	0.000	0.000
rpart~19+20	0.666	0.000	0.735	0.500	0.459	0.766	0.001	0.003
svm~4+42	0.671	0.000	0.588	0.669	0.506	0.738	0.000	0.012
svm~16+26	0.670	0.000	0.412	0.788	0.528	0.699	0.001	0.000
knn~15+16	0.666	0.000	0.750	0.466	0.447	0.764	0.003	0.002
svm~16+10	0.670	0.000	0.676	0.627	0.511	0.771	0.000	0.033
svm~17+19	0.670	0.000	0.485	0.754	0.532	0.718	0.000	0.001
nb~41+6	0.670	0.000	0.441	0.814	0.577	0.716	0.000	0.016
nb~40+28	0.670	0.000	0.662	0.661	0.529	0.772	0.000	0.028
svm~15+40	0.670	0.000	0.485	0.661	0.452	0.690	0.040	0.565
rf~4+8	0.670	0.000	0.721	0.492	0.450	0.753	0.003	0.001
knn~10+19	0.665	0.000	0.382	0.881	0.650	0.712	0.000	0.000
nb~37+19	0.669	0.000	0.544	0.678	0.493	0.721	0.000	0.000
knn~4+31	0.665	0.000	0.544	0.712	0.521	0.730	0.000	0.002
nb~33+6	0.669	0.000	0.544	0.763	0.569	0.744	0.000	0.029
nb~20+22	0.669	0.000	0.603	0.619	0.477	0.730	0.001	0.001
rf~8+26	0.669	0.000	0.574	0.695	0.520	0.739	0.000	0.002
svm~33+19	0.669	0.000	0.574	0.627	0.470	0.718	0.003	0.000
nb~19+6	0.669	0.000	0.515	0.780	0.574	0.736	0.000	0.001
nb~4+18	0.669	0.000	0.485	0.771	0.550	0.722	0.000	0.004
svm~4+18	0.668	0.000	0.441	0.797	0.556	0.712	0.000	0.016
knn~15+13	0.665	0.000	0.735	0.517	0.467	0.772	0.001	0.235
svm~4+39	0.668	0.000	0.544	0.729	0.536	0.735	0.000	0.000
svm~42+15	0.668	0.000	0.471	0.720	0.492	0.702	0.006	0.638
svm~10+6	0.668	0.000	0.485	0.797	0.579	0.729	0.000	0.004
rf~4+24	0.668	0.000	0.574	0.678	0.506	0.734	0.000	0.000
svm~19+6	0.668	0.000	0.559	0.720	0.535	0.739	0.000	0.001
nb~1+6	0.667	0.000	0.485	0.771	0.550	0.722	0.000	0.007
nb~15+33	0.667	0.000	0.471	0.737	0.508	0.707	0.003	0.452
svm~12+6	0.667	0.000	0.544	0.703	0.514	0.728	0.000	0.002
nb~15+31	0.667	0.000	0.412	0.788	0.528	0.699	0.002	0.155

rpart~15+31	0.662	0.000	0.324	0.890	0.629	0.695	0.000	0.155
knn~4+22	0.664	0.000	0.735	0.475	0.446	0.757	0.002	0.005
svm~40+24	0.667	0.000	0.632	0.653	0.512	0.755	0.000	0.006
nb~12+6	0.667	0.000	0.618	0.644	0.500	0.745	0.000	0.002
nb~18+28	0.667	0.000	0.515	0.661	0.467	0.703	0.012	0.005
knn~15+31	0.663	0.000	0.706	0.585	0.495	0.775	0.000	0.060
svm~4+24	0.667	0.000	0.426	0.864	0.644	0.723	0.000	0.000
nb~42+22	0.667	0.000	0.647	0.525	0.440	0.721	0.021	0.032
rpart~4+34	0.666	0.000	0.618	0.602	0.472	0.732	0.002	0.063
svm~4+37	0.667	0.000	0.574	0.686	0.513	0.736	0.000	0.003
svm~4+2	0.667	0.000	0.662	0.678	0.542	0.777	0.000	0.077
nb~22+6	0.667	0.000	0.559	0.695	0.514	0.732	0.000	0.004
nb~42+15	0.666	0.000	0.485	0.712	0.493	0.706	0.005	0.521
svm~40+22	0.666	0.000	0.721	0.475	0.441	0.747	0.013	0.086
knn~29+18	0.662	0.000	0.529	0.695	0.500	0.719	0.002	0.029
nb~12+22	0.666	0.000	0.559	0.669	0.494	0.725	0.000	0.001
svm~10+22	0.666	0.000	0.544	0.678	0.493	0.721	0.002	0.015
svm~35+22	0.666	0.000	0.456	0.771	0.534	0.711	0.000	0.024
svm~8+26	0.666	0.000	0.441	0.780	0.536	0.708	0.001	0.006
nb~4+25	0.666	0.000	0.515	0.805	0.603	0.742	0.000	0.002
nb~17+6	0.666	0.000	0.588	0.661	0.500	0.736	0.000	0.002
svm~26+22	0.666	0.000	0.500	0.720	0.507	0.714	0.001	0.005
nb~38+28	0.666	0.000	0.559	0.703	0.521	0.735	0.000	0.023
nb~18+13	0.666	0.000	0.618	0.559	0.447	0.717	0.024	0.011
nb~37+6	0.666	0.000	0.588	0.678	0.513	0.741	0.000	0.016
rf~4+13	0.666	0.000	0.471	0.771	0.542	0.717	0.000	0.002
nb~4+7	0.666	0.000	0.456	0.771	0.534	0.711	0.001	0.028
nb~4+10	0.666	0.000	0.353	0.924	0.727	0.712	0.000	0.003
svm~24+6	0.666	0.000	0.426	0.788	0.537	0.705	0.000	0.018
rf~4+39	0.665	0.000	0.662	0.602	0.489	0.755	0.000	0.002
nb~19+22	0.665	0.000	0.706	0.568	0.485	0.770	0.000	0.000
svm~26+28	0.665	0.000	0.426	0.797	0.547	0.707	0.000	0.004
nb~33+19	0.665	0.000	0.721	0.568	0.490	0.779	0.000	0.016
rf~4+42	0.665	0.000	0.588	0.644	0.488	0.731	0.002	0.015
svm~24+19	0.665	0.000	0.456	0.814	0.585	0.722	0.000	0.002
nb~4+26	0.665	0.000	0.426	0.856	0.630	0.721	0.000	0.001
nb~15+10	0.665	0.000	0.706	0.483	0.440	0.740	0.018	0.404
knn~15+19	0.661	0.000	0.794	0.398	0.432	0.770	0.006	0.003
nb~19+20	0.665	0.000	0.706	0.517	0.457	0.753	0.001	0.000
rf~15+2	0.665	0.000	0.647	0.619	0.494	0.753	0.000	0.846
svm~40+28	0.665	0.000	0.676	0.602	0.495	0.763	0.000	0.039
nb~1+22	0.664	0.000	0.603	0.610	0.471	0.727	0.003	0.008
svm~15+24	0.664	0.000	0.338	0.890	0.639	0.700	0.000	0.135
rpart~4+20	0.640	0.000	0.765	0.508	0.473	0.789	0.000	0.001
svm~18+2	0.664	0.000	0.632	0.610	0.483	0.742	0.002	0.252
svm~37+22	0.664	0.000	0.632	0.636	0.500	0.750	0.000	0.042
nb~34+6	0.664	0.000	0.500	0.703	0.493	0.709	0.002	0.012

rpart~1+20	0.659	0.000	0.779	0.483	0.465	0.792	0.000	0.000
nb~4+39	0.664	0.000	0.515	0.814	0.614	0.744	0.000	0.004
nb~31+6	0.664	0.000	0.515	0.729	0.522	0.723	0.000	0.007
svm~2+28	0.664	0.000	0.647	0.602	0.484	0.747	0.001	0.039
knn~24+22	0.659	0.000	0.485	0.771	0.550	0.722	0.000	0.014
nb~18+6	0.664	0.000	0.544	0.712	0.521	0.730	0.000	0.009
rf~26+22	0.663	0.000	0.618	0.669	0.519	0.752	0.000	0.015
svm~31+6	0.663	0.000	0.544	0.661	0.481	0.716	0.004	0.044
nb~20+6	0.663	0.000	0.544	0.678	0.493	0.721	0.001	0.001
nb~4+43	0.663	0.000	0.397	0.873	0.643	0.715	0.000	0.006
svm~1+22	0.663	0.000	0.500	0.771	0.557	0.728	0.000	0.006
nb~40+17	0.663	0.000	0.632	0.610	0.483	0.742	0.001	0.140
nb~37+28	0.663	0.000	0.603	0.653	0.500	0.740	0.000	0.019
nb~17+8	0.663	0.000	0.559	0.686	0.507	0.730	0.001	0.017
svm~12+19	0.663	0.000	0.588	0.678	0.513	0.741	0.000	0.004
nb~27+6	0.663	0.000	0.588	0.636	0.482	0.728	0.001	0.012
nb~32+22	0.663	0.000	0.559	0.627	0.463	0.712	0.006	0.002
rf~42+19	0.663	0.000	0.662	0.593	0.484	0.753	0.000	0.000
nb~2+28	0.663	0.000	0.529	0.669	0.480	0.712	0.005	0.101
rpart~4+24	0.655	0.000	0.412	0.805	0.549	0.704	0.000	0.001
svm~18+19	0.663	0.000	0.603	0.669	0.513	0.745	0.000	0.002
knn~9+19	0.659	0.000	0.691	0.576	0.485	0.764	0.000	0.005
svm~38+22	0.663	0.000	0.632	0.712	0.558	0.771	0.000	0.035
rf~4+38	0.662	0.000	0.515	0.703	0.500	0.716	0.001	0.024
nb~17+22	0.662	0.000	0.662	0.568	0.469	0.744	0.001	0.002
nb~10+6	0.662	0.000	0.412	0.847	0.609	0.714	0.000	0.012
rpart~4+6	0.658	0.000	0.574	0.703	0.527	0.741	0.000	0.012
knn~35+19	0.658	0.000	0.824	0.424	0.452	0.806	0.001	0.011
rpart~20+6	0.660	0.000	0.574	0.627	0.470	0.718	0.003	0.000
nb~2+20	0.662	0.000	0.603	0.678	0.519	0.748	0.000	0.078
knn~16+10	0.655	0.000	0.824	0.432	0.455	0.810	0.001	0.031
svm~10+28	0.662	0.000	0.559	0.686	0.507	0.730	0.000	0.022
svm~2+22	0.662	0.000	0.691	0.542	0.465	0.753	0.001	0.179
svm~10+19	0.662	0.000	0.559	0.712	0.528	0.737	0.000	0.000
knn~4+38	0.658	0.000	0.750	0.475	0.451	0.767	0.002	0.002
svm~19+32	0.661	0.000	0.485	0.771	0.550	0.722	0.000	0.001
nb~15+12	0.661	0.000	0.485	0.720	0.500	0.708	0.002	0.013
nb~17+13	0.661	0.000	0.618	0.619	0.483	0.737	0.001	0.014
nb~18+22	0.661	0.000	0.662	0.610	0.495	0.758	0.000	0.005
rf~4+41	0.660	0.000	0.588	0.636	0.482	0.728	0.002	0.007
rpart~4+35	0.652	0.000	0.544	0.737	0.544	0.737	0.000	0.016
rpart~24+19	0.654	0.000	0.603	0.593	0.461	0.722	0.003	0.002
knn~16+19	0.658	0.000	0.647	0.610	0.489	0.750	0.000	0.000
nb~33+22	0.660	0.000	0.706	0.492	0.444	0.744	0.007	0.031
svm~24+28	0.659	0.000	0.250	0.890	0.567	0.673	0.001	0.012
nb~19+32	0.659	0.000	0.515	0.720	0.515	0.720	0.000	0.000
rf~39+32	0.659	0.000	0.676	0.559	0.469	0.750	0.001	0.000

svm~42+6	0.659	0.000	0.574	0.661	0.494	0.729	0.001	0.012
nb~24+19	0.659	0.000	0.574	0.712	0.534	0.743	0.000	0.000
rf~15+28	0.659	0.000	0.618	0.585	0.462	0.726	0.004	0.204
rpart~4+38	0.658	0.000	0.603	0.661	0.506	0.743	0.000	0.045
knn~4+34	0.655	0.000	0.765	0.415	0.430	0.754	0.008	0.009
nb~41+22	0.659	0.000	0.603	0.636	0.488	0.735	0.001	0.027
rpart~35+20	0.657	0.000	0.603	0.644	0.494	0.738	0.001	0.050
rf~31+19	0.659	0.000	0.676	0.542	0.460	0.744	0.002	0.000
rpart~5+28	0.651	0.000	0.706	0.602	0.505	0.780	0.000	0.029
rf~35+6	0.658	0.000	0.618	0.585	0.462	0.726	0.009	0.007
nb~24+20	0.658	0.000	0.662	0.517	0.441	0.726	0.007	0.000
rpart~24+10	0.638	0.000	0.382	0.839	0.578	0.702	0.000	0.005
nb~12+28	0.658	0.000	0.632	0.669	0.524	0.760	0.000	0.001
svm~4+22	0.658	0.000	0.544	0.771	0.578	0.746	0.000	0.002
nb~36+6	0.658	0.000	0.485	0.754	0.532	0.718	0.000	0.010
nb~34+22	0.658	0.000	0.618	0.576	0.457	0.723	0.009	0.012
knn~16+38	0.653	0.000	0.824	0.373	0.431	0.786	0.007	0.206
svm~29+6	0.658	0.000	0.529	0.746	0.545	0.733	0.000	0.009
nb~38+6	0.658	0.000	0.500	0.746	0.531	0.721	0.000	0.061
svm~1+19	0.658	0.000	0.603	0.636	0.488	0.735	0.000	0.003
nb~16+32	0.658	0.000	0.515	0.729	0.522	0.723	0.000	0.005
svm~38+28	0.658	0.000	0.632	0.695	0.544	0.766	0.000	0.008
rpart~20+22	0.654	0.000	0.515	0.703	0.500	0.716	0.001	0.005
svm~15+39	0.658	0.000	0.500	0.780	0.567	0.730	0.000	0.153
nb~41+28	0.658	0.000	0.559	0.602	0.447	0.703	0.024	0.008
rpart~8+19	0.655	0.000	0.618	0.644	0.500	0.745	0.000	0.001
nb~31+19	0.657	0.000	0.603	0.695	0.532	0.752	0.000	0.002
rpart~15+8	0.656	0.000	0.426	0.763	0.509	0.698	0.003	0.243
rf~15+8	0.657	0.000	0.529	0.686	0.493	0.717	0.002	0.788
rf~7+19	0.657	0.000	0.735	0.551	0.485	0.783	0.000	0.016
rf~29+19	0.657	0.000	0.676	0.602	0.495	0.763	0.000	0.000
nb~35+17	0.657	0.000	0.618	0.610	0.477	0.735	0.002	0.135
svm~16+17	0.657	0.000	0.515	0.737	0.530	0.725	0.000	0.004
knn~18+28	0.653	0.000	0.735	0.441	0.431	0.743	0.010	0.002
nb~16+2	0.657	0.000	0.632	0.678	0.531	0.762	0.000	0.422
nb~26+28	0.656	0.000	0.544	0.678	0.493	0.721	0.001	0.002
rf~16+18	0.656	0.000	0.632	0.678	0.531	0.762	0.000	0.008
svm~4+25	0.656	0.000	0.588	0.653	0.494	0.733	0.000	0.031
nb~15+41	0.656	0.000	0.574	0.602	0.453	0.710	0.019	0.212
rpart~40+24	0.650	0.000	0.471	0.771	0.542	0.717	0.000	0.005
nb~17+19	0.656	0.000	0.706	0.610	0.511	0.783	0.000	0.000
svm~27+6	0.656	0.000	0.588	0.619	0.471	0.723	0.002	0.034
svm~19+34	0.656	0.000	0.588	0.610	0.465	0.720	0.002	0.001
rpart~16+28	0.655	0.000	0.515	0.669	0.473	0.705	0.011	0.009
rf~7+6	0.656	0.000	0.691	0.585	0.490	0.767	0.000	0.022
knn~29+6	0.652	0.000	0.529	0.695	0.500	0.719	0.001	0.022
knn~4+1	0.652	0.000	0.750	0.381	0.411	0.726	0.072	0.004

rpart~24+5	0.654	0.000	0.485	0.746	0.524	0.715	0.001	0.007
nb~32+6	0.656	0.000	0.412	0.847	0.609	0.714	0.000	0.004
nb~10+22	0.656	0.000	0.632	0.534	0.439	0.716	0.030	0.024
rpart~23+19	0.648	0.000	0.721	0.466	0.438	0.743	0.008	0.021
rpart~4+12	0.652	0.000	0.603	0.653	0.500	0.740	0.000	0.004
rf~4+14	0.656	0.000	0.544	0.678	0.493	0.721	0.001	0.007
nb~33+20	0.656	0.000	0.824	0.398	0.441	0.797	0.003	0.013
knn~4+35	0.652	0.000	0.471	0.746	0.516	0.710	0.001	0.050
rf~4+20	0.655	0.000	0.618	0.551	0.442	0.714	0.018	0.005
nb~18+8	0.655	0.000	0.485	0.695	0.478	0.701	0.018	0.023
svm~5+28	0.655	0.000	0.603	0.678	0.519	0.748	0.000	0.024
rf~10+19	0.655	0.000	0.574	0.686	0.513	0.736	0.000	0.000
svm~28+22	0.655	0.000	0.515	0.763	0.556	0.732	0.000	0.001
rpart~10+22	0.652	0.000	0.500	0.678	0.472	0.702	0.020	0.048
rf~4+18	0.655	0.000	0.603	0.661	0.506	0.743	0.000	0.006
nb~16+37	0.655	0.000	0.647	0.593	0.478	0.745	0.001	0.085
nb~19+34	0.655	0.000	0.574	0.686	0.513	0.736	0.000	0.001
rpart~4+25	0.652	0.000	0.706	0.534	0.466	0.759	0.001	0.024
knn~26+22	0.650	0.000	0.735	0.492	0.455	0.763	0.002	0.002
rf~35+19	0.654	0.000	0.618	0.636	0.494	0.743	0.000	0.010
rpart~15+3	0.647	0.000	0.279	0.890	0.594	0.682	0.000	0.294
svm~15+22	0.654	0.000	0.426	0.805	0.558	0.709	0.000	0.004
nb~28+32	0.654	0.000	0.544	0.644	0.468	0.710	0.003	0.004
svm~22+6	0.654	0.000	0.426	0.746	0.492	0.693	0.008	0.006
knn~42+19	0.649	0.000	0.721	0.551	0.480	0.774	0.000	0.005
nb~24+32	0.654	0.000	0.235	0.873	0.516	0.665	0.009	0.000
nb~16+35	0.654	0.000	0.515	0.737	0.530	0.725	0.001	0.205
nb~37+20	0.654	0.000	0.559	0.602	0.447	0.703	0.013	0.002
rpart~40+19	0.648	0.000	0.853	0.364	0.436	0.811	0.002	0.056
rpart~4+9	0.651	0.001	0.588	0.720	0.548	0.752	0.000	0.006
rf~15+39	0.653	0.001	0.544	0.720	0.529	0.733	0.000	0.221
svm~4+33	0.653	0.001	0.544	0.729	0.536	0.735	0.000	0.016
nb~13+26	0.653	0.001	0.662	0.483	0.425	0.713	0.051	0.002
svm~27+19	0.653	0.001	0.588	0.610	0.465	0.720	0.004	0.005
svm~15+37	0.653	0.001	0.412	0.805	0.549	0.704	0.000	0.070
nb~16+38	0.653	0.001	0.471	0.729	0.500	0.705	0.005	0.079
rpart~16+6	0.645	0.001	0.471	0.695	0.471	0.695	0.009	0.098
rpart~4+5	0.647	0.001	0.603	0.653	0.500	0.740	0.001	0.023
svm~2+19	0.653	0.001	0.676	0.500	0.438	0.728	0.011	0.019
rpart~24+20	0.644	0.001	0.529	0.712	0.514	0.724	0.000	0.001
svm~14+22	0.653	0.001	0.515	0.729	0.522	0.723	0.000	0.009
nb~36+22	0.653	0.001	0.632	0.576	0.462	0.731	0.003	0.013
rpart~26+28	0.649	0.001	0.456	0.746	0.508	0.704	0.001	0.001
rf~15+9	0.652	0.001	0.544	0.695	0.507	0.726	0.001	0.451
knn~24+19	0.648	0.001	0.824	0.373	0.431	0.786	0.004	0.002
nb~23+6	0.652	0.001	0.500	0.754	0.540	0.724	0.000	0.158
svm~34+22	0.652	0.001	0.632	0.576	0.462	0.731	0.003	0.007

nb~18+37	0.652	0.001	0.500	0.695	0.486	0.707	0.006	0.144
svm~31+22	0.652	0.001	0.574	0.619	0.464	0.716	0.009	0.011
rpart~18+13	0.651	0.001	0.559	0.602	0.447	0.703	0.037	0.050
knn~16+20	0.649	0.001	0.779	0.483	0.465	0.792	0.000	0.032
nb~40+24	0.652	0.001	0.529	0.636	0.456	0.701	0.023	0.005
nb~15+34	0.652	0.001	0.397	0.797	0.529	0.696	0.001	0.129
svm~16+24	0.652	0.001	0.265	0.890	0.581	0.677	0.000	0.005
svm~35+28	0.652	0.001	0.412	0.814	0.560	0.706	0.000	0.271
nb~26+6	0.652	0.001	0.559	0.703	0.521	0.735	0.000	0.003
nb~20+32	0.652	0.001	0.618	0.525	0.429	0.705	0.029	0.001
rpart~4+27	0.641	0.001	0.559	0.712	0.528	0.737	0.000	0.001
nb~26+22	0.652	0.001	0.676	0.602	0.495	0.763	0.000	0.002
rpart~13+26	0.647	0.001	0.500	0.788	0.576	0.732	0.000	0.000
rpart~7+20	0.644	0.001	0.735	0.475	0.446	0.757	0.005	0.052
svm~15+17	0.652	0.001	0.397	0.754	0.482	0.685	0.005	0.033
nb~16+9	0.652	0.001	0.471	0.703	0.478	0.697	0.022	0.058
rpart~39+19	0.644	0.001	0.735	0.458	0.439	0.750	0.004	0.010
svm~18+28	0.652	0.001	0.485	0.686	0.471	0.698	0.009	0.010
nb~26+19	0.652	0.001	0.691	0.542	0.465	0.753	0.001	0.001
knn~16+18	0.648	0.001	0.779	0.373	0.417	0.746	0.038	0.004
nb~17+32	0.651	0.001	0.515	0.678	0.479	0.708	0.002	0.002
svm~28+6	0.651	0.001	0.500	0.720	0.507	0.714	0.001	0.002
rf~16+19	0.651	0.001	0.603	0.585	0.456	0.719	0.007	0.001
nb~4+5	0.651	0.001	0.456	0.797	0.564	0.718	0.000	0.006
svm~42+19	0.651	0.001	0.500	0.712	0.500	0.712	0.001	0.002
svm~35+17	0.651	0.001	0.515	0.712	0.507	0.718	0.001	0.217
nb~1+28	0.651	0.001	0.529	0.729	0.529	0.729	0.000	0.007
nb~12+18	0.651	0.001	0.500	0.686	0.479	0.704	0.005	0.004
nb~9+28	0.651	0.001	0.500	0.720	0.507	0.714	0.001	0.021
nb~18+19	0.651	0.001	0.647	0.602	0.484	0.747	0.000	0.002
knn~16+28	0.648	0.001	0.838	0.364	0.432	0.796	0.003	0.001
knn~16+6	0.648	0.001	0.515	0.661	0.467	0.703	0.016	0.038
nb~33+28	0.651	0.001	0.603	0.585	0.456	0.719	0.014	0.036
svm~35+20	0.651	0.001	0.618	0.585	0.462	0.726	0.005	0.030
svm~24+8	0.651	0.001	0.338	0.831	0.535	0.685	0.003	0.002
knn~4+8	0.647	0.001	0.794	0.381	0.425	0.763	0.010	0.004
rpart~4+21	0.648	0.001	0.426	0.771	0.518	0.700	0.003	0.044
rf~16+38	0.651	0.001	0.632	0.627	0.494	0.747	0.000	0.244
knn~2+20	0.648	0.001	0.779	0.432	0.442	0.773	0.003	0.013
svm~24+13	0.650	0.001	0.353	0.864	0.600	0.699	0.000	0.000
rf~8+22	0.650	0.001	0.647	0.610	0.489	0.750	0.000	0.029
knn~35+6	0.646	0.001	0.647	0.534	0.444	0.724	0.017	0.012
rpart~8+28	0.646	0.001	0.574	0.678	0.506	0.734	0.000	0.079
knn~37+6	0.647	0.001	0.721	0.432	0.422	0.729	0.032	0.006
nb~43+6	0.650	0.001	0.382	0.797	0.520	0.691	0.002	0.052
rpart~15+14	0.646	0.001	0.338	0.814	0.511	0.681	0.004	0.614
nb~1+15	0.650	0.001	0.412	0.695	0.438	0.672	0.106	0.161

nb~12+19	0.650	0.001	0.632	0.602	0.478	0.740	0.001	0.000
svm~32+6	0.650	0.001	0.456	0.780	0.544	0.713	0.000	0.003
rpart~18+8	0.644	0.001	0.588	0.686	0.519	0.743	0.000	0.047
knn~38+22	0.648	0.001	0.559	0.644	0.475	0.717	0.002	0.007
rpart~4+40	0.649	0.001	0.603	0.593	0.461	0.722	0.006	0.159
nb~16+13	0.650	0.001	0.485	0.669	0.458	0.693	0.029	0.032
nb~18+20	0.650	0.001	0.632	0.525	0.434	0.713	0.019	0.003
svm~4+26	0.650	0.001	0.397	0.907	0.711	0.723	0.000	0.002
svm~17+8	0.650	0.001	0.471	0.805	0.582	0.725	0.000	0.019
nb~18+2	0.650	0.001	0.485	0.686	0.471	0.698	0.030	0.390
rf~4+34	0.650	0.001	0.765	0.441	0.441	0.765	0.005	0.022
rpart~9+20	0.643	0.001	0.721	0.500	0.454	0.756	0.003	0.055
svm~17+13	0.650	0.001	0.441	0.729	0.484	0.694	0.008	0.020
nb~15+14	0.650	0.001	0.324	0.831	0.524	0.681	0.003	0.310
rpart~26+22	0.642	0.001	0.485	0.763	0.541	0.720	0.000	0.004
knn~4+2	0.646	0.001	0.779	0.424	0.438	0.769	0.003	0.083
nb~42+19	0.649	0.001	0.574	0.644	0.481	0.724	0.001	0.003
svm~29+28	0.649	0.001	0.397	0.763	0.491	0.687	0.010	0.009
nb~42+28	0.649	0.001	0.529	0.686	0.493	0.717	0.001	0.025
knn~39+19	0.646	0.001	0.647	0.619	0.494	0.753	0.000	0.000
rf~4+32	0.649	0.001	0.544	0.653	0.474	0.713	0.004	0.004
svm~16+8	0.649	0.001	0.485	0.703	0.485	0.703	0.006	0.309
svm~17+28	0.649	0.001	0.485	0.695	0.478	0.701	0.002	0.003
svm~41+22	0.649	0.001	0.544	0.669	0.487	0.718	0.003	0.019
rpart~14+20	0.634	0.001	0.735	0.551	0.485	0.783	0.000	0.001
svm~16+13	0.649	0.001	0.471	0.686	0.464	0.692	0.027	0.069
svm~28+32	0.649	0.001	0.441	0.771	0.526	0.705	0.000	0.006
svm~19+21	0.648	0.001	0.500	0.763	0.548	0.726	0.000	0.004
knn~42+18	0.643	0.001	0.632	0.602	0.478	0.740	0.004	0.016
nb~38+22	0.648	0.001	0.529	0.695	0.500	0.719	0.001	0.060
knn~4+41	0.645	0.001	0.456	0.746	0.508	0.704	0.002	0.007
rpart~15+24	0.638	0.001	0.721	0.517	0.462	0.763	0.001	0.064
rpart~10+28	0.640	0.001	0.441	0.746	0.500	0.698	0.011	0.086
rf~15+41	0.648	0.001	0.603	0.703	0.539	0.755	0.000	0.701
svm~33+22	0.648	0.001	0.544	0.610	0.446	0.699	0.024	0.061
rpart~33+28	0.645	0.001	0.603	0.593	0.461	0.722	0.006	0.211
rpart~2+22	0.640	0.001	0.706	0.508	0.453	0.750	0.003	0.125
nb~17+9	0.648	0.001	0.559	0.703	0.521	0.735	0.000	0.044
svm~16+29	0.648	0.001	0.368	0.873	0.625	0.705	0.000	0.005
svm~37+28	0.648	0.001	0.603	0.627	0.482	0.733	0.001	0.035
knn~32+6	0.645	0.001	0.500	0.653	0.453	0.694	0.024	0.008
nb~16+8	0.648	0.001	0.500	0.686	0.479	0.704	0.012	0.042
rpart~4+14	0.644	0.001	0.515	0.780	0.574	0.736	0.000	0.001
knn~5+19	0.644	0.001	0.647	0.585	0.473	0.742	0.001	0.003
nb~27+22	0.647	0.001	0.706	0.534	0.466	0.759	0.001	0.016
svm~4+14	0.647	0.001	0.456	0.822	0.596	0.724	0.000	0.002
nb~12+20	0.647	0.001	0.662	0.500	0.433	0.720	0.015	0.001

svm~16+31	0.647	0.001	0.426	0.754	0.500	0.695	0.007	0.267
nb~24+8	0.647	0.001	0.618	0.568	0.452	0.720	0.008	0.000
nb~35+26	0.647	0.001	0.603	0.602	0.466	0.724	0.012	0.007
rpart~18+22	0.638	0.001	0.426	0.771	0.518	0.700	0.002	0.049
nb~16+40	0.647	0.001	0.500	0.720	0.507	0.714	0.003	0.173
svm~18+6	0.647	0.001	0.456	0.737	0.500	0.702	0.003	0.046
svm~7+6	0.647	0.001	0.618	0.653	0.506	0.748	0.000	0.025
svm~40+17	0.647	0.001	0.603	0.644	0.494	0.738	0.000	0.059
rpart~16+22	0.644	0.001	0.574	0.636	0.476	0.721	0.003	0.042
rf~8+19	0.647	0.001	0.441	0.737	0.492	0.696	0.002	0.004
nb~4+11	0.647	0.001	0.382	0.941	0.788	0.725	0.000	0.009
nb~40+18	0.647	0.001	0.618	0.534	0.433	0.708	0.051	0.230
nb~17+24	0.647	0.001	0.515	0.678	0.479	0.708	0.002	0.000
svm~18+37	0.647	0.001	0.441	0.754	0.508	0.701	0.004	0.011
nb~20+34	0.647	0.001	0.691	0.542	0.465	0.753	0.001	0.004
svm~4+34	0.646	0.001	0.471	0.754	0.525	0.712	0.000	0.014
nb~29+6	0.646	0.001	0.500	0.763	0.548	0.726	0.000	0.032
rpart~25+19	0.640	0.001	0.647	0.542	0.449	0.727	0.005	0.014
rpart~29+20	0.632	0.001	0.706	0.534	0.466	0.759	0.001	0.004
rf~13+22	0.646	0.001	0.676	0.568	0.474	0.753	0.001	0.080
nb~18+9	0.646	0.001	0.588	0.602	0.460	0.717	0.023	0.068
svm~38+6	0.646	0.001	0.574	0.712	0.534	0.743	0.000	0.021
rpart~4+26	0.644	0.001	0.485	0.678	0.465	0.696	0.016	0.005
knn~17+22	0.643	0.001	0.559	0.661	0.487	0.722	0.001	0.036
knn~37+22	0.643	0.001	0.750	0.432	0.432	0.750	0.014	0.001
svm~18+13	0.646	0.001	0.559	0.661	0.487	0.722	0.002	0.006
nb~43+22	0.646	0.001	0.691	0.559	0.475	0.759	0.001	0.054
rpart~41+20	0.635	0.001	0.794	0.398	0.432	0.770	0.008	0.054
knn~4+27	0.643	0.001	0.529	0.619	0.444	0.695	0.038	0.061
svm~12+18	0.646	0.001	0.485	0.669	0.458	0.693	0.018	0.018
svm~1+6	0.645	0.001	0.515	0.720	0.515	0.720	0.000	0.008
svm~12+22	0.645	0.001	0.559	0.644	0.475	0.717	0.002	0.006
svm~39+22	0.645	0.001	0.588	0.593	0.455	0.714	0.008	0.024
nb~31+28	0.645	0.001	0.574	0.661	0.494	0.729	0.001	0.009
svm~34+6	0.645	0.001	0.603	0.619	0.477	0.730	0.001	0.005
knn~15+9	0.642	0.001	0.382	0.805	0.531	0.693	0.001	0.050
nb~16+5	0.645	0.001	0.662	0.534	0.450	0.733	0.011	0.023
rpart~17+22	0.640	0.001	0.515	0.669	0.473	0.705	0.007	0.390
svm~4+11	0.645	0.001	0.441	0.873	0.667	0.730	0.000	0.004
svm~32+22	0.645	0.001	0.456	0.737	0.500	0.702	0.002	0.002
rf~4+7	0.645	0.001	0.588	0.610	0.465	0.720	0.009	0.016
svm~35+24	0.645	0.001	0.279	0.873	0.559	0.678	0.005	0.031
svm~7+19	0.645	0.001	0.691	0.551	0.470	0.756	0.001	0.017
nb~35+18	0.645	0.001	0.559	0.602	0.447	0.703	0.036	0.086
nb~17+37	0.645	0.001	0.618	0.661	0.512	0.750	0.000	0.111
knn~20+6	0.642	0.001	0.676	0.525	0.451	0.738	0.005	0.001
knn~4+6	0.641	0.001	0.544	0.737	0.544	0.737	0.000	0.003

rf~24+19	0.644	0.001	0.515	0.703	0.500	0.716	0.000	0.000
knn~4+32	0.642	0.001	0.618	0.653	0.506	0.748	0.000	0.077
nb~26+2	0.644	0.001	0.397	0.771	0.500	0.689	0.018	0.213
rpart~4+37	0.626	0.001	0.412	0.763	0.500	0.692	0.005	0.002
nb~29+22	0.644	0.001	0.515	0.720	0.515	0.720	0.001	0.035
nb~39+6	0.644	0.001	0.485	0.712	0.493	0.706	0.002	0.030
rf~33+19	0.644	0.001	0.647	0.483	0.419	0.704	0.051	0.009
nb~35+24	0.644	0.001	0.471	0.763	0.533	0.714	0.000	0.010
rpart~1+19	0.639	0.001	0.632	0.602	0.478	0.740	0.000	0.003
knn~4+14	0.642	0.001	0.529	0.712	0.514	0.724	0.000	0.005
rf~12+31	0.644	0.001	0.588	0.551	0.430	0.699	0.045	0.144
nb~15+36	0.644	0.001	0.500	0.754	0.540	0.724	0.000	0.267
nb~36+19	0.644	0.001	0.706	0.542	0.471	0.762	0.000	0.003
svm~27+22	0.644	0.001	0.588	0.636	0.482	0.728	0.002	0.023
svm~1+28	0.644	0.001	0.515	0.780	0.574	0.736	0.000	0.003
knn~4+9	0.641	0.001	0.529	0.712	0.514	0.724	0.000	0.007
knn~4+36	0.641	0.001	0.721	0.373	0.398	0.698	0.099	0.002
knn~39+22	0.641	0.001	0.632	0.627	0.494	0.747	0.000	0.161
rpart~24+32	0.641	0.001	0.353	0.831	0.545	0.690	0.001	0.000
rpart~12+18	0.642	0.001	0.618	0.551	0.442	0.714	0.022	0.039
svm~16+21	0.643	0.001	0.559	0.669	0.494	0.725	0.001	0.442
svm~17+6	0.643	0.001	0.471	0.712	0.485	0.700	0.004	0.012
nb~24+18	0.643	0.001	0.456	0.678	0.449	0.684	0.042	0.001
nb~15+43	0.643	0.001	0.485	0.703	0.485	0.703	0.005	0.444
svm~5+6	0.643	0.001	0.471	0.703	0.478	0.697	0.011	0.015
knn~26+19	0.640	0.001	0.794	0.364	0.419	0.754	0.018	0.048
nb~16+41	0.643	0.001	0.368	0.729	0.439	0.667	0.149	0.188
rf~20+22	0.643	0.001	0.485	0.661	0.452	0.690	0.032	0.021
knn~9+22	0.640	0.001	0.574	0.695	0.520	0.739	0.000	0.022
nb~4+14	0.643	0.001	0.397	0.890	0.675	0.719	0.000	0.004
nb~10+28	0.643	0.001	0.397	0.797	0.529	0.696	0.001	0.035
rf~15+19	0.643	0.001	0.574	0.636	0.476	0.721	0.005	0.021
nb~15+27	0.643	0.001	0.471	0.669	0.451	0.687	0.025	0.181
nb~16+31	0.643	0.001	0.471	0.720	0.492	0.702	0.007	0.059
knn~24+2	0.639	0.001	0.735	0.475	0.446	0.757	0.005	0.202
knn~13+26	0.638	0.001	0.662	0.483	0.425	0.713	0.045	0.002
knn~18+13	0.639	0.001	0.779	0.398	0.427	0.758	0.016	0.042
svm~15+29	0.642	0.001	0.397	0.822	0.563	0.703	0.000	0.371
svm~17+2	0.642	0.001	0.544	0.661	0.481	0.716	0.005	0.196
knn~37+19	0.639	0.001	0.853	0.314	0.417	0.787	0.008	0.011
rpart~18+28	0.641	0.001	0.485	0.729	0.508	0.711	0.001	0.016
svm~42+22	0.642	0.001	0.559	0.636	0.469	0.714	0.004	0.027
svm~33+28	0.642	0.001	0.588	0.568	0.440	0.705	0.040	0.015
rpart~24+8	0.637	0.001	0.324	0.814	0.500	0.676	0.009	0.003
svm~43+19	0.642	0.001	0.515	0.720	0.515	0.720	0.000	0.064
nb~23+20	0.642	0.001	0.765	0.466	0.452	0.775	0.002	0.095
nb~35+32	0.642	0.001	0.500	0.695	0.486	0.707	0.003	0.050

svm~4+21	0.642	0.001	0.441	0.839	0.612	0.723	0.000	0.026
rpart~24+2	0.637	0.001	0.382	0.856	0.605	0.706	0.000	0.005
nb~15+38	0.642	0.001	0.412	0.746	0.483	0.688	0.018	0.369
nb~7+6	0.642	0.001	0.515	0.695	0.493	0.713	0.002	0.077
nb~8+26	0.642	0.001	0.750	0.381	0.411	0.726	0.068	0.003
knn~4+37	0.639	0.001	0.779	0.390	0.424	0.754	0.011	0.006
svm~15+7	0.642	0.001	0.456	0.712	0.477	0.694	0.010	0.662
knn~15+24	0.637	0.001	0.632	0.542	0.443	0.719	0.019	0.072
rf~1+22	0.641	0.001	0.632	0.610	0.483	0.742	0.001	0.010
rpart~24+33	0.635	0.001	0.368	0.788	0.500	0.684	0.005	0.002
rpart~8+6	0.639	0.001	0.529	0.703	0.507	0.722	0.001	0.016
rpart~2+28	0.639	0.001	0.574	0.686	0.513	0.736	0.000	0.336
svm~41+19	0.641	0.001	0.441	0.746	0.500	0.698	0.004	0.034
rpart~1+2	0.640	0.001	0.529	0.712	0.514	0.724	0.002	0.188
rpart~31+22	0.634	0.001	0.544	0.686	0.500	0.723	0.001	0.002
svm~4+17	0.641	0.001	0.426	0.780	0.527	0.702	0.001	0.003
rpart~16+10	0.628	0.001	0.515	0.763	0.556	0.732	0.000	0.033
rpart~32+6	0.637	0.001	0.485	0.678	0.465	0.696	0.020	0.021
rpart~16+33	0.640	0.001	0.603	0.636	0.488	0.735	0.001	0.732
knn~4+11	0.637	0.001	0.441	0.771	0.526	0.705	0.001	0.014
svm~14+19	0.641	0.001	0.471	0.712	0.485	0.700	0.002	0.006
svm~35+18	0.641	0.001	0.382	0.754	0.473	0.679	0.053	0.027
rpart~15+12	0.637	0.001	0.324	0.746	0.423	0.657	0.179	0.348
rpart~4+33	0.639	0.001	0.618	0.568	0.452	0.720	0.009	0.007
nb~28+34	0.641	0.001	0.574	0.653	0.488	0.726	0.001	0.009
knn~28+21	0.636	0.001	0.779	0.398	0.427	0.758	0.015	0.017
nb~17+2	0.640	0.001	0.529	0.686	0.493	0.717	0.004	0.465
rpart~20+38	0.632	0.001	0.706	0.508	0.453	0.750	0.003	0.194
rf~18+8	0.640	0.001	0.632	0.602	0.478	0.740	0.002	0.011
svm~15+20	0.640	0.001	0.559	0.644	0.475	0.717	0.002	0.058
nb~18+32	0.640	0.001	0.500	0.703	0.493	0.709	0.002	0.005
rpart~14+22	0.633	0.001	0.441	0.754	0.508	0.701	0.001	0.013
rf~15+20	0.640	0.001	0.647	0.559	0.458	0.733	0.009	0.512
svm~41+28	0.640	0.001	0.471	0.669	0.451	0.687	0.043	0.013
rf~19+3	0.640	0.001	0.603	0.619	0.477	0.730	0.001	0.001

Table 51: pairwise biomarkers from the 43 biomarker panel with significance for Wilcoxon P-value (auc.pvalue<=0.05) and other metrics for the PCSM event endpoint.

Auc.pvalue : Wilcoxon Test P-value. MFD: Median Fold Difference. KM: Kaplan Meier curves. mvaHRPval: Multivariable Analysis Hazard Ratio P-value.

Classifier	auc	auc. pvalue	Sensitivity	Specificity	Pos. Pred. Value	Neg. Pred. Value	KM P- value	Mva HRPval
svm~31+19	0.80	0.00	0.78	0.61	0.33	0.92	0.00	0.00
nb~16+19	0.79	0.00	0.83	0.65	0.36	0.94	0.00	0.00
svm~4+16	0.78	0.00	0.64	0.72	0.35	0.89	0.00	0.02
nb~4+16	0.78	0.00	0.61	0.85	0.49	0.90	0.00	0.01

svm~16+19	0.78	0.00	0.75	0.63	0.33	0.91	0.00	0.00
nb~16+22	0.77	0.00	0.78	0.68	0.37	0.93	0.00	0.01
nb~16+18	0.77	0.00	0.78	0.63	0.34	0.92	0.00	0.01
svm~40+19	0.77	0.00	0.83	0.59	0.33	0.94	0.00	0.01
nb~4+28	0.77	0.00	0.58	0.79	0.40	0.89	0.00	0.01
svm~35+19	0.77	0.00	0.69	0.71	0.36	0.91	0.00	0.01
nb~16+28	0.77	0.00	0.81	0.61	0.33	0.93	0.00	0.00
nb~16+20	0.77	0.00	0.81	0.53	0.29	0.92	0.00	0.00
nb~16+6	0.77	0.00	0.72	0.71	0.38	0.91	0.00	0.00
rpart~4+16	0.76	0.00	0.72	0.68	0.35	0.91	0.00	0.04
svm~39+19	0.77	0.00	0.81	0.59	0.32	0.93	0.00	0.00
svm~16+28	0.77	0.00	0.67	0.73	0.38	0.90	0.00	0.04
svm~16+18	0.77	0.00	0.75	0.73	0.40	0.92	0.00	0.01
nb~40+28	0.76	0.00	0.83	0.63	0.35	0.94	0.00	0.01
nb~28+6	0.76	0.00	0.75	0.69	0.37	0.92	0.00	0.00
nb~40+19	0.76	0.00	0.86	0.52	0.30	0.94	0.00	0.01
nb~12+28	0.76	0.00	0.81	0.65	0.35	0.93	0.00	0.00
svm~43+19	0.76	0.00	0.69	0.71	0.37	0.91	0.00	0.00
nb~43+19	0.76	0.00	0.94	0.51	0.32	0.97	0.00	0.00
nb~4+24	0.76	0.00	0.53	0.87	0.49	0.88	0.00	0.00
nb~24+28	0.76	0.00	0.58	0.73	0.34	0.88	0.00	0.00
nb~15+28	0.76	0.00	0.58	0.77	0.38	0.89	0.00	0.01
svm~13+22	0.76	0.00	0.81	0.66	0.36	0.93	0.00	0.04
knn~16+18	0.75	0.00	0.92	0.37	0.26	0.95	0.00	0.02
svm~4+24	0.76	0.00	0.56	0.83	0.44	0.89	0.00	0.00
nb~19+28	0.76	0.00	0.81	0.63	0.34	0.93	0.00	0.00
nb~4+12	0.75	0.00	0.64	0.79	0.42	0.90	0.00	0.01
nb~28+22	0.75	0.00	0.75	0.66	0.35	0.92	0.00	0.01
svm~16+22	0.75	0.00	0.75	0.63	0.33	0.91	0.00	0.02
nb~12+22	0.75	0.00	0.75	0.67	0.35	0.92	0.00	0.01
nb~4+35	0.75	0.00	0.61	0.85	0.49	0.90	0.00	0.03
svm~29+19	0.75	0.00	0.69	0.68	0.34	0.90	0.00	0.00
nb~35+19	0.75	0.00	0.81	0.53	0.29	0.92	0.00	0.01
nb~4+19	0.75	0.00	0.61	0.78	0.40	0.89	0.00	0.01
nb~16+24	0.75	0.00	0.67	0.70	0.35	0.90	0.00	0.00
nb~20+28	0.75	0.00	0.75	0.59	0.30	0.91	0.00	0.00
nb~18+28	0.75	0.00	0.64	0.65	0.31	0.88	0.00	0.01
nb~43+6	0.75	0.00	0.47	0.78	0.34	0.86	0.00	0.01
nb~35+6	0.75	0.00	0.61	0.74	0.36	0.89	0.00	0.01
nb~35+20	0.75	0.00	0.89	0.41	0.26	0.94	0.00	0.00
svm~8+22	0.75	0.00	0.67	0.71	0.36	0.90	0.00	0.01
nb~16+26	0.75	0.00	0.58	0.73	0.34	0.88	0.00	0.00
nb~12+6	0.75	0.00	0.78	0.63	0.33	0.92	0.00	0.01
nb~40+24	0.74	0.00	0.64	0.63	0.29	0.88	0.00	0.00
rpart~20+22	0.74	0.00	0.61	0.68	0.31	0.88	0.00	0.01
nb~4+43	0.74	0.00	0.53	0.85	0.45	0.88	0.00	0.01
nb~12+18	0.74	0.00	0.69	0.69	0.35	0.90	0.00	0.02

svm~16+6	0.74	0.00	0.75	0.67	0.35	0.92	0.00	0.00
svm~4+12	0.74	0.00	0.64	0.79	0.42	0.90	0.00	0.04
rpart~8+28	0.74	0.00	0.75	0.67	0.35	0.92	0.00	0.01
nb~40+22	0.74	0.00	0.72	0.56	0.28	0.89	0.00	0.07
svm~13+28	0.74	0.00	0.64	0.65	0.30	0.88	0.00	0.02
nb~26+28	0.74	0.00	0.67	0.66	0.32	0.89	0.00	0.00
nb~40+6	0.74	0.00	0.61	0.74	0.36	0.89	0.00	0.03
svm~12+6	0.74	0.00	0.67	0.68	0.33	0.89	0.00	0.00
knn~24+22	0.73	0.00	0.67	0.76	0.40	0.90	0.00	0.04
rpart~4+38	0.74	0.00	0.75	0.64	0.33	0.91	0.00	0.05
svm~19+22	0.74	0.00	0.58	0.70	0.32	0.88	0.00	0.01
svm~40+28	0.74	0.00	0.83	0.58	0.32	0.94	0.00	0.02
rpart~4+24	0.73	0.00	0.56	0.79	0.39	0.88	0.00	0.01
svm~19+28	0.74	0.00	0.69	0.71	0.36	0.91	0.00	0.00
svm~4+31	0.74	0.00	0.69	0.68	0.34	0.90	0.00	0.04
nb~4+20	0.74	0.00	0.69	0.72	0.37	0.91	0.00	0.01
nb~4+15	0.74	0.00	0.56	0.79	0.39	0.88	0.00	0.03
svm~33+19	0.74	0.00	0.64	0.60	0.28	0.87	0.00	0.00
nb~24+22	0.74	0.00	0.72	0.59	0.30	0.90	0.00	0.00
nb~12+19	0.74	0.00	0.75	0.58	0.30	0.91	0.00	0.00
nb~4+23	0.74	0.00	0.61	0.77	0.39	0.89	0.00	0.06
nb~4+31	0.74	0.00	0.56	0.79	0.38	0.88	0.00	0.03
svm~13+19	0.74	0.00	0.83	0.50	0.29	0.93	0.00	0.03
nb~4+6	0.74	0.00	0.58	0.77	0.38	0.88	0.00	0.04
nb~43+28	0.74	0.00	0.69	0.68	0.34	0.90	0.00	0.00
nb~28+32	0.74	0.00	0.67	0.63	0.30	0.89	0.00	0.02
nb~19+6	0.74	0.00	0.61	0.74	0.36	0.89	0.00	0.00
knn~4+16	0.73	0.00	0.78	0.59	0.31	0.92	0.00	0.02
nb~13+22	0.74	0.00	0.75	0.67	0.35	0.92	0.00	0.07
rf~31+19	0.74	0.00	0.81	0.53	0.29	0.92	0.00	0.00
nb~43+22	0.74	0.00	0.83	0.54	0.30	0.93	0.00	0.02
nb~4+8	0.73	0.00	0.53	0.87	0.50	0.89	0.00	0.03
nb~4+32	0.73	0.00	0.61	0.82	0.45	0.90	0.00	0.05
nb~4+40	0.73	0.00	0.58	0.87	0.53	0.90	0.00	0.04
svm~4+13	0.73	0.00	0.61	0.83	0.46	0.90	0.00	0.01
rpart~4+39	0.72	0.00	0.67	0.73	0.37	0.90	0.00	0.00
svm~29+22	0.73	0.00	0.69	0.58	0.28	0.89	0.00	0.04
nb~40+20	0.73	0.00	0.78	0.53	0.28	0.91	0.00	0.01
nb~35+22	0.73	0.00	0.81	0.48	0.27	0.91	0.00	0.03
rf~13+26	0.73	0.00	0.72	0.66	0.34	0.91	0.00	0.02
svm~8+19	0.73	0.00	0.72	0.62	0.31	0.90	0.00	0.00
nb~24+20	0.73	0.00	0.78	0.51	0.27	0.90	0.00	0.00
nb~15+6	0.73	0.00	0.42	0.79	0.33	0.85	0.00	0.03
svm~35+22	0.73	0.00	0.58	0.75	0.36	0.88	0.00	0.09
nb~8+19	0.73	0.00	0.72	0.65	0.33	0.91	0.00	0.01
nb~4+22	0.73	0.00	0.61	0.77	0.39	0.89	0.00	0.05
svm~4+40	0.73	0.00	0.72	0.58	0.29	0.90	0.00	0.18

svm~4+8	0.73	0.00	0.64	0.81	0.45	0.90	0.00	0.00
nb~13+19	0.73	0.00	0.83	0.51	0.29	0.93	0.00	0.02
svm~4+29	0.73	0.00	0.56	0.83	0.44	0.89	0.00	0.01
svm~4+38	0.73	0.00	0.64	0.77	0.40	0.90	0.00	0.01
nb~19+32	0.73	0.00	0.67	0.71	0.35	0.90	0.00	0.01
nb~13+28	0.73	0.00	0.61	0.68	0.31	0.88	0.00	0.01
nb~26+19	0.73	0.00	0.83	0.53	0.30	0.93	0.00	0.01
nb~35+28	0.73	0.00	0.64	0.65	0.31	0.88	0.00	0.01
nb~24+6	0.73	0.00	0.44	0.82	0.37	0.86	0.00	0.00
svm~19+6	0.73	0.00	0.67	0.69	0.34	0.90	0.00	0.01
nb~19+22	0.73	0.00	0.81	0.53	0.29	0.92	0.00	0.01
nb~24+19	0.73	0.00	0.67	0.67	0.33	0.89	0.00	0.00
nb~4+13	0.73	0.00	0.56	0.88	0.53	0.89	0.00	0.03
svm~4+15	0.73	0.00	0.44	0.83	0.38	0.86	0.00	0.04
nb~8+28	0.73	0.00	0.72	0.63	0.32	0.90	0.00	0.01
svm~37+19	0.73	0.00	0.72	0.55	0.28	0.89	0.00	0.01
nb~12+24	0.73	0.00	0.64	0.77	0.40	0.90	0.00	0.00
nb~13+6	0.73	0.00	0.69	0.68	0.34	0.90	0.00	0.02
nb~20+6	0.73	0.00	0.67	0.66	0.32	0.89	0.00	0.00
svm~4+14	0.73	0.00	0.58	0.79	0.40	0.89	0.00	0.02
knn~40+6	0.72	0.00	0.94	0.29	0.24	0.96	0.00	0.02
nb~4+26	0.73	0.00	0.56	0.83	0.43	0.89	0.00	0.02
nb~32+6	0.73	0.00	0.50	0.81	0.39	0.87	0.00	0.03
svm~38+28	0.73	0.00	0.69	0.64	0.32	0.90	0.00	0.01
rpart~13+6	0.72	0.00	0.72	0.67	0.34	0.91	0.00	0.05
svm~4+35	0.73	0.00	0.61	0.77	0.39	0.89	0.00	0.05
nb~4+18	0.73	0.00	0.58	0.74	0.35	0.88	0.00	0.05
nb~12+26	0.73	0.00	0.58	0.77	0.38	0.89	0.00	0.01
rf~24+22	0.73	0.00	0.69	0.67	0.34	0.90	0.00	0.02
svm~19+38	0.73	0.00	0.72	0.63	0.32	0.90	0.00	0.02
nb~19+20	0.73	0.00	0.78	0.49	0.27	0.90	0.00	0.01
nb~31+28	0.73	0.00	0.78	0.66	0.35	0.93	0.00	0.00
svm~40+24	0.73	0.00	0.78	0.63	0.33	0.92	0.00	0.02
svm~12+28	0.73	0.00	0.64	0.68	0.32	0.89	0.00	0.08
knn~18+32	0.72	0.00	0.89	0.39	0.26	0.94	0.00	0.03
nb~4+33	0.72	0.00	0.56	0.85	0.48	0.89	0.00	0.07
nb~31+19	0.72	0.00	0.75	0.67	0.35	0.92	0.00	0.01
nb~8+22	0.72	0.00	0.78	0.57	0.30	0.91	0.00	0.06
svm~14+19	0.72	0.00	0.58	0.70	0.32	0.88	0.00	0.01
nb~32+22	0.72	0.00	0.67	0.61	0.29	0.88	0.00	0.05
nb~4+36	0.72	0.00	0.50	0.89	0.51	0.88	0.00	0.03
svm~40+6	0.72	0.00	0.81	0.55	0.30	0.92	0.00	0.08
svm~39+22	0.72	0.00	0.75	0.59	0.31	0.91	0.00	0.03
rpart~16+6	0.71	0.00	0.61	0.69	0.32	0.88	0.00	0.04
knn~13+19	0.72	0.00	0.50	0.75	0.32	0.86	0.00	0.07
rpart~4+31	0.72	0.00	0.75	0.66	0.35	0.92	0.00	0.04
svm~13+6	0.72	0.00	0.69	0.69	0.35	0.90	0.00	0.04

svm~4+42	0.72	0.00	0.69	0.64	0.32	0.90	0.00	0.09
nb~12+20	0.72	0.00	0.75	0.49	0.26	0.89	0.00	0.00
nb~22+6	0.72	0.00	0.64	0.66	0.31	0.88	0.00	0.02
rpart~4+43	0.72	0.00	0.56	0.71	0.32	0.87	0.00	0.01
rf~13+22	0.72	0.00	0.78	0.54	0.29	0.91	0.00	0.45
nb~26+6	0.72	0.00	0.69	0.68	0.34	0.90	0.00	0.01
svm~35+6	0.72	0.00	0.58	0.74	0.35	0.88	0.00	0.05
nb~20+22	0.72	0.00	0.69	0.59	0.29	0.89	0.00	0.01
rf~4+12	0.72	0.00	0.69	0.57	0.28	0.89	0.00	0.02
nb~14+28	0.72	0.00	0.61	0.75	0.37	0.89	0.00	0.01
rpart~24+38	0.71	0.00	0.61	0.77	0.39	0.89	0.00	0.00
svm~4+28	0.72	0.00	0.61	0.74	0.36	0.89	0.00	0.04
svm~24+13	0.72	0.00	0.42	0.83	0.38	0.86	0.00	0.02
svm~19+21	0.72	0.00	0.64	0.74	0.37	0.90	0.00	0.01
nb~18+6	0.72	0.00	0.64	0.68	0.32	0.89	0.00	0.02
svm~13+26	0.72	0.00	0.53	0.86	0.48	0.88	0.00	0.18
nb~17+28	0.72	0.00	0.64	0.67	0.32	0.88	0.00	0.00
rpart~39+28	0.71	0.00	0.78	0.64	0.34	0.92	0.00	0.01
nb~37+28	0.72	0.00	0.69	0.62	0.30	0.89	0.00	0.02
nb~24+43	0.72	0.00	0.61	0.67	0.31	0.88	0.00	0.00
rf~16+19	0.72	0.00	0.72	0.57	0.29	0.90	0.00	0.01
svm~15+28	0.72	0.00	0.56	0.78	0.38	0.88	0.00	0.02
svm~31+22	0.72	0.00	0.69	0.61	0.30	0.89	0.00	0.05
rpart~31+19	0.71	0.00	0.86	0.54	0.31	0.94	0.00	0.01
nb~16+17	0.72	0.00	0.61	0.75	0.37	0.89	0.00	0.02
rpart~26+22	0.71	0.00	0.61	0.74	0.36	0.89	0.00	0.03
svm~16+24	0.72	0.00	0.39	0.89	0.45	0.86	0.00	0.02
svm~40+26	0.72	0.00	0.75	0.59	0.30	0.91	0.00	0.05
nb~43+20	0.72	0.00	0.78	0.50	0.27	0.90	0.00	0.00
svm~12+19	0.72	0.00	0.72	0.65	0.33	0.91	0.00	0.03
rpart~24+32	0.71	0.00	0.50	0.83	0.41	0.87	0.00	0.02
svm~31+28	0.72	0.00	0.81	0.63	0.34	0.93	0.00	0.01
nb~20+32	0.72	0.00	0.75	0.53	0.28	0.90	0.00	0.02
rpart~16+20	0.71	0.00	0.78	0.52	0.28	0.91	0.00	0.04
rpart~4+13	0.71	0.00	0.64	0.67	0.32	0.89	0.00	0.04
nb~24+26	0.72	0.00	0.72	0.67	0.34	0.91	0.00	0.00
rpart~24+22	0.71	0.00	0.64	0.73	0.37	0.89	0.00	0.02
rpart~8+19	0.71	0.00	0.75	0.62	0.32	0.91	0.00	0.00
nb~15+22	0.72	0.00	0.50	0.74	0.32	0.86	0.00	0.06
svm~28+32	0.72	0.00	0.53	0.75	0.33	0.87	0.00	0.09
svm~4+41	0.72	0.00	0.42	0.82	0.36	0.85	0.00	0.01
svm~4+19	0.72	0.00	0.81	0.68	0.38	0.94	0.00	0.02
knn~12+22	0.71	0.00	0.67	0.68	0.33	0.89	0.00	0.05
nb~16+32	0.72	0.00	0.64	0.71	0.34	0.89	0.00	0.06
nb~26+22	0.72	0.00	0.78	0.57	0.30	0.91	0.00	0.03
svm~12+18	0.72	0.00	0.67	0.68	0.33	0.89	0.00	0.05
nb~8+6	0.72	0.00	0.58	0.72	0.33	0.88	0.00	0.03

svm~18+19	0.72	0.00	0.72	0.64	0.33	0.91	0.00	0.01
rf~33+19	0.72	0.00	0.75	0.48	0.26	0.89	0.01	0.00
svm~26+19	0.72	0.00	0.64	0.76	0.39	0.90	0.00	0.01
nb~15+16	0.72	0.00	0.53	0.73	0.32	0.87	0.00	0.05
nb~42+6	0.71	0.00	0.61	0.75	0.37	0.89	0.00	0.04
nb~18+22	0.71	0.00	0.81	0.59	0.32	0.93	0.00	0.05
nb~14+19	0.71	0.00	0.81	0.45	0.26	0.91	0.00	0.01
rpart~33+28	0.71	0.00	0.72	0.58	0.29	0.90	0.00	0.15
svm~4+1	0.71	0.00	0.56	0.81	0.41	0.88	0.00	0.03
svm~24+19	0.71	0.00	0.58	0.79	0.40	0.89	0.00	0.01
nb~33+6	0.71	0.00	0.64	0.72	0.35	0.89	0.00	0.07
nb~42+28	0.71	0.00	0.61	0.66	0.30	0.88	0.00	0.02
knn~15+16	0.71	0.00	0.81	0.43	0.25	0.90	0.00	0.07
svm~16+26	0.71	0.00	0.56	0.78	0.38	0.88	0.00	0.03
rpart~24+28	0.71	0.00	0.44	0.77	0.31	0.85	0.00	0.02
nb~31+6	0.71	0.00	0.64	0.71	0.34	0.89	0.00	0.01
svm~12+22	0.71	0.00	0.67	0.63	0.30	0.89	0.00	0.08
nb~15+19	0.71	0.00	0.53	0.77	0.36	0.87	0.00	0.03
nb~18+19	0.71	0.00	0.72	0.57	0.29	0.89	0.00	0.02
nb~23+20	0.71	0.00	0.89	0.45	0.28	0.94	0.00	0.01
knn~4+32	0.71	0.00	0.78	0.63	0.34	0.92	0.00	0.37
knn~40+19	0.71	0.00	0.83	0.48	0.28	0.92	0.00	0.02
svm~15+19	0.71	0.00	0.47	0.81	0.37	0.86	0.00	0.07
nb~4+41	0.71	0.00	0.53	0.79	0.38	0.88	0.00	0.05
rpart~18+22	0.70	0.00	0.53	0.75	0.34	0.87	0.00	0.12
rf~13+19	0.71	0.00	0.89	0.35	0.25	0.93	0.01	0.05
nb~15+24	0.71	0.00	0.58	0.73	0.34	0.88	0.00	0.01
rpart~20+28	0.70	0.00	0.81	0.47	0.27	0.91	0.00	0.01
knn~31+19	0.71	0.00	0.78	0.53	0.28	0.91	0.00	0.01
svm~7+19	0.71	0.00	0.78	0.52	0.28	0.91	0.00	0.05
rf~40+28	0.71	0.00	0.86	0.49	0.29	0.94	0.00	0.10
knn~40+28	0.71	0.00	0.58	0.77	0.38	0.89	0.00	0.01
rpart~4+32	0.71	0.00	0.61	0.71	0.33	0.88	0.00	0.19
nb~4+42	0.71	0.00	0.53	0.83	0.43	0.88	0.00	0.07
svm~8+28	0.71	0.00	0.69	0.65	0.32	0.90	0.00	0.02
rf~12+19	0.71	0.00	0.64	0.66	0.31	0.88	0.00	0.01
nb~42+22	0.71	0.00	0.72	0.51	0.26	0.88	0.01	0.16
nb~4+11	0.71	0.00	0.47	0.89	0.52	0.88	0.00	0.09
nb~40+18	0.71	0.00	0.75	0.53	0.28	0.90	0.00	0.16
nb~15+32	0.71	0.00	0.33	0.84	0.33	0.84	0.00	0.15
svm~4+32	0.71	0.00	0.61	0.73	0.35	0.89	0.00	0.13
svm~29+28	0.71	0.00	0.47	0.75	0.31	0.85	0.00	0.02
knn~16+19	0.71	0.00	0.81	0.59	0.32	0.93	0.00	0.00
nb~4+29	0.71	0.00	0.58	0.73	0.34	0.88	0.00	0.10
svm~4+39	0.71	0.00	0.64	0.69	0.33	0.89	0.00	0.00
knn~18+13	0.71	0.00	0.89	0.39	0.26	0.94	0.00	0.43
svm~19+32	0.71	0.00	0.61	0.75	0.37	0.89	0.00	0.01

svm~28+22	0.71	0.00	0.64	0.73	0.37	0.89	0.00	0.01
svm~8+6	0.71	0.00	0.67	0.67	0.33	0.89	0.00	0.02
nb~4+14	0.71	0.00	0.50	0.85	0.45	0.88	0.00	0.03
rf~24+13	0.71	0.00	0.64	0.57	0.26	0.87	0.01	0.01
rf~9+19	0.71	0.00	0.83	0.57	0.32	0.93	0.00	0.00
nb~41+28	0.71	0.00	0.67	0.59	0.28	0.88	0.00	0.02
nb~42+19	0.71	0.00	0.69	0.63	0.31	0.90	0.00	0.04
nb~4+1	0.71	0.00	0.58	0.79	0.40	0.89	0.00	0.05
svm~1+19	0.71	0.00	0.69	0.61	0.30	0.89	0.00	0.00
knn~35+19	0.70	0.00	0.89	0.39	0.26	0.94	0.00	0.00
svm~4+11	0.71	0.00	0.53	0.83	0.42	0.88	0.00	0.04
nb~18+32	0.71	0.00	0.61	0.69	0.32	0.88	0.00	0.12
nb~24+32	0.71	0.00	0.42	0.89	0.48	0.86	0.00	0.01
nb~33+28	0.71	0.00	0.72	0.57	0.29	0.90	0.00	0.02
rpart~4+18	0.70	0.00	0.67	0.67	0.33	0.89	0.00	0.03
svm~4+18	0.71	0.00	0.53	0.77	0.35	0.87	0.00	0.16
svm~2+28	0.71	0.00	0.75	0.57	0.30	0.91	0.00	0.03
svm~16+29	0.71	0.00	0.44	0.84	0.40	0.86	0.00	0.01
nb~4+39	0.71	0.00	0.58	0.76	0.37	0.88	0.00	0.04
svm~24+31	0.71	0.00	0.44	0.84	0.40	0.86	0.00	0.00
svm~39+28	0.71	0.00	0.69	0.67	0.34	0.90	0.00	0.01
nb~14+22	0.71	0.00	0.75	0.56	0.29	0.90	0.00	0.05
knn~4+42	0.70	0.00	0.89	0.29	0.23	0.92	0.02	0.02
knn~16+17	0.70	0.00	0.64	0.69	0.33	0.89	0.00	0.03
svm~32+22	0.71	0.00	0.58	0.73	0.34	0.88	0.00	0.04
rpart~14+28	0.68	0.00	0.53	0.80	0.39	0.88	0.00	0.07
rpart~15+33	0.70	0.00	0.42	0.85	0.39	0.86	0.00	0.78
rpart~14+24	0.70	0.00	0.47	0.79	0.35	0.86	0.00	0.02
svm~42+19	0.71	0.00	0.58	0.69	0.31	0.87	0.00	0.11
nb~18+20	0.71	0.00	0.72	0.51	0.26	0.89	0.00	0.02
rpart~4+42	0.70	0.00	0.75	0.58	0.30	0.91	0.00	0.12
svm~12+24	0.71	0.00	0.39	0.87	0.41	0.86	0.00	0.04
rpart~32+22	0.70	0.00	0.61	0.73	0.35	0.89	0.00	0.17
nb~4+25	0.71	0.00	0.64	0.77	0.40	0.90	0.00	0.14
nb~24+18	0.71	0.00	0.56	0.67	0.29	0.86	0.00	0.01
svm~43+6	0.71	0.00	0.47	0.77	0.33	0.86	0.00	0.03
rpart~4+11	0.67	0.00	0.53	0.77	0.35	0.87	0.00	0.04
nb~4+37	0.71	0.00	0.58	0.79	0.40	0.89	0.00	0.06
svm~19+3	0.71	0.00	0.56	0.77	0.37	0.88	0.00	0.13
rpart~33+19	0.67	0.00	0.67	0.68	0.33	0.89	0.00	0.01
nb~37+22	0.71	0.00	0.67	0.59	0.28	0.88	0.00	0.11
nb~8+20	0.71	0.00	0.75	0.47	0.25	0.89	0.01	0.01
rpart~12+24	0.70	0.00	0.47	0.83	0.40	0.87	0.00	0.00
rpart~9+19	0.69	0.00	0.78	0.53	0.28	0.91	0.00	0.01
nb~4+38	0.70	0.00	0.67	0.74	0.38	0.90	0.00	0.02
svm~17+19	0.70	0.00	0.56	0.72	0.32	0.87	0.00	0.01
nb~4+9	0.70	0.00	0.61	0.78	0.40	0.89	0.00	0.06

nb~23+6	0.70	0.00	0.58	0.72	0.33	0.88	0.00	0.03
rpart~25+19	0.69	0.00	0.78	0.53	0.29	0.91	0.00	0.02
knn~4+12	0.70	0.00	0.53	0.82	0.41	0.88	0.00	0.07
nb~17+6	0.70	0.00	0.67	0.63	0.30	0.89	0.00	0.01
svm~31+6	0.70	0.00	0.67	0.65	0.31	0.89	0.00	0.03
svm~21+22	0.70	0.00	0.58	0.69	0.31	0.87	0.00	0.07
rpart~14+22	0.69	0.00	0.53	0.73	0.32	0.87	0.00	0.05
nb~37+19	0.70	0.00	0.61	0.65	0.29	0.87	0.00	0.01
nb~26+20	0.70	0.00	0.75	0.52	0.27	0.90	0.00	0.01
rpart~40+26	0.69	0.00	0.64	0.63	0.29	0.88	0.01	0.03
svm~26+22	0.70	0.00	0.61	0.70	0.33	0.88	0.00	0.04
svm~24+26	0.70	0.00	0.31	0.92	0.48	0.85	0.00	0.00
svm~28+6	0.70	0.00	0.64	0.71	0.34	0.89	0.00	0.00
nb~40+26	0.70	0.00	0.78	0.47	0.26	0.90	0.01	0.08
rpart~42+22	0.69	0.00	0.67	0.59	0.28	0.88	0.00	0.36
nb~36+6	0.70	0.00	0.58	0.73	0.34	0.88	0.00	0.02
nb~36+22	0.70	0.00	0.72	0.55	0.28	0.89	0.00	0.08
nb~16+40	0.70	0.00	0.58	0.69	0.31	0.87	0.00	0.09
svm~18+6	0.70	0.00	0.56	0.72	0.32	0.87	0.00	0.08
nb~41+6	0.70	0.00	0.53	0.78	0.37	0.87	0.00	0.05
svm~16+31	0.70	0.00	0.53	0.74	0.33	0.87	0.00	0.15
nb~12+17	0.70	0.00	0.53	0.77	0.36	0.87	0.00	0.02
nb~36+28	0.70	0.00	0.72	0.59	0.30	0.90	0.00	0.01
rpart~16+19	0.69	0.00	0.83	0.56	0.31	0.93	0.00	0.00
knn~40+24	0.70	0.00	0.86	0.41	0.26	0.93	0.00	0.01
svm~37+22	0.70	0.00	0.69	0.59	0.29	0.89	0.00	0.51
rpart~24+5	0.70	0.00	0.58	0.72	0.33	0.88	0.00	0.01
rf~4+39	0.70	0.00	0.75	0.57	0.29	0.90	0.00	0.00
nb~4+34	0.70	0.00	0.53	0.80	0.39	0.88	0.00	0.05
nb~17+19	0.70	0.00	0.78	0.56	0.30	0.91	0.00	0.01
rf~16+18	0.70	0.00	0.67	0.62	0.30	0.89	0.00	0.19
svm~14+22	0.70	0.00	0.53	0.68	0.28	0.86	0.01	0.06
svm~18+28	0.70	0.00	0.64	0.69	0.33	0.89	0.00	0.01
rpart~7+20	0.69	0.00	0.81	0.45	0.26	0.91	0.00	0.03
svm~42+6	0.70	0.00	0.67	0.63	0.30	0.89	0.00	0.03
nb~4+27	0.70	0.00	0.67	0.66	0.32	0.89	0.00	0.07
nb~11+6	0.70	0.00	0.50	0.81	0.39	0.87	0.00	0.06
rf~35+19	0.70	0.00	0.72	0.61	0.31	0.90	0.00	0.01
svm~26+28	0.70	0.00	0.53	0.77	0.36	0.87	0.00	0.02
nb~1+28	0.70	0.00	0.61	0.69	0.32	0.88	0.00	0.01
nb~11+28	0.70	0.00	0.56	0.71	0.31	0.87	0.00	0.05
rf~4+32	0.70	0.00	0.64	0.63	0.29	0.88	0.00	0.23
rpart~4+26	0.70	0.00	0.58	0.67	0.30	0.87	0.00	0.02
nb~13+20	0.70	0.00	0.69	0.57	0.28	0.89	0.00	0.02
nb~37+6	0.70	0.00	0.69	0.65	0.32	0.90	0.00	0.08
svm~25+28	0.70	0.00	0.72	0.59	0.30	0.90	0.00	0.09
svm~40+18	0.70	0.00	0.72	0.55	0.28	0.89	0.00	0.10

nb~14+20	0.70	0.00	0.78	0.51	0.28	0.91	0.00	0.01
knn~32+22	0.70	0.00	0.64	0.69	0.33	0.89	0.00	0.06
rpart~19+20	0.69	0.00	0.81	0.47	0.27	0.91	0.00	0.02
rf~4+31	0.70	0.00	0.61	0.64	0.29	0.87	0.00	0.05
rpart~4+28	0.70	0.00	0.58	0.73	0.34	0.88	0.00	0.03
svm~24+22	0.70	0.00	0.42	0.83	0.38	0.86	0.00	0.05
knn~4+19	0.70	0.00	0.72	0.65	0.33	0.91	0.00	0.07
nb~4+17	0.70	0.00	0.58	0.79	0.40	0.89	0.00	0.05
svm~12+16	0.70	0.00	0.39	0.87	0.42	0.86	0.00	0.08
rpart~4+1	0.69	0.00	0.69	0.51	0.25	0.87	0.01	0.09
svm~24+6	0.70	0.00	0.56	0.77	0.37	0.88	0.00	0.03
knn~39+22	0.70	0.00	0.78	0.61	0.32	0.92	0.00	0.38
rpart~4+23	0.69	0.00	0.67	0.67	0.33	0.89	0.00	0.03
svm~29+6	0.70	0.00	0.64	0.71	0.35	0.89	0.00	0.01
knn~4+31	0.69	0.00	0.61	0.67	0.31	0.88	0.00	0.01
knn~35+28	0.69	0.00	0.89	0.43	0.27	0.94	0.00	0.12
nb~4+2	0.70	0.00	0.64	0.71	0.35	0.89	0.00	0.15
nb~17+22	0.70	0.00	0.69	0.53	0.26	0.88	0.01	0.04
nb~26+32	0.70	0.00	0.67	0.59	0.28	0.88	0.00	0.05
knn~29+6	0.69	0.00	0.61	0.67	0.31	0.88	0.00	0.03
svm~38+22	0.70	0.00	0.67	0.65	0.31	0.89	0.00	0.11
svm~34+22	0.70	0.00	0.64	0.53	0.25	0.86	0.03	0.01
nb~33+19	0.70	0.00	0.81	0.53	0.29	0.92	0.00	0.05
rpart~31+22	0.69	0.00	0.64	0.66	0.31	0.88	0.00	0.01
svm~12+32	0.70	0.00	0.44	0.83	0.38	0.86	0.00	0.10
rpart~28+34	0.69	0.00	0.56	0.66	0.28	0.86	0.00	0.06
knn~4+34	0.69	0.00	0.81	0.39	0.24	0.89	0.02	0.15
svm~21+6	0.70	0.00	0.61	0.65	0.30	0.88	0.00	0.02
nb~15+20	0.70	0.00	0.75	0.57	0.30	0.91	0.00	0.02
svm~4+43	0.70	0.00	0.50	0.83	0.42	0.87	0.00	0.01
knn~12+19	0.69	0.00	0.67	0.59	0.28	0.88	0.00	0.01
rpart~24+31	0.69	0.00	0.47	0.83	0.40	0.87	0.00	0.00
svm~4+6	0.70	0.00	0.64	0.73	0.37	0.89	0.00	0.14
nb~14+6	0.70	0.00	0.64	0.74	0.37	0.90	0.00	0.02
rpart~40+18	0.69	0.00	0.81	0.45	0.26	0.91	0.01	0.07
rf~4+38	0.70	0.00	0.58	0.67	0.30	0.87	0.00	0.07
rpart~23+19	0.69	0.00	0.81	0.45	0.26	0.91	0.00	0.01
rpart~18+32	0.69	0.00	0.69	0.62	0.30	0.89	0.00	0.11
svm~1+22	0.70	0.00	0.58	0.73	0.34	0.88	0.00	0.02
svm~4+22	0.70	0.00	0.64	0.73	0.36	0.89	0.00	0.16
rpart~4+6	0.69	0.00	0.61	0.65	0.30	0.88	0.00	0.11
svm~4+25	0.70	0.00	0.67	0.62	0.30	0.89	0.00	0.33
svm~42+22	0.70	0.00	0.64	0.61	0.28	0.88	0.00	0.07
nb~16+43	0.70	0.00	0.58	0.67	0.30	0.87	0.01	0.01
knn~4+20	0.69	0.00	0.72	0.53	0.27	0.89	0.00	0.02
svm~19+34	0.70	0.00	0.75	0.61	0.31	0.91	0.00	0.00
svm~4+21	0.70	0.00	0.58	0.81	0.43	0.89	0.00	0.11

rf~12+22	0.70	0.00	0.64	0.66	0.31	0.88	0.00	0.04
rpart~4+17	0.69	0.00	0.58	0.67	0.30	0.87	0.00	0.02
knn~17+22	0.69	0.00	0.67	0.64	0.31	0.89	0.00	0.11
rf~24+19	0.70	0.00	0.58	0.67	0.30	0.87	0.00	0.00
nb~9+6	0.70	0.00	0.69	0.57	0.28	0.89	0.00	0.07
svm~9+19	0.70	0.00	0.78	0.59	0.31	0.92	0.00	0.01
rpart~4+29	0.69	0.00	0.64	0.65	0.30	0.88	0.00	0.01
svm~27+19	0.69	0.00	0.67	0.59	0.28	0.88	0.00	0.03
svm~13+32	0.69	0.00	0.47	0.79	0.35	0.86	0.00	0.31
svm~36+28	0.69	0.00	0.61	0.64	0.29	0.87	0.00	0.02
svm~11+28	0.69	0.00	0.61	0.69	0.32	0.88	0.00	0.46
nb~28+34	0.69	0.00	0.61	0.61	0.28	0.87	0.00	0.01
nb~18+43	0.69	0.00	0.61	0.67	0.31	0.88	0.00	0.09
rf~4+16	0.69	0.00	0.75	0.55	0.29	0.90	0.00	0.21
svm~15+22	0.69	0.00	0.50	0.77	0.35	0.87	0.00	0.05
nb~28+21	0.69	0.00	0.53	0.71	0.30	0.86	0.00	0.00
rf~38+28	0.69	0.00	0.69	0.58	0.28	0.89	0.00	0.47
svm~4+33	0.69	0.00	0.64	0.69	0.33	0.89	0.00	0.04
nb~4+3	0.69	0.00	0.50	0.81	0.39	0.87	0.00	0.10
rpart~28+22	0.68	0.00	0.67	0.62	0.30	0.89	0.00	0.12
svm~1+28	0.69	0.00	0.61	0.74	0.36	0.89	0.00	0.00
knn~13+26	0.69	0.00	0.75	0.47	0.25	0.89	0.01	0.08
nb~40+32	0.69	0.00	0.64	0.65	0.31	0.88	0.00	0.31
rf~26+22	0.69	0.00	0.67	0.62	0.30	0.89	0.00	0.12
svm~15+40	0.69	0.00	0.58	0.65	0.29	0.87	0.01	0.85
knn~4+43	0.69	0.00	0.58	0.69	0.31	0.87	0.00	0.08
rf~40+24	0.69	0.00	0.67	0.62	0.30	0.89	0.00	0.03
nb~12+16	0.69	0.00	0.58	0.73	0.34	0.88	0.00	0.05
rf~4+13	0.69	0.00	0.56	0.74	0.34	0.87	0.00	0.09
knn~24+13	0.69	0.00	0.81	0.52	0.29	0.92	0.00	0.06
knn~4+37	0.69	0.00	0.86	0.37	0.25	0.92	0.01	0.02
rf~4+14	0.69	0.00	0.64	0.65	0.31	0.88	0.00	0.01
rpart~16+18	0.65	0.00	0.47	0.82	0.39	0.87	0.00	0.03
nb~34+6	0.69	0.00	0.56	0.67	0.29	0.86	0.00	0.03
svm~12+13	0.69	0.00	0.31	0.83	0.31	0.83	0.03	0.07
nb~16+13	0.69	0.00	0.58	0.66	0.29	0.87	0.01	0.20
svm~39+6	0.69	0.00	0.61	0.73	0.35	0.89	0.00	0.07
knn~24+43	0.69	0.00	0.67	0.57	0.27	0.88	0.02	0.00
nb~42+20	0.69	0.00	0.72	0.52	0.27	0.89	0.00	0.04
svm~28+21	0.69	0.00	0.64	0.72	0.35	0.89	0.00	0.02
svm~14+28	0.69	0.00	0.53	0.76	0.35	0.87	0.00	0.05
rpart~17+22	0.68	0.00	0.58	0.65	0.28	0.87	0.00	0.41
nb~9+19	0.69	0.00	0.78	0.55	0.29	0.91	0.00	0.02
rpart~25+22	0.69	0.00	0.72	0.50	0.26	0.88	0.01	0.22
nb~9+22	0.69	0.00	0.58	0.69	0.31	0.87	0.00	0.12
svm~43+22	0.69	0.00	0.53	0.73	0.32	0.87	0.00	0.04
svm~18+32	0.69	0.00	0.58	0.68	0.30	0.87	0.00	0.23

rpart~39+19	0.68	0.00	0.83	0.44	0.26	0.92	0.00	0.01
nb~39+6	0.69	0.00	0.56	0.69	0.30	0.87	0.00	0.04
rpart~24+20	0.68	0.00	0.67	0.69	0.34	0.90	0.00	0.01
nb~38+28	0.69	0.00	0.61	0.66	0.30	0.88	0.00	0.02
nb~16+31	0.69	0.00	0.56	0.70	0.31	0.87	0.00	0.11
rpart~20+38	0.68	0.00	0.78	0.48	0.26	0.90	0.00	0.07
rpart~4+40	0.69	0.00	0.67	0.57	0.27	0.88	0.01	0.25
rpart~24+19	0.68	0.00	0.69	0.57	0.28	0.89	0.00	0.01
nb~11+22	0.69	0.00	0.83	0.52	0.29	0.93	0.00	0.13
knn~37+6	0.69	0.00	0.81	0.42	0.25	0.90	0.01	0.01
knn~13+22	0.69	0.00	0.89	0.37	0.25	0.93	0.00	0.33
nb~4+7	0.69	0.00	0.56	0.75	0.34	0.88	0.00	0.08
nb~25+6	0.69	0.00	0.56	0.73	0.33	0.87	0.00	0.16
knn~28+21	0.68	0.00	0.92	0.39	0.27	0.95	0.00	0.05
nb~15+12	0.69	0.00	0.56	0.69	0.30	0.87	0.00	0.06
nb~33+22	0.69	0.00	0.78	0.47	0.26	0.90	0.01	0.17
svm~3+28	0.69	0.00	0.39	0.81	0.33	0.85	0.00	0.17
nb~12+32	0.69	0.00	0.64	0.69	0.33	0.89	0.00	0.05
nb~27+28	0.69	0.00	0.78	0.54	0.29	0.91	0.00	0.03
nb~39+28	0.69	0.00	0.44	0.71	0.27	0.84	0.03	0.01
nb~3+6	0.69	0.00	0.42	0.81	0.35	0.85	0.00	0.05
knn~12+6	0.69	0.00	0.64	0.67	0.32	0.88	0.00	0.02
nb~15+26	0.69	0.00	0.53	0.73	0.32	0.87	0.00	0.11
nb~16+14	0.69	0.00	0.61	0.71	0.33	0.88	0.00	0.05
rf~19+3	0.69	0.00	0.69	0.59	0.29	0.89	0.00	0.00
svm~33+28	0.69	0.00	0.69	0.56	0.27	0.88	0.00	0.04
nb~23+19	0.69	0.00	0.67	0.64	0.31	0.89	0.00	0.04
svm~30+19	0.69	0.00	0.64	0.63	0.29	0.88	0.00	0.00
rpart~13+26	0.68	0.00	0.61	0.75	0.37	0.89	0.00	0.07
svm~23+6	0.69	0.00	0.58	0.70	0.32	0.88	0.00	0.01
svm~12+26	0.69	0.00	0.47	0.83	0.40	0.87	0.00	0.10
svm~24+38	0.69	0.00	0.42	0.83	0.37	0.86	0.00	0.00
rpart~4+25	0.69	0.00	0.78	0.50	0.27	0.90	0.00	0.03
svm~33+22	0.69	0.00	0.67	0.61	0.29	0.88	0.00	0.08
rpart~43+19	0.69	0.00	0.72	0.59	0.30	0.90	0.00	0.01
nb~17+24	0.69	0.00	0.67	0.67	0.33	0.89	0.00	0.00
nb~36+19	0.69	0.00	0.81	0.51	0.28	0.92	0.00	0.02
rpart~37+28	0.68	0.00	0.69	0.61	0.30	0.89	0.00	0.16
knn~37+22	0.68	0.00	0.86	0.42	0.26	0.93	0.00	0.01
knn~33+19	0.68	0.00	0.44	0.78	0.33	0.85	0.00	0.07
nb~9+28	0.69	0.00	0.53	0.68	0.28	0.86	0.01	0.03
svm~34+6	0.69	0.00	0.72	0.60	0.30	0.90	0.00	0.00
rf~4+43	0.69	0.00	0.69	0.62	0.30	0.89	0.00	0.08
nb~25+28	0.69	0.00	0.58	0.67	0.30	0.87	0.00	0.04
knn~24+19	0.68	0.00	0.89	0.35	0.25	0.93	0.00	0.02
svm~2+19	0.69	0.00	0.72	0.47	0.25	0.88	0.02	0.06
nb~21+6	0.69	0.00	0.61	0.69	0.32	0.88	0.00	0.02

rpart~1+19	0.68	0.00	0.75	0.58	0.30	0.91	0.00	0.01
nb~1+6	0.69	0.00	0.56	0.73	0.33	0.87	0.00	0.03
svm~16+21	0.69	0.00	0.58	0.63	0.27	0.86	0.01	0.05
svm~33+6	0.69	0.00	0.58	0.67	0.30	0.87	0.00	0.09
rpart~16+22	0.68	0.00	0.64	0.61	0.28	0.88	0.00	0.28
svm~4+26	0.69	0.00	0.50	0.87	0.47	0.88	0.00	0.04
rpart~8+26	0.68	0.00	0.42	0.83	0.38	0.86	0.00	0.00
knn~29+32	0.68	0.00	0.83	0.38	0.24	0.90	0.01	0.02
rpart~26+28	0.68	0.00	0.56	0.73	0.33	0.87	0.00	0.01
nb~15+18	0.69	0.00	0.58	0.71	0.32	0.88	0.00	0.15
rf~39+24	0.69	0.00	0.72	0.54	0.27	0.89	0.00	0.01
nb~33+20	0.69	0.00	0.89	0.37	0.25	0.93	0.00	0.02
svm~29+18	0.69	0.00	0.36	0.81	0.31	0.84	0.02	0.10
knn~39+24	0.68	0.00	0.75	0.59	0.30	0.91	0.00	0.00
nb~11+20	0.69	0.00	0.78	0.45	0.25	0.89	0.01	0.03
svm~40+22	0.69	0.00	0.78	0.45	0.25	0.89	0.02	0.27
svm~16+32	0.69	0.00	0.50	0.78	0.35	0.87	0.00	0.26
nb~25+19	0.69	0.00	0.67	0.65	0.32	0.89	0.00	0.12
rf~4+24	0.69	0.00	0.64	0.64	0.30	0.88	0.00	0.02
nb~27+6	0.69	0.00	0.64	0.60	0.28	0.87	0.00	0.05
svm~12+40	0.69	0.00	0.61	0.60	0.27	0.87	0.05	0.12
knn~17+19	0.68	0.00	0.44	0.79	0.34	0.86	0.00	0.04
nb~13+26	0.69	0.00	0.78	0.48	0.26	0.90	0.01	0.24
rpart~41+20	0.67	0.00	0.83	0.37	0.24	0.90	0.01	0.04
knn~35+22	0.68	0.00	0.75	0.50	0.26	0.89	0.01	0.22
rpart~24+33	0.68	0.00	0.44	0.77	0.32	0.85	0.00	0.01
nb~16+8	0.69	0.00	0.58	0.67	0.30	0.87	0.01	0.13
nb~17+43	0.69	0.00	0.56	0.69	0.30	0.87	0.00	0.05
nb~12+40	0.69	0.00	0.53	0.71	0.30	0.86	0.01	0.07
rf~4+19	0.68	0.00	0.64	0.63	0.29	0.88	0.00	0.05
nb~18+13	0.68	0.00	0.69	0.54	0.27	0.88	0.01	0.48
nb~23+22	0.68	0.00	0.67	0.65	0.31	0.89	0.00	0.07
rpart~1+22	0.67	0.00	0.42	0.79	0.33	0.85	0.00	0.09
svm~17+6	0.68	0.00	0.56	0.69	0.30	0.87	0.00	0.04
nb~7+6	0.68	0.00	0.56	0.66	0.28	0.86	0.01	0.05
nb~4+30	0.68	0.00	0.56	0.78	0.38	0.88	0.00	0.02
rpart~12+32	0.68	0.00	0.69	0.69	0.35	0.90	0.00	0.53
rpart~35+6	0.68	0.00	0.56	0.69	0.30	0.87	0.00	0.26
svm~24+28	0.68	0.00	0.36	0.89	0.43	0.85	0.00	0.02
knn~43+22	0.68	0.00	0.81	0.45	0.26	0.91	0.00	0.01
nb~34+22	0.68	0.00	0.67	0.55	0.26	0.87	0.01	0.07
nb~29+6	0.68	0.00	0.61	0.73	0.35	0.89	0.00	0.07
nb~21+22	0.68	0.00	0.69	0.61	0.30	0.89	0.00	0.03
nb~29+28	0.68	0.00	0.61	0.67	0.31	0.88	0.00	0.05
rpart~14+20	0.67	0.00	0.78	0.50	0.27	0.90	0.00	0.01
rpart~29+20	0.67	0.00	0.78	0.50	0.27	0.90	0.00	0.01
nb~10+6	0.68	0.00	0.50	0.81	0.39	0.87	0.00	0.05

nb~41+22	0.68	0.00	0.64	0.59	0.27	0.87	0.01	0.14
nb~23+28	0.68	0.00	0.47	0.75	0.31	0.85	0.01	0.02
svm~43+28	0.68	0.00	0.58	0.72	0.33	0.88	0.00	0.01
knn~4+13	0.68	0.00	0.67	0.69	0.34	0.90	0.00	0.59
nb~17+32	0.68	0.00	0.67	0.67	0.33	0.89	0.00	0.10
svm~37+6	0.68	0.00	0.69	0.62	0.30	0.89	0.00	0.14
svm~7+28	0.68	0.00	0.58	0.60	0.26	0.86	0.03	0.26
svm~32+6	0.68	0.00	0.58	0.76	0.37	0.88	0.00	0.01
nb~31+22	0.68	0.00	0.72	0.55	0.28	0.89	0.00	0.06
svm~38+6	0.68	0.00	0.64	0.67	0.32	0.88	0.00	0.03
nb~11+19	0.68	0.00	0.69	0.62	0.30	0.89	0.00	0.07
nb~19+21	0.68	0.00	0.72	0.61	0.31	0.90	0.00	0.01
rpart~4+8	0.68	0.00	0.69	0.62	0.30	0.89	0.00	0.02
nb~15+43	0.68	0.00	0.56	0.68	0.29	0.86	0.01	0.08
svm~22+6	0.68	0.00	0.53	0.73	0.32	0.87	0.00	0.03
nb~24+31	0.68	0.00	0.53	0.76	0.35	0.87	0.00	0.00
svm~28+34	0.68	0.00	0.58	0.65	0.29	0.87	0.00	0.16
rpart~4+37	0.66	0.00	0.53	0.75	0.34	0.87	0.00	0.01
rf~4+40	0.68	0.00	0.69	0.49	0.25	0.87	0.04	0.07
svm~25+6	0.68	0.00	0.67	0.55	0.26	0.87	0.01	0.22
svm~42+16	0.68	0.00	0.47	0.73	0.29	0.85	0.02	0.12
nb~2+28	0.68	0.00	0.56	0.63	0.27	0.86	0.02	0.04
svm~35+28	0.68	0.00	0.50	0.79	0.36	0.87	0.00	0.39
nb~3+28	0.68	0.00	0.47	0.71	0.28	0.85	0.01	0.04
svm~12+39	0.68	0.00	0.36	0.81	0.31	0.84	0.02	0.12
rf~4+42	0.68	0.00	0.64	0.61	0.28	0.88	0.01	0.20
nb~29+22	0.68	0.00	0.58	0.69	0.31	0.87	0.00	0.18
nb~10+28	0.68	0.00	0.47	0.77	0.33	0.86	0.00	0.06
svm~11+22	0.68	0.00	0.61	0.69	0.32	0.88	0.00	0.40
rpart~24+34	0.67	0.00	0.36	0.89	0.43	0.85	0.00	0.00
rf~32+22	0.68	0.00	0.61	0.65	0.29	0.87	0.00	0.25
rf~24+28	0.68	0.00	0.61	0.61	0.27	0.87	0.01	0.02
nb~1+22	0.68	0.00	0.64	0.57	0.26	0.87	0.01	0.08
nb~36+20	0.68	0.00	0.78	0.55	0.29	0.91	0.00	0.01
knn~15+22	0.68	0.00	0.81	0.46	0.26	0.91	0.00	0.32
svm~10+6	0.68	0.00	0.56	0.75	0.35	0.88	0.00	0.06
nb~10+22	0.68	0.00	0.69	0.51	0.26	0.88	0.02	0.23
nb~19+34	0.68	0.00	0.69	0.66	0.33	0.90	0.00	0.01
svm~17+28	0.68	0.00	0.56	0.67	0.29	0.86	0.00	0.02
svm~37+28	0.68	0.00	0.67	0.59	0.28	0.88	0.00	0.08
nb~4+21	0.68	0.00	0.58	0.81	0.43	0.89	0.00	0.03
nb~37+20	0.68	0.00	0.64	0.59	0.27	0.87	0.00	0.01
svm~42+28	0.68	0.00	0.81	0.59	0.32	0.93	0.00	0.26
knn~4+40	0.67	0.00	0.75	0.51	0.27	0.90	0.01	0.23
knn~12+40	0.67	0.00	0.75	0.57	0.30	0.91	0.00	0.22
nb~18+26	0.68	0.00	0.69	0.63	0.31	0.90	0.00	0.12
rpart~15+24	0.67	0.00	0.78	0.48	0.26	0.90	0.00	0.08

nb~15+40	0.68	0.00	0.42	0.81	0.35	0.85	0.00	0.30
svm~10+19	0.68	0.00	0.64	0.67	0.32	0.89	0.00	0.01
svm~12+29	0.68	0.00	0.44	0.79	0.34	0.86	0.00	0.01
rpart~4+33	0.68	0.00	0.67	0.54	0.26	0.87	0.02	0.00
rpart~24+25	0.67	0.00	0.50	0.75	0.33	0.86	0.00	0.00
knn~15+19	0.67	0.00	0.89	0.38	0.26	0.93	0.00	0.06
knn~8+6	0.67	0.00	0.75	0.49	0.26	0.89	0.01	0.01
nb~39+22	0.68	0.00	0.72	0.47	0.25	0.88	0.02	0.08
nb~31+20	0.68	0.00	0.72	0.49	0.25	0.88	0.01	0.01
rpart~13+22	0.68	0.00	0.78	0.52	0.28	0.91	0.00	0.36
knn~4+38	0.67	0.00	0.75	0.43	0.24	0.88	0.03	0.04
rf~15+28	0.68	0.00	0.69	0.56	0.27	0.88	0.00	0.17
svm~9+22	0.68	0.00	0.56	0.72	0.32	0.87	0.00	0.16
knn~37+19	0.67	0.00	0.94	0.30	0.24	0.96	0.00	0.01
svm~15+16	0.68	0.00	0.50	0.77	0.35	0.87	0.00	0.23
nb~16+21	0.68	0.00	0.61	0.62	0.28	0.87	0.01	0.01
rf~19+6	0.68	0.00	0.67	0.66	0.32	0.89	0.00	0.01
nb~41+19	0.68	0.00	0.69	0.59	0.29	0.89	0.00	0.05
svm~7+22	0.68	0.00	0.67	0.59	0.28	0.88	0.00	0.28
nb~31+32	0.68	0.00	0.39	0.75	0.27	0.84	0.05	0.28
rf~7+22	0.68	0.00	0.75	0.49	0.26	0.89	0.01	0.14
rpart~1+24	0.67	0.00	0.58	0.77	0.38	0.88	0.00	0.00
rf~16+24	0.68	0.00	0.64	0.59	0.27	0.87	0.01	0.02
svm~16+13	0.68	0.00	0.53	0.67	0.28	0.85	0.03	0.33
rf~18+22	0.68	0.00	0.69	0.60	0.29	0.89	0.00	0.22
rf~31+22	0.68	0.00	0.75	0.56	0.29	0.90	0.00	0.10
knn~19+21	0.67	0.00	0.78	0.57	0.30	0.91	0.00	0.00

Table 52: pairwise biomarkers from the 43 biomarker panel with significance for Wilcoxon P-value (auc.pvalue≤0.05) and other metrics for the psaDT endpoint.
Auc.pvalue : Wilcoxon Test P-value. MFD: Median Fold Difference. KM: Kaplan Meier curves. mvaHRPval: Multivariable Analysis Hazard Ratio P-value.

Classifier	auc	auc. pvalue	Sensitivity	Specificity	Pos.Pred. Value	Neg.Pred .Value	mvaPval
svm~4+12	0.71	0.00	0.15	0.56	0.16	0.54	0.00
rpart~24+32	0.70	0.00	0.07	0.65	0.09	0.55	0.00
rpart~15+14	0.69	0.00	0.09	0.63	0.12	0.55	0.03
svm~12+24	0.70	0.00	0.04	0.71	0.08	0.57	0.01
knn~12+26	0.31	0.00	0.02	0.73	0.04	0.57	0.00
svm~15+24	0.69	0.00	0.00	0.83	0.00	0.60	0.01
nb~12+19	0.69	0.00	0.28	0.50	0.24	0.55	0.00
rf~4+12	0.69	0.00	0.24	0.41	0.19	0.49	0.01
knn~12+18	0.68	0.00	0.33	0.45	0.25	0.54	0.00
svm~12+26	0.69	0.00	0.11	0.70	0.17	0.58	0.01
nb~15+24	0.69	0.00	0.15	0.59	0.17	0.55	0.00
nb~16+19	0.69	0.00	0.20	0.52	0.19	0.54	0.01

nb~12+24	0.68	0.00	0.04	0.68	0.07	0.56	0.00
rpart~12+24	0.68	0.00	0.09	0.65	0.12	0.56	0.00
rf~12+22	0.68	0.00	0.22	0.44	0.18	0.50	0.00
nb~12+6	0.68	0.00	0.37	0.44	0.27	0.55	0.00
nb~12+26	0.68	0.00	0.15	0.60	0.18	0.56	0.00
rf~12+26	0.68	0.00	0.20	0.65	0.24	0.59	0.00
nb~12+18	0.68	0.00	0.15	0.57	0.17	0.55	0.00
svm~16+24	0.68	0.00	0.07	0.71	0.11	0.57	0.01
nb~37+19	0.68	0.00	0.33	0.49	0.26	0.56	0.08
knn~12+22	0.68	0.00	0.28	0.45	0.22	0.53	0.01
svm~15+12	0.68	0.00	0.04	0.70	0.07	0.56	0.01
svm~16+19	0.68	0.00	0.35	0.48	0.27	0.57	0.02
rpart~12+6	0.67	0.00	0.37	0.43	0.27	0.55	0.03
rpart~1+24	0.67	0.00	0.17	0.57	0.19	0.55	0.01
rpart~4+16	0.67	0.00	0.35	0.48	0.27	0.57	0.03
knn~4+12	0.67	0.00	0.07	0.62	0.09	0.54	0.01
nb~15+12	0.67	0.00	0.20	0.59	0.21	0.56	0.00
svm~16+21	0.67	0.00	0.20	0.56	0.20	0.55	0.01
rf~42+19	0.67	0.00	0.41	0.34	0.26	0.51	0.16
rpart~15+24	0.66	0.00	0.46	0.34	0.28	0.53	0.04
rpart~1+6	0.67	0.00	0.35	0.46	0.27	0.56	0.14
svm~24+10	0.67	0.00	0.09	0.71	0.14	0.58	0.01
knn~24+13	0.66	0.00	0.37	0.30	0.23	0.46	0.11
rf~12+31	0.67	0.00	0.33	0.54	0.28	0.59	0.03
svm~24+8	0.66	0.00	0.13	0.72	0.21	0.60	0.30
svm~12+28	0.66	0.00	0.30	0.56	0.28	0.59	0.08
svm~12+18	0.66	0.00	0.17	0.54	0.17	0.54	0.01
svm~12+37	0.66	0.00	0.33	0.49	0.26	0.56	0.14
svm~15+38	0.66	0.00	0.15	0.61	0.18	0.56	0.01
rpart~4+32	0.66	0.00	0.24	0.50	0.21	0.54	0.05
rf~4+24	0.66	0.00	0.28	0.45	0.22	0.53	0.03
rf~12+18	0.66	0.00	0.30	0.51	0.26	0.57	0.01
nb~4+12	0.66	0.00	0.15	0.57	0.17	0.55	0.01
nb~16+24	0.66	0.00	0.13	0.65	0.17	0.57	0.00
nb~15+28	0.66	0.00	0.26	0.55	0.24	0.57	0.08
nb~24+28	0.66	0.00	0.26	0.56	0.25	0.58	0.08
nb~12+22	0.66	0.00	0.30	0.51	0.26	0.57	0.01
svm~1+12	0.66	0.00	0.26	0.55	0.24	0.57	0.01
svm~15+10	0.66	0.00	0.17	0.63	0.21	0.58	0.01
nb~24+37	0.66	0.00	0.28	0.49	0.24	0.55	0.09
nb~12+28	0.66	0.00	0.39	0.48	0.30	0.58	0.02
knn~15+35	0.65	0.00	0.15	0.68	0.21	0.59	0.12
nb~10+19	0.65	0.00	0.41	0.40	0.28	0.55	0.04
svm~8+19	0.65	0.00	0.33	0.43	0.24	0.53	0.03
svm~26+19	0.65	0.00	0.22	0.55	0.21	0.56	0.03
knn~1+24	0.65	0.00	0.39	0.35	0.25	0.51	0.01
rpart~15+12	0.65	0.00	0.15	0.60	0.18	0.56	0.02

svm~13+26	0.65	0.00	0.13	0.67	0.18	0.58	0.05
knn~15+17	0.65	0.00	0.22	0.59	0.23	0.57	0.02
nb~15+14	0.65	0.00	0.09	0.71	0.14	0.58	0.04
nb~12+20	0.65	0.00	0.48	0.37	0.30	0.56	0.01
knn~4+32	0.65	0.00	0.35	0.44	0.26	0.55	0.40
rf~12+20	0.65	0.00	0.46	0.41	0.30	0.58	0.16
rf~12+19	0.65	0.00	0.33	0.50	0.27	0.57	0.01
knn~17+24	0.64	0.00	0.30	0.48	0.25	0.55	0.01
nb~16+6	0.65	0.00	0.30	0.50	0.25	0.56	0.02
nb~15+16	0.65	0.00	0.17	0.65	0.22	0.58	0.01
svm~13+19	0.65	0.00	0.48	0.30	0.28	0.51	0.31
svm~1+19	0.65	0.00	0.26	0.49	0.22	0.54	0.01
svm~24+13	0.65	0.01	0.07	0.65	0.09	0.55	0.01
knn~16+28	0.65	0.01	0.39	0.40	0.27	0.54	0.06
nb~13+19	0.65	0.01	0.52	0.32	0.30	0.54	0.11
nb~24+6	0.65	0.01	0.13	0.67	0.18	0.58	0.03
rf~4+43	0.65	0.01	0.35	0.44	0.26	0.55	0.26
knn~18+13	0.64	0.01	0.57	0.21	0.29	0.46	0.38
knn~24+43	0.64	0.01	0.35	0.45	0.26	0.55	0.04
rpart~4+15	0.64	0.01	0.15	0.59	0.17	0.55	0.04
rf~9+19	0.65	0.01	0.41	0.37	0.27	0.53	0.03
nb~16+26	0.65	0.01	0.20	0.60	0.21	0.57	0.01
knn~4+16	0.64	0.01	0.43	0.40	0.29	0.56	0.06
knn~1+28	0.64	0.01	0.57	0.17	0.28	0.41	0.15
knn~40+24	0.64	0.01	0.50	0.30	0.29	0.52	0.01
rpart~28+34	0.64	0.01	0.33	0.55	0.29	0.59	0.38
nb~16+18	0.65	0.01	0.28	0.50	0.24	0.55	0.01
nb~15+10	0.65	0.01	0.52	0.35	0.31	0.57	0.01
svm~42+16	0.65	0.01	0.17	0.61	0.20	0.57	0.01
rf~4+32	0.65	0.01	0.26	0.50	0.23	0.55	0.05
nb~35+19	0.65	0.01	0.24	0.54	0.22	0.56	0.15
nb~28+6	0.65	0.01	0.35	0.50	0.28	0.58	0.23
nb~4+24	0.65	0.01	0.13	0.67	0.18	0.58	0.04
nb~16+21	0.65	0.01	0.26	0.52	0.24	0.56	0.03
rpart~43+22	0.64	0.01	0.28	0.49	0.24	0.55	0.09
svm~37+22	0.64	0.01	0.37	0.48	0.28	0.57	0.67
svm~15+13	0.64	0.01	0.26	0.52	0.24	0.56	0.10
rpart~24+8	0.64	0.01	0.20	0.73	0.29	0.62	0.21
svm~42+24	0.64	0.01	0.04	0.73	0.08	0.58	0.09
rpart~12+5	0.64	0.01	0.33	0.41	0.24	0.52	0.00
knn~4+17	0.64	0.01	0.24	0.49	0.21	0.53	0.04
svm~4+16	0.64	0.01	0.22	0.51	0.20	0.54	0.05
rf~39+19	0.64	0.01	0.50	0.33	0.29	0.54	0.03
nb~12+17	0.64	0.01	0.11	0.59	0.13	0.54	0.01
svm~12+13	0.64	0.01	0.07	0.73	0.12	0.58	0.01
nb~36+19	0.64	0.01	0.67	0.22	0.33	0.55	0.05
rf~7+19	0.64	0.01	0.52	0.29	0.29	0.52	0.18

nb~19+6	0.64	0.01	0.24	0.61	0.26	0.59	0.07
knn~4+34	0.64	0.01	0.35	0.44	0.26	0.55	0.70
nb~11+6	0.64	0.01	0.20	0.62	0.23	0.58	0.15
rpart~4+10	0.64	0.01	0.24	0.57	0.24	0.57	0.01
knn~15+37	0.64	0.01	0.48	0.29	0.28	0.50	0.11
nb~15+13	0.64	0.01	0.33	0.50	0.27	0.57	0.04
svm~12+22	0.64	0.01	0.39	0.48	0.30	0.58	0.06
rf~15+17	0.64	0.01	0.30	0.52	0.26	0.57	0.06
nb~37+6	0.64	0.01	0.24	0.59	0.24	0.58	0.14
rf~15+26	0.64	0.01	0.33	0.55	0.29	0.59	0.01
knn~15+24	0.64	0.01	0.43	0.35	0.27	0.53	0.04
nb~4+19	0.64	0.01	0.26	0.59	0.26	0.59	0.15
rpart~12+26	0.39	0.01	0.09	0.68	0.13	0.57	0.01
rpart~24+31	0.63	0.01	0.11	0.71	0.17	0.59	0.01
svm~15+16	0.64	0.01	0.15	0.65	0.19	0.58	0.01
nb~21+6	0.64	0.01	0.26	0.52	0.24	0.56	0.12
rf~4+15	0.64	0.01	0.22	0.57	0.22	0.57	0.08
nb~16+20	0.64	0.01	0.46	0.38	0.29	0.55	0.03
rf~4+16	0.64	0.01	0.41	0.41	0.28	0.56	0.23
knn~13+19	0.63	0.01	0.24	0.63	0.27	0.60	0.14
knn~4+24	0.63	0.01	0.20	0.60	0.21	0.57	0.21
knn~38+22	0.63	0.01	0.33	0.44	0.25	0.54	0.25
knn~32+22	0.63	0.01	0.26	0.48	0.22	0.53	0.11
nb~11+28	0.64	0.01	0.24	0.63	0.27	0.60	0.71
nb~12+16	0.64	0.01	0.17	0.57	0.19	0.55	0.01
rpart~24+34	0.63	0.01	0.07	0.79	0.15	0.60	0.05
nb~13+6	0.64	0.01	0.43	0.44	0.30	0.58	0.12
rf~19+21	0.63	0.01	0.33	0.37	0.22	0.49	0.01
knn~15+8	0.63	0.01	0.48	0.32	0.28	0.52	0.19
nb~15+37	0.63	0.01	0.20	0.61	0.22	0.57	0.06
nb~12+37	0.63	0.01	0.37	0.46	0.28	0.57	0.08
knn~16+19	0.63	0.01	0.41	0.40	0.28	0.55	0.01
rf~39+22	0.63	0.01	0.35	0.50	0.28	0.58	0.08
rf~15+35	0.63	0.01	0.26	0.55	0.24	0.57	0.12
rf~4+42	0.63	0.01	0.37	0.49	0.29	0.58	0.23
nb~4+28	0.63	0.01	0.22	0.60	0.23	0.58	0.39
rpart~15+9	0.62	0.01	0.15	0.60	0.18	0.56	0.08
knn~12+19	0.63	0.01	0.37	0.46	0.28	0.57	0.01
rf~4+39	0.63	0.01	0.33	0.49	0.26	0.56	0.04
rpart~17+13	0.39	0.01	0.13	0.68	0.19	0.58	0.05
rpart~15+16	0.40	0.01	0.07	0.74	0.13	0.59	0.06
rpart~12+17	0.62	0.01	0.24	0.50	0.21	0.54	0.02
nb~16+17	0.63	0.01	0.17	0.65	0.22	0.58	0.01
svm~37+6	0.63	0.01	0.37	0.45	0.27	0.56	0.37
knn~12+31	0.63	0.01	0.63	0.30	0.34	0.60	0.03
rpart~4+13	0.63	0.01	0.35	0.51	0.29	0.58	0.10
rf~42+26	0.63	0.01	0.57	0.30	0.31	0.56	0.32

rf~32+22	0.63	0.01	0.30	0.46	0.24	0.54	0.06
rf~16+10	0.63	0.01	0.22	0.60	0.23	0.58	0.02
nb~37+28	0.63	0.01	0.28	0.55	0.26	0.58	0.69
nb~12+32	0.63	0.01	0.17	0.55	0.18	0.54	0.01
rf~37+19	0.63	0.01	0.41	0.37	0.27	0.53	0.20
rpart~16+41	0.63	0.01	0.24	0.55	0.23	0.56	0.01
svm~35+19	0.63	0.01	0.30	0.54	0.27	0.58	0.28
nb~4+17	0.63	0.01	0.22	0.62	0.24	0.59	0.11
knn~12+6	0.63	0.01	0.28	0.44	0.22	0.52	0.03
svm~10+19	0.63	0.01	0.28	0.51	0.25	0.56	0.00
rf~24+28	0.63	0.01	0.35	0.50	0.28	0.58	0.04
rf~24+13	0.63	0.01	0.37	0.48	0.28	0.57	0.14
rpart~4+24	0.62	0.02	0.20	0.62	0.23	0.58	0.08
knn~24+28	0.63	0.02	0.17	0.65	0.22	0.58	0.04
rpart~15+8	0.63	0.02	0.20	0.59	0.21	0.56	0.42
nb~25+6	0.63	0.02	0.33	0.52	0.28	0.58	0.09
svm~12+10	0.63	0.02	0.20	0.61	0.22	0.57	0.01
rpart~15+13	0.63	0.02	0.26	0.62	0.28	0.60	0.10
svm~19+28	0.63	0.02	0.37	0.54	0.31	0.60	0.26
svm~24+37	0.63	0.02	0.22	0.63	0.25	0.59	0.71
rpart~16+6	0.62	0.02	0.26	0.52	0.24	0.56	0.06
rpart~16+22	0.63	0.02	0.37	0.44	0.27	0.55	0.02
svm~40+19	0.63	0.02	0.37	0.44	0.27	0.55	0.16
svm~4+24	0.63	0.02	0.15	0.63	0.19	0.57	0.02
rpart~11+22	0.38	0.02	0.22	0.57	0.22	0.57	0.49
rf~12+6	0.63	0.02	0.33	0.39	0.23	0.51	0.01
nb~4+16	0.63	0.02	0.17	0.63	0.21	0.58	0.06
nb~16+28	0.63	0.02	0.39	0.48	0.30	0.58	0.11
svm~11+28	0.63	0.02	0.24	0.59	0.24	0.58	0.85
knn~9+6	0.63	0.02	0.48	0.30	0.28	0.51	0.26
svm~13+6	0.63	0.02	0.39	0.50	0.31	0.59	0.63
svm~28+32	0.63	0.02	0.33	0.66	0.35	0.64	0.40
svm~40+24	0.63	0.02	0.35	0.46	0.27	0.56	0.08
rpart~14+24	0.62	0.02	0.07	0.74	0.13	0.59	0.05
rpart~16+26	0.63	0.02	0.22	0.62	0.24	0.59	0.05
knn~16+29	0.38	0.02	0.26	0.56	0.25	0.58	0.02
nb~15+6	0.63	0.02	0.15	0.66	0.20	0.58	0.03
rf~29+19	0.63	0.02	0.37	0.41	0.26	0.54	0.00
rf~4+21	0.63	0.02	0.33	0.54	0.28	0.59	0.51
nb~4+15	0.63	0.02	0.11	0.61	0.14	0.55	0.07
rf~24+19	0.63	0.02	0.26	0.56	0.25	0.58	0.02
nb~9+19	0.63	0.02	0.35	0.48	0.27	0.57	0.70
svm~21+6	0.63	0.02	0.33	0.49	0.26	0.56	0.16
rf~15+10	0.63	0.02	0.30	0.52	0.26	0.57	0.01
knn~17+37	0.62	0.02	0.65	0.26	0.33	0.57	0.28
rpart~17+18	0.39	0.02	0.22	0.56	0.22	0.56	0.14
nb~1+19	0.63	0.02	0.57	0.30	0.31	0.56	0.04

svm~1+16	0.63	0.02	0.09	0.74	0.16	0.59	0.03
rpart~42+15	0.62	0.02	0.22	0.56	0.22	0.56	0.33
rpart~4+12	0.62	0.02	0.35	0.44	0.26	0.55	0.00
rf~15+19	0.63	0.02	0.30	0.56	0.28	0.59	0.00
rf~15+24	0.63	0.02	0.30	0.50	0.25	0.56	0.06
nb~26+6	0.63	0.02	0.26	0.59	0.26	0.59	0.08
svm~16+18	0.62	0.02	0.22	0.55	0.21	0.56	0.03
nb~16+22	0.62	0.02	0.35	0.52	0.29	0.59	0.06
nb~17+6	0.62	0.02	0.28	0.63	0.30	0.61	0.10
nb~24+13	0.62	0.02	0.17	0.66	0.22	0.59	0.05
knn~12+10	0.62	0.02	0.50	0.29	0.28	0.51	0.02
knn~9+19	0.62	0.02	0.48	0.35	0.29	0.55	0.79
svm~16+26	0.62	0.02	0.20	0.60	0.21	0.57	0.02
rf~4+8	0.62	0.02	0.59	0.29	0.32	0.56	0.14
rf~10+22	0.62	0.02	0.37	0.43	0.27	0.55	0.03
nb~37+22	0.62	0.02	0.37	0.48	0.28	0.57	0.45
svm~13+28	0.62	0.02	0.35	0.46	0.27	0.56	0.42
rf~1+19	0.62	0.02	0.41	0.46	0.30	0.58	0.18
nb~15+35	0.62	0.02	0.30	0.56	0.28	0.59	0.07
svm~4+25	0.62	0.02	0.37	0.45	0.27	0.56	0.28
nb~12+13	0.62	0.02	0.26	0.59	0.26	0.59	0.04
nb~24+10	0.62	0.02	0.39	0.43	0.28	0.56	0.02
rf~10+19	0.62	0.02	0.37	0.44	0.27	0.55	0.02
rpart~16+10	0.61	0.02	0.24	0.55	0.23	0.56	0.00
svm~12+5	0.62	0.02	0.39	0.41	0.27	0.55	0.06
svm~9+19	0.62	0.02	0.35	0.40	0.25	0.52	0.24
svm~32+22	0.62	0.02	0.26	0.57	0.26	0.58	0.03
knn~15+28	0.62	0.02	0.17	0.65	0.22	0.58	0.19
nb~16+32	0.62	0.02	0.26	0.55	0.24	0.57	0.03
rpart~42+24	0.62	0.02	0.17	0.68	0.24	0.60	0.07
nb~14+6	0.62	0.02	0.24	0.61	0.26	0.59	0.16
nb~12+38	0.62	0.02	0.20	0.59	0.21	0.56	0.00
rf~13+19	0.62	0.02	0.57	0.33	0.32	0.57	0.13
nb~16+37	0.62	0.02	0.33	0.44	0.25	0.54	0.21
svm~4+42	0.62	0.02	0.39	0.44	0.28	0.56	0.22
rpart~37+22	0.61	0.03	0.33	0.48	0.26	0.56	0.72
knn~18+10	0.38	0.03	0.54	0.23	0.28	0.48	0.13
rf~4+10	0.62	0.03	0.17	0.66	0.22	0.59	0.34
svm~4+28	0.62	0.03	0.30	0.59	0.29	0.60	0.58
nb~18+6	0.62	0.03	0.33	0.56	0.29	0.60	0.13
nb~12+41	0.62	0.03	0.15	0.63	0.19	0.57	0.06
nb~12+10	0.62	0.03	0.35	0.56	0.31	0.61	0.02
svm~11+22	0.62	0.03	0.33	0.54	0.28	0.59	0.71
svm~8+28	0.62	0.03	0.30	0.46	0.24	0.54	0.10
nb~10+6	0.62	0.03	0.17	0.63	0.21	0.58	0.05
rf~31+19	0.62	0.03	0.41	0.39	0.28	0.54	0.05
rf~12+2	0.62	0.03	0.33	0.49	0.26	0.56	0.04

svm~16+38	0.62	0.03	0.22	0.56	0.22	0.56	0.01
nb~39+6	0.62	0.03	0.24	0.59	0.24	0.58	0.06
rf~16+19	0.62	0.03	0.41	0.44	0.29	0.57	0.01
svm~12+6	0.62	0.03	0.30	0.49	0.25	0.56	0.01
svm~16+34	0.62	0.03	0.28	0.60	0.28	0.60	0.05
rf~15+8	0.62	0.03	0.28	0.51	0.25	0.56	0.15
nb~10+28	0.62	0.03	0.22	0.65	0.26	0.60	0.31
nb~10+20	0.62	0.03	0.37	0.45	0.27	0.56	0.10
rpart~4+18	0.61	0.03	0.35	0.51	0.29	0.58	0.89
knn~35+19	0.39	0.03	0.57	0.24	0.30	0.50	0.14
rpart~18+32	0.62	0.03	0.39	0.45	0.29	0.57	0.09
svm~7+28	0.62	0.03	0.39	0.52	0.32	0.61	0.76
knn~1+22	0.39	0.03	0.37	0.51	0.30	0.59	0.02
rpart~4+41	0.61	0.03	0.22	0.61	0.24	0.58	0.08
svm~43+22	0.62	0.03	0.22	0.62	0.24	0.59	0.25
rpart~1+28	0.62	0.03	0.33	0.48	0.26	0.56	0.60
rpart~12+31	0.62	0.03	0.28	0.59	0.28	0.59	0.05
rpart~10+22	0.61	0.03	0.33	0.50	0.27	0.57	0.01
nb~40+24	0.62	0.03	0.28	0.54	0.25	0.57	0.07
svm~4+10	0.62	0.03	0.15	0.61	0.18	0.56	0.05
svm~13+32	0.62	0.03	0.24	0.71	0.31	0.62	0.52
rpart~4+1	0.39	0.03	0.52	0.35	0.31	0.57	0.35
rf~16+24	0.62	0.03	0.30	0.55	0.27	0.58	0.16
rf~4+19	0.62	0.03	0.37	0.45	0.27	0.56	0.05
rpart~24+10	0.40	0.03	0.20	0.67	0.25	0.60	0.00
svm~19+6	0.62	0.03	0.37	0.52	0.30	0.60	0.14
nb~15+36	0.62	0.03	0.26	0.55	0.24	0.57	0.01
knn~43+22	0.61	0.03	0.43	0.24	0.24	0.43	0.13
knn~4+7	0.61	0.03	0.22	0.67	0.27	0.60	0.22
nb~20+6	0.62	0.03	0.28	0.55	0.26	0.58	0.19
rpart~24+38	0.61	0.03	0.24	0.62	0.26	0.59	0.15
svm~24+25	0.61	0.03	0.20	0.66	0.24	0.59	0.07
knn~11+28	0.61	0.03	0.59	0.23	0.30	0.50	0.78
rf~24+43	0.61	0.03	0.17	0.67	0.23	0.59	0.05
rf~9+22	0.61	0.03	0.28	0.51	0.25	0.56	0.10
knn~26+2	0.61	0.03	0.59	0.21	0.29	0.47	0.22
knn~24+20	0.39	0.03	0.17	0.78	0.31	0.63	0.07
rf~24+10	0.61	0.03	0.30	0.55	0.27	0.58	0.02
svm~29+22	0.61	0.03	0.46	0.46	0.32	0.60	0.24
nb~43+6	0.61	0.03	0.20	0.62	0.23	0.58	0.11
rpart~1+15	0.61	0.03	0.22	0.63	0.25	0.59	0.05
rpart~38+22	0.61	0.03	0.39	0.40	0.27	0.54	0.87
rpart~18+13	0.61	0.03	0.43	0.44	0.30	0.58	0.95
nb~16+38	0.61	0.03	0.28	0.61	0.29	0.60	0.01
nb~18+13	0.61	0.03	0.37	0.48	0.28	0.57	0.26
nb~24+31	0.61	0.03	0.26	0.56	0.25	0.58	0.01
svm~26+37	0.61	0.03	0.15	0.68	0.21	0.59	0.95

knn~4+42	0.39	0.03	0.70	0.21	0.33	0.55	0.08
svm~16+8	0.61	0.03	0.26	0.55	0.24	0.57	0.02
rf~18+13	0.61	0.03	0.48	0.43	0.32	0.59	0.95
nb~13+28	0.61	0.04	0.33	0.54	0.28	0.59	0.61
rf~19+28	0.61	0.04	0.41	0.39	0.28	0.54	0.03
svm~36+19	0.61	0.04	0.30	0.50	0.25	0.56	0.02
svm~12+9	0.61	0.04	0.26	0.60	0.27	0.59	0.14
svm~12+27	0.61	0.04	0.30	0.52	0.26	0.57	0.01
rpart~16+3	0.41	0.04	0.11	0.82	0.25	0.62	0.67
rf~10+28	0.61	0.04	0.50	0.44	0.33	0.61	0.41
nb~35+6	0.61	0.04	0.24	0.56	0.23	0.57	0.12
knn~4+10	0.39	0.04	0.22	0.60	0.23	0.58	0.14
svm~4+11	0.61	0.04	0.13	0.63	0.17	0.57	0.20
nb~16+11	0.61	0.04	0.35	0.57	0.31	0.61	0.17
knn~37+22	0.61	0.04	0.54	0.27	0.29	0.51	0.26
rpart~16+25	0.60	0.04	0.41	0.45	0.30	0.58	0.26
nb~15+31	0.61	0.04	0.26	0.60	0.27	0.59	0.02
knn~12+28	0.61	0.04	0.15	0.63	0.19	0.57	0.19
knn~4+43	0.39	0.04	0.33	0.52	0.28	0.58	0.41
svm~16+22	0.61	0.04	0.37	0.50	0.29	0.59	0.15
svm~16+28	0.61	0.04	0.33	0.51	0.27	0.58	0.19
nb~4+10	0.61	0.04	0.11	0.71	0.17	0.59	0.13
knn~16+18	0.61	0.04	0.28	0.45	0.22	0.53	0.14
knn~8+19	0.61	0.04	0.37	0.44	0.27	0.55	0.23
nb~18+37	0.61	0.04	0.35	0.49	0.28	0.57	0.41
svm~24+2	0.61	0.04	0.22	0.60	0.23	0.58	0.74
knn~18+20	0.61	0.04	0.17	0.70	0.24	0.60	0.24
knn~26+20	0.61	0.04	0.48	0.43	0.32	0.59	0.10
nb~16+13	0.61	0.04	0.26	0.54	0.24	0.56	0.14
nb~14+28	0.61	0.04	0.28	0.61	0.29	0.60	0.66
svm~42+15	0.61	0.04	0.26	0.61	0.27	0.60	0.13
svm~4+21	0.61	0.04	0.22	0.63	0.25	0.59	0.64
rpart~24+33	0.60	0.04	0.17	0.67	0.23	0.59	0.23
rpart~13+22	0.61	0.04	0.48	0.34	0.29	0.54	0.50
rf~1+28	0.61	0.04	0.37	0.39	0.25	0.52	0.21
knn~24+10	0.61	0.04	0.37	0.41	0.26	0.54	0.01
rf~40+24	0.61	0.04	0.33	0.54	0.28	0.59	0.03
knn~4+20	0.61	0.04	0.46	0.38	0.29	0.55	0.20
rpart~20+28	0.60	0.04	0.54	0.33	0.31	0.56	0.30
rf~15+16	0.61	0.04	0.17	0.61	0.20	0.57	0.01
svm~31+28	0.61	0.04	0.43	0.49	0.32	0.61	0.26
nb~10+22	0.61	0.04	0.33	0.56	0.29	0.60	0.19
knn~4+8	0.61	0.04	0.13	0.71	0.20	0.59	0.11
svm~4+19	0.61	0.04	0.35	0.43	0.25	0.54	0.19
knn~29+19	0.61	0.04	0.17	0.65	0.22	0.58	0.03
nb~38+28	0.61	0.04	0.30	0.49	0.25	0.56	0.04
svm~16+31	0.61	0.04	0.20	0.61	0.22	0.57	0.03

nb~16+29	0.61	0.04	0.26	0.63	0.29	0.60	0.09
knn~26+19	0.61	0.05	0.41	0.43	0.29	0.56	0.03
nb~22+6	0.61	0.05	0.35	0.52	0.29	0.59	0.19
svm~2+28	0.61	0.05	0.35	0.43	0.25	0.54	0.65
svm~37+28	0.61	0.05	0.37	0.46	0.28	0.57	0.99
rf~19+34	0.61	0.05	0.33	0.44	0.25	0.54	0.02
svm~4+14	0.61	0.05	0.15	0.60	0.18	0.56	0.27
svm~28+21	0.61	0.05	0.33	0.56	0.29	0.60	0.67
rpart~29+6	0.60	0.05	0.33	0.54	0.28	0.59	0.09
svm~16+13	0.61	0.05	0.24	0.57	0.24	0.57	0.09
rpart~15+6	0.60	0.05	0.33	0.52	0.28	0.58	0.31
rpart~31+6	0.60	0.05	0.39	0.50	0.31	0.59	0.40
nb~4+6	0.61	0.05	0.24	0.57	0.24	0.57	0.33
svm~15+22	0.61	0.05	0.22	0.60	0.23	0.58	0.16
svm~15+37	0.61	0.05	0.17	0.66	0.22	0.59	0.21
svm~16+32	0.61	0.05	0.13	0.67	0.18	0.58	0.02
knn~4+15	0.40	0.05	0.24	0.56	0.23	0.57	0.06
knn~12+2	0.60	0.05	0.39	0.49	0.30	0.59	0.24
nb~15+34	0.61	0.05	0.20	0.68	0.26	0.60	0.07
svm~8+32	0.61	0.05	0.22	0.66	0.26	0.60	0.03
nb~1+6	0.61	0.05	0.26	0.60	0.27	0.59	0.09
nb~12+5	0.61	0.05	0.59	0.28	0.31	0.55	0.04
svm~35+6	0.61	0.05	0.24	0.59	0.24	0.58	0.48
nb~16+31	0.61	0.05	0.24	0.59	0.24	0.58	0.05
svm~4+37	0.61	0.05	0.30	0.50	0.25	0.56	0.51
nb~12+35	0.61	0.05	0.20	0.61	0.22	0.57	0.08
rpart~10+32	0.60	0.05	0.24	0.68	0.30	0.62	0.02
svm~15+35	0.60	0.05	0.20	0.67	0.25	0.60	0.62
svm~14+6	0.60	0.05	0.37	0.59	0.33	0.62	0.25
rf~24+22	0.60	0.05	0.30	0.48	0.25	0.55	0.14

Example 13: A 2,040 Biomarker Library for Prostate Cancer Progression

[0546] In order to define, from the entire set of 1.4 million features, a comprehensive library of biomarkers that presents prognostic ability, the Discovery Set (Training and Testing) presented in Example 1 was processed as follows. First, all features with a probe count lower than 4 or with cross-hybridizing probes as defined by affymetrix (<http://www.affymetrix.com>) were removed. Second, a background filter was applied in order to ensure signal in the expression capture for each feature. To achieve this, features that had a median expression value in the group of *met*s patients and in the group of non-*met*s patients (separately) lower than 1.2 times the background signal (captured by the control antigenomic probes defined by affymetrix (<http://www.affymetrix.com>)) were removed. Third, the statistical significance of the differential expression observed between the *met*s and non-*met*s groups was assessed using the Kolmogorov-Smirnov test for each feature. Those features

with a p-value greater than 0.05 were removed. Last, a Random forest variable importance was calculated by building a random forest with 450,000 trees. Features with Mean Decrease Gini (or MDG) ≤ 0 were discarded and features with MDG $> 6.5e-3$ and Mean Decrease in Accuracy (or MDA) > 0 were selected, reducing the feature set to 2,040 features. MDA is defined as the average difference in accuracy of the true variable vs the variable randomized for trees in the forest. MDG is defined as the mean of the change in gini between a parent node and a child node when splitting on a variable across the whole forest.

[0547] These represent the most important features (based on MDG and MDA) that are statistically significant (based on Kolmogorov-Smirnov Test) for the differential expression between *mets* and non-*mets* patients (Table 55) and provides a biomarker library for prostate cancer progression.

[0548] In tables 53 and 54, those biomarkers from the 2,040 in the library that were found statistically significant in the training and testing sets based on a Wilcoxon test (p-value ≤ 0.05) for the Area under the ROC curve (AUC) metric, are shown for Biochemical Recurrence Event (BCR) and Metastasis Event (Mets Event). Whereas results are shown for the testing set (as defined in Example 1), these biomarkers were significant also in the training set of the discovery study.

[0549] Further significance of the selected features was evidenced by multiple metrics and are also listed in tables 53 and 54. Metrics are defined in Example 12.

These results demonstrate, based on the multiple metrics shown, that the library of biomarkers built has the ability to capture the biology underlying the progression of prostate cancer, as defined by diverse clinical variables.

Table 53: biomarkers from the 2,040 biomarker library with significance for Wilcoxon P-value (auc.pvalue<=0.05) and other metrics for the BCR event endpoint. Auc.pvalue : Wilcoxon Test P-value. KM: Kaplan Meier curves. mvaHRPval: Multivariable Analysis Hazard Ratio P-value.

SEQ ID NO.	auc	auc. pvalue	Sensitivity	Specificity	Pos. Pred. Value	Neg. Pred. Value	KM P-value	Mva HRPval
55	0.60	0.03	0.62	0.52	0.74	0.38	0.10	0.02
58	0.59	0.04	0.55	0.48	0.70	0.33	0.22	0.00
90	0.59	0.05	0.66	0.31	0.68	0.29	0.80	0.04
97	0.62	0.01	0.51	0.67	0.77	0.38	0.02	0.00
107	0.62	0.01	0.53	0.62	0.76	0.38	0.07	0.35
109	0.60	0.02	0.42	0.43	0.62	0.25	0.11	0.73
117	0.60	0.04	0.66	0.45	0.73	0.38	0.06	0.38
125	0.61	0.02	0.65	0.17	0.63	0.18	0.02	0.47
165	0.59	0.04	0.45	0.64	0.73	0.35	0.06	0.55
170	0.61	0.02	0.42	0.71	0.76	0.36	0.01	0.92
176	0.61	0.02	0.63	0.55	0.76	0.41	0.01	0.00
178	0.61	0.01	0.35	0.79	0.79	0.36	0.03	0.74
179	0.61	0.02	0.45	0.69	0.76	0.36	0.01	0.73
183	0.59	0.05	0.73	0.28	0.69	0.31	0.68	0.29
208	0.61	0.02	0.67	0.47	0.74	0.39	0.03	0.01
228	0.60	0.02	0.48	0.66	0.75	0.36	0.01	0.55
246	0.65	0.00	0.70	0.53	0.77	0.45	0.00	0.00
251	0.59	0.04	0.45	0.43	0.63	0.26	0.05	0.22
311	0.61	0.02	0.39	0.71	0.75	0.34	0.13	0.33
315	0.59	0.05	0.59	0.53	0.74	0.37	0.09	0.40
316	0.61	0.02	0.65	0.50	0.74	0.39	0.03	0.06
317	0.61	0.02	0.33	0.78	0.76	0.34	0.03	0.38
339	0.60	0.03	0.55	0.33	0.64	0.25	0.26	0.87
357	0.63	0.00	0.51	0.71	0.79	0.39	0.00	0.41
437	0.65	0.00	0.42	0.78	0.81	0.38	0.00	0.36
465	0.60	0.03	0.48	0.71	0.78	0.38	0.00	0.98
473	0.60	0.03	0.70	0.48	0.75	0.42	0.01	0.29
522	0.59	0.05	0.63	0.52	0.74	0.38	0.02	0.01
582	0.60	0.03	0.40	0.79	0.81	0.37	0.00	0.07
615	0.59	0.04	0.40	0.47	0.62	0.26	0.02	0.00
643	0.62	0.01	0.54	0.67	0.78	0.40	0.00	0.00
693	0.63	0.00	0.62	0.59	0.77	0.41	0.01	0.01
696	0.59	0.04	0.63	0.45	0.72	0.36	0.17	0.15
791	0.61	0.02	0.73	0.41	0.73	0.41	0.02	0.12
836	0.59	0.04	0.52	0.38	0.65	0.27	0.14	0.49
981	0.63	0.00	0.52	0.31	0.63	0.23	0.02	0.03
1024	0.59	0.04	0.58	0.48	0.71	0.34	0.12	0.00
1062	0.60	0.02	0.63	0.52	0.74	0.39	0.06	0.42
1094	0.60	0.02	0.48	0.34	0.62	0.23	0.03	0.52
1247	0.62	0.01	0.69	0.40	0.72	0.37	0.22	0.01

1249	0.61	0.02	0.48	0.41	0.64	0.26	0.03	0.17
1251	0.59	0.04	0.59	0.57	0.75	0.39	0.01	0.53
1270	0.59	0.04	0.47	0.67	0.76	0.36	0.05	0.16
1285	0.60	0.03	0.54	0.66	0.78	0.39	0.01	0.68
1378	0.61	0.02	0.36	0.53	0.63	0.27	0.06	0.02
1485	0.59	0.05	0.73	0.16	0.66	0.21	0.19	0.75
1509	0.60	0.03	0.43	0.36	0.60	0.22	0.02	0.02
1517	0.59	0.04	0.37	0.55	0.64	0.28	0.22	0.07
1537	0.60	0.02	0.57	0.59	0.75	0.38	0.00	0.45
1540	0.61	0.02	0.36	0.50	0.61	0.26	0.06	0.00
1541	0.62	0.01	0.69	0.50	0.75	0.42	0.01	0.01
1576	0.62	0.01	0.49	0.69	0.78	0.38	0.01	0.29
1581	0.59	0.05	0.52	0.60	0.74	0.36	0.18	0.24
1634	0.64	0.00	0.54	0.66	0.78	0.39	0.03	0.00
1656	0.60	0.03	0.36	0.76	0.77	0.35	0.02	0.54
1706	0.60	0.02	0.41	0.43	0.62	0.25	0.06	0.64
1719	0.60	0.02	0.50	0.64	0.75	0.37	0.00	0.17
1721	0.61	0.02	0.57	0.59	0.75	0.38	0.01	0.05
1783	0.61	0.02	0.63	0.53	0.75	0.39	0.02	0.83
1801	0.61	0.02	0.60	0.53	0.74	0.38	0.24	0.18
1823	0.61	0.02	0.37	0.48	0.61	0.26	0.05	0.21
1902	0.64	0.00	0.53	0.71	0.80	0.41	0.00	0.02
1958	0.60	0.03	0.67	0.50	0.75	0.41	0.00	0.00
1964	0.60	0.03	0.70	0.36	0.71	0.35	0.14	0.01
1965	0.62	0.01	0.47	0.71	0.78	0.38	0.00	0.84
2014	0.61	0.02	0.59	0.53	0.74	0.37	0.09	0.01

Table 54: biomarkers from the 2,040 biomarker library with significance for Wilcoxon P-value (auc.pvalue<=0.05) and other metrics for the MET event endpoint. Auc.pvalue : Wilcoxon Test P-value. KM: Kaplan Meier curves. mvaHRPval: Multivariable Analysis Hazard Ratio P-value.

SEQ ID NO.	auc	auc. pvalue	Sensitivity	Specificity	Pos. Pred. Value	Neg. Pred. Value	KM P-value	Mva HRPval
50	0.65	0.00	0.32	0.42	0.24	0.52	0.00	0.14
51	0.64	0.00	0.59	0.58	0.45	0.71	0.01	0.02
53	0.69	0.00	0.78	0.47	0.46	0.79	0.00	0.00
55	0.60	0.02	0.65	0.47	0.41	0.70	0.11	0.10
58	0.65	0.00	0.63	0.51	0.43	0.71	0.03	0.00
59	0.63	0.00	0.76	0.44	0.44	0.76	0.00	0.39
60	0.63	0.00	0.71	0.50	0.45	0.75	0.01	0.05
63	0.60	0.03	0.59	0.55	0.43	0.70	0.04	0.15
68	0.59	0.04	0.81	0.40	0.44	0.78	0.00	0.46
71	0.60	0.02	0.46	0.42	0.31	0.57	0.06	0.09
76	0.60	0.03	0.81	0.37	0.43	0.77	0.01	0.25
82	0.63	0.00	0.68	0.55	0.46	0.75	0.00	0.03
87	0.59	0.05	0.82	0.31	0.41	0.75	0.03	0.04
90	0.63	0.00	0.74	0.37	0.40	0.71	0.08	0.07
96	0.62	0.01	0.78	0.38	0.42	0.75	0.01	0.02
97	0.67	0.00	0.60	0.64	0.49	0.74	0.00	0.00
100	0.63	0.00	0.32	0.42	0.24	0.52	0.00	0.07
102	0.60	0.02	0.66	0.45	0.41	0.70	0.09	0.00
107	0.61	0.01	0.57	0.57	0.43	0.70	0.09	0.10
108	0.60	0.02	0.50	0.66	0.46	0.70	0.01	0.13
117	0.61	0.01	0.71	0.42	0.41	0.71	0.06	0.02
119	0.61	0.01	0.75	0.41	0.42	0.74	0.02	0.04
120	0.59	0.05	0.76	0.36	0.41	0.73	0.04	0.19
126	0.59	0.04	0.46	0.37	0.30	0.54	0.02	0.28
130	0.63	0.00	0.65	0.56	0.46	0.73	0.00	0.12
131	0.59	0.05	0.60	0.53	0.42	0.70	0.04	0.02
137	0.60	0.02	0.43	0.69	0.45	0.68	0.09	0.13
144	0.59	0.05	0.63	0.54	0.44	0.72	0.02	0.73
151	0.63	0.00	0.56	0.70	0.52	0.73	0.00	0.23
152	0.69	0.00	0.60	0.63	0.48	0.73	0.00	0.00
155	0.61	0.01	0.56	0.49	0.39	0.66	0.68	0.24
163	0.61	0.02	0.63	0.54	0.44	0.72	0.03	0.14
165	0.65	0.00	0.53	0.64	0.46	0.70	0.02	0.04
169	0.59	0.04	0.68	0.52	0.45	0.73	0.01	0.08
170	0.63	0.00	0.51	0.69	0.49	0.71	0.00	0.13
175	0.59	0.04	0.74	0.40	0.41	0.72	0.05	0.02
176	0.60	0.02	0.69	0.49	0.44	0.73	0.01	0.01
179	0.66	0.00	0.57	0.69	0.51	0.74	0.00	0.36
183	0.60	0.02	0.79	0.31	0.40	0.73	0.08	0.07
187	0.62	0.01	0.76	0.40	0.42	0.75	0.02	0.01

188	0.61	0.01	0.43	0.40	0.29	0.55	0.03	0.88
192	0.64	0.00	0.35	0.40	0.25	0.52	0.00	0.12
197	0.60	0.02	0.53	0.61	0.44	0.69	0.02	0.01
204	0.59	0.05	0.79	0.30	0.39	0.71	0.22	0.94
213	0.59	0.04	0.68	0.48	0.43	0.72	0.02	0.01
225	0.64	0.00	0.74	0.47	0.44	0.75	0.01	0.02
228	0.64	0.00	0.59	0.65	0.49	0.73	0.00	0.06
230	0.61	0.01	0.40	0.45	0.29	0.56	0.06	0.39
239	0.61	0.02	0.69	0.47	0.43	0.73	0.01	0.02
241	0.59	0.03	0.50	0.37	0.31	0.56	0.10	0.93
246	0.65	0.00	0.82	0.48	0.48	0.83	0.00	0.01
251	0.59	0.05	0.37	0.45	0.28	0.55	0.02	0.30
255	0.60	0.02	0.62	0.60	0.47	0.73	0.00	0.34
268	0.59	0.05	0.65	0.51	0.43	0.71	0.02	0.10
269	0.59	0.04	0.72	0.42	0.42	0.72	0.03	0.02
271	0.63	0.00	0.41	0.41	0.29	0.55	0.01	0.51
273	0.59	0.04	0.40	0.44	0.29	0.56	0.03	0.20
275	0.59	0.05	0.38	0.51	0.31	0.59	0.11	0.05
277	0.60	0.02	0.47	0.45	0.33	0.60	0.25	0.02
285	0.65	0.00	0.38	0.36	0.25	0.50	0.00	0.47
288	0.62	0.01	0.53	0.57	0.41	0.68	0.13	0.05
291	0.61	0.02	0.59	0.53	0.42	0.69	0.08	0.19
292	0.63	0.00	0.54	0.28	0.30	0.52	0.01	0.02
293	0.59	0.04	0.54	0.38	0.34	0.59	0.35	0.62
299	0.59	0.05	0.62	0.53	0.43	0.71	0.04	0.08
314	0.60	0.03	0.34	0.53	0.29	0.58	0.06	0.01
317	0.66	0.00	0.41	0.77	0.51	0.69	0.00	0.07
333	0.60	0.02	0.75	0.27	0.37	0.65	0.61	0.05
336	0.60	0.02	0.56	0.35	0.33	0.58	0.28	0.42
344	0.60	0.03	0.78	0.37	0.42	0.75	0.02	0.00
350	0.60	0.03	0.59	0.57	0.44	0.71	0.02	0.18
352	0.61	0.01	0.43	0.41	0.29	0.55	0.02	0.00
356	0.60	0.02	0.71	0.42	0.41	0.71	0.09	0.11
357	0.64	0.00	0.54	0.62	0.45	0.70	0.02	0.03
360	0.60	0.02	0.50	0.36	0.31	0.55	0.05	0.92
362	0.65	0.00	0.62	0.59	0.47	0.73	0.00	0.04
367	0.60	0.02	0.59	0.51	0.41	0.68	0.14	0.09
371	0.60	0.02	0.50	0.33	0.30	0.53	0.01	0.04
373	0.60	0.03	0.75	0.31	0.38	0.68	0.39	0.08
383	0.62	0.01	0.50	0.62	0.43	0.68	0.13	0.15
394	0.60	0.03	0.54	0.31	0.31	0.54	0.06	0.43
397	0.61	0.01	0.59	0.57	0.44	0.71	0.04	0.14
400	0.60	0.03	0.69	0.45	0.42	0.72	0.05	0.24
409	0.60	0.02	0.54	0.58	0.43	0.69	0.03	0.10
418	0.62	0.01	0.68	0.47	0.42	0.71	0.02	0.01
419	0.64	0.00	0.69	0.57	0.48	0.76	0.00	0.01
425	0.59	0.04	0.60	0.47	0.40	0.67	0.25	0.08

441	0.61	0.02	0.81	0.34	0.41	0.75	0.03	0.10
445	0.60	0.02	0.59	0.53	0.42	0.69	0.06	0.22
447	0.62	0.01	0.60	0.58	0.45	0.72	0.01	0.08
459	0.59	0.05	0.44	0.46	0.32	0.59	0.27	0.22
466	0.59	0.04	0.28	0.58	0.28	0.58	0.05	0.03
473	0.59	0.04	0.76	0.42	0.43	0.76	0.01	0.48
477	0.61	0.01	0.46	0.75	0.52	0.71	0.00	0.12
478	0.60	0.02	0.66	0.47	0.42	0.71	0.04	0.04
484	0.62	0.01	0.75	0.44	0.44	0.75	0.01	0.10
485	0.61	0.02	0.29	0.53	0.26	0.56	0.02	0.19
493	0.61	0.01	0.59	0.55	0.43	0.70	0.03	0.40
494	0.61	0.01	0.74	0.36	0.40	0.70	0.13	0.23
500	0.59	0.05	0.71	0.39	0.40	0.70	0.17	0.08
509	0.60	0.03	0.32	0.50	0.27	0.56	0.02	0.58
516	0.65	0.00	0.28	0.53	0.25	0.56	0.01	0.03
517	0.59	0.04	0.62	0.52	0.42	0.70	0.04	0.05
522	0.62	0.01	0.69	0.48	0.44	0.73	0.01	0.14
539	0.66	0.00	0.75	0.45	0.44	0.76	0.00	0.00
548	0.61	0.01	0.71	0.42	0.41	0.71	0.08	0.07
552	0.61	0.01	0.68	0.47	0.42	0.71	0.03	0.03
559	0.62	0.01	0.37	0.40	0.26	0.52	0.00	0.00
563	0.59	0.04	0.35	0.46	0.27	0.55	0.01	0.68
568	0.61	0.01	0.75	0.37	0.41	0.72	0.06	0.07
571	0.60	0.02	0.72	0.41	0.41	0.72	0.04	0.07
572	0.65	0.00	0.65	0.56	0.46	0.73	0.00	0.01
579	0.60	0.02	0.72	0.42	0.42	0.72	0.03	0.03
582	0.68	0.00	0.54	0.78	0.59	0.75	0.00	0.00
586	0.61	0.02	0.44	0.38	0.29	0.54	0.02	0.04
589	0.60	0.02	0.49	0.39	0.31	0.57	0.14	0.91
614	0.64	0.00	0.75	0.44	0.44	0.75	0.01	0.11
616	0.61	0.01	0.63	0.54	0.44	0.72	0.01	0.87
618	0.62	0.01	0.60	0.54	0.43	0.70	0.04	0.01
639	0.63	0.00	0.66	0.56	0.46	0.74	0.00	0.03
643	0.60	0.03	0.57	0.58	0.44	0.70	0.02	0.00
645	0.64	0.00	0.53	0.61	0.44	0.69	0.04	0.04
650	0.63	0.00	0.35	0.43	0.26	0.54	0.01	0.37
671	0.62	0.01	0.43	0.37	0.28	0.53	0.01	0.08
688	0.59	0.05	0.72	0.41	0.41	0.72	0.05	0.00
693	0.64	0.00	0.68	0.52	0.45	0.73	0.01	0.00
695	0.60	0.03	0.63	0.50	0.42	0.70	0.03	0.11
696	0.64	0.00	0.71	0.45	0.42	0.73	0.04	0.02
698	0.59	0.04	0.68	0.48	0.43	0.72	0.02	0.02
704	0.59	0.03	0.76	0.36	0.41	0.72	0.05	0.02
707	0.59	0.03	0.50	0.32	0.30	0.53	0.01	0.99
717	0.59	0.04	0.54	0.34	0.32	0.56	0.07	0.33
721	0.63	0.00	0.82	0.34	0.42	0.77	0.02	0.00
724	0.60	0.03	0.38	0.51	0.31	0.59	0.11	0.51

729	0.60	0.02	0.43	0.41	0.29	0.55	0.02	0.11
733	0.59	0.04	0.60	0.56	0.44	0.71	0.01	0.16
737	0.60	0.02	0.26	0.60	0.28	0.59	0.05	0.07
752	0.60	0.03	0.56	0.31	0.32	0.55	0.09	0.09
760	0.60	0.03	0.66	0.52	0.44	0.73	0.02	0.91
761	0.62	0.01	0.68	0.49	0.43	0.73	0.02	0.24
772	0.66	0.00	0.71	0.55	0.48	0.76	0.00	0.00
799	0.60	0.02	0.68	0.47	0.43	0.72	0.05	0.75
802	0.59	0.04	0.72	0.41	0.41	0.72	0.09	0.02
804	0.60	0.02	0.29	0.58	0.29	0.59	0.08	0.01
816	0.59	0.05	0.62	0.56	0.45	0.72	0.03	0.41
821	0.59	0.04	0.71	0.34	0.38	0.67	0.42	0.11
825	0.59	0.03	0.62	0.50	0.42	0.69	0.06	0.29
826	0.61	0.01	0.65	0.58	0.47	0.74	0.00	0.12
830	0.59	0.03	0.29	0.58	0.29	0.59	0.04	0.11
836	0.61	0.01	0.47	0.40	0.31	0.57	0.09	0.13
840	0.62	0.00	0.75	0.37	0.41	0.72	0.05	0.03
845	0.64	0.00	0.59	0.62	0.47	0.72	0.01	0.04
863	0.60	0.03	0.79	0.29	0.39	0.71	0.20	0.21
864	0.64	0.00	0.68	0.55	0.46	0.75	0.00	0.01
884	0.59	0.04	0.65	0.49	0.42	0.71	0.08	0.08
887	0.61	0.01	0.53	0.57	0.41	0.68	0.15	0.00
889	0.61	0.01	0.38	0.49	0.30	0.58	0.11	0.59
892	0.59	0.03	0.56	0.57	0.43	0.69	0.11	0.11
901	0.59	0.04	0.49	0.60	0.41	0.67	0.18	0.06
913	0.62	0.01	0.72	0.41	0.41	0.72	0.04	0.01
920	0.61	0.01	0.84	0.21	0.38	0.69	0.34	0.08
921	0.60	0.02	0.25	0.53	0.23	0.55	0.00	0.82
924	0.61	0.02	0.75	0.42	0.43	0.75	0.01	0.28
950	0.59	0.03	0.69	0.44	0.42	0.71	0.07	0.09
959	0.66	0.00	0.54	0.30	0.31	0.53	0.03	0.21
967	0.59	0.04	0.65	0.47	0.41	0.70	0.13	0.05
971	0.62	0.00	0.24	0.53	0.23	0.55	0.00	0.34
977	0.59	0.04	0.41	0.42	0.29	0.55	0.02	0.10
979	0.59	0.04	0.57	0.31	0.32	0.55	0.10	0.55
981	0.62	0.01	0.46	0.36	0.29	0.53	0.01	0.44
988	0.64	0.00	0.56	0.62	0.46	0.71	0.01	0.01
993	0.61	0.01	0.66	0.54	0.45	0.74	0.00	0.00
997	0.59	0.04	0.51	0.31	0.30	0.53	0.01	0.07
1001	0.63	0.00	0.66	0.58	0.47	0.75	0.00	0.08
1005	0.63	0.00	0.68	0.45	0.41	0.71	0.13	0.62
1008	0.61	0.01	0.62	0.53	0.43	0.71	0.04	0.09
1024	0.59	0.04	0.59	0.46	0.38	0.66	0.29	0.02
1032	0.60	0.02	0.38	0.43	0.28	0.55	0.01	0.14
1036	0.61	0.01	0.65	0.48	0.42	0.70	0.04	0.01
1047	0.59	0.04	0.50	0.35	0.31	0.55	0.03	0.00
1051	0.63	0.00	0.43	0.39	0.29	0.54	0.01	0.12

1055	0.64	0.00	0.68	0.52	0.45	0.73	0.01	0.08
1066	0.59	0.04	0.72	0.42	0.42	0.72	0.04	0.05
1070	0.60	0.03	0.68	0.37	0.38	0.67	0.28	0.14
1078	0.61	0.01	0.49	0.65	0.45	0.69	0.10	0.00
1079	0.64	0.00	0.79	0.42	0.44	0.78	0.00	0.02
1084	0.60	0.02	0.75	0.41	0.42	0.74	0.02	0.27
1094	0.63	0.00	0.40	0.38	0.27	0.52	0.00	0.91
1104	0.60	0.02	0.34	0.50	0.28	0.57	0.04	0.18
1116	0.59	0.04	0.62	0.47	0.40	0.68	0.22	0.50
1122	0.63	0.00	0.69	0.37	0.39	0.68	0.26	0.02
1130	0.61	0.01	0.41	0.46	0.30	0.57	0.09	0.61
1145	0.61	0.01	0.75	0.39	0.41	0.73	0.04	0.06
1161	0.62	0.01	0.57	0.60	0.45	0.71	0.02	0.00
1164	0.65	0.00	0.71	0.53	0.46	0.76	0.00	0.00
1166	0.61	0.01	0.56	0.61	0.45	0.71	0.02	0.01
1169	0.60	0.03	0.82	0.27	0.39	0.73	0.08	0.03
1171	0.60	0.03	0.28	0.52	0.25	0.55	0.01	0.78
1194	0.59	0.04	0.75	0.41	0.42	0.74	0.04	0.64
1200	0.59	0.04	0.62	0.51	0.42	0.70	0.07	0.02
1203	0.62	0.00	0.34	0.47	0.27	0.55	0.01	0.77
1206	0.61	0.01	0.74	0.40	0.41	0.72	0.09	0.09
1215	0.63	0.00	0.65	0.53	0.44	0.72	0.01	0.13
1227	0.60	0.02	0.66	0.47	0.42	0.71	0.03	0.13
1241	0.59	0.04	0.46	0.41	0.31	0.56	0.11	0.78
1249	0.60	0.02	0.40	0.42	0.28	0.55	0.01	0.16
1251	0.64	0.00	0.68	0.53	0.46	0.74	0.01	0.17
1257	0.61	0.02	0.51	0.34	0.31	0.55	0.05	0.91
1259	0.60	0.03	0.65	0.53	0.44	0.72	0.01	0.02
1270	0.60	0.02	0.50	0.62	0.43	0.68	0.05	0.02
1277	0.60	0.02	0.76	0.38	0.42	0.74	0.05	0.24
1290	0.60	0.03	0.68	0.53	0.45	0.74	0.01	0.05
1291	0.60	0.02	0.46	0.42	0.31	0.57	0.09	0.38
1294	0.61	0.02	0.75	0.27	0.37	0.65	0.52	0.06
1299	0.60	0.02	0.53	0.29	0.30	0.52	0.01	0.07
1307	0.59	0.04	0.75	0.35	0.40	0.71	0.09	0.11
1311	0.60	0.02	0.71	0.39	0.40	0.70	0.10	0.02
1319	0.59	0.05	0.87	0.19	0.38	0.72	0.19	0.11
1323	0.62	0.01	0.57	0.57	0.43	0.70	0.09	0.32
1324	0.66	0.00	0.59	0.60	0.46	0.72	0.02	0.15
1332	0.59	0.04	0.44	0.40	0.30	0.55	0.01	0.01
1336	0.59	0.04	0.69	0.43	0.41	0.71	0.08	0.09
1337	0.59	0.05	0.65	0.48	0.42	0.70	0.06	0.29
1339	0.64	0.00	0.82	0.34	0.42	0.77	0.01	0.04
1343	0.60	0.02	0.84	0.31	0.41	0.77	0.02	0.15
1348	0.61	0.01	0.21	0.56	0.21	0.55	0.00	0.87
1355	0.62	0.01	0.59	0.31	0.33	0.56	0.13	0.36
1366	0.61	0.01	0.78	0.41	0.43	0.76	0.01	0.09

1369	0.66	0.00	0.62	0.56	0.45	0.72	0.02	0.26
1378	0.64	0.00	0.25	0.53	0.23	0.55	0.00	0.01
1379	0.61	0.02	0.60	0.52	0.42	0.69	0.06	0.18
1380	0.60	0.02	0.63	0.48	0.41	0.70	0.11	0.13
1383	0.60	0.02	0.38	0.72	0.44	0.67	0.11	0.08
1388	0.61	0.02	0.68	0.42	0.40	0.69	0.17	0.12
1403	0.62	0.01	0.22	0.66	0.27	0.60	0.09	0.23
1405	0.60	0.02	0.78	0.34	0.40	0.73	0.07	0.24
1408	0.60	0.03	0.69	0.41	0.40	0.70	0.10	0.06
1413	0.61	0.02	0.65	0.55	0.45	0.73	0.00	0.11
1417	0.61	0.01	0.38	0.37	0.26	0.51	0.00	0.41
1421	0.60	0.02	0.68	0.47	0.42	0.71	0.02	0.01
1428	0.59	0.04	0.43	0.42	0.30	0.56	0.03	0.01
1439	0.60	0.02	0.47	0.42	0.32	0.58	0.19	0.97
1447	0.59	0.04	0.59	0.31	0.33	0.56	0.07	0.43
1451	0.63	0.00	0.74	0.43	0.43	0.74	0.01	0.19
1458	0.59	0.05	0.50	0.42	0.33	0.60	0.30	0.61
1465	0.61	0.01	0.40	0.47	0.30	0.58	0.06	0.00
1477	0.61	0.01	0.41	0.43	0.29	0.56	0.06	0.12
1480	0.59	0.04	0.62	0.50	0.42	0.69	0.09	0.21
1491	0.63	0.00	0.46	0.37	0.30	0.54	0.03	0.01
1500	0.60	0.03	0.63	0.53	0.44	0.72	0.01	0.21
1502	0.60	0.02	0.68	0.46	0.42	0.71	0.04	0.02
1509	0.65	0.00	0.34	0.42	0.25	0.52	0.00	0.03
1514	0.59	0.04	0.57	0.58	0.44	0.70	0.04	0.30
1517	0.63	0.00	0.28	0.54	0.26	0.57	0.02	0.04
1523	0.59	0.05	0.43	0.45	0.31	0.58	0.04	0.06
1524	0.66	0.00	0.49	0.71	0.49	0.71	0.00	0.03
1528	0.60	0.02	0.57	0.51	0.40	0.67	0.25	0.02
1535	0.61	0.01	0.60	0.64	0.49	0.74	0.00	0.27
1537	0.63	0.00	0.65	0.55	0.45	0.73	0.01	0.10
1540	0.62	0.01	0.31	0.54	0.28	0.58	0.05	0.00
1541	0.62	0.00	0.75	0.44	0.44	0.75	0.00	0.01
1543	0.59	0.04	0.57	0.52	0.41	0.68	0.20	0.15
1547	0.67	0.00	0.60	0.67	0.51	0.75	0.00	0.00
1549	0.63	0.00	0.59	0.58	0.45	0.71	0.02	0.14
1554	0.59	0.05	0.59	0.47	0.39	0.67	0.34	0.22
1558	0.60	0.02	0.66	0.46	0.41	0.70	0.09	0.12
1559	0.64	0.00	0.66	0.57	0.47	0.74	0.00	0.00
1563	0.61	0.02	0.68	0.44	0.41	0.70	0.09	0.06
1566	0.62	0.00	0.38	0.47	0.29	0.57	0.04	0.04
1576	0.59	0.04	0.49	0.59	0.41	0.67	0.18	0.13
1578	0.64	0.00	0.44	0.72	0.48	0.69	0.02	0.10
1580	0.60	0.02	0.66	0.47	0.42	0.71	0.13	0.14
1583	0.61	0.01	0.81	0.34	0.41	0.75	0.03	0.04
1586	0.59	0.04	0.63	0.47	0.41	0.69	0.20	0.02
1588	0.60	0.02	0.62	0.47	0.40	0.68	0.15	0.00

1593	0.64	0.00	0.59	0.69	0.52	0.74	0.00	0.16
1595	0.61	0.01	0.65	0.47	0.42	0.70	0.07	0.01
1600	0.61	0.02	0.66	0.51	0.44	0.72	0.02	0.03
1606	0.61	0.01	0.38	0.42	0.27	0.54	0.01	0.49
1615	0.61	0.01	0.60	0.49	0.41	0.68	0.15	0.03
1623	0.59	0.05	0.41	0.48	0.31	0.59	0.16	0.79
1628	0.61	0.01	0.29	0.51	0.26	0.56	0.01	0.85
1634	0.64	0.00	0.59	0.58	0.45	0.71	0.02	0.00
1642	0.63	0.00	0.75	0.43	0.43	0.75	0.01	0.24
1646	0.60	0.02	0.78	0.42	0.43	0.77	0.00	0.06
1651	0.60	0.03	0.50	0.42	0.33	0.59	0.17	0.84
1656	0.61	0.01	0.47	0.76	0.53	0.71	0.00	0.12
1660	0.59	0.04	0.78	0.39	0.42	0.75	0.01	0.09
1663	0.60	0.02	0.57	0.61	0.46	0.71	0.01	0.11
1671	0.61	0.01	0.68	0.52	0.45	0.73	0.00	0.04
1681	0.61	0.01	0.65	0.57	0.46	0.74	0.00	0.31
1683	0.60	0.03	0.72	0.45	0.43	0.74	0.01	0.07
1691	0.63	0.00	0.87	0.24	0.40	0.76	0.08	0.00
1694	0.59	0.04	0.71	0.45	0.42	0.73	0.03	0.38
1704	0.62	0.01	0.41	0.80	0.54	0.70	0.00	0.69
1705	0.61	0.01	0.43	0.42	0.30	0.56	0.05	0.79
1712	0.62	0.00	0.74	0.51	0.46	0.77	0.00	0.06
1718	0.63	0.00	0.50	0.64	0.44	0.69	0.04	0.00
1719	0.64	0.00	0.57	0.61	0.46	0.71	0.01	0.09
1720	0.62	0.01	0.54	0.23	0.29	0.47	0.00	0.17
1721	0.64	0.00	0.65	0.55	0.45	0.73	0.00	0.02
1722	0.59	0.04	0.57	0.51	0.40	0.67	0.31	0.05
1734	0.60	0.02	0.49	0.63	0.43	0.68	0.08	0.06
1738	0.61	0.01	0.79	0.35	0.41	0.75	0.02	0.05
1742	0.64	0.00	0.63	0.57	0.46	0.73	0.00	0.03
1756	0.60	0.03	0.56	0.63	0.46	0.71	0.01	0.00
1757	0.61	0.02	0.57	0.56	0.43	0.69	0.04	0.02
1764	0.59	0.05	0.85	0.26	0.40	0.76	0.07	0.02
1778	0.60	0.03	0.76	0.32	0.39	0.70	0.19	0.03
1782	0.62	0.01	0.69	0.49	0.44	0.73	0.01	0.01
1783	0.66	0.00	0.74	0.52	0.47	0.77	0.00	0.00
1784	0.59	0.03	0.76	0.36	0.41	0.72	0.04	0.02
1790	0.63	0.00	0.72	0.52	0.46	0.76	0.00	0.03
1798	0.59	0.04	0.56	0.64	0.48	0.72	0.00	0.04
1806	0.61	0.01	0.28	0.50	0.24	0.55	0.00	0.31
1814	0.63	0.00	0.43	0.35	0.27	0.51	0.00	0.20
1816	0.63	0.00	0.62	0.58	0.46	0.73	0.00	0.04
1819	0.61	0.01	0.71	0.48	0.44	0.74	0.00	0.12
1820	0.62	0.01	0.49	0.66	0.45	0.69	0.02	0.07
1821	0.59	0.05	0.57	0.59	0.45	0.71	0.03	0.44
1823	0.64	0.00	0.28	0.51	0.25	0.55	0.00	0.16
1824	0.61	0.01	0.49	0.67	0.46	0.69	0.01	0.08

1833	0.63	0.00	0.76	0.43	0.44	0.76	0.00	0.00
1836	0.60	0.03	0.68	0.43	0.41	0.70	0.09	0.02
1837	0.61	0.01	0.54	0.59	0.44	0.69	0.07	0.06
1838	0.59	0.04	0.50	0.64	0.44	0.69	0.05	0.46
1843	0.64	0.00	0.68	0.50	0.44	0.73	0.01	0.00
1844	0.61	0.02	0.63	0.58	0.46	0.73	0.01	0.60
1845	0.64	0.00	0.60	0.61	0.47	0.73	0.00	0.04
1852	0.62	0.01	0.51	0.63	0.44	0.69	0.05	0.10
1853	0.63	0.00	0.68	0.47	0.42	0.71	0.03	0.01
1858	0.61	0.01	0.65	0.58	0.47	0.74	0.00	0.06
1859	0.60	0.02	0.75	0.44	0.44	0.75	0.00	0.00
1864	0.59	0.05	0.53	0.60	0.43	0.69	0.08	0.34
1866	0.62	0.01	0.54	0.68	0.49	0.72	0.00	0.06
1872	0.63	0.00	0.65	0.51	0.43	0.71	0.02	0.04
1874	0.59	0.03	0.54	0.54	0.41	0.67	0.14	0.03
1877	0.59	0.04	0.51	0.67	0.47	0.71	0.01	0.08
1879	0.59	0.04	0.66	0.44	0.41	0.69	0.09	0.02
1880	0.64	0.00	0.84	0.41	0.45	0.81	0.00	0.00
1882	0.60	0.03	0.62	0.53	0.43	0.71	0.03	0.29
1902	0.62	0.01	0.60	0.63	0.48	0.73	0.00	0.38
1904	0.60	0.02	0.65	0.53	0.44	0.72	0.02	0.23
1907	0.59	0.04	0.71	0.45	0.42	0.73	0.03	0.22
1908	0.61	0.02	0.56	0.61	0.45	0.71	0.02	0.01
1912	0.61	0.01	0.79	0.36	0.42	0.75	0.01	0.06
1915	0.63	0.00	0.63	0.52	0.43	0.71	0.03	0.00
1916	0.62	0.01	0.59	0.61	0.47	0.72	0.00	0.04
1921	0.64	0.00	0.59	0.53	0.42	0.69	0.05	0.09
1922	0.60	0.02	0.65	0.54	0.45	0.73	0.00	0.13
1926	0.61	0.01	0.69	0.46	0.42	0.72	0.04	0.02
1927	0.59	0.05	0.76	0.38	0.42	0.74	0.03	0.01
1930	0.59	0.04	0.29	0.55	0.27	0.58	0.02	0.90
1932	0.59	0.03	0.50	0.61	0.43	0.68	0.06	0.00
1934	0.61	0.01	0.60	0.59	0.46	0.72	0.01	0.22
1936	0.63	0.00	0.66	0.53	0.45	0.73	0.01	0.02
1938	0.60	0.02	0.79	0.36	0.42	0.75	0.02	0.18
1939	0.59	0.05	0.47	0.48	0.34	0.61	0.51	0.04
1941	0.61	0.02	0.69	0.44	0.42	0.71	0.04	0.04
1945	0.61	0.02	0.50	0.58	0.41	0.67	0.35	0.00
1946	0.60	0.02	0.74	0.42	0.42	0.73	0.02	0.05
1948	0.60	0.02	0.65	0.50	0.43	0.71	0.02	0.03
1949	0.60	0.03	0.56	0.60	0.45	0.70	0.02	0.10
1950	0.63	0.00	0.66	0.59	0.48	0.75	0.00	0.02
1953	0.62	0.01	0.72	0.42	0.42	0.72	0.03	0.01
1957	0.59	0.04	0.75	0.44	0.44	0.75	0.01	0.31
1958	0.61	0.01	0.71	0.43	0.42	0.72	0.03	0.03
1959	0.61	0.02	0.72	0.46	0.43	0.74	0.01	0.02
1963	0.70	0.00	0.29	0.42	0.22	0.51	0.00	0.00

1964	0.64	0.00	0.76	0.37	0.41	0.73	0.04	0.01
1965	0.67	0.00	0.54	0.66	0.48	0.72	0.00	0.02
1967	0.62	0.01	0.56	0.59	0.44	0.70	0.03	0.01
1970	0.59	0.05	0.69	0.52	0.45	0.74	0.00	0.12
1971	0.60	0.02	0.59	0.56	0.43	0.70	0.03	0.01
1972	0.66	0.00	0.62	0.62	0.48	0.74	0.00	0.00
1976	0.59	0.05	0.66	0.48	0.42	0.71	0.05	0.09
1977	0.59	0.05	0.54	0.57	0.42	0.68	0.11	0.11
1978	0.60	0.02	0.65	0.47	0.42	0.70	0.04	0.09
1980	0.61	0.01	0.63	0.53	0.43	0.71	0.04	0.31
1981	0.59	0.04	0.60	0.55	0.44	0.71	0.03	0.58
1984	0.63	0.00	0.41	0.85	0.61	0.71	0.00	0.10
1986	0.63	0.00	0.69	0.49	0.44	0.73	0.01	0.06
1988	0.60	0.03	0.72	0.46	0.43	0.74	0.01	0.00
1990	0.62	0.01	0.56	0.62	0.46	0.71	0.01	0.01
1991	0.59	0.05	0.59	0.54	0.43	0.70	0.06	0.64
1992	0.64	0.00	0.74	0.45	0.43	0.75	0.01	0.01
1994	0.59	0.03	0.56	0.55	0.42	0.68	0.12	0.31
1998	0.66	0.00	0.60	0.60	0.47	0.72	0.00	0.00
1999	0.60	0.02	0.66	0.46	0.41	0.70	0.05	0.00
2004	0.60	0.02	0.71	0.43	0.42	0.72	0.05	0.02
2005	0.67	0.00	0.63	0.65	0.51	0.75	0.00	0.01
2007	0.62	0.01	0.54	0.62	0.45	0.70	0.01	0.02
2009	0.60	0.02	0.60	0.53	0.42	0.70	0.04	0.00
2012	0.61	0.02	0.71	0.45	0.42	0.73	0.02	0.01
2013	0.59	0.04	0.53	0.61	0.44	0.69	0.03	0.09
2014	0.59	0.04	0.59	0.47	0.39	0.67	0.36	0.21
2016	0.60	0.02	0.68	0.42	0.40	0.69	0.13	0.28
2018	0.59	0.04	0.63	0.50	0.42	0.70	0.05	0.44
2019	0.65	0.00	0.71	0.52	0.46	0.75	0.00	0.01
2023	0.61	0.02	0.57	0.59	0.45	0.71	0.01	0.00
2024	0.59	0.04	0.65	0.50	0.43	0.71	0.06	0.07
2025	0.59	0.03	0.69	0.48	0.44	0.73	0.01	0.03
2027	0.61	0.01	0.68	0.53	0.45	0.74	0.00	0.00
2030	0.61	0.01	0.66	0.47	0.42	0.71	0.04	0.01
2032	0.59	0.05	0.59	0.57	0.44	0.71	0.02	0.05
2033	0.63	0.00	0.66	0.55	0.46	0.74	0.00	0.68
2034	0.60	0.03	0.41	0.70	0.44	0.67	0.11	0.10
2036	0.62	0.01	0.68	0.47	0.42	0.71	0.04	0.17
2037	0.59	0.03	0.59	0.48	0.40	0.67	0.30	0.38
2039	0.64	0.00	0.69	0.57	0.48	0.76	0.00	0.00
2042	0.59	0.05	0.78	0.35	0.41	0.73	0.04	0.59
2043	0.63	0.00	0.56	0.65	0.48	0.72	0.01	0.01
2044	0.63	0.00	0.63	0.49	0.42	0.70	0.08	0.01
2046	0.61	0.01	0.66	0.53	0.45	0.73	0.01	0.06
2048	0.62	0.01	0.69	0.51	0.45	0.74	0.01	0.96
2050	0.59	0.05	0.57	0.61	0.46	0.71	0.01	0.01

2052	0.64	0.00	0.76	0.46	0.45	0.77	0.00	0.01
2054	0.61	0.01	0.74	0.47	0.45	0.76	0.00	0.05
2056	0.62	0.01	0.71	0.48	0.44	0.74	0.00	0.01
2058	0.63	0.00	0.72	0.46	0.43	0.74	0.01	0.02
2060	0.62	0.01	0.74	0.47	0.44	0.75	0.00	0.00
2061	0.62	0.01	0.72	0.48	0.45	0.75	0.00	0.06
2062	0.59	0.04	0.82	0.31	0.41	0.76	0.04	0.42
2063	0.61	0.01	0.63	0.50	0.42	0.70	0.06	0.09
2064	0.62	0.00	0.63	0.57	0.46	0.73	0.00	0.01
2067	0.62	0.01	0.62	0.55	0.44	0.71	0.02	0.09
2068	0.60	0.02	0.53	0.58	0.42	0.68	0.07	0.11
2069	0.62	0.01	0.85	0.28	0.41	0.77	0.02	0.08
2070	0.66	0.00	0.54	0.64	0.46	0.71	0.02	0.10
2071	0.65	0.00	0.69	0.54	0.47	0.75	0.00	0.01
2072	0.59	0.04	0.74	0.38	0.41	0.71	0.07	0.06
2073	0.63	0.00	0.50	0.61	0.43	0.68	0.12	0.01
2074	0.60	0.02	0.66	0.47	0.42	0.71	0.06	0.29
2076	0.62	0.01	0.75	0.46	0.44	0.76	0.00	0.12
2080	0.60	0.03	0.75	0.42	0.43	0.75	0.01	0.01
2081	0.60	0.02	0.72	0.43	0.42	0.73	0.02	0.01
2082	0.61	0.01	0.72	0.38	0.40	0.70	0.12	0.24

Table 11. List of Target Sequences

SEQ ID NO:	SEQUENCE
SEQ ID NO: 1	ATACCCTTCGCCATGTTATCAGCCAGACAGGAGGATACAGTGATGGACTCGCAGCCAGTCAGATGTACAGTCCGCAGGGCATCA
SEQ ID NO: 2	TCCCTGGTCCAAAATCAAGATACCGAATTAGAGTTGAGGGTAAAAAACA CATCTTGATCATAGAGGGAGCAACAAAGGCTGATGCTGCAGAATATTCA GTAATGACAACAGGAGGACAATCATCTGCTAAACTTAGTG
SEQ ID NO: 3	GCAAAGGTTTCAGCGTAGTGGCAGACACGCCCGAGCTCCAGAGAATCAA
SEQ ID NO: 4	CAGCTGGTGTGCCTTAAGAGAATCCCTATAAATAACAGAAAAGACACTC CAAGCATTCCTGTACGTGGACTCAGAGCACAGAGAAAAGAACTAAAAT GCCTTTTGGCATTTCAAGATATTTGGCACTCTTGTGATTACATTTTTTTAC AGTCCATTAAAGAGAATAAACTGACATAATATTAGAGAAATAAACAGGC TGCTCACACAACAGACTGCAAGGGGAAGTTAGAAAAAGCTCAAGCATTT TTTTCTTTGTTTTTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT TTTTCTGACATAAAAAATGTGTCCATTTGCATTAACCTGGGCAGATAGCT TGCAGCAACAAAGAAACACAAGCTTTACAACCTCATTTTAAAATAAAATC TTTTCTATGTATCATTCCTTAGAAAAGTTCTCTTCTTGTTTTAAACACATT CCTGATAACTTCTAAAGATGACCAAAAATAAAACAGAATATCTACAGAGA TCATTTTCTGAATTTTTTGTACATCCAAGGATAACAACATAAAAAAAATA AAACTGGACAGCATTTACATCCAAGTGCACAGAACCATTTTTGCAAGA TTAAATAATGTAAACATTGGGAACAGCCAAATCAGCGAAGAATGCCAAC ACCTCAAAACACCTGGTGTGCGCGCTTCATTAAGTGGTTCAAAATCCAGA TCTATAATTGCGCAATATTCACCGTATATAAAAAGAAATGGATATTAATT TTGACAAATAGCTGCAACTGAGACTTCTTTTTATTTCTTTATATGTGTATA TAGTGAATTTTTATTATTTTTAAAATTTTATTTATTTTTTTATTTTTATTTT TGCAGAGGAGCCCAGAGCCTTCTCCTCCTCCTCCTCCTCCTCCTCGCCTCA TCTGTCTCCCGGCCTGATACCAGATACAGGTTGTTGATTTCATCGTGGGT AGCAAGCTAGTAATAAATTTCAAAGTGCTTTCTCTTTTCATGCTTTTTGCC AATAACTGTTACCGCCGTTCTTATTCTCTCCCTTAACTCATTGTCTTTGGG GGAGTTAGACACCAGGAGGTGCCTTGTCGGTCATATTTTTTCAGCACGTCA TC
SEQ ID NO: 5	CTCCTGTGTCCTTAAAGTAGTCATGGGCTGGGAATGTTTCGGTTAATATCC CGGGTGATAGCACTGTCCTGGGGAGACTCCTGTGGAAACATAAGGAAAG AGAGGGTTTAGTTAGGTAAATCATGTAAACTCTTATTCAGGTTTAGGCAA GGTCTTCTCATTTACACACTTTAAATGTTGCAGGGACATACATACACATA TGTATGCCCATAGTTACTGCCTCTTCAGG
SEQ ID NO: 6	TATACAAGGGCTCAACCGAGGCTTAATTTAAAAGACAAAAACAAAACA AAAATACCACAGCTCAAGATAAAGAGTCCTATACAGAAATCACAAAAA GGACAGACCATCTAAGGAAAAATTAAAAAGACGACACAAGGACAGGCT GGGCAGCCTGGGTCAGGGCTCCTGGCTGGTGACCTGCTTTGAGTAGGTTT CTTGCAGGTACTTCTTAAAAGC
SEQ ID NO: 7	GCTGAGGCACCAATCATACCCTATACAGACAGCTAAGCACATTGTGTAA GGCAGATGTTGCCCACTCAGCCCATTAGAGAGCTCATGCACCATCA AACCCAGAATAAAGCAATAAGCCCAATGGTGATCCAACCCTTG
SEQ ID NO: 8	TCAGGCTTCTGTTGCAAGCCAATGTAGGGAACCA

SEQ ID NO:	SEQUENCE
SEQ ID NO: 9	GCTTTCATACTTGGAGCTCTACTGATTTTCCATCCAAGCCAACTTGTAGG GTTTTTTCCTTCCTATCACCAGAGGAGACAGGGTTTAGGGGAATCCAAG AAGGTTGAAGTCAGCACT
SEQ ID NO: 10	GGGTTATCTTCTAGTCCACATGTCACATAATATGTACCTTTATTTACCTTT TAAACTGAAGTTTTTAAAACCTGGGTTTTTAAAAAGAGAACAACCTACCCAT CAGCAATTACAGAAGACAAAGGAACTTGTGTGTCTGAAGACTGAGTGTT ATTTAGCAGCTCTTTGGTCAGCTTGGATTGGTCACATATGTGGAACTGG GAAATAATAGGGGCTACTTACACTGGAGAAGAACACTACAAATGGTGTA AAGAGTGGTTTTGGAATGTATCCAGACTTCCTTCTAAAATAAAAAATTTAA ACAGCTGTGTTTGAGAGATGGGTATGCACAATTCTTGTAAGAAAGACTG TGATAGATGTTTGAGGTCCCCTTAGTCCCTGATGCTACCATTGTTCC
SEQ ID NO: 11	GGGCAAAATATTCCTGGAGTGCTGAGCAATACATGTCACAGTCTCCAAT TTTTTTTTTATTCTTACGTTAGTTCAGATTCCACTGTATCCAATATGTGCT TGAGAGTGAAAATTGTATTAGTTTCTATTGTAATCTATCTCCATTTGCGCT CGAGAAAAATTA
SEQ ID NO: 12	TGTCGAGGCCCGGTTGGCTTTCAGAGGCGTATCCATGGGAGTAGGTGTC ATGTATCAAATAGGAGATTCAAAGTCAGCTGTTACCACGGCTACAGAAA TGCCAGTCTTTTCCTAAGAGTGCGAA
SEQ ID NO: 13	CCGGGTATCAGATGGTTATTATCCGACC
SEQ ID NO: 14	GTTGCAACTATCTATGCTGCCTGTAGCAGACACACTCCAGCTCTAAGGAT ACATATAGAATGAAAGTAAAGGGATGAAAAGAAGATGCTCCATGCAAA TGGAACAAAGACGGTAGGGGTGGCTATACTTACATCAGGCAAAAT AGACTTTTAGTCAAAAATTATAACAAGAGACAAAGGAGCTCACTATATA ATTATAAAGGGCTAATTCATCAAGAGGATATAAAAATTATAAGTACATA TGCACATAATGTCAGAGCACCTAAATATATAATTTACATAACTGAAG GGAGAAACAGCAATATAATAATCGTAGCGGACTTCAGTA
SEQ ID NO: 15	CCTTGACCTGGGAAAGCCATTACTCTTGTGTCTGCTACTGCCCTCCCACA GTCACCCCAATATTACAAGCACTGCCCCAGCGGCTTGATTTCCCCTCTGC CTTCCTTCTCTCTGCACTCCCACAAAGCCAGGGCCAGGCTCCCCATCCCT ACCTCCCCTGTCATCAGCAGTGGGTGTTCTGCCCCTCCTGAGTCTAGGC AGCTCTGCTGCTGTGATCTGCACACCCTCCAACCTGGGCAGGGACTGGG GGGATGCAGTGTGTGTTAGTGCCCATGTGGCATTGTGGCACTGTTGCCCC CCATGGCGGCATGGGCAAGATGACCTTCCATTAGCTTCAAGTCTTGTTCT CTTGTCTGTGGTCTGTTTAATATGTGGGTCACTAGGGTATTTATTCTTTCT CCCATCCTTACACTCTGGATCATTGTGCAGACTTAATCAGGGTTTTAACG CTTTCATTTTTTTTTTTTTTTTTTTTTTTTTTTTGTAGCTCAAAGAGAGTTCTCAT TTTCCCTATTCAAATAATACCCATGCCGTGTTTTTTACCTTGGAATTTAAA GTCACCTTAGGTTGGGGCAACAGATTCTCACTCATGTTTA
SEQ ID NO: 15	TTCGAATGTTTCAGAGCGCAGGGCCGTTCTCCCTCGTGTCTCTGGACCC ACCCGCCCCCTTCCCTGCCCTGTTTGCGCAGGGACATCACCCACATGCCCA GCTCTCGGACCCTGCAGCTCTGTGTCCCAGGCCACAGCAAAGGTCTGTTG AACCCCTCCCTCCATTCCCAGTTATCTGGGTCTCTGGATTCTTCTGTTTC TTGAATCAGGCTCTGCTTTCCCCCTAGCCACTACAGGCAGCCTCTGACAG TGCCGCTTTACTTGCAATTCTGCAGCAATTACATGTGTCTTTTGATCCTTG CCCAACTTCCCTCCCTCTCCAGCTCCTGGCCCCCTGGCCCAGGGCCCCCTC TTGCTGTTTTTACCTCTGTTCTTGGGGCCTAGTACCCAGCAAGCACCCA

SEQ ID NO:	SEQUENCE
	AATGGGGGAGGTTTTGGGATGAGAGGAGGAAACGTGTATACCTGTAACA TCTGGTGGCTCTTCCCCCAGAAGTTTGTGTTCATACATAATTGTTTTCCAC GCTGGATCATAATGTGACGTGCAGTTCTGCCCTGTGCTGGGGAGCCACA TGAAGCTTCCCCTGGCTAACTTGCTACCCCGCAGCAATCCCAGTGTGGCC GTCTGCTTGCTAAAAAATG
SEQ ID NO: 17	TCACGATGAAGCATGCTAGAAGCTGTAACAGAATACATAGAGAATAATG AGGAGTTTATGATGGAACCTTAAATATATAATGTTGCCAGCGATTTTAGT TCAATATTTGTTACTGTTATCTATCTGCTGTATATGGAATTCTTTTAATTC AAACGCTGAAAAGAATCAGCATTTAGTCTTGCCAGGCACACCCAATAAT CAGTCATGTGTAATATGCACAAGTTTGTTTTTGTGTTTTTTTTGTTG GTTGGTTTGTGTTTTTTGCTTTAAGTTGCATGATCTTTCTGCAGGAAATAGT CACTCATCCCCTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTCT GATGATGGATAGGGGGCAAATCTTTTTCCCCTTTCTGTTAATAGTCATCA CATTTCTATGCCAAACAGGAACAATCCATAACTTTAGTCTTAATGTACAC ATTGCATTTTGATAAAATTAATTTTGTGTTTCCTTTGAGGTTGATCGTTG TGTTGTTGTTTTGCTGCACCTTTTACTTTTTTGCGTGTGGAGCTGTATTCC CGAGACCAACG
SEQ ID NO: 18	GTCCATCGAGGTGTTTCATAAGTTTTTTGGTGTGTTTTCTGGGTCGTCTAT GTGTCATATGGTTTTACTTTTCTCTCCTTTTTCGTTTTCAGAACATTTTTCT GTCTGTTTTGGATTCACTGCTTCCATTTTACAGAATGTCACTCTTTAGACT CTCAGTCCATCATGCCATCGGGTACTCTTGTTGCAGTGTAATTTTTATTAC ATGCGGTTATTTCCCTAACGATGTGCTATTCACGTTTCATCTTCAAACCTCA TTTTCCATCAGCCAGTGTCTACTATTTAGTGCCCTGGCTCTATTTCCGGTCC TCCTCCCCGGGCTTTCCCTGGCTGCTGTGCTGGCCAAAAGCATGGGCTTT ATTCTCTCCATTGGCTGCTGCTCCACCTTAGAGGTGTGACCTCACTAGCG TTGACTG
SEQ ID NO: 19	CCCACTTTAGTCACGAGATCTTTTTCTGCTAACTGTTCATAGTCTGTGTAG TGTCATGGGTTCTTCATGTGCTATGATCTCTGAAAAGACGTTATCACCT TAAAGCTCAAATTCTTTGGGATGGTTTTTACTTAAGTCCATTAACAATTC AGGTTTCTAACGAGACCCATCCTAAAATTCTGTTTCTAGATTTTTAATGT CAAGTTCCCAAGTTCCCCCTGCTGGTTCTAATATTAACAGAACTGCAGTC TTCTGCTAGCCAATAGCATTACCTGATGGCAGCTAGTTATGCAAGCTTC AGGAGAATTTGAACAATAACAAGAATAGGGTAAGCTGGGATAGAAAGG CCACCTCTTCACTCTCTATAGAATATAGTAACCTTTATGAAACGGGGCCA TATAGTTTGGTTATGACATCAATATTTACCTAGGTGAAATTGTTTAGGC TTATGTACCTTCGTTCAAATA
SEQ ID NO: 20	ATTAGCAGCCATATTCCACAGTTCCTATAATTTTTACTGGGGGGGATTTG TGATAGGAAAGTCCTTGGGAAACATTTCCAATCTTTCAAAATATTATTGT GTATCTTAAGAAGTATAGGAACCTTGATGTTGAAATGTTGTATGGTAGTT CTTGTATAGTTAAATAATAATCTTTTTAAGAGTTAATGATAAGCATATGT TATGTGCATTATTAATAAAATAGTGGCCACTTAGGTAATACCCACTTTTA TCTTGTGTGCTGGGTACTCTGGTTACTGAGATAAATAAGGCACTGGACAT CCTCACGTGGAGTTCACAGGCTCATCAGTGAATTCTGTACCACATTTCAA CCTTGTTTATTTTAGTTAATGGAATATACATTCTTAGTATTGCCTGATTA TTTAAATTTGTTGAGGGGGATTGCATGTTGCTTTATTGGCCTGTAAAAAT AGCTAGTTTGGTAAGATTTGGTCTCGCACCTTCCATCTTTGCTACCACAT TAAAGATGAGCTTGTTAAAAAGGAAAGCATATTTCTCTGATTGCCCTTAT

SEQ ID NO:	SEQUENCE
	GGAGAAATA
SEQ ID NO: 21	GGCTTCTGACGCCAAATGGGCTTCCCATGGTCACCCTGGACAAGGAGGC AACCACCCACCTCCCCGTAGGAGCAGAGAGCACCTGGTGTGGGGGCG AGTGGGTTCCTCCACAACCCCGCTTCTGTGTGATTCTGGGGAAGTCCCGGC CCCTCTCTGGGCCTCAGTAGGGCTCCCAGGCTGCAAGGGGTGGACTGTG GGATGCATGCCCTGGCAACATTGAAGTTCGATCATGG
SEQ ID NO: 22	GTGATTTCTGTATAGGACTCTTTATCTTGAGCTGTG
SEQ ID NO: 23	AGAGGATGTCCATGTTCAATCACCCTGTCCAAATTCAGAAGCTCAGAA CGCTGGACTCTCCCTTTGCAG
SEQ ID NO: 24	AGAAGTAGCATGTCTTCGTGGCCGATTTGACAAGGGCAATATATGGAGT GCAGAAAAAGGCGGAACTCAAA
SEQ ID NO: 25	AAGACCACCCAGGAAACCATCGACAAGACTGCTAACCAG
SEQ ID NO: 26	GTGTCTTGCTTCATCCCACTGACTGCTGGGAGAGAGCCTCTGGGACTTTT CTTTGGGGCATCATTTTGTCTTTTCGTAGCAGGGAAAGGATATGAC AATGGGGAGGACAGTTCTTTTGGAGGTTGGAGGGGGCCAAGCCAAGGAC AGGAGCAAGTGTGCCCTCATTTTGTTC
SEQ ID NO: 27	CGTTTACGGCTTCCACTTGAGTATATGGCAATCTGTGCCCTTTGTGCAAA AGATCCTGTAAAGGAGAGAAGAGCTCATGCTAGGCAATGTTTGGTGAAA AATATAAATGTAAGGCGGGAGTATCTGAAGC
SEQ ID NO: 28	AACAAGATGAACAAGTCGGACTTCCTGGGAAAGGGGGGAAGGCCAAGG GGAAAAAACACAAATGGCTGAAGTTTGCCTTCTCCGCGTGGTCAAAG AGTCATTCCACGAATAACCATAGAAATGAA
SEQ ID NO: 29	GTCCCAGGCGGTCTAGCAGTGATGAGCAGGGCCTCTCGTATTCATCTT
SEQ ID NO: 30	AAGAGATACTCAGAGATGGATGATCATTATGAGTGCTTGAATAGATTGT CTCTTGAC
SEQ ID NO: 31	AGCCAATCTTGGCTCGGATTCAGGAGGACCGCACTGTGATTGTGTCTCCT GTGTTTGACAACATTCGTTTTGACACCTTCAAAGTGGATAAGTATGAACT GGCAGTTGATGGGTTTAACTGGGAAGTCTGGTGCCGCTACGATGCACTG CCACAAG
SEQ ID NO: 32	ATTAATTAAAGTTCTGATTCAGAGGGGATATGATTCGGATCCTGTGAAG GC
SEQ ID NO: 33	AAACGCTGGCGTCCGTTTCTGCTGAGAGCGTGGGGCTTTCTCTGCAAGTG GGGGGTGGGAGATGAGGGTTTGGATGAGGGTGTGGGAGGACCCTAAAC TGATTCCCATGCTAGTTGGAGAAAGAAAGGTGTGGATGAGGATAAAGTT TTCATGGTGACCAGGGTGACCCTCCGCTCAGAGGGACGAGCGGAGCCCG GCAAAACCAGTCACTGCCTTGTAGTTCCAAGCTTTGGGGATGATCAGCTC CCAAGAAATTGCTGTGGGGTGCAGGGGGCTGTGGGTGACCCAAATTGGGC AGAGGGCCTACAGGTCTGAGGCTGCCTGCACA
SEQ ID NO: 34	CATTTCTCTCTGGTGTGGCGAGCCGAGCAGATCGCTGGGAGAGAAATCG GAAAAGGGGGGAGAGGAAAAGGAAAAGGGGACTTGAGAGAGACTTT GTGCTTCAATGTTTC
SEQ ID NO: 35	TTTGAGTCAGGTTATCTCTGTCGCTCAAGCT

SEQ ID NO:	SEQUENCE
SEQ ID NO: 36	ACATTTGTCTGCTTGGGCTGTCATAACAAAATACCATCGACTAGTGTA AATAAAAATCTATTATCTCTCAGTTCTGGATGCTAGAAGTCCCAGAGTAA GGTGTCCATATATTTAGTTTCTGGCGAAGGCTCTTCCTGGCTTGTAGTCA GTGCCTTCTCTGTCTGCCCTCACTTGGCCTATCCACCTGTGAACACAAAT AAATATCTCTGTTGTTTTTTTCCTCTCCTTATGTGAACATGTGTCCTATGG AATTAGGGCCTCACTCTTGTGACTTCA
SEQ ID NO: 37	AGTGAGACATTGTGGCCTGGAAGTCTTTCAGACACCCACTCAGAGAAGT CAAGTTTAAAGTGGATGTTCTTCAGAGAATTTTTCATTTCTGAAAATGTG TTTTGCTTATAGAATATAACAGAGTTGACTAGAAAGAGAGAAACAACCTG CATACTAATCTTTTAAAGCCTTTAACAGTTGCTTTTAACTTTCTTTTAA ATGTTTCATGACTCTTCACCTATTTTTTTTTTAAATGGGGACGAAGAGATA TGAAAACCTGAGACATAAGACAAATACCTAGAAACCTCTAAGACTGCACA TATGATTTGGTAGAAGTCTGAAGGTATACACATTGTAAGAGGCAGACCT A
SEQ ID NO: 38	CAGGGTGCTAATCATGATATTTGGTTACA
SEQ ID NO: 39	CTGGCCCTGTGATATAACACAGATCAGCAATGGATTCCAACTACTCTCTG GCTATGTGACAACAAGATGCAGGTCACCCAGCAACTCGACACTTCCTCA GACCACTACAGGTCAAAGTCAATTCCTGATCCAAGTAAATGTCACGA ACATGCCTTTCAGATG
SEQ ID NO: 40	GATGAGACTAGGCAGGGTGACAAGGTGGGCTGACCGGGAGTAGGAGCA GTTTTAGGGTGGCAGGCGGAAAGGGGGCAAGAAAAAGCGGAGTTAACC CTTACTAAGCATTTACCCTGGGCTTC
SEQ ID NO: 41	TTCTTTTTATGTCAACGACGCCCATAG
SEQ ID NO: 42	ATGAGGACAGGCCTTGAGTCTGTCCTGGTCTCTGGAATCACGGTGTCTAG TAGAGGCCAGCACACAGCAAATATATAAATGTACAAATGAGTGAATGA AGAGAATCTGATTGGCCTTAAGGAACTTACGCACTTAAAATAATTGGGC AGAAGAGAAGCAGTGAAGGAGTGCAGAGGCATCACCTGA
SEQ ID NO: 43	AGCACAATGGCTGGAGGTCAGATGCCCACTAGGAGATGCT

Table 55.

Affymetrix Probeset ID = Aff P-ID						
A = Category: 1 = Non_Coding (Intergenic); 2 = Non_Coding (Utr); 3 = NON_CODING (Nctranscript); 4 = Non_Coding (Intronic); 5 = Non_Coding (Cds_Antisense); 6 = Non_Coding (Non_Unique); 7 = Non_Coding (Utr_antisense); 8 = Non_Coding (Intronic_Antisense); 9 = Coding						
B = Associated Gene; C = Kolmogorov Smirnov p-value; D = Mean Decrease Gini; E = Mean Decrease Accuracy						
SEQ ID NO	Aff P-ID	A	B	C	D	E
313	2315652	1		0.013881148	0.009628618	4.57E-06
1865	2318066	1		0.000124059	0.007038957	3.54E-06
851	2318095	2	KCNAB2	0.017721275	0.008633649	5.18E-06
375	2320530	3	NPPA-AS1	0.017194217	0.009820199	7.40E-06
1289	2321544	4	KAZN	0.015428709	0.007819131	3.23E-06
1326	2324753	9	ZBTB40	0.0060277	0.007357121	4.99E-06
2077	2324895	2	C1QB	0.001253978	0.006841561	3.40E-06
418	2326211	5	STMN1	7.48E-05	0.021492165	1.52E-05
1954	2326780	2	SFN	0.000243178	0.00786279	3.51E-06
1304	2327444	4	PHACTR4	0.002984774	0.006653744	2.06E-06
1385	2329291	4	ZNF362	0.012844897	0.007545796	4.23E-06
135	2329991	5	CLSPN	0.001302035	0.022069922	1.50E-05
143	2329993	3	RP11-435D7.3	9.91E-07	0.026064562	2.95E-05
56	2329994	3	RP11-435D7.3	4.78E-07	0.046754573	5.18E-05
1342	2330255	4	ADPRHL2	0.000235082	0.00711415	4.83E-06
1861	2330579	5	GRIK3	0.003259761	0.007150962	7.11E-06
1747	2330744	2	DNALI1	0.001040005	0.007171718	4.91E-06
403	2332283	2	FOXO6	0.000604099	0.012992693	6.72E-06
1225	2332781	4	C1orf50	0.021592904	0.006558798	3.37E-06
976	2334624	2	TSPAN1	0.018262733	0.006574417	5.96E-06
1628	2337238	9	HEATR8	0.000113163	0.008182282	4.36E-06
104	2337538	3	RP11-90C4.1	0.000731459	0.018213477	1.45E-05
832	2337700	5	PPAP2B	0.00035324	0.006977438	4.81E-06
451	2338845	4	NFIA	0.002123679	0.009137592	7.92E-06
414	2343884	4	LPHN2	6.92E-05	0.01266909	6.27E-06
1141	2344229	6		0.000731459	0.006584977	4.40E-06
1197	2345198	9	HS2ST1	0.005416181	0.007195699	2.34E-06
2026	2345779	7	GBP4	0.000276837	0.007850394	6.56E-06
668	2348920	4	CDC14A	0.023196567	0.007069116	4.57E-06
761	2348926	4	CDC14A	0.015428709	0.007499352	5.74E-06
1586	2349294	8	RP5-936J12.1	0.0015655	0.006876156	5.64E-06
1770	2350297	3	PRPF38B	0.000683093	0.006540911	5.89E-06
734	2351311	4	KCNC4	0.000115017	0.008419847	6.31E-06
583	2351412	6		0.000118813	0.013583363	8.53E-06
593	2351598	3	RP11-96K19.2	0.010913939	0.012701614	1.35E-05
932	2352425	6		6.62E-06	0.01526752	1.41E-05

SEQ ID NO	Aff P-ID	A	B	C	D	E
474	2352537	9	LRIG2	0.000177948	0.011098091	8.26E-06
796	2353802	4	TTF2	0.005280805	0.007398234	4.66E-06
1426	2354664	4	PHGDH	0.00022254	0.008825131	7.03E-06
859	2354667	3	PHGDH	0.001151831	0.007373918	4.66E-06
61	2355118	6		0.033605237	0.024962916	4.91E-05
717	2356711	5	FMO5	0.00032469	0.011169866	8.71E-06
1815	2358768	4	PIP5K1A	0.001426456	0.006739963	5.31E-06
1906	2358817	4	PIP5K1A	0.00011347	0.008659372	2.79E-06
1344	2358866	9	ZNF687	0.047189944	0.007896143	2.93E-06
318	2359022	4	TUFT1	0.008412239	0.019281699	2.24E-05
1991	2359172	7	S100A10	2.46E-05	0.008579579	1.13E-05
1973	2360177	9	HAX1	0.000475873	0.007177691	5.19E-06
619	2361306	4	LMNA	9.15E-05	0.010680811	5.62E-06
60	2361561	7	IQGAP3	6.53E-05	0.052285286	7.62E-05
591	2361774	9	NTRK1	0.001689593	0.009588501	9.17E-06
1397	2361937	1		0.008429307	0.011369338	9.16E-06
1609	2362760	2	SLAMF8	0.000293755	0.008851971	3.93E-06
415	2362943	2	ATP1A2	0.000931652	0.010267038	8.99E-06
1121	2363443	7	RP11-297K8.2	0.000105163	0.008348104	5.02E-06
1478	2363596	2	TOMM40L	0.001351803	0.006766808	2.02E-06
1807	2363918	2	DUSP12	6.39E-06	0.008024841	5.36E-06
1775	2364168	9	UHMK1	9.30E-05	0.006583588	3.54E-06
1636	2365136	4	MGST3	0.001286836	0.006751106	3.74E-06
1433	2367711	8	AL645568.1	1.65E-05	0.009625929	4.05E-06
1255	2368310	8	KIAA0040	0.000252191	0.006744191	4.61E-06
1258	2369335	4	C1orf49;C1orf220;AL513013.1	0.004267545	0.007220492	2.75E-06
1571	2370215	9	KIAA1614	0.004407176	0.006575102	1.91E-06
1835	2371053	2	DHX9	0.001027681	0.009724721	7.95E-06
1246	2371206	7	NMNAT2	0.000742232	0.007072308	5.66E-06
1968	2373881	4	PTPRC	0.003830941	0.008142194	4.66E-06
1910	2374274	1		1.92E-05	0.007591419	3.48E-06
251	2375421	3	RP11-480I12.3	2.80E-05	0.014753778	1.93E-05
1405	2376434	5	KLHDC8A	3.24E-05	0.008440933	7.36E-06
276	2376513	1		0.000310846	0.011470781	7.56E-06
1891	2376804	4	IKBKE	4.25E-05	0.006524562	4.11E-06
1161	2377129	2	PFKFB2	2.67E-05	0.01046144	7.14E-06
261	2378098	9	HSD11B1	0.012161553	0.014861289	1.03E-05
358	2379173	9	FAM71A	6.53E-05	0.012088903	5.38E-06
467	2379454	9	RPS6KC1	0.015937432	0.011695155	1.18E-05
811	2379471	4	RPS6KC1	6.60E-05	0.011990906	1.17E-05
572	2379903	9	CENPF	2.09E-05	0.019043146	1.94E-05
845	2379907	9	CENPF	4.92E-05	0.016468854	9.51E-06
525	2381284	4	MOSC2	0.000881522	0.01234807	6.65E-06
539	2382372	9	DEGS1	3.86E-06	0.020088544	1.45E-05
316	2382373	4	DEGS1	6.13E-05	0.019451886	1.79E-05
1948	2382443	2	CNIH4	0.000243178	0.008587751	4.58E-06

SEQ ID NO	Aff P-ID	A	B	C	D	E
1652	2382480	4	CNIH3	0.002187152	0.006827297	3.25E-06
1435	2383093	5	PARP1	0.017390197	0.00692499	4.35E-06
743	2384613	5	C1orf96	0.00026838	0.007981474	5.05E-06
1238	2386188	5	IRF2BP2	0.000108061	0.008100112	2.38E-06
1678	2386782	4	GPR137B	0.001757031	0.007939934	4.07E-06
1381	2389967	1		2.60E-06	0.008282347	6.16E-06
908	2391060	4	C1orf159	9.88E-05	0.011500656	5.14E-06
825	2391846	2	GNB1	0.000128482	0.014644576	1.14E-05
529	2393322	1		0.010386073	0.008019303	4.22E-06
606	2395510	9	ENO1	0.000156233	0.019298761	2.09E-05
333	2396027	9	LZIC	1.95E-06	0.020081931	2.37E-05
348	2397591	5	KAZN	1.81E-06	0.015572111	1.63E-05
695	2398901	6		7.23E-06	0.016623913	1.75E-05
1507	2399450	9	UBR4	3.56E-05	0.008422828	4.92E-06
1181	2400148	3	RP4-749H3.1	0.001221904	0.010206572	5.86E-06
152	2400178	2	CAMK2N1	9.01E-06	0.026063706	2.59E-05
582	2400179	2	CAMK2N1	4.47E-05	0.01559515	9.45E-06
97	2400180	2	CAMK2N1	3.66E-06	0.031824392	3.10E-05
58	2400181	9	CAMK2N1	0.000198282	0.038963268	4.21E-05
575	2400707	9	RAP1GAP	0.003098917	0.010613844	6.50E-06
1813	2401703	4	MYOM3;R P11-293P20.3	7.38E-05	0.006696158	3.40E-06
1753	2402420	2	C1orf135	0.00010346	0.009232187	3.30E-06
643	2402463	2	STMN1	2.42E-06	0.018080299	1.07E-05
484	2402464	9	STMN1	0.000363271	0.023971946	2.62E-05
1879	2402466	9	STMN1	4.53E-05	0.010009361	5.91E-06
1581	2406442	9	CLSPN	0.000150908	0.010372461	7.04E-06
1799	2406443	9	CLSPN	0.000126082	0.008736274	4.61E-06
1562	2406607	3	TRAPPC3	0.002919457	0.007068394	3.93E-06
450	2409634	4	ERI3	0.00060261	0.008504212	4.47E-06
139	2410530	2	POMGNT1	0.004360173	0.017748354	1.83E-05
1411	2413541	4	HSPB11	0.011398396	0.006601892	4.14E-06
1011	2414409	4	PPAP2B	0.003064934	0.007911982	5.54E-06
754	2414437	5	PRKAA2	4.32E-05	0.011624453	7.82E-06
1378	2415125	1		1.22E-05	0.00685264	1.64E-06
222	2415666	5	NFIA	0.013961818	0.010182727	9.23E-06
234	2420021	1		0.022075503	0.011356751	8.96E-06
1362	2423947	3	RP11-86H7.6	0.000333103	0.006732521	4.49E-06
544	2423977	1		0.002202047	0.009340892	1.02E-05
203	2425002	5	PALMD	0.001460097	0.011648419	1.24E-05
708	2425301	5	CDC14A	0.028404922	0.006591512	4.33E-06
1886	2425955	7	AMY2B;AC TG1P4	0.000731459	0.007223839	4.52E-06
1256	2428116	2	KCND3	0.003923309	0.00762346	5.07E-06
866	2428148	4	KCND3	0.000333956	0.00838534	4.70E-06
1653	2428490	6		1.05E-05	0.006690888	3.07E-06
1030	2428505	2	SLC16A1	8.27E-06	0.012777404	7.84E-06

SEQ ID NO	Aff P-ID	A	B	C	D	E
1824	2428507	9	SLC16A1	0.000131632	0.007514531	2.97E-06
536	2431143	9	NOTCH2	3.08E-05	0.012700774	8.14E-06
1737	2432473	6		5.28E-06	0.007929227	4.32E-06
1109	2432882	6		0.002356255	0.006664499	3.11E-06
699	2433254	2	FMO5	0.00580501	0.009377878	2.79E-06
1560	2433880	4	RP11-744H18.2	0.000454879	0.006744412	3.44E-06
964	2434001	6		3.58E-06	0.013245904	1.02E-05
1858	2434095	1		0.001705241	0.006866301	4.85E-06
1432	2434340	5	CA14;snoU13.115;CA14	0.008706715	0.006743011	5.10E-06
1647	2435365	4	THEM4	6.81E-05	0.006800674	2.64E-06
2045	2435391	2	S100A10	2.12E-05	0.007179441	6.15E-06
138	2435392	9	S100A10	1.64E-06	0.029375761	3.58E-05
420	2436400	5	CREB3L4	0.010140998	0.009145342	7.79E-06
2046	2436718	2	UBE2Q1	1.24E-05	0.008826572	5.71E-06
1559	2436760	9	ADAR	0.000333103	0.007188607	4.31E-06
2081	2436777	9	ADAR	0.00055537	0.006511312	3.94E-06
1816	2438283	2	IQGAP3	0.019281916	0.007219209	5.36E-06
1403	2438403	4	RP11-284F21.7	0.009861702	0.007020494	4.83E-06
702	2439112	9	FCRL1	0.00180613	0.010454141	6.09E-06
697	2439713	1		0.018818925	0.009054474	6.05E-06
713	2440486	9	F11R	0.002951948	0.009184105	4.04E-06
1854	2440934	6		0.000329714	0.009574997	9.06E-06
1880	2441254	7	UHMK1	0.000674778	0.007808112	7.85E-06
479	2441293	1		0.04486637	0.007065833	3.64E-06
52	2442609	9	CD247	1.32E-08	0.058186499	7.57E-05
146	2442711	4	CREG1	0.044564191	0.016459758	1.51E-05
1139	2443145	2	DPT	0.001689593	0.008816218	5.73E-06
1553	2445386	9	ASTN1	0.00081399	0.007829511	7.28E-06
201	2445439	4	ASTN1	0.000986793	0.015663776	1.28E-05
1306	2445596	1		2.37E-05	0.008143377	5.57E-06
1045	2445659	4	AL359075.1;SEC16B	2.89E-05	0.008115986	5.64E-06
2059	2446213	2	TOR1AIP2	0.000701725	0.006905728	3.97E-06
1017	2449595	9	ASPM	0.00028481	0.011214528	1.13E-05
1479	2450707	7	IGFN1	0.008126841	0.006840666	3.17E-06
1990	2452640	2	NUCKS1	6.19E-05	0.006513548	4.46E-06
1907	2452665	9	NUCKS1	1.22E-05	0.00700385	2.12E-06
226	2453257	3	C1orf132	0.003864295	0.015604689	1.46E-05
856	2454934	7	VASH2	9.17E-05	0.01002888	5.93E-06
1742	2455571	5	CENPF	0.000909538	0.012399382	9.59E-06
1382	2455740	9	USH2A	6.92E-05	0.008670255	3.56E-06
367	2458002	4	PARP1	8.76E-05	0.022724911	2.24E-05
494	2458051	9	PARP1;NV L	0.000839994	0.018192256	2.19E-05
614	2458059	9	PARP1;NV L	0.001013073	0.018177128	2.33E-05

SEQ ID NO	Aff P-ID	A	B	C	D	E
772	2458061	9	PARP1;NV L	0.000120755	0.016719436	1.39E-05
371	2460770	7	RP5-865N13.2	0.030881616	0.013148273	1.70E-05
240	2461554	1		1.71E-05	0.015540624	6.99E-06
647	2461808	3	ARID4B	1.85E-05	0.009733544	4.19E-06
1888	2461983	2	GNG4	2.45E-05	0.006679482	3.66E-06
987	2462132	4	LYST	0.005853836	0.008761152	3.61E-06
646	2462390	5	EDARADD	0.009608615	0.008062889	5.07E-06
391	2462402	6		0.024995647	0.013921384	1.34E-05
148	2463199	4	GREM2	5.31E-05	0.020014135	1.68E-05
1688	2463907	6		3.87E-05	0.009135293	5.78E-06
480	2464645	5	KIF26B	0.000394997	0.01015051	6.15E-06
1745	2464725	5	KIF26B	0.02996467	0.007436111	2.41E-06
961	2465112	4	SMYD3	0.000740426	0.00859054	3.68E-06
1228	2468077	1		0.001320494	0.008632826	6.05E-06
1438	2468096	1		0.00199727	0.006948306	3.18E-06
1499	2468976	2	IAH1	6.79E-05	0.009755437	5.56E-06
1773	2469870	9	GREB1	0.005601625	0.007192075	3.14E-06
369	2469885	4	GREB1	0.004872298	0.010268236	8.27E-06
660	2470495	2	FAM84A	0.028813689	0.01106141	8.18E-06
1270	2470675	9	DDX1	0.000126422	0.011859396	8.45E-06
807	2471816	1		0.003031295	0.011034735	1.03E-05
1190	2472863	4	KLHL29	0.00028481	0.008335196	6.23E-06
1359	2472904	5	ATAD2B	7.63E-05	0.010695906	5.99E-06
822	2473804	4	EPT1	0.00515944	0.009520516	5.10E-06
604	2473817	2	EPT1	0.000162598	0.009646651	3.60E-06
740	2473976	2	C2orf18;CE NPA	0.000228432	0.008345388	4.46E-06
1033	2473979	2	C2orf18;CE NPA	0.001106343	0.006681413	3.51E-06
1926	2474461	4	TRIM54	2.15E-05	0.006718124	3.84E-06
1650	2475693	2	LBH;AC104 698.1	2.46E-05	0.010241028	5.98E-06
291	2475695	2	LBH;AC104 698.1	9.56E-07	0.016675474	1.27E-05
1191	2477478	1		0.000269075	0.00759234	2.13E-06
857	2480873	5	CALM2;C2 orf61	2.34E-05	0.007532819	2.91E-06
1481	2483422	1		0.000297559	0.008805039	2.45E-06
641	2484202	5	BCL11A	0.015223504	0.008222288	7.55E-06
732	2485722	2	CEP68	0.000146537	0.008285681	2.36E-06
1594	2487212	2	ANTXR1	0.006898401	0.008932501	1.10E-05
1005	2487217	2	ANTXR1	0.000374519	0.013610335	2.20E-05
1684	2487383	4	AC092431.1	0.000701725	0.007954263	5.49E-06
432	2488699	4	SMYD5	7.87E-05	0.015768425	1.14E-05
1395	2489016	4	ACTG2	0.022775596	0.007854953	6.38E-06
982	2489925	1		0.004689092	0.006770824	1.87E-06
169	2491288	2	TMSB10	1.18E-07	0.02981693	4.03E-05
1034	2492588	6		1.82E-05	0.009689749	6.82E-06

SEQ ID NO	Aff P-ID	A	B	C	D	E
1538	2492639	6		0.00115456	0.007687908	5.59E-06
1697	2496842	9	MAP4K4	0.000896506	0.006816041	2.44E-06
719	2500274	4	BCL2L11	0.000106893	0.013001365	7.72E-06
129	2500383	6		0.000862602	0.031191838	3.41E-05
1098	2500950	4	SLC20A1	0.016212799	0.007999574	6.76E-06
1080	2502419	1		0.009101689	0.00713435	5.92E-06
942	2503248	1		0.032905271	0.009185376	8.32E-06
1587	2504114	4	CNTNAP5	0.020351547	0.006559961	4.15E-06
1404	2504466	1		0.001732949	0.007924953	6.78E-06
1730	2505547	3	PTPN18	0.033429032	0.007152644	5.39E-06
736	2508938	5	ZEB2;ZEB2 ;AC009951.1	0.000595218	0.008601963	6.26E-06
302	2510012	4	LYPD6B	0.001713115	0.010465528	8.12E-06
1633	2511767	4	UPP2	0.000134132	0.009381362	4.93E-06
1883	2512731	9	PSMD14	2.46E-05	0.008283694	5.51E-06
1140	2514422	9	BBS5;RP11 - 724O16.1;K BTBD10	0.000293755	0.012231572	7.96E-06
241	2514660	9	UBR3	0.043299568	0.009434778	9.95E-06
303	2515814	2	RAPGEF4	5.13E-05	0.012849118	1.19E-05
849	2516546	8	ATF2	0.049782645	0.008503428	5.55E-06
170	2518113	8	AC009478.1	3.25E-07	0.026250826	2.61E-05
1251	2518123	1		6.28E-06	0.013391344	1.23E-05
317	2518126	1		2.05E-05	0.020141631	1.48E-05
1537	2518128	1		0.000144203	0.008894878	3.10E-06
1719	2518146	1		3.51E-05	0.00934739	5.22E-06
1852	2518152	1		0.009120022	0.007551326	5.14E-06
1965	2518159	1		9.59E-05	0.006815639	4.29E-06
357	2518161	1		2.94E-05	0.018291423	1.92E-05
1470	2519298	4	FAM171B	0.000281159	0.008194504	4.50E-06
2016	2519657	2	COL3A1	4.06E-05	0.008943244	6.69E-06
2051	2519667	5	COL5A2	0.000620704	0.007056377	5.54E-06
1620	2521265	2	CCDC150	0.01434388	0.007186124	3.87E-06
1321	2522030	4	C2orf47	0.000509079	0.007679796	4.01E-06
84	2522842	7	ALS2CR4	0.003428273	0.021356529	1.53E-05
492	2523250	9	BMPR2	3.28E-05	0.012246342	1.00E-05
1635	2524751	4	FASTKD2	0.000873066	0.00892817	5.63E-06
915	2527797	3	CTDSP1	0.00051035	0.00707731	4.80E-06
198	2528111	9	CYP27A1	0.006771364	0.012183336	1.06E-05
1455	2529187	5	EPHA4	0.001895132	0.006902755	5.45E-06
850	2533263	3	TRPM8	0.006310467	0.008444188	3.54E-06
1064	2533688	4	AGAP1	0.005613406	0.008401337	5.08E-06
682	2534019	2	CXCR7	0.007173756	0.01141102	7.05E-06
1657	2534732	9	FAM132B	1.12E-05	0.009726611	8.21E-06
728	2535587	1		6.50E-05	0.008364795	5.93E-06
862	2535780	4	GPC1	0.04726916	0.007338948	3.68E-06
354	2536222	9	ANO7	2.05E-05	0.014644119	1.34E-05
71	2536223	9	ANO7	0.000206799	0.028782637	2.44E-05

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485	2536224	2	ANO7	0.000570716	0.011820556	1.20E-05
277	2536236	9	ANO7	2.42E-05	0.016689851	1.24E-05
140	2536237	9	ANO7	0.017291959	0.017903985	1.67E-05
109	2536238	9	ANO7	0.000173296	0.024766753	2.94E-05
1491	2536242	3	ANO7	0.012572419	0.006741049	3.26E-06
321	2536250	4	ANO7	0.000142667	0.018967199	1.42E-05
1449	2536358	2	SEPT2	9.99E-06	0.009644912	8.09E-06
1198	2537304	1		0.002329878	0.00823596	5.31E-06
768	2537460	5	SNTG2	0.000192114	0.010858597	5.00E-06
803	2537866	8	MYT1L	0.021197932	0.006898528	6.62E-06
502	2538478	1		0.000173296	0.013636136	1.07E-05
1472	2539249	5	RNF144A	4.58E-05	0.00662945	5.00E-06
162	2539540	4	KIDINS220	2.33E-06	0.018153181	1.91E-05
258	2540638	5	GREB1	0.004267545	0.016181776	1.93E-05
278	2542638	8	AC013400.2	0.00877735	0.010171152	9.08E-06
182	2543788	8	KLHL29	1.26E-06	0.021121055	2.52E-05
722	2544499	4	ADCY3	0.000333956	0.012620568	6.33E-06
911	2545313	1		0.001054975	0.009808729	6.93E-06
721	2545500	4	CGREF1	0.008310486	0.008345871	6.14E-06
1808	2546680	5	LBH	0.000150908	0.00755128	3.85E-06
694	2548823	4	ATL2	0.002912998	0.009530356	6.26E-06
1266	2552574	1		0.016649629	0.007187407	7.40E-06
2053	2555538	3	XPO1	0.001173835	0.007493161	3.61E-06
1439	2556553	1		0.001280802	0.006668129	4.29E-06
293	2556767	4	SPRED2	0.000188103	0.013452402	9.14E-06
897	2558656	4	TGFA	0.02996467	0.007536374	5.60E-06
1414	2559989	9	DCTN1	0.037954575	0.006518274	3.07E-06
1229	2567271	4	CHST10	0.001429788	0.007566499	4.27E-06
1634	2570887	4	AC068491.1	0.001219026	0.008462262	3.38E-06
1058	2571158	6		0.00022254	0.008954674	6.74E-06
1477	2571255	7	ZC3H6	2.01E-05	0.007653159	2.75E-06
114	2572052	1		0.000364196	0.019834692	2.14E-05
776	2573159	5	AC069154.2	0.000205715	0.0076573	4.39E-06
903	2573284	1		9.46E-05	0.009345976	3.05E-06
812	2574817	9	MAP3K2	0.000425014	0.013698999	8.31E-06
1592	2576618	6		3.46E-05	0.008938034	4.32E-06
1985	2576850	6		3.58E-06	0.006932694	7.40E-06
830	2577477	5	MGAT5	0.002388272	0.007909049	6.65E-06
1839	2577916	9	MCM6	3.19E-05	0.009421871	2.84E-06
795	2577927	9	MCM6	1.29E-05	0.013004413	6.45E-06
675	2579064	4	LRP1B	0.016903952	0.007936997	7.43E-06
1368	2580293	5	ACVR2A	0.001709174	0.007527767	3.54E-06
1127	2581981	1		0.001070147	0.011265964	9.12E-06
1097	2582242	3	AC021849.1	0.010636495	0.006584575	2.40E-06
677	2582451	2	CYTIP	0.0015655	0.011798932	1.18E-05
1739	2587120	1		0.000260166	0.006806629	3.86E-06
194	2587539	4	SP3	0.009861702	0.012931293	1.26E-05
1176	2589145	3	PDE11A;A C011998.1	0.019718284	0.011752117	1.04E-05

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1794	2590293	1		0.004699102	0.007499753	4.42E-06
1734	2590313	4	AC009478.1	3.34E-05	0.008654695	7.53E-06
1642	2590317	4	AC009478.1	4.52E-05	0.008749677	5.73E-06
179	2590322	4	AC009478.1	1.05E-07	0.023171685	2.54E-05
1578	2590330	1		0.007866301	0.00767295	6.39E-06
1656	2590333	1		0.000194662	0.008938714	7.05E-06
228	2590342	4	AC009478.1	5.66E-07	0.021717658	1.52E-05
1524	2590346	1		3.04E-05	0.009745903	8.95E-06
477	2590349	1		1.31E-05	0.015351436	1.07E-05
1108	2590723	9	FRZB	4.39E-05	0.00810083	4.99E-06
836	2591456	4	TFPI	0.009724683	0.007478175	2.86E-06
2062	2591636	5	COL3A1	0.00028925	0.007114892	8.20E-06
345	2591688	9	COL5A2	0.000442481	0.007495535	6.23E-06
1066	2592274	4	STAT1	0.000449203	0.00766067	5.93E-06
1338	2592645	4	TMEFF2	0.014482591	0.009295027	5.86E-06
118	2592648	9	TMEFF2	0.013588933	0.024063565	2.28E-05
535	2595779	1		6.19E-05	0.010523583	4.82E-06
1974	2597276	2	C2orf67	0.035105592	0.006946012	7.83E-06
781	2599275	4	TNS1	9.17E-05	0.008975208	8.42E-06
1632	2599476	2	USP37	0.029541528	0.006562388	4.64E-06
910	2599863	1		4.52E-05	0.008829888	5.90E-06
965	2599915	9	C2orf24	0.000742232	0.007348425	2.98E-06
335	2600704	9	EPHA4	1.55E-05	0.018536235	1.63E-05
378	2600943	1		0.014566395	0.008784565	3.86E-06
1809	2601389	4	WDFY1	0.000306094	0.007084701	3.35E-06
154	2601681	9	DOCK10	7.88E-06	0.02628921	2.68E-05
1081	2602465	3	5S_rRNA.4 24	0.000144203	0.007318832	2.05E-06
1234	2602539	4	SPHKAP	9.28E-05	0.008361255	2.05E-06
1157	2602918	9	TRIP12	1.47E-05	0.008997078	6.95E-06
2061	2602948	9	TRIP12	0.000753154	0.007525896	5.35E-06
396	2603204	1		0.012720391	0.008693728	8.76E-06
723	2603264	5	CAB39	0.011153791	0.00928397	4.96E-06
286	2605670	5	FAM132B; AC016757.1	0.003288508	0.011313889	6.50E-06
788	2605785	9	PER2	0.000524526	0.009752043	4.77E-06
1004	2606698	1		5.32E-05	0.011144864	8.01E-06
1695	2606919	9	KIF1A	0.042209752	0.006760359	3.63E-06
2067	2608200	3	TRNT1	5.06E-05	0.007942636	2.32E-06
1430	2608310	8	SUMF1	0.000664925	0.010575278	7.69E-06
1942	2608320	4	LRRN1	0.006310467	0.007137097	3.69E-06
155	2608321	2	LRRN1	0.000173296	0.019550721	1.90E-05
1549	2608324	9	LRRN1	0.000363271	0.011008854	7.59E-06
645	2608325	2	LRRN1	6.21E-05	0.019434045	1.39E-05
1008	2608339	5	SUMF1	2.54E-05	0.012507145	5.22E-06
1746	2608671	9	ITPR1	0.000933891	0.006561627	5.98E-06
1597	2611429	1		0.000611594	0.007531947	4.72E-06
1532	2612685	5	RFTN1	0.000197241	0.007072248	3.46E-06
1419	2616182	4	CRTAP	0.001052466	0.006830214	3.37E-06

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916	2617484	9	DLEC1	0.013431886	0.008587469	5.38E-06
816	2617540	9	DLEC1	0.017888918	0.007446384	3.41E-06
1694	2618614	2	EIF1B	6.41E-05	0.006862005	2.47E-06
98	2619175	9	TRAK1	0.004114217	0.025408058	2.25E-05
269	2622081	7	RHOA	2.76E-05	0.023574859	3.36E-05
545	2623385	5	IQCF1	0.00071035	0.008401967	6.10E-06
690	2626663	8	FHIT	0.007866301	0.010201017	7.71E-06
1156	2627422	9	ATXN7	8.27E-06	0.012122322	1.25E-05
651	2629053	5	FOXP1	0.000436951	0.011217143	6.81E-06
409	2629551	7	RYBP	0.001173835	0.015072362	1.96E-05
738	2629744	4	PPP4R2	0.04726916	0.008537673	9.19E-06
1410	2630507	4	ROBO2	0.001302035	0.008310638	3.52E-06
1748	2635824	9	PLCXD2	3.62E-05	0.008886785	7.53E-06
1166	2636575	6		0.002123679	0.009197633	9.18E-06
423	2638147	9	C3orf15	0.009193693	0.007970185	8.90E-06
1233	2638761	2	SLC15A2	0.000352341	0.00718282	1.84E-06
1834	2642793	4	DNAJC13	0.045938047	0.007033282	3.08E-06
184	2643246	4	TFP1;TF	0.018126	0.010721006	8.87E-06
1052	2643765	1		0.000108061	0.008880817	1.02E-05
510	2644440	9	CLDN18	0.003266926	0.017008691	1.45E-05
1523	2647113	4	CPA3	6.21E-05	0.008005576	4.00E-06
1771	2647816	6		1.85E-05	0.010052151	7.45E-06
952	2647934	9	MED12L	0.004800285	0.007000581	2.37E-06
1723	2648885	9	GMPS	0.000172838	0.007554839	3.61E-06
1035	2649525	1		8.59E-05	0.007182612	3.53E-06
934	2649935	2	IQCJ-SCHIP1;AC063955.1	6.02E-05	0.010720906	8.75E-06
1421	2650228	9	SMC4	3.17E-06	0.016266742	1.10E-05
2003	2650244	9	SMC4	1.68E-05	0.00695319	2.52E-06
907	2651198	3	RP11-298O21.6;R P11-298O21.2	5.24E-07	0.013460027	1.71E-05
1508	2651858	4	GPR160	1.95E-05	0.008579857	3.86E-06
1855	2652236	5	TNIK	9.17E-05	0.007559912	2.17E-06
1823	2652297	1		3.08E-05	0.006668549	3.20E-06
526	2653422	8	TBL1XR1	0.003210012	0.010540491	6.82E-06
445	2655291	5	ABCC5	6.39E-06	0.015888528	1.09E-05
1939	2658515	1		3.13E-05	0.007764126	4.87E-06
1213	2658524	1		0.002147887	0.007985716	5.27E-06
93	2658918	5	C3orf21	0.000102061	0.020156465	1.03E-05
616	2660844	4	SUMF1	0.002052564	0.013982945	1.22E-05
1801	2660916	4	SUMF1	0.006537209	0.006595054	4.89E-06
296	2661905	4	AC087859.1	7.38E-05	0.010850848	7.91E-06
757	2662405	3	RPUSD3	0.011000613	0.009676955	5.52E-06
1357	2663942	3	GRIP2	0.003473534	0.00850067	5.57E-06
1027	2664336	2	COLQ	0.000769819	0.007370036	1.10E-06
963	2666262	3	THRB;AC112217.2	2.79E-05	0.009236679	6.52E-06

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696	2666522	9	TOP2B	2.38E-06	0.013163028	1.15E-05
1149	2666743	1		0.005051331	0.008825818	3.83E-06
883	2667008	1		6.41E-05	0.007673324	2.51E-06
1552	2670412	1		0.004140901	0.008171632	8.16E-06
2022	2673028	9	MAP4	2.38E-06	0.007570706	7.03E-06
113	2673623	9	CELSR3	0.003413307	0.016791865	2.15E-05
704	2674247	2	RHOA	3.07E-06	0.018909578	2.10E-05
1602	2676932	2	RP11-884K10.5	0.003181899	0.006579698	2.72E-06
512	2676993	5	CACNA2D3	0.013302264	0.012413878	1.18E-05
1547	2677357	2	WNT5A	0.000483071	0.008107545	3.23E-06
774	2678668	1		0.000183201	0.013190267	1.35E-05
1371	2678742	2	FHIT	5.15E-05	0.008580237	6.43E-06
1189	2678879	4	FHIT	0.034438352	0.007911619	3.61E-06
829	2679967	9	PRICKLE2	0.000250234	0.010916403	6.29E-06
1847	2680050	2	ADAMTS9	6.62E-06	0.008282353	5.23E-06
1085	2680626	4	LRIG1	0.001040005	0.00879174	3.90E-06
264	2682971	9	CNTN3	0.015576799	0.011505616	5.10E-06
770	2685234	3	RP11-91A15.1	0.008044591	0.00862745	5.44E-06
470	2686545	9	ABI3BP	0.000628393	0.011468681	7.23E-06
751	2687361	1		0.002066608	0.007528671	2.37E-06
2023	2688904	4	C3orf17	0.000438052	0.00735558	2.33E-06
975	2689033	5	BOC	0.000143818	0.008308479	5.46E-06
1755	2689214	6		1.57E-05	0.007486134	3.62E-06
106	2689313	9	KIAA1407	0.015311147	0.019661807	1.60E-05
382	2691686	9	HCLS1	0.039015171	0.014788972	1.95E-05
1669	2692363	4	ADCY5	0.00180613	0.0065665	2.64E-06
1037	2693582	4	ZXDC	0.047746878	0.008220293	6.80E-06
1354	2694294	1		0.000674778	0.00923119	7.11E-06
996	2696131	9	SLCO2A1	0.003217076	0.010887966	6.31E-06
1099	2698045	5	CLSTN2	6.11E-05	0.007604148	1.93E-06
372	2698593	9	TFDP2	2.19E-05	0.010880081	5.99E-06
1117	2699041	2	PCOLCE2	0.008011904	0.009640861	1.01E-05
581	2699705	9	PLSCR2	4.99E-05	0.013537973	1.13E-05
1699	2701408	1		8.76E-05	0.006644833	2.64E-06
1866	2701986	6		0.000461778	0.009788617	6.40E-06
780	2703842	9	SLITRK3	0.002842819	0.00956677	5.48E-06
1928	2704213	9	PDCD10	0.000203565	0.008620506	6.27E-06
532	2705096	5	CLDN11	0.000256815	0.01098403	7.29E-06
809	2706654	6		2.79E-05	0.009580406	3.21E-06
547	2706734	3	RP11-385J1.2	0.000413384	0.014860356	8.42E-06
805	2708067	2	KLHL6	0.009399078	0.008372295	5.09E-06
373	2708335	2	ABCC5	7.23E-06	0.021678507	2.02E-05
939	2708654	1		0.029020011	0.007307342	7.26E-06
624	2708847	3	TMEM41A	0.001685702	0.010692634	7.69E-06
671	2710829	1		0.000480661	0.012195242	9.06E-06
1884	2711363	1		6.02E-05	0.006846258	7.64E-07

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824	2711369	1		0.00250353	0.008479945	8.04E-06
74	2712860	2	UBXN7	0.00020038	0.035827272	4.83E-05
1006	2713195	2	DLG1	0.005359393	0.008326261	5.45E-06
1146	2713748	6		0.000151311	0.012719493	1.44E-05
1806	2714218	3	MYL5	0.005051331	0.007306045	2.72E-06
1527	2714265	9	PCGF3	0.00055537	0.006717865	2.23E-06
810	2714497	2	FGFRL1	0.000131632	0.009136359	6.17E-06
1686	2715217	2	C4orf48	5.66E-05	0.009995655	4.38E-06
361	2715538	4	FAM193A	0.014622507	0.010400399	1.38E-05
1143	2715773	4	GRK4	1.60E-05	0.008298962	6.27E-06
947	2717272	4	SORCS2	0.013148205	0.007377617	5.17E-06
312	2717882	9	GPR78;CPZ	0.038548018	0.010132666	9.20E-06
1025	2718833	1		0.038548018	0.006597734	7.31E-06
1651	2719625	9	BST1	0.000130223	0.008372717	2.39E-06
1639	2719826	1		0.000909538	0.007775232	3.00E-06
94	2720275	9	NCAPG	2.38E-05	0.025732286	2.34E-05
1227	2720285	9	NCAPG	1.10E-05	0.010793838	5.59E-06
210	2720599	4	SLIT2	0.000279712	0.011956609	7.08E-06
838	2720737	2	PACRGL	0.000111639	0.008424719	2.21E-06
1040	2721165	4	RP11- 412P11.1	0.011398396	0.009482342	5.16E-06
592	2724294	4	WDR19	4.25E-05	0.009963907	5.26E-06
1193	2725201	4	LIMCH1	0.00081399	0.007780391	4.53E-06
2034	2725364	2	TMEM33	0.000760518	0.007417092	5.94E-06
1848	2728354	7	HOPX	2.26E-05	0.009545719	6.32E-06
337	2728905	1		0.03372316	0.015384819	1.83E-05
622	2731160	4	RP11- 692D12.1	0.000158328	0.011497866	7.81E-06
1018	2731449	4	MTHFD2L	0.000391017	0.00826973	4.23E-06
594	2732857	9	ANXA3	0.000487927	0.008250723	5.40E-06
1273	2733095	4	RP11- 438E5.1	0.000314052	0.00752303	3.35E-06
426	2734127	8	RP11-8L2.1	0.002481187	0.014163778	1.48E-05
1873	2735462	4	HERC3	0.004105357	0.007182623	6.66E-06
674	2736504	9	BMPRI1B	0.000254163	0.013616013	1.23E-05
933	2736527	4	BMPRI1B	0.009101689	0.006962968	2.94E-06
1950	2737930	5	CENPE	0.000664925	0.007944468	5.90E-06
176	2737932	5	CENPE	2.22E-06	0.026656504	2.45E-05
867	2737940	5	CENPE	4.53E-05	0.015521495	1.13E-05
1447	2740920	4	NDST3	0.001339198	0.008462414	8.23E-06
1930	2746264	1		0.000292246	0.006691996	4.00E-06
280	2746800	9	ARHGAP10	0.000356857	0.010703669	8.03E-06
161	2746996	1		0.006154763	0.011745989	6.30E-06
238	2747807	1		0.004167745	0.012491376	6.74E-06
700	2750636	4	CPE	0.013148205	0.013210393	1.20E-05
1147	2750647	4	CPE	0.00059375	0.011114732	9.38E-06
1003	2751964	4	GALNT7	0.000111337	0.006519285	3.50E-06
1259	2751997	5	HMGB2	0.000731459	0.014936895	1.55E-05
1860	2754413	5	MLF1IP	0.000257482	0.008133228	5.30E-06
1274	2757410	1		0.000310049	0.008014173	7.49E-06

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1130	2757591	4	WHSC2	0.012547908	0.007213149	4.68E-06
88	2758470	1		0.003071703	0.024935438	2.95E-05
385	2759511	5	SORCS2	0.000790656	0.006915943	5.83E-06
504	2759598	2	AFAP1	0.021792834	0.006631939	1.53E-06
1327	2762889	5	SLIT2	0.025498894	0.007381634	3.06E-06
1676	2763219	4	KCNIP4	9.72E-05	0.007286607	5.33E-06
231	2763921	9	CCDC149	4.35E-07	0.020155155	2.18E-05
275	2767308	4	BEND4	0.002052564	0.017199346	1.77E-05
475	2769840	9	KDR	0.000199853	0.007321611	4.45E-06
489	2771025	5	LPHN3	0.000172838	0.01109885	9.41E-06
574	2771634	4	RP11- 584P21.2	0.003428273	0.009027656	3.62E-06
1248	2772766	5	SLC4A4	5.40E-05	0.009353946	6.89E-06
573	2773378	1		0.000425014	0.008077849	2.20E-06
817	2775033	4	ANTXR2	0.002641545	0.011265019	7.43E-06
814	2775038	9	ANTXR2	0.045938047	0.010132648	2.35E-06
340	2775115	1		0.000146929	0.015266238	9.71E-06
948	2776793	3	MAPK10	0.001522517	0.00974321	4.48E-06
1164	2776796	2	MAPK10	0.003534738	0.007120783	3.70E-06
555	2778529	4	UNC5C	0.005485054	0.009116757	6.23E-06
45	2780211	9	CENPE	7.94E-08	0.085631944	0.000102736
821	2780715	3	RP11- 710F7.2	0.004749446	0.009335921	7.74E-06
565	2781004	2	PAPSS1	0.002537394	0.011813474	8.67E-06
1966	2782139	1		0.000402054	0.006574721	2.46E-06
1129	2788582	1		0.014042909	0.007952057	7.05E-06
1902	2790298	5	KIAA0922	2.67E-05	0.008591867	4.35E-06
1604	2792487	5	CPE	0.00241526	0.007846726	2.23E-06
840	2793953	2	HMGB2	1.54E-05	0.017289428	1.47E-05
730	2794726	4	ASB5	0.024147101	0.007418717	7.68E-06
861	2795876	1		0.029646817	0.009793545	8.29E-06
1119	2796405	4	IRF2	0.003781407	0.008632721	4.33E-06
1330	2798289	1		0.001108971	0.00695949	1.53E-06
1703	2798596	4	PDCD6	0.003906364	0.006523124	7.17E-06
801	2799905	1		0.026532368	0.007637195	7.17E-06
1047	2800042	9	ADAMTS1 6	0.049865614	0.007127301	7.62E-06
909	2801585	1		0.001054975	0.009377942	6.51E-06
1356	2803060	4	FBXL7	0.001602179	0.007148233	4.28E-06
1721	2803194	7	FAM134B	0.000412342	0.009777832	1.19E-05
1961	2806221	4	TTC23L	0.003181899	0.007438554	4.93E-06
1031	2807753	9	C7	0.001320494	0.009484133	6.00E-06
2057	2810394	2	MAP3K1	0.00010346	0.006765207	3.83E-06
199	2810960	5	PDE4D	0.000625307	0.017332263	1.85E-05
520	2811016	5	PDE4D	0.000249584	0.013631798	1.22E-05
127	2811062	5	PDE4D	1.71E-05	0.024255342	2.78E-05
1137	2811064	5	PDE4D	0.009608615	0.007519077	2.39E-06
1158	2811075	3	CTD- 2254N19.1	0.001065067	0.007478452	5.17E-06
1896	2811116	8	PDE4D	0.005601625	0.006976064	4.08E-06

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1743	2811117	8	PDE4D	0.00811033	0.007133926	2.86E-06
1644	2811124	8	PDE4D	0.001463501	0.006801354	4.84E-06
875	2811133	8	PDE4D	0.004194748	0.011585515	1.06E-05
1374	2811137	8	PDE4D	0.008310486	0.00749324	3.24E-06
587	2814538	6		0.003217076	0.009592647	6.55E-06
679	2814695	9	CARTPT	0.001127536	0.009790303	8.15E-06
1334	2818565	9	VCAN	4.84E-05	0.014054659	1.35E-05
951	2818582	2	VCAN	2.99E-05	0.013285949	1.06E-05
1039	2819807	3	GPR98	0.000212853	0.010053274	4.60E-06
711	2820736	5	MCTP1	0.000175608	0.010900573	6.10E-06
215	2820823	3	FAM81B	0.027553244	0.01114295	1.20E-05
1601	2820990	4	RHOBTB3	0.013562644	0.007317207	7.76E-06
831	2821794	2	RGMB	0.000373569	0.013055543	9.09E-06
1496	2822927	1		0.000189098	0.008702002	3.67E-06
164	2823841	9	WDR36	2.38E-06	0.01812122	1.20E-05
827	2824081	1		0.000280435	0.009511252	5.20E-06
1781	2824971	1		0.046795588	0.006732733	6.92E-06
1124	2827090	4	GRAMD3	0.008480701	0.006592995	5.52E-06
550	2827181	9	C5orf48	0.000701725	0.010009205	4.36E-06
309	2827382	2	MEGF10	0.00195225	0.012497339	9.89E-06
1752	2827801	9	ADAMTS1 9	3.34E-05	0.008103524	2.94E-06
1361	2828481	2	SLC22A4	0.015786268	0.007598853	6.85E-06
570	2828804	2	LEAP2	0.021355142	0.006802107	3.41E-06
1010	2829040	1		4.84E-06	0.011084794	9.79E-06
1841	2829806	4	CTC- 321K16.1	2.01E-05	0.007691385	6.15E-06
1053	2829898	5	IL9	0.000185636	0.007264838	4.67E-06
1184	2830875	9	EGR1	0.012281121	0.006583967	3.65E-06
128	2832532	7	TAF7;AC00 5618.1	0.001173835	0.021583374	2.37E-05
466	2834899	4	ABLIM3	4.52E-06	0.012756132	5.66E-06
680	2835934	7	SPARC	1.72E-06	0.018740722	2.49E-05
1483	2836555	4	GALNT10	0.001171064	0.007953627	3.86E-06
2012	2836811	9	LARP1	5.49E-05	0.008860871	6.50E-06
904	2840276	4	KCNIP1	0.003724362	0.007065134	1.81E-06
1911	2840930	7	FBXW11	0.000269075	0.007625411	4.11E-06
455	2842772	4	UNC5A	0.001157296	0.011866543	6.61E-06
1798	2844247	2	CANX	9.77E-05	0.009485266	1.11E-05
1222	2844255	4	CANX	0.000636171	0.00806974	3.62E-06
1615	2844539	2	SQSTM1	0.002162534	0.008729973	9.01E-06
211	2844540	2	SQSTM1	0.036159066	0.011382357	7.36E-06
1645	2844718	4	CNOT6	6.32E-05	0.006891649	2.87E-06
1525	2845394	4	SLC9A3	0.000104877	0.007173792	4.58E-06
635	2845607	4	BRD9	0.001877871	0.010609655	7.35E-06
1484	2845672	5	NKD2	0.001354972	0.007318934	3.90E-06
1221	2845675	5	NKD2	0.009101689	0.009826739	8.25E-06
1536	2846862	1		4.46E-05	0.007535106	1.50E-06
1185	2847247	1		0.033429032	0.007973611	7.35E-06
1897	2847334	6		0.001587412	0.006770776	3.66E-06

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818	2848815	9	CTNND2	0.000155817	0.007745231	4.67E-06
1032	2849087	9	DNAH5	8.61E-05	0.00794934	5.03E-06
1333	2849099	9	DNAH5	0.040101547	0.007167069	3.66E-06
1285	2849102	9	DNAH5	0.002537394	0.006928127	3.69E-06
841	2849152	9	DNAH5	0.013562644	0.007538097	6.90E-06
145	2849177	3	DNAH5	0.000297559	0.019731072	9.73E-06
460	2849511	4	ANKH	0.006926925	0.010661478	7.13E-06
1611	2849802	5	FBXL7	0.001124866	0.006581459	5.10E-06
117	2849995	2	FAM134B	0.00014459	0.026361181	3.38E-05
1701	2850497	6		0.008143382	0.007243822	3.72E-06
503	2851189	1		0.000191608	0.011471627	7.40E-06
944	2854889	2	HEATR7B2	0.030501101	0.007657939	3.05E-06
1012	2856493	4	MOCS2	0.000310049	0.007523726	3.12E-06
739	2856671	4	ARL15	0.001095886	0.007898792	4.05E-06
1390	2857094	4	RP11- 528L24.3	0.003174906	0.006645723	3.59E-06
1101	2858235	4	PDE4D	0.001709174	0.007746921	6.08E-06
476	2858299	4	PDE4D	0.016744596	0.010941528	4.86E-06
368	2858312	4	PDE4D	0.007144307	0.010799351	6.79E-06
436	2858317	4	PDE4D	0.000553994	0.012556713	8.30E-06
469	2858354	4	PDE4D	0.000367918	0.014805117	1.60E-05
1605	2858355	4	PDE4D	0.01732465	0.007281016	1.82E-06
1360	2858366	4	PDE4D	0.006926925	0.009640878	7.22E-06
1445	2858387	4	PDE4D	0.001543869	0.009130611	7.79E-06
1392	2858392	4	PDE4D	0.000931652	0.008377171	7.70E-06
1867	2858399	4	PDE4D	0.001283816	0.006649943	4.90E-06
507	2858418	4	PDE4D	0.000328031	0.013378586	4.08E-06
835	2858532	4	PDE4D	0.000984436	0.01321077	1.06E-05
1720	2858540	4	PDE4D	0.000720832	0.00689557	3.83E-06
398	2858550	4	PDE4D	0.000175143	0.015741974	1.65E-05
563	2858551	4	PDE4D	0.00160589	0.011660697	6.79E-06
1566	2858567	4	PDE4D	0.001752996	0.008574915	4.99E-06
360	2858575	4	PDE4D	0.000142286	0.016665493	1.59E-05
973	2858577	4	PDE4D	4.53E-05	0.013041407	1.47E-05
1466	2858619	9	DEPDC1B	0.019828743	0.007090047	4.33E-06
384	2860275	3	RP11- 83M16.5	0.038217335	0.014699721	1.45E-05
262	2860360	1		0.004426107	0.013556498	1.14E-05
1372	2863463	2	ZBED3	2.19E-05	0.008828438	5.87E-06
253	2863936	4	LHFPL2	1.57E-06	0.015136691	1.37E-05
374	2864082	4	ARSB	0.001480634	0.012463709	7.11E-06
336	2864402	1		0.004699102	0.012757132	1.00E-05
1733	2869244	7	PAM	0.042209752	0.008127007	4.53E-06
1424	2869909	4	EFNA5	0.000722593	0.010990528	7.75E-06
756	2870559	1		0.004851623	0.009976688	7.50E-06
1979	2871561	5	KCNN2	0.017956371	0.007538282	3.77E-06
304	2873260	7	CSNK1G3	0.001286836	0.013895424	1.35E-05
1503	2873713	4	RP11- 114J13.1	8.45E-05	0.006843065	4.69E-06
2056	2873861	7	LMNB1	0.001797859	0.008557564	6.17E-06

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540	2874627	4	CTC-575N7.1	0.007850273	0.012194012	1.37E-05
1019	2876122	5	SEC24A	1.65E-05	0.008469393	7.83E-06
891	2877487	4	ETF1	0.002849134	0.008531733	6.73E-06
1558	2877961	2	DNAJC18	0.003692121	0.007016632	2.32E-06
692	2878005	2	TMEM173	8.12E-06	0.010978292	9.08E-06
775	2880995	4	CSNK1A1	0.000385118	0.010477403	7.49E-06
684	2881838	1		0.00021174	0.007683315	6.31E-06
1997	2882121	2	SPARC	3.72E-05	0.008293392	7.47E-06
115	2882122	2	SPARC	5.12E-06	0.032841204	3.86E-05
2054	2882125	2	SPARC	1.71E-05	0.007415852	3.23E-06
2079	2882128	9	SPARC	1.47E-05	0.00652917	2.77E-06
1643	2882142	9	SPARC	3.85E-06	0.012687273	1.48E-05
518	2884192	4	EBF1	0.000885779	0.011197582	6.32E-06
792	2885859	5	ODZ2	0.002565937	0.007653162	8.95E-06
1554	2886153	9	PANK3	1.62E-05	0.008848725	5.11E-06
1353	2887118	9	STK10	0.000160023	0.008064688	4.64E-06
365	2887495	2	STC2	0.000619177	0.018246493	2.35E-05
1188	2887512	4	STC2	0.039351871	0.008021546	4.68E-06
546	2888080	1		4.89E-05	0.010112214	5.90E-06
1727	2888742	2	F12	0.000183201	0.007635791	5.72E-06
1209	2889481	1		0.000292999	0.0077346	3.92E-06
227	2890130	5	RUFY1	0.003458386	0.015862344	1.98E-05
1442	2890334	9	TBC1D9B	0.01496327	0.007323032	1.43E-06
767	2891058	4	GNB2L1	0.016586586	0.006763538	5.07E-06
1346	2891302	4	DUSP22	0.000958852	0.007004444	1.00E-06
1000	2893481	3	RP1-80N2.2	0.049041286	0.007653208	3.62E-06
957	2893660	4	RREB1	1.26E-05	0.010296887	6.32E-06
1217	2894668	2	PAK1IP1	0.000323032	0.00766513	2.99E-06
147	2896936	9	CAP2	0.032161453	0.02300686	3.11E-05
1783	2898612	3	GMNN	0.01160212	0.01009499	9.29E-06
1595	2898626	2	GMNN	6.42E-05	0.009780056	3.60E-06
1239	2899122	4	HFE	3.62E-05	0.007219004	2.43E-06
2043	2901929	2	TUBB	0.003390971	0.008049603	8.03E-06
1186	2902700	5	VAR5	0.000252847	0.00748735	2.36E-06
1007	2902874	3	CFB;XXbac - BPG116M5.17	0.016243657	0.006650439	4.11E-06
936	2903195	9	HLA-DRA	0.000384143	0.013596025	1.40E-05
216	2903200	9	HLA-DRA	0.000226058	0.023137572	2.88E-05
1913	2903425	9	HLA-DPB1	0.019535405	0.007421118	6.20E-06
1810	2903456	3	HLA-DPB2	0.001140973	0.007189358	4.98E-06
1173	2903747	4	SYNGAP1	0.006813471	0.006836913	3.73E-06
914	2904304	9	UHRF1BP1	0.009512851	0.008610073	5.37E-06
1311	2905788	2	ZFAND3	0.000250234	0.009189307	1.18E-05
1522	2906151	1		0.027602711	0.006514376	3.25E-06
753	2907867	4	TTBK1	2.23E-05	0.010219124	7.77E-06
1617	2909086	5	RCAN2	0.000200907	0.007185162	2.21E-06
424	2909642	1		0.016461142	0.010554498	4.48E-06

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292	2909752	1		0.022567667	0.011174444	1.02E-05
967	2910038	1		0.000792576	0.007667081	3.42E-06
720	2916447	6		1.19E-06	0.013525256	1.66E-05
1842	2918773	3	RP11-14I4.3	3.52E-05	0.008939061	7.01E-06
1845	2919791	4	AIM1	0.000116584	0.007440145	4.92E-06
650	2923986	2	CLVS2	2.50E-05	0.014201609	9.88E-06
1180	2926824	9	MYB	0.000449203	0.006598249	3.58E-06
1550	2927252	1		3.56E-05	0.006844416	4.85E-06
1446	2929703	1		0.000272577	0.008755676	5.51E-06
229	2934526	4	SLC22A3	0.000205715	0.018234968	1.72E-05
1291	2934538	9	SLC22A3	0.00362841	0.009917021	1.07E-05
1427	2934539	9	SLC22A3	0.001777336	0.007323945	3.98E-06
266	2934543	4	SLC22A3	6.72E-05	0.017329092	1.57E-05
1565	2934557	4	SLC22A3	0.000509079	0.00868456	8.95E-06
180	2934569	4	SLC22A3	4.44E-05	0.022037658	2.59E-05
513	2934571	4	SLC22A3	0.000771692	0.013671209	1.16E-05
1174	2934586	4	SLC22A3	0.02563769	0.010772341	8.50E-06
990	2934942	8	AGPAT4	0.000540412	0.00716353	4.90E-06
787	2935707	1		5.15E-05	0.011241051	7.14E-06
584	2936726	3	RP11-568A7.2	0.02244372	0.011771471	1.03E-05
1366	2937410	4	XXyac-YX65C7_A.2	1.83E-05	0.014910823	1.15E-05
925	2937411	4	XXyac-YX65C7_A.2	3.03E-05	0.017161552	9.44E-06
895	2937484	5	WDR27	0.039759255	0.008047812	5.15E-06
741	2938547	7	FOXF2	0.000412342	0.008173684	5.12E-06
381	2938741	9	GMDS	0.014877417	0.008255843	7.22E-06
412	2941607	7	TMEM14C	0.000933891	0.019147592	1.94E-05
672	2941759	6		0.000378341	0.00855831	5.95E-06
174	2941893	2	NEDD9	0.006757381	0.017550027	2.12E-05
1631	2943773	5	CAP2	0.023624431	0.006508257	4.92E-06
1179	2944071	2	DEK	1.41E-06	0.012319789	1.03E-05
246	2945999	5	LRRC16A	2.93E-05	0.01735269	1.41E-05
1712	2948594	7	TUBB	0.002029355	0.013237004	7.19E-06
537	2949541	3	EHMT2	0.033900726	0.007162816	5.30E-06
1358	2949792	4	PRRT1	3.41E-05	0.010959106	4.97E-06
954	2950359	3	HLA-DPA2	0.0264846	0.006794213	5.43E-06
1074	2950628	1		0.002531721	0.007373825	5.32E-06
1957	2951240	9	C6orf106	0.000742232	0.006740159	2.55E-06
1705	2951657	2	FKBP5	0.01612054	0.006552065	5.39E-06
1150	2952044	4	CPNE5	0.000292246	0.007034962	1.80E-06
270	2952341	9	MDGA1	0.029384212	0.01770572	1.92E-05
437	2952713	5	DNAH8	0.000896506	0.012004253	1.16E-05
1280	2954808	3	GTPBP2	0.008619147	0.009128367	6.34E-06
1607	2956143	5	GPR115	0.004167745	0.007592338	4.65E-06
1918	2965266	1		7.04E-05	0.006704181	4.77E-06
89	2965642	1		2.62E-05	0.025473063	1.96E-05

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1267	2968105	4	SEC63	0.002641545	0.00762644	6.71E-06
1406	2969569	1		7.50E-05	0.009287234	7.32E-06
1046	2970405	1		1.39E-06	0.012220589	9.68E-06
1903	2974773	1		0.000450333	0.006875027	2.38E-06
869	2976265	1		0.000148906	0.008014361	2.11E-06
1216	2980527	9	CNKS3	0.006618995	0.010696705	8.84E-06
779	2980896	4	NOX3	0.044188955	0.0069985	8.86E-06
763	2982371	4	SOD2	0.000562297	0.007631489	4.53E-06
1154	2982612	5	SLC22A3	0.00199727	0.007947392	5.12E-06
1299	2982619	5	SLC22A3	0.000394997	0.009799409	9.65E-06
598	2982626	5	SLC22A3	0.008884278	0.009911085	7.59E-06
1038	2983744	1		0.025498894	0.008506019	9.12E-06
1545	2985812	2	THBS2	9.90E-05	0.012219435	9.02E-06
173	2985814	2	THBS2	7.38E-07	0.023947968	2.18E-05
1365	2985815	2	THBS2	4.36E-06	0.0130199	8.34E-06
257	2985821	9	THBS2	5.55E-05	0.019474651	1.88E-05
912	2985825	9	THBS2	0.000212296	0.009058079	5.43E-06
55	2985827	9	THBS2	2.10E-08	0.04925015	6.11E-05
1672	2985830	9	THBS2	0.00060261	0.008283886	6.83E-06
1900	2985852	4	THBS2	1.07E-05	0.006706587	7.05E-07
1263	2986383	4	DLL1	0.00076237	0.006667557	2.62E-06
1041	2986512	4	PSMB1	0.012305161	0.007787863	2.74E-06
1517	2987970	6		0.000701725	0.008122069	6.02E-06
1160	2988685	5	FBXL18	2.14E-06	0.013965334	9.39E-06
301	2988989	9	USP42	5.20E-06	0.018386695	1.25E-05
1278	2989490	5	COL28A1	0.003684101	0.006751514	1.06E-06
1425	2989606	4	AC006465.3 ;GLCCII	0.024995647	0.00697113	4.25E-06
893	2990835	5	AGMO	0.000106893	0.008642024	4.81E-06
1859	2993333	7	CYCS	1.63E-05	0.009327163	5.44E-06
558	2993375	1		0.000920533	0.009480199	2.07E-06
465	2993385	1		0.000496534	0.011230659	7.84E-06
1709	2994249	1		0.000611594	0.008053291	5.10E-06
1065	2994656	4	CREB5	2.98E-05	0.00904156	8.03E-06
1001	2995111	7	SCRN1	0.000242546	0.006895394	4.13E-06
1026	2995377	1		4.39E-05	0.00926322	5.50E-06
1782	2995444	9	GARS	5.76E-05	0.011995848	8.82E-06
404	2997012	1		0.000118492	0.012317168	6.55E-06
370	2997133	4	SEPT7	7.71E-05	0.010482923	5.22E-06
444	2997175	6		0.009101689	0.013517476	1.49E-05
1450	2997383	4	ANLN	0.023754148	0.009205054	7.66E-06
79	2997407	9	ANLN	1.29E-05	0.027389498	2.57E-05
628	2997645	5	ELMO1	0.021002867	0.009159887	6.97E-06
1779	2998743	4	C7orf10	0.00011347	0.007120881	5.41E-06
2070	2998957	7	AC005027.3 ;INHBA	6.01E-05	0.006964308	2.98E-06
718	2999112	5	GLI3	0.001466913	0.009358662	6.89E-06
2058	3000529	7	IGFBP3	0.000391017	0.006979675	2.90E-06
823	3006506	1		1.22E-05	0.009439851	9.16E-06

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1980	3010073	5	TMEM60	0.00041969	0.006577928	3.02E-06
991	3010612	5	SEMA3C	0.001082945	0.009528208	6.30E-06
446	3011436	9	RUNDC3B	5.65E-05	0.009499059	7.55E-06
1463	3012549	9	ANKIB1	0.000586459	0.008029494	2.20E-06
548	3013157	9	COL1A2	1.66E-06	0.017474811	1.42E-05
1418	3013369	4	PPP1R9A	4.61E-05	0.009215595	3.64E-06
1622	3013678	4	DYNC1I1	0.029646817	0.006940481	2.98E-06
1796	3014762	2	BUD31	0.000120755	0.007722082	4.42E-06
1626	3015101	6		0.002212029	0.00893252	8.09E-06
1793	3015540	2	PILRA	3.04E-05	0.006597037	4.97E-06
497	3017037	4	LRRC17	0.000200907	0.013948871	7.99E-06
1269	3017439	4	LHFPL3	0.011739756	0.006799509	2.22E-06
1890	3017590	9	MLL5	0.000333103	0.008691028	6.56E-06
585	3017615	9	MLL5	0.004464194	0.007736726	6.92E-06
1218	3018430	9	HBP1	0.005019305	0.006977198	6.61E-06
900	3020009	4	MDFIC	3.41E-05	0.013179927	1.10E-05
209	3022789	7	IMPDH1	0.037823788	0.01275585	1.46E-05
1057	3023361	9	SMO	0.000729678	0.007489073	4.24E-06
1196	3023750	4	KLHDC10	9.02E-05	0.009325147	9.03E-06
1696	3024264	8	AC058791.2	0.000454879	0.006967013	4.72E-06
1829	3024911	5	CHCHD3	0.01615124	0.006700971	3.74E-06
1726	3027105	4	CLEC2L	2.22E-05	0.007139137	3.31E-06
1885	3027444	1		0.008028233	0.006511512	4.30E-06
487	3027586	5	BRAF	5.28E-06	0.01350394	8.95E-06
1485	3028591	1		0.000945161	0.007818806	4.35E-06
1153	3029904	2	CNTNAP2	0.006827559	0.006900031	5.28E-06
1529	3030862	1		4.47E-05	0.010863593	6.72E-06
747	3030882	3	SSPO	0.001705241	0.008747664	3.19E-06
323	3031189	4	ATP6V0E2	5.87E-06	0.015735604	8.36E-06
1310	3031580	3	GIMAP5	0.003557945	0.007082989	2.22E-06
1452	3031668	9	ABP1	0.002849134	0.00784346	4.34E-06
764	3032568	1		0.001797859	0.006590099	2.66E-06
417	3033649	1		3.28E-05	0.016185129	1.54E-05
1497	3034150	5	PTPRN2	0.001268815	0.006942742	3.14E-06
1400	3034165	5	PTPRN2	0.000142286	0.007604817	5.46E-06
62	3034212	5	PTPRN2	5.67E-06	0.041004965	4.35E-05
1509	3034226	5	PTPRN2	4.26E-05	0.009473058	6.04E-06
449	3034229	5	PTPRN2	7.50E-05	0.01521519	1.17E-05
1769	3034583	6		0.001374129	0.007171184	4.35E-06
1792	3034982	5	SUN1;GET 4	0.003031295	0.008267621	3.22E-06
1925	3034996	4	ADAP1;CO X19	0.001925692	0.007392579	3.91E-06
1260	3035770	3	GRIFIN	0.000180795	0.007217638	2.93E-06
1115	3036697	5	WIPI2	0.000167867	0.00903808	4.79E-06
1516	3036972	6		9.88E-05	0.007741062	6.32E-06
1683	3037200	9	EIF2AK1	2.49E-05	0.007813506	5.78E-06
1958	3037328	6		5.98E-06	0.008945527	7.37E-06
1464	3037738	1		0.006389661	0.007386167	4.59E-06

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784	3039035	5	SCIN	7.97E-05	0.009191604	2.92E-06
1383	3039818	2	AGR2	0.000128137	0.011486351	1.09E-05
629	3041213	4	AC099759.1	0.004590062	0.011694926	8.46E-06
254	3042471	3	HNRNPA2 B1	0.003098917	0.012381991	9.24E-06
1118	3043075	7	RP5-110315.1;A C004009.3	0.000701725	0.010817936	7.40E-06
1457	3043108	8	RP5-110315.1;A C004009.3	0.013431886	0.008758105	6.86E-06
330	3044438	1		0.000224879	0.011215692	7.96E-06
1448	3044555	1		0.032104854	0.006681803	7.10E-06
136	3044692	9	PDE1C	3.19E-05	0.020143883	1.83E-05
255	3046448	2	SFRP4	1.66E-06	0.023764559	2.43E-05
350	3046449	2	SFRP4	6.33E-07	0.020534054	3.08E-05
868	3046453	9	SFRP4	8.12E-06	0.017228888	1.44E-05
630	3046457	9	SFRP4	4.28E-06	0.01509688	1.74E-05
49	3046459	9	SFRP4	2.62E-09	0.069643156	0.000104049
1318	3047600	2	AC005027.3;INHBA	0.000729678	0.012639164	1.27E-05
943	3047613	4	AC005027.3;INHBA	0.000339114	0.011103507	3.96E-06
1475	3049299	9	IGFBP3	0.002537394	0.011328252	9.82E-06
284	3050416	9	DDC	0.02980537	0.010140623	1.36E-05
1163	3051219	1		0.00102279	0.00821568	4.94E-06
559	3052483	6		0.005952617	0.012033356	1.36E-05
742	3052982	6		0.032963108	0.009953901	6.39E-06
1444	3056252	4	STX1A	7.08E-06	0.007013993	4.56E-06
1204	3058806	4	SEMA3C	0.01496327	0.007578283	3.96E-06
1125	3062164	5	DYNC11I	0.000553994	0.007395291	5.33E-06
567	3062175	5	DYNC11I	0.000837966	0.007293075	6.55E-06
1257	3063591	2	AZGP1	0.007770575	0.010789364	8.53E-06
889	3063598	9	AZGP1	0.002481187	0.013545858	1.28E-05
1094	3063601	9	AZGP1	0.001219026	0.010779914	8.76E-06
724	3063605	6		0.001184984	0.012200652	1.10E-05
376	3064449	1		0.004304377	0.007354949	4.54E-06
979	3065014	9	ALKBH4	0.003217076	0.007568557	3.61E-06
625	3066949	4	CTB-111H14.1	0.012043037	0.006585706	3.61E-06
1988	3067307	9	LAMB1	1.96E-05	0.009872566	7.52E-06
1658	3067310	9	LAMB1	5.38E-06	0.011224347	8.31E-06
1606	3067585	4	NRCAM	0.000354141	0.009376832	8.46E-06
1443	3068373	6		0.004416632	0.006818008	5.24E-06
416	3070220	9	AASS	0.016398739	0.0070476	9.29E-06
440	3072337	4	UBE2H	4.44E-05	0.011046023	6.90E-06
2064	3074661	6		5.67E-06	0.007879089	7.19E-06
778	3075021	4	DGKI	0.002232119	0.007232854	4.83E-06
1949	3076101	9	SLC37A3	0.001173835	0.008365773	5.62E-06
1637	3077525	2	FAM115A	0.006757381	0.006736752	1.22E-06

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363	3077790	4	TPK1	0.026532368	0.009554661	1.31E-05
1531	3081037	7	INSIG1	2.94E-05	0.011796154	8.27E-06
2060	3082100	7	DNAJB6	0.011785961	0.007939522	6.41E-06
813	3082532	1		0.000206799	0.008814925	6.04E-06
1096	3082626	5	ERICH1	4.91E-05	0.009444815	6.17E-06
1132	3083218	5	CSMD1	0.003855932	0.008232629	5.74E-06
1384	3084878	1		0.003420783	0.008068285	1.37E-06
448	3090530	4	DOCK5	0.02092529	0.006719573	4.33E-06
1077	3090561	4	DOCK5	0.011465942	0.007494898	6.10E-06
553	3090589	9	DOCK5	0.00084815	0.008174387	6.42E-06
955	3090592	4	DOCK5	0.042066262	0.007251473	6.58E-06
1060	3093827	9	KCNU1	2.12E-05	0.012045129	4.30E-06
1249	3094697	5	FGFR1	0.000120755	0.006868788	3.88E-06
578	3097271	1		0.006687861	0.010902639	1.13E-05
1107	3099025	4	LYN	0.000180795	0.007929824	4.64E-06
1711	3100547	3	CLVS1	0.031155964	0.008689629	4.81E-06
2000	3101370	7	ARMC1	0.001873579	0.008741283	4.65E-06
1952	3102393	9	SULF1	0.00035324	0.009114519	5.56E-06
1870	3102402	4	SULF1	0.000740426	0.007834969	3.81E-06
1343	3102414	9	SULF1	0.000462937	0.012550374	8.12E-06
828	3102439	9	SULF1	2.80E-06	0.015931026	1.68E-05
2010	3102445	9	SULF1	0.000194662	0.008480409	5.98E-06
1759	3102461	2	SULF1	0.000177948	0.009249871	6.69E-06
2037	3102463	2	SULF1	0.000131986	0.008176341	7.53E-06
1982	3102464	2	SULF1	4.81E-05	0.008098921	4.23E-06
1380	3103453	5	UBE2W	5.92E-05	0.010791524	6.97E-06
1576	3103632	2	GDAP1	0.000629941	0.011534464	8.50E-06
218	3103710	4	PII5	0.000674778	0.015711899	1.73E-05
1528	3104056	4	ZFHX4	0.0001169	0.006655882	2.13E-06
2071	3104305	2	PKIA	0.001547455	0.007394509	6.93E-06
1986	3104626	5	TPD52	1.85E-05	0.008255373	5.59E-06
1893	3104778	7	ZNF704	0.037111478	0.006548322	6.22E-06
1577	3105433	9	LRRCC1	0.000172838	0.007157123	2.51E-06
1183	3105924	9	CPNE3	0.009861702	0.007692419	7.28E-06
1055	3106288	9	OSGIN2	3.12E-06	0.012037745	1.11E-05
1802	3106314	4	DECR1	0.004800285	0.007172927	6.53E-06
881	3107647	6		2.38E-05	0.016569088	1.45E-05
612	3107695	3	INTS8	0.004639335	0.010553457	9.22E-06
1316	3107732	4	C8orf38	5.22E-05	0.008155705	5.18E-06
1812	3107789	4	C8orf38	0.000450333	0.007765135	5.80E-06
499	3107876	4	KB-1047C11.2	0.033900726	0.007197605	3.82E-06
1670	3108459	9	MTDH	0.006687861	0.00668549	3.67E-06
2039	3108479	2	MTDH	2.93E-05	0.006961325	4.37E-06
1345	3108839	5	STK3	1.98E-05	0.011035218	8.64E-06
1016	3108873	4	OSR2	0.002531721	0.006675267	5.33E-06
533	3109199	2	POLR2K	5.32E-05	0.017958214	1.73E-05
1500	3109252	3	SPAG1	0.000306094	0.010773506	7.30E-06
1916	3109448	6		9.77E-05	0.012137832	1.07E-05

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797	3109660	8	KB-1930G5.4	0.009842021	0.007123883	3.92E-06
1704	3109903	7	UBR5	0.000260842	0.007334514	3.82E-06
1805	3109920	5	UBR5	0.000103742	0.009519129	5.07E-06
1049	3110126	4	KB-1507C5.2;K B-1507C5.3	0.025777155	0.007009345	8.94E-06
439	3110185	9	ATP6V1C1	4.20E-06	0.017215388	9.26E-06
213	3110198	2	ATP6V1C1	1.58E-05	0.023734636	1.63E-05
1975	3110329	9	CTHRC1	0.000134132	0.00898655	5.05E-06
1548	3110790	4	RP11-127H5.1	0.000101783	0.00824034	1.85E-06
441	3112570	4	UTP23	9.04E-06	0.021427543	1.64E-05
1043	3112714	1		0.00160589	0.009852004	4.57E-06
1363	3112879	5	EXT1	0.027405312	0.009431374	7.50E-06
858	3113688	3	HAS2-AS1	0.000219649	0.012595807	9.78E-06
1062	3114046	3	RP11-557C18.3	1.20E-05	0.011270582	7.70E-06
1476	3114081	9	WDR67	0.000280435	0.013530226	1.04E-05
633	3114092	9	WDR67	8.88E-05	0.013744083	7.95E-06
1909	3114096	9	WDR67	0.000862602	0.008984675	8.61E-06
1551	3114703	5	MTSS1	0.002997998	0.0115069	6.12E-06
1708	3114847	9	SQLE	0.001236387	0.009381479	7.07E-06
1837	3115587	3	PVT1	0.000212296	0.007279185	1.96E-06
1661	3115998	4	RP11-473O4.5	0.000553994	0.011864556	1.23E-05
411	3117908	6		0.002991379	0.011194815	2.75E-06
339	3118152	1		0.010386073	0.011188769	6.80E-06
1168	3118707	3	DENND3	0.001965656	0.007321616	4.60E-06
185	3119251	2	C8orf55	1.42E-05	0.015914535	1.24E-05
137	3119919	7	EPPK1	4.35E-06	0.028826853	2.57E-05
560	3119979	9	SPATC1	0.0060277	0.013334373	1.31E-05
1300	3120764	5	ARHGAP39	0.000122727	0.010438117	4.98E-06
806	3124365	2	AF131216.2	1.77E-05	0.01362045	1.26E-05
1947	3124528	5	FDFT1	0.023281585	0.007309709	5.45E-06
848	3125600	9	MSR1	0.000181274	0.017085539	1.35E-05
929	3127573	1		0.048959505	0.007288313	3.51E-06
664	3129039	9	CHRNA2	0.002388272	0.011092138	6.33E-06
1458	3129619	4	KIF13B	0.001135581	0.00738277	4.70E-06
386	3132919	1		0.005684569	0.01383766	1.03E-05
2042	3134154	9	PRKDC	7.26E-05	0.00675565	4.66E-06
1629	3135385	1		0.002024742	0.008228586	4.97E-06
902	3135419	1		0.002543079	0.009783809	9.62E-06
2052	3138424	2	ARMC1	3.35E-05	0.009405851	3.32E-06
1488	3138480	9	PDE7A	0.01575619	0.011220854	1.37E-05
1971	3138675	7	RRS1;ADH FE1	0.006898401	0.006687195	5.87E-06
1983	3138814	9	VCPIP1	5.66E-05	0.007953518	1.54E-06
2063	3139046	2	ARFGEF1	0.000629941	0.007275746	6.32E-06
984	3139077	4	ARFGEF1	0.001852254	0.008893133	6.29E-06

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119	3139107	9	ARFGEF1	6.61E-08	0.033566027	3.81E-05
1079	3139108	9	ARFGEF1	1.18E-05	0.015040305	6.57E-06
265	3139551	5	SULF1	2.63E-05	0.021575493	2.25E-05
1236	3139562	7	SULF1	2.88E-05	0.01622433	1.99E-05
1337	3139607	9	SLCO5A1	0.01612054	0.00752669	5.63E-06
186	3139630	9	SLCO5A1	0.000367918	0.011111055	1.14E-05
1706	3139726	2	NCOA2	3.46E-05	0.009051694	5.98E-06
1822	3139788	9	NCOA2	1.08E-05	0.008651908	6.79E-06
820	3139840	4	NCOA2	6.21E-05	0.016208818	1.23E-05
256	3139841	4	NCOA2	1.77E-05	0.014482929	1.28E-05
1585	3139843	3	NCOA2	0.004639335	0.007233204	3.77E-06
1969	3139907	2	TRAM1	6.51E-05	0.008461955	5.00E-06
1944	3139925	9	TRAM1	0.002671169	0.007740888	7.55E-06
2001	3139926	9	TRAM1	1.31E-05	0.008848099	5.28E-06
447	3140775	2	UBE2W	0.001052466	0.017989974	1.81E-05
1526	3140795	4	UBE2W	0.005613406	0.009006123	6.57E-06
1830	3141853	4	MRPS28	0.003636318	0.00677358	3.50E-06
1663	3141865	2	TPD52	0.000637737	0.011384196	1.16E-05
1959	3141883	9	TPD52	4.84E-05	0.007772796	7.02E-06
1920	3141894	4	TPD52	0.000961152	0.007445917	4.49E-06
638	3142136	2	ZNF704	0.025498894	0.012518258	1.63E-05
1838	3142146	2	ZNF704	6.13E-05	0.006851634	5.15E-06
1460	3142170	2	ZNF704	0.000357766	0.009437061	6.74E-06
716	3142182	9	ZNF704	0.002612225	0.011108751	5.96E-06
1022	3143340	4	FAM82B	5.59E-05	0.01435305	9.55E-06
325	3143470	4	CNGB3	2.71E-05	0.017979346	2.25E-05
1584	3143922	4	RP11-37B2.1	3.87E-05	0.007023854	5.38E-06
2036	3144771	9	RBM12B	0.001852254	0.007359204	5.57E-06
1393	3145100	6		0.011131791	0.007702451	5.96E-06
777	3145187	5	C8orf38	0.000468776	0.009489743	4.21E-06
204	3145592	9	MTERFD1	2.95E-06	0.023094718	1.57E-05
454	3145807	2	TSPYL5	0.001925692	0.011918826	6.99E-06
102	3145886	5	MTDH	3.41E-05	0.03013173	3.38E-05
130	3145888	7	MTDH	2.84E-05	0.027153197	2.73E-05
149	3145890	7	MTDH	0.000101783	0.020297858	2.08E-05
1811	3145981	2	HRSP12	4.53E-05	0.009789405	6.30E-06
1722	3146344	4	RP11-410L14.2	2.08E-05	0.008830151	5.09E-06
1738	3146442	9	COX6C	0.000110135	0.010882068	6.38E-06
1244	3146529	9	FBXO43	0.003390971	0.011341658	9.24E-06
1215	3146566	2	RNF19A	0.000148906	0.010441166	1.00E-05
362	3146569	9	RNF19A	0.00010545	0.021503954	1.92E-05
2019	3146577	9	RNF19A	0.000885779	0.006579631	3.15E-06
478	3146675	2	ANKRD46	3.35E-05	0.019301227	1.64E-05
1945	3146698	3	ANKRD46	0.006376399	0.006617936	4.09E-06
639	3146904	6		1.45E-05	0.020079582	2.10E-05
1126	3147061	2	ZNF706	0.002671169	0.009051504	4.43E-06
1323	3147137	5	GRHL2	5.83E-05	0.007715533	3.80E-06

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1821	3147154	5	GRHL2	0.000250234	0.006855299	2.16E-06
1778	3147288	2	RRM2B	0.000691504	0.00650489	5.26E-06
1312	3147309	4	RRM2B	0.002509145	0.006651229	1.26E-06
133	3147316	8	KB-431C1.4	1.68E-05	0.02024896	1.20E-05
95	3147353	9	UBR5	1.40E-05	0.029777153	2.71E-05
1951	3147355	9	UBR5	4.38E-05	0.008446581	2.80E-06
57	3147362	9	UBR5	3.58E-05	0.042037758	5.21E-05
693	3147378	4	UBR5	1.55E-05	0.014008764	7.94E-06
1937	3147416	4	UBR5	1.05E-05	0.007966735	3.42E-06
571	3147425	9	UBR5	0.000504026	0.016922667	1.60E-05
90	3147426	9	UBR5	3.18E-06	0.031095942	3.24E-05
175	3147427	9	UBR5	5.48E-06	0.025869674	1.89E-05
1992	3147613	9	AZIN1	0.000264928	0.007282996	6.61E-06
1750	3147677	7	ATP6V1C1	0.02057934	0.007555028	6.58E-06
793	3148720	9	TMEM74	0.007582294	0.010273983	6.22E-06
1693	3148899	4	SYBU	4.91E-05	0.006815011	2.32E-06
1953	3149782	3	EIF3H	4.99E-05	0.006519112	2.50E-06
1978	3149863	9	RAD21	3.09E-05	0.010598225	6.84E-06
2069	3149864	9	RAD21	0.000142286	0.006938925	5.44E-06
96	3149866	9	RAD21	5.86E-05	0.032413212	3.97E-05
566	3150181	4	EXT1	0.007337714	0.011167989	7.79E-06
200	3150260	1		0.005450518	0.009774559	1.03E-05
1535	3150537	4	RP11-4K16.2	1.59E-05	0.012061709	7.83E-06
1956	3150666	9	TAF2	2.80E-05	0.007484629	3.54E-06
221	3151057	1		1.19E-06	0.016560632	1.54E-05
1758	3151568	4	ATAD2	0.000958852	0.006912877	2.11E-06
1148	3151571	9	ATAD2	2.14E-06	0.01249276	1.03E-05
1530	3151576	9	ATAD2	0.021434136	0.007350183	7.31E-06
1931	3151874	1		0.00010865	0.008065512	2.97E-06
1544	3151880	1		0.000986793	0.007880354	4.89E-06
1541	3151942	5	RNF139	0.000302186	0.01206077	9.57E-06
725	3151996	9	MTSS1	2.75E-05	0.013085414	6.46E-06
2011	3152016	9	MTSS1	0.001921299	0.006534607	2.49E-06
1564	3152038	4	MTSS1	0.002514771	0.006782061	3.70E-06
1573	3152088	9	MTSS1	0.038614454	0.007217448	6.83E-06
1877	3152261	9	KIAA0196	0.000153344	0.008032919	2.64E-06
1042	3152298	5	NSMCE2	0.031432454	0.00702341	4.58E-06
496	3152302	5	NSMCE2	0.000199853	0.012091556	8.22E-06
1029	3152910	8	PVT1	0.025177619	0.00679582	3.81E-06
874	3152978	8	PVT1	0.018228464	0.007100921	6.91E-06
157	3153331	2	FAM49B	8.86E-07	0.031562714	3.42E-05
481	3153338	4	FAM49B	0.000449203	0.008890397	4.61E-06
1474	3153369	2	FAM49B	0.016492423	0.010486458	6.26E-06
542	3153531	9	ASAP1	0.000611594	0.015079374	1.42E-05
791	3153572	4	ASAP1	0.000563692	0.013482063	1.03E-05
1713	3153586	4	ASAP1	0.003557945	0.007447963	1.39E-06
517	3155043	5	KHDRBS3	0.000319739	0.010247178	7.03E-06
1984	3155047	5	KHDRBS3	0.000192114	0.006667798	4.43E-06

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1262	3155524	4	FAM135B	0.00247563	0.006678738	3.02E-06
490	3156104	4	TRAPPC9	0.000636171	0.01047113	6.63E-06
1914	3156387	9	PTK2	0.036159066	0.008448362	6.92E-06
958	3156443	4	PTK2	0.000130223	0.010054359	6.30E-06
388	3158057	5	SPATC1	5.48E-05	0.018175287	1.55E-05
745	3158586	9	SLC39A4	0.000385118	0.010205084	4.89E-06
1461	3158698	2	CYHR1	0.004759574	0.010659625	7.27E-06
239	3158768	2	AC084125.3;RECQL4	0.000189098	0.02025759	2.25E-05
332	3160259	8	KIAA0020	0.009010521	0.018759046	1.78E-05
205	3162826	5	NFIB	0.000288505	0.016847222	1.49E-05
1420	3163197	7	PSIP1	7.08E-06	0.009902923	2.89E-06
2041	3164984	4	MTAP;CDK N2B-AS1	0.01575619	0.006644381	4.63E-06
644	3165859	9	TEK	0.001040005	0.011526316	8.47E-06
1214	3168684	4	RP11-220I1.1	0.008902214	0.008733067	7.44E-06
876	3173552	6		0.001890803	0.008001967	7.79E-06
886	3173564	4	PGM5	0.001187787	0.007799223	4.99E-06
1281	3173991	4	FAM189A2	0.022116149	0.007416716	3.04E-06
1349	3174918	3	RP11-549A6.1	0.007322669	0.00657993	4.06E-06
524	3175377	9	PCSK5	0.015107347	0.00744564	4.09E-06
1864	3179420	4	CENPP	8.56E-06	0.008122664	4.87E-06
1878	3180308	6		7.16E-05	0.006665582	1.89E-06
878	3180982	2	HABP4	0.000525832	0.014120969	1.08E-05
1598	3183013	4	NIPSNAP3 B	0.027405312	0.006936068	3.26E-06
953	3184500	2	PALM2;PALM2-AKAP2;AKAP2	0.001852254	0.008987807	5.92E-06
1871	3184589	2	PALM2-AKAP2;AKAP2	0.000408197	0.009970306	8.46E-06
413	3184813	5	LPAR1	0.002868156	0.010363738	7.70E-06
1922	3184980	2	DNAJC25;DNAJC25-GNG10;GNG10	1.35E-05	0.009724691	6.25E-06
969	3187623	9	CEP110	0.041709394	0.008605407	4.58E-06
1741	3187835	1		2.54E-05	0.007378865	4.73E-06
1429	3188396	3	RABGAP1	0.000570716	0.006841685	6.73E-06
315	3188421	5	STRBP	0.000850201	0.01607902	1.45E-05
712	3188741	4	NEK6	0.000100405	0.010689095	8.10E-06
534	3189377	9	PBX3	0.006232171	0.00879012	7.47E-06
989	3190108	3	RP11-228B15.4	0.005040635	0.006714995	6.12E-06
405	3191266	5	FNBP1	0.023538302	0.014455398	1.63E-05
1151	3193448	1		0.011131791	0.009354179	9.05E-06

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399	3196844	2	RFX3	0.002978182	0.009216545	4.49E-06
2047	3203380	6		6.62E-06	0.006812633	5.06E-06
698	3203820	3	UBAP2	0.002817689	0.016552722	1.81E-05
1386	3204770	9	TLN1	0.035351019	0.008277517	1.13E-05
167	3204782	9	TLN1	0.023971749	0.016308237	1.76E-05
429	3205204	4	RNF38	4.84E-05	0.013951133	8.09E-06
245	3205740	2	SHB	0.002743526	0.0122041	1.11E-05
1054	3208576	8	PIP5K1B	0.003024609	0.006720951	4.71E-06
1241	3210613	4	PRUNE2	0.007218138	0.007096218	4.96E-06
259	3212839	7	PHBP7	4.89E-05	0.017439809	1.18E-05
2048	3214846	2	ASPN	0.00021566	0.007049369	3.82E-06
1938	3214862	9	ASPN	6.07E-06	0.006832329	4.54E-06
1023	3215437	5	PTPDC1	0.027851225	0.007438226	1.37E-06
1504	3219170	5	RAD23B	0.001095886	0.007364521	2.15E-06
250	3220872	2	SUSD1	0.009531934	0.011306015	8.69E-06
1917	3221558	2	CDC26	0.00011347	0.006784429	2.24E-06
1172	3222049	5	ATP6V1G1	0.00160961	0.011736719	9.61E-06
1561	3223277	1		0.0264846	0.006904205	5.16E-06
656	3223629	9	FBXW2	4.32E-05	0.012411705	9.21E-06
1833	3224597	9	STRBP	0.000148906	0.008661385	4.92E-06
1784	3224614	2	STRBP	6.13E-05	0.007866017	4.57E-06
195	3224665	4	DENND1A	0.00877735	0.010604445	9.39E-06
595	3224695	4	DENND1A	8.71E-06	0.010346806	7.49E-06
64	3224721	4	DENND1A	0.000204101	0.030370222	2.60E-05
2055	3225482	9	MAPKAP1	0.000357766	0.007505626	3.36E-06
683	3225668	1		0.015967819	0.007726744	4.05E-06
662	3226162	9	ST6GALNA C6	0.008619147	0.010328204	3.83E-06
235	3226361	2	PTGES2	0.000332253	0.01043034	6.55E-06
1724	3227198	9	FNBP1	0.019499011	0.006759972	5.10E-06
972	3227514	1		0.029020011	0.007096129	5.16E-06
1145	3227768	4	RAPGEF1	0.003105755	0.009440612	3.72E-06
663	3228519	4	RALGDS	0.012305161	0.00667609	3.78E-06
1401	3228844	4	SARDH	0.001647248	0.007061409	3.19E-06
1195	3229079	9	BRD3	0.004454644	0.010177232	9.25E-06
1325	3232245	1		0.000288505	0.006672542	4.35E-06
383	3233209	4	NET1	0.000490372	0.014676043	1.08E-05
1600	3233220	6		0.005404779	0.011800116	1.59E-05
1768	3233333	4	C10orf18	0.002531721	0.006884206	4.90E-06
1219	3233453	9	FBXO18	0.003781407	0.008479823	5.51E-06
1791	3233454	4	FBXO18	0.006245159	0.006903255	5.00E-06
678	3237409	9	CACNB2	0.006442959	0.009187946	6.21E-06
1367	3238738	9	ARMC3	0.001558259	0.006682987	5.03E-06
219	3238928	1		0.048552369	0.014256799	5.10E-06
1264	3242177	5	PARD3	0.044114238	0.007389697	4.64E-06
609	3243790	1		0.004987466	0.009165899	5.63E-06
706	3245925	4	WDFY4	0.000481864	0.010700417	3.49E-06
983	3245926	4	WDFY4	0.001628328	0.007000229	3.48E-06
1301	3246011	3	RP11-	0.003133247	0.007051697	5.62E-06

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			507P23.3			
906	3247960	1		0.008412239	0.007147019	6.25E-06
846	3248990	1		0.001314314	0.007676396	8.78E-06
1981	3250089	9	DDX21	0.007597824	0.007720875	6.45E-06
1728	3251407	2	DDIT4	0.002001825	0.00976791	1.12E-05
1895	3251899	2	SEC24C	0.009861702	0.006512534	6.03E-06
1279	3253147	5	KCNMA1	3.45E-05	0.008675527	4.82E-06
1817	3256044	9	LDB3	0.002743526	0.00667878	5.31E-06
2065	3257391	9	KIF20B	0.00010865	0.006823504	5.42E-06
1211	3258781	9	TMEM20	0.006523669	0.007770014	6.38E-06
949	3258921	4	HELLS	0.003504013	0.009449736	7.75E-06
272	3258959	2	HELLS;RP1 1-119K6.6	9.61E-05	0.020646723	1.09E-05
1666	3260203	1		0.014792007	0.007368352	7.25E-06
1616	3260608	6		0.000117217	0.009690655	4.08E-06
790	3260609	2	SCD;AL139 819.1	0.000153753	0.01256466	6.16E-06
1827	3261067	9	TLX1	0.000620704	0.007366558	7.93E-06
1319	3261680	9	NFKB2	0.00620627	0.007045917	5.59E-06
1087	3262195	7	USMG5	1.18E-05	0.011314813	4.65E-06
1308	3262201	9	PDCD11	0.003266926	0.008070873	4.26E-06
714	3263441	1		0.000273283	0.011872655	6.77E-06
1994	3263816	9	SMC3	2.66E-05	0.00676427	4.02E-06
2066	3263824	9	SMC3	0.000146929	0.007441363	6.30E-06
297	3265208	9	TDRD1	0.011264381	0.012192501	1.62E-05
2080	3266824	7	C10orf46	1.60E-05	0.006900786	2.85E-06
1340	3268609	9	ACADSB	0.00453157	0.007532844	4.87E-06
2072	3268687	6		0.000408197	0.006896832	5.98E-06
549	3270603	1		0.001587412	0.010264099	7.78E-06
1608	3270778	1		3.33E-05	0.00732201	4.59E-06
2033	3271719	9	PPP2R2D	1.57E-05	0.006604433	4.28E-06
752	3271859	9	JAKMIP3	0.007566793	0.009133827	1.66E-06
1317	3273492	2	LARP4B	0.000163031	0.008013788	4.84E-06
1831	3273589	7	IDI2-AS1	0.045476068	0.007550062	5.19E-06
1134	3273785	9	ADARB2	0.041003559	0.007815956	5.26E-06
1465	3274485	1		0.015428709	0.009244812	1.10E-05
1682	3276980	1		0.024015481	0.007284984	4.12E-06
1116	3277460	1		8.36E-05	0.007347087	4.76E-06
468	3280630	2	NEBL	0.00349637	0.007402615	5.15E-06
1232	3281132	4	PIP4K2A	0.000412342	0.008458062	6.54E-07
1093	3281422	7	KIAA1217	0.000272577	0.00776324	3.40E-06
926	3281437	1		0.00877735	0.010032762	6.39E-06
2017	3282231	9	YME1L1	4.43E-06	0.006735584	3.51E-06
1970	3283993	2	KIF5B	0.000784922	0.007852174	3.97E-06
1820	3283995	2	KIF5B	5.94E-05	0.008521667	5.86E-06
1621	3284211	9	ITGB1	1.31E-05	0.01042158	1.05E-05
1648	3284305	9	NRPI	0.006429597	0.011846842	1.13E-05
1762	3284324	9	NRPI	6.28E-06	0.008755286	5.38E-06
110	3289058	9	TIMM23	2.58E-05	0.018804344	1.65E-05

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673	3289482	2	A1CF	0.04509417	0.00800955	7.31E-06
1757	3290799	9	CCDC6	1.95E-05	0.009372214	7.09E-06
1999	3290817	9	CCDC6	6.16E-06	0.007807125	6.97E-06
920	3292591	2	PBLD	0.000264928	0.00979269	6.69E-06
1732	3292766	4	SLC25A16	0.000164774	0.006568018	1.05E-06
193	3293219	9	TYSND1	0.037563396	0.014951746	2.22E-05
1413	3293539	2	PCBD1	0.00020953	0.012455715	5.62E-06
905	3293767	2	PSAP	6.74E-06	0.014379385	1.31E-05
1194	3294169	2	P4HA1	3.50E-05	0.008388232	5.05E-06
884	3294190	9	P4HA1	0.000151311	0.012053017	9.96E-06
1767	3294612	9	USP54	0.002152759	0.006663838	5.69E-06
1582	3295307	7	SAMD8	7.16E-05	0.008856807	3.98E-06
1502	3295752	5	C10orf11	0.003914828	0.008579333	3.46E-06
177	3296861	8	ZMIZ1	0.000850201	0.017485614	1.56E-05
1341	3297947	5	NRG3	0.014905986	0.006924227	7.73E-06
392	3298214	1		0.000954268	0.009857566	6.07E-06
839	3298765	9	WAPAL	0.023239041	0.007619348	8.04E-06
1856	3301491	4	SORBS1	0.020694087	0.006725547	5.24E-06
2018	3301871	9	TM9SF3	0.000358678	0.010592662	6.42E-06
602	3301947	9	PIK3AP1	0.040239182	0.009496091	6.27E-06
407	3302849	2	HPS1	0.000475873	0.011980131	1.06E-05
1940	3303460	6		0.000933891	0.006757907	5.65E-06
108	3303461	6		6.24E-07	0.02895629	2.30E-05
597	3304424	4	ACTR1A	0.004749446	0.008965086	8.27E-06
125	3305521	5	SORCS3	0.002324635	0.016042517	9.05E-06
1575	3306389	8	ADD3	0.04624829	0.00697595	7.55E-06
2038	3306415	8	ADD3	0.000862602	0.00712363	4.55E-06
667	3306762	4	BBIP1	0.001080374	0.007248372	4.19E-06
759	3307486	1		0.005416181	0.008128483	3.67E-06
69	3308170	1		1.05E-05	0.037128898	3.04E-05
131	3309791	9	MCMBP	1.23E-05	0.026269881	2.80E-05
843	3309876	1		0.024015481	0.008960388	5.20E-06
1350	3310831	1		0.000802243	0.006806731	3.45E-06
53	3312502	9	MKI67	4.20E-06	0.060126952	7.13E-05
1716	3312508	9	MKI67	0.004061321	0.007855735	5.63E-06
48	3312516	9	MKI67	1.16E-08	0.076247204	0.00010532
307	3312517	9	MKI67	3.35E-06	0.022040564	1.75E-05
322	3312528	9	MKI67	0.000276123	0.011794395	7.23E-06
1192	3316579	3	RP13- 870H17.3	4.46E-05	0.007081656	4.90E-06
456	3317399	4	KCNQ1	0.006154763	0.010928167	7.03E-06
2082	3318045	2	RRM1	0.0001169	0.00747355	4.30E-06
77	3319231	5	CYB5R2	0.007337714	0.028273098	4.44E-05
731	3320141	2	ADM	0.000194662	0.007431738	2.85E-06
1849	3321317	2	FAR1	0.00094743	0.00693472	6.58E-06
1231	3322467	4	OTOG	0.00877735	0.007993957	8.02E-06
343	3326990	4	LDLRAD3	0.008566991	0.009998305	9.60E-06
346	3329359	9	MDK	0.000111942	0.019795601	2.22E-05
1760	3329848	7	CELF1	0.005225318	0.007191149	5.91E-06

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1309	3329913	2	NDUFS3	0.02450122	0.006617557	5.96E-06
236	3331846	3	GLYATL1	0.002099724	NA	NA
279	3331847	9	GLYATL1	0.003636318	0.013971736	1.16E-05
488	3331877	6		0.040446406	0.011268756	7.13E-06
1593	3331913	2	FAM111B	1.74E-05	0.009308618	5.06E-06
1489	3332111	3	AP000442.1	0.011353565	0.006946152	3.91E-06
168	3332705	2	CD6	6.62E-06	0.024221205	2.00E-05
654	3332877	4	DAK;RP11-286N22.3	4.74E-05	0.008544328	3.23E-06
2009	3333236	6		0.000457168	0.009182253	5.87E-06
632	3333240	7	FADS1	9.43E-05	0.014572418	1.23E-05
1972	3333487	2	ASRGL1	0.001265835	0.006689375	4.50E-06
187	3333728	2	SLC3A2	3.46E-05	0.02137965	1.84E-05
1679	3334217	5	MACROD1	0.000438052	0.007910565	3.13E-06
1889	3334931	2	MRPL49	9.46E-05	0.00816066	3.93E-06
1744	3335187	3	MALAT1	2.12E-05	0.006711132	4.85E-06
2032	3335239	3	NEAT1	0.000296032	0.007557915	4.73E-06
1640	3335344	4	SSSCA1;FA M89B	4.05E-05	0.007034036	6.22E-06
283	3335444	9	PCNXL3	0.009647164	0.012006177	6.85E-06
2035	3335570	1		7.50E-05	0.006753736	2.46E-06
2078	3335635	6		5.37E-05	0.007183286	6.76E-06
1624	3335777	9	SART1	0.000133772	0.007144549	4.34E-06
1764	3336464	5	RBM4B	0.00271316	0.009071279	8.82E-06
669	3336491	4	C11orf80	0.000122396	0.008642129	3.62E-06
183	3336510	4	C11orf80	2.67E-05	0.021906893	2.50E-05
248	3336517	4	C11orf80	0.000611594	0.017681213	2.55E-05
473	3336722	4	KDM2A	6.62E-06	0.015914087	1.54E-05
1202	3336851	2	ADRBK1	0.005203274	0.007814406	2.76E-06
1009	3337064	9	CARNS1	0.005348101	0.00726324	2.93E-06
1226	3338508	9	PPFIA1	0.043299568	0.006560039	7.24E-06
873	3339046	6		0.003098917	0.007737485	4.79E-06
815	3339248	9	RNF121	0.000337386	0.006535423	3.33E-06
1599	3339697	5	FCHSD2	0.000228432	0.006761278	4.54E-06
794	3339872	2	ARHGEF17	0.034740252	0.006686228	3.12E-06
92	3340087	4	PAAF1	2.10E-06	0.030966825	3.44E-05
1268	3340183	9	PPME1	0.002514771	0.007854617	3.58E-06
111	3340387	4	SPCS2	6.42E-05	0.027924152	2.54E-05
758	3340768	4	UVRAG	0.006855816	0.012411782	9.19E-06
1787	3340811	4	UVRAG	7.63E-05	0.008875995	5.36E-06
1574	3341181	9	CAPN5	0.000496534	0.009800362	6.74E-06
1294	3341189	2	CAPN5	0.009436864	0.015307962	1.31E-05
1857	3341212	4	CAPN5	2.80E-05	0.006838246	3.07E-06
617	3345158	4	PIWIL4	0.006687861	0.010150886	6.44E-06
2013	3345244	9	AMOTL1	0.001689593	0.006558789	5.28E-06
1534	3345406	3	SRSF8	0.010080553	0.006911306	3.45E-06
82	3345480	4	RP11-712B9.2	1.81E-08	0.037576248	4.27E-05
1964	3345483	4	RP11-712B9.2	1.05E-05	0.010257851	4.80E-06

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959	3345752	5	MAML2	0.001302035	0.007036077	1.13E-06
1290	3346491	4	YAP1	0.000368854	0.008650836	4.28E-06
401	3348854	2	DLAT	0.025452776	0.011991906	1.01E-05
349	3349774	4	ZBTB16	0.017855277	0.010864318	6.21E-06
1915	3350647	6		0.00028925	0.007811622	4.02E-06
1210	3350849	6		0.038283273	0.007497037	3.10E-06
1024	3351637	4	UBE4A	0.0001886	0.013100313	9.63E-06
1511	3351903	3	C2CD2L	0.000138152	0.006533071	1.21E-06
83	3352135	7	MFRP;AP0 03396.1;C1 QTNF5	1.97E-07	0.031497369	3.10E-05
992	3352315	1		0.000142286	0.008881946	2.42E-06
1718	3354757	6		0.00050277	0.011369051	1.04E-05
482	3355746	4	FLI1	0.018924879	0.010554527	5.80E-06
554	3355776	9	FLI1	0.010763744	0.009348037	6.32E-06
1467	3355783	9	FLI1	0.000731459	0.00654568	4.54E-06
971	3357277	4	RP11- 700F16.3	0.000111639	0.013337881	8.58E-06
516	3357313	3	ACAD8	2.85E-06	0.014817037	1.29E-05
1814	3357388	2	GLB1L3	0.00180613	0.008448428	5.79E-06
1086	3359084	3	H19	2.99E-05	0.013078059	7.77E-06
528	3359501	3	NAP1L4	9.46E-05	0.014646313	1.11E-05
842	3360089	3	OR55B1P	0.006167603	0.010590966	7.17E-06
1780	3360163	1		0.002951948	0.006890013	7.80E-06
430	3360381	9	OR52A1	0.000412342	0.009965671	3.84E-06
611	3360900	1		0.000148906	0.009149581	4.11E-06
230	3361622	5	TUB	0.000457168	0.017258817	1.23E-05
1111	3361630	2	RIC3	0.010262873	0.007017678	4.08E-06
91	3361748	1		0.001151831	0.018169375	1.73E-05
122	3362161	2	NRIP3	0.007173756	0.01771743	1.45E-05
649	3364941	9	ABCC8	0.001173835	0.011380468	9.19E-06
242	3365534	2	SPTY2D1	0.000208981	0.010413807	5.07E-06
1417	3366734	5	LUZP2	1.89E-05	0.00914798	8.89E-06
457	3369637	5	LDLRAD3	0.00020038	0.010462696	7.14E-06
425	3370248	6		0.008126841	0.0128565	1.47E-05
887	3370702	3	RP11- 384E5.2	0.0007279	0.006946076	3.70E-06
735	3370815	6		1.54E-06	0.013058631	1.33E-05
505	3371611	9	AMBRA1	0.004360173	0.007627791	2.57E-06
434	3372262	2	CELF1	1.18E-05	0.011210977	4.51E-06
427	3374540	4	RP11- 142C4.6	0.000148906	0.011207134	8.37E-06
634	3374581	4	RP11- 142C4.6	0.013588933	0.010869048	7.19E-06
1090	3375092	2	SLC15A3	0.000358678	0.009310369	7.70E-06
160	3375544	2	FADS1	2.85E-06	0.023685263	2.93E-05
1749	3375547	2	FADS1	0.002152759	0.00685867	2.62E-06
2074	3375864	2	MTA2	0.000461778	0.007768584	5.69E-06
1462	3376302	3	SNHG1	0.000579253	0.008432056	3.82E-06
495	3376751	9	MACROD1	0.001974641	0.014172182	1.21E-05

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126	3377027	9	PYGM	0.00035324	0.01933795	1.59E-05
1872	3377621	7	NEAT1	2.62E-05	0.008003529	4.98E-06
442	3377625	7	NEAT1	1.99E-06	0.018865238	1.97E-05
85	3377627	7	NEAT1	0.002805201	0.030343821	4.67E-05
1514	3377629	7	NEAT1	8.09E-05	0.009289123	3.99E-06
826	3377633	7	NEAT1	3.71E-06	0.014719313	1.56E-05
1790	3377635	7	NEAT1	0.000417578	0.006683799	4.19E-06
1329	3377637	7	NEAT1	9.78E-06	0.011817785	1.08E-05
1646	3377641	7	NEAT1	0.000129873	0.010091592	9.01E-06
1590	3377659	7	MALAT1	3.52E-06	0.009063684	6.47E-06
760	3378515	3	RP11-658F2.3	1.71E-05	0.011361311	9.90E-06
894	3379539	8	PPP6R3	3.93E-05	0.011032576	9.23E-06
580	3379566	5	PPP6R3	0.006456347	0.011482378	1.43E-05
395	3379697	1		0.001001048	0.01468751	1.53E-05
290	3379916	1		0.002099724	0.00944787	5.89E-06
1596	3380081	2	ORAOV1	0.000102061	0.006925599	2.34E-06
68	3380323	4	AP000487.6	0.000119134	0.03317763	4.24E-05
1302	3380437	4	SHANK2;A P001271.5	0.000378341	0.006723456	4.70E-06
217	3381818	2	UCP2	5.30E-06	0.022035487	2.14E-05
997	3383041	2	RSF1	0.039284329	0.007912749	2.11E-06
2007	3386740	6		8.24E-05	0.00957179	7.94E-06
864	3387255	2	SESN3	1.75E-06	0.014386509	9.69E-06
1050	3389367	9	CASP1	0.005684569	0.008445273	5.16E-06
150	3391911	8	ZBTB16	0.005359393	0.01781851	1.50E-05
1501	3392582	8	AP000797.3	0.00060261	0.007086086	3.38E-06
880	3393305	8	CEP164	2.01E-05	0.008257925	3.45E-06
1627	3394419	9	THY1	0.00080419	0.007549673	4.89E-06
1415	3397595	2	ETS1	0.042209752	0.009491646	1.11E-05
387	3398942	5	NTM	0.005672651	0.012339334	1.02E-05
319	3399568	4	NCAPD3	0.005792861	0.010903697	8.85E-06
921	3399590	9	NCAPD3	0.001666372	0.010212699	6.68E-06
1171	3399602	9	NCAPD3	0.001095886	0.008878141	5.06E-06
1498	3401999	4	KCNA1;RP 3-377H17.1	0.030501101	0.00691775	4.16E-06
431	3402336	3	CD9	0.000194662	0.013880303	7.94E-06
172	3402965	2	RPL13P5;L RRC23	0.000284076	0.015901702	1.90E-05
596	3404455	4	CLEC2D	0.004749446	0.013360002	1.34E-05
501	3405316	4	LOH12CR1	0.008884278	0.011806462	6.56E-06
237	3405606	2	GPRC5A	2.19E-05	0.020038313	1.78E-05
802	3406085	9	ATF7IP	6.62E-06	0.012402676	9.80E-06
1245	3406450	8	EPS8	0.043006584	0.007576256	5.93E-06
590	3408793	7	BHLHE41	0.000617654	0.008783782	3.44E-06
855	3409273	4	PPFIBP1	0.030178237	0.007142121	5.18E-06
727	3411330	9	LRRK2	0.008812862	0.008052347	5.33E-06
1021	3412547	6		0.001543869	0.010561963	5.59E-06
988	3413308	2	TMEM106C	3.81E-05	0.017324674	1.55E-05
2027	3413826	9	TUBA1C	1.38E-05	0.009416863	6.80E-06

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607	3414084	4	RP11-133N21.2	0.01309721	0.011337491	8.76E-06
116	3415017	9	SCN8A	0.005756556	0.027631416	3.31E-05
922	3415243	4	NR4A1	0.004790078	0.00857609	7.18E-06
919	3415245	2	NR4A1	0.036791598	0.008209899	4.22E-06
511	3415254	9	NR4A1	0.000146537	0.010832039	6.60E-06
1131	3415256	4	NR4A1	0.00421284	0.007543327	3.79E-06
486	3415264	4	NR4A1	4.81E-05	0.013327502	1.58E-05
1619	3416307	4	AC012531.1;HOXC6	1.54E-05	0.007942225	4.10E-06
1692	3418367	9	ARHGEF25	0.000310049	0.007360913	4.16E-06
1520	3419870	9	TBK1	0.000261519	0.008358427	3.52E-06
888	3419989	2	TBC1D30	0.000436951	0.0081496	9.21E-06
1662	3420374	4	HMGA2	0.00051035	0.007578034	4.27E-06
985	3421317	3	MDM2	0.000444711	0.013007873	1.22E-05
710	3421365	7	CPM	0.002052564	0.011613351	1.08E-05
613	3421368	7	CPM	0.017687915	0.008834732	8.09E-06
1331	3422466	9	TRHDE	0.003428273	0.007617866	7.06E-06
112	3426457	1		0.015458225	0.015811581	9.94E-06
923	3426889	1		0.000389041	0.006909422	6.41E-07
1072	3426905	1		0.002836517	0.006581456	3.08E-06
783	3427524	4	RMST	0.001689593	0.009272144	3.88E-06
273	3428610	9	MYBPC1	0.000102061	0.019860486	1.97E-05
121	3428624	9	MYBPC1	0.000138152	0.025277716	2.87E-05
50	3428626	9	MYBPC1	2.14E-07	0.070836699	9.91E-05
421	3428630	9	MYBPC1	5.22E-05	0.012819523	8.90E-06
509	3428631	9	MYBPC1	0.001171064	0.014030378	9.24E-06
1901	3428639	9	MYBPC1	4.76E-05	0.007216313	4.05E-06
1440	3428640	9	MYBPC1	0.011488537	0.007374662	2.66E-06
100	3428641	9	MYBPC1	7.61E-05	0.029360211	3.68E-05
498	3428643	9	MYBPC1	0.000547163	0.014490122	1.22E-05
1495	3428647	9	MYBPC1	0.005280805	0.008215244	3.64E-06
459	3428651	9	MYBPC1	0.000664925	0.015153353	1.32E-05
355	3428655	9	MYBPC1	0.000579253	0.015754106	1.72E-05
202	3428665	9	MYBPC1	0.003339377	0.020953424	2.12E-05
970	3429167	9	STAB2	0.045322973	0.007449469	6.24E-06
1104	3430743	2	FICD	0.00551979	0.008200033	5.38E-06
1313	3431048	9	ACACB	0.001298982	0.006971522	3.36E-06
1840	3431135	6		0.00023941	0.010844051	5.73E-06
224	3432191	5	TMEM116	0.003302969	0.016329795	1.27E-05
899	3433246	1		0.01286993	0.008994596	7.50E-06
627	3433531	1		0.000170561	0.015569748	1.05E-05
1825	3435731	8	PITPNM2	0.001877871	0.007175536	7.03E-06
1654	3436139	9	DNAH10	0.009627872	0.006840034	6.70E-06
271	3439162	2	P2RX2	0.000425014	0.015078838	9.02E-06
334	3439330	1		0.001332936	0.008574024	3.79E-06
1199	3440108	4	CACNA2D4	0.000318921	0.007172134	3.04E-06
1555	3440184	3	RP5-1096D14.2	0.012305161	0.008586488	8.01E-06

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81	3440944	6		0.00180613	0.026417303	3.09E-05
1169	3442059	9	CHD4	0.000570716	0.009351255	8.12E-06
1114	3448127	8	SSPN	0.011131791	0.007354431	5.34E-06
379	3448205	4	ITPR2	0.003147077	0.013261635	1.12E-05
107	3449806	9	DENND5B	0.001925692	0.017715275	1.68E-05
626	3452385	1		9.00E-05	0.009592315	3.89E-06
1819	3452862	7	TMEM106C	0.000319739	0.008530675	3.81E-06
993	3453875	6		1.50E-05	0.017942905	1.38E-05
2014	3454060	4	FMNL3	0.000984436	0.006743349	4.61E-06
1908	3454236	9	RACGAP1	0.000165652	0.008552193	5.05E-06
1892	3454247	9	RACGAP1	0.007337714	0.008243299	4.88E-06
1591	3454249	9	RACGAP1	0.004304377	0.011117041	8.17E-06
1689	3454251	4	RACGAP1	0.00076237	0.010799497	7.64E-06
1797	3454663	2	CSRNP2	0.026058101	0.006874234	7.89E-06
377	3455102	5	NR4A1	0.000708617	0.013562634	1.16E-05
994	3455119	1		0.034019558	0.007187542	3.36E-06
1468	3455129	1		0.024191116	0.006911722	5.22E-06
389	3455389	1		0.014179003	0.010346618	6.20E-06
1436	3456343	1		0.013379902	0.008092246	3.37E-06
1977	3457204	2	SARNP	0.00011347	0.007559171	2.29E-06
924	3457859	9	TIMELESS	7.10E-06	0.011459793	8.55E-06
1048	3461394	4	CPM	0.000172838	0.008653889	5.97E-06
1453	3462104	2	ZFC3H1	0.002887295	0.008108262	5.31E-06
2025	3462988	9	OSBPL8	0.000563692	0.006950222	6.46E-06
2040	3462998	9	OSBPL8	0.015311147	0.007361228	4.24E-06
749	3465245	1		0.000552621	0.006681797	3.72E-06
589	3468064	5	MYBPC1	0.000873066	0.012604826	6.35E-06
192	3468071	5	MYBPC1	4.98E-05	0.018785189	1.97E-05
419	3468104	2	GNPTAB	0.000655208	0.015552323	1.51E-05
1936	3468105	9	GNPTAB	1.12E-05	0.007894032	6.49E-06
1843	3468121	9	GNPTAB	9.90E-05	0.010165009	7.09E-06
618	3468122	9	GNPTAB	6.95E-06	0.011918652	7.85E-06
1921	3468125	9	GNPTAB	0.00020953	0.007617622	6.03E-06
579	3468126	9	GNPTAB	3.85E-06	0.014435127	1.06E-05
1015	3469401	1		0.003557945	0.008173686	6.81E-06
1076	3469805	5	RIC8B	0.025498894	0.009095378	6.52E-06
73	3470260	4	SART3	0.01575619	0.021496487	3.64E-05
189	3470958	4	TRPV4	3.23E-05	0.013118108	8.19E-06
543	3471602	4	ATXN2	0.001339198	0.012656175	7.58E-06
1136	3471633	9	ATXN2	0.004061321	0.008273273	6.75E-06
1028	3471764	5	MAPKAPK 5	0.001705241	0.007376753	3.38E-06
687	3472790	4	TBX3	0.002880903	0.008033958	6.27E-06
556	3473370	5	RNFT2	2.29E-06	0.012094303	1.14E-05
1518	3473458	9	TESC	4.91E-05	0.007870352	2.49E-06
47	3473622	9	KSR2	4.80E-07	0.065638753	8.65E-05
311	3473690	9	KSR2	0.000664925	0.013784107	1.32E-05
557	3473708	1		0.046404092	0.008792034	8.42E-06
452	3474192	9	CIT	0.001852254	0.018785154	1.33E-05

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1441	3474713	3	AC069214.1	0.002217036	0.008112305	5.71E-06
364	3474739	4	AC069214.1	0.01809196	0.007620008	2.94E-06
72	3475900	2	ABCB9;RP11-197N18.4	0.000368854	0.025422078	2.24E-05
931	3475981	2	PITPNM2	0.00592778	0.007346276	5.13E-06
267	3476305	5	ATP6V0A2	0.040585072	0.011750362	7.01E-06
347	3476911	8	TMEM132B	0.001093286	0.011585565	1.01E-05
366	3481437	4	TNFRSF19	0.001095886	0.012314567	6.70E-06
798	3481446	4	TNFRSF19	4.12E-05	0.011301562	3.72E-06
945	3481456	9	TNFRSF19	2.53E-05	0.009087909	6.89E-06
1490	3482106	6		0.009647164	0.006783836	4.16E-06
879	3484182	1		0.00587839	0.006816243	3.47E-06
1905	3485957	7	POSTN	0.000905174	0.006832111	4.62E-06
1492	3487850	4	SERP2	1.77E-05	0.009359098	3.89E-06
1469	3492720	5	PCDH9	4.68E-05	0.008721471	8.18E-06
551	3494195	4	LMO7	0.000367918	0.009638476	5.96E-06
1976	3494747	1		0.001265835	0.006763304	1.25E-06
1887	3497274	3	DNAJC3;RP11-10E18.2	3.19E-05	0.009677701	3.97E-06
87	3497377	4	HS6ST3	7.38E-05	0.027178585	2.76E-05
1082	3497692	2	RAP2A	0.008795089	0.007805083	5.00E-06
1882	3499158	9	ITGBL1	9.32E-06	0.009461541	7.12E-06
1993	3499164	9	ITGBL1	1.12E-05	0.007754542	4.29E-06
521	3499195	9	ITGBL1	0.002350957	0.016058117	1.81E-05
1459	3499197	2	ITGBL1	0.000475873	0.009854259	3.60E-06
1261	3499203	4	RP11-397O8.4	0.013881148	0.006923667	2.88E-06
163	3499919	1		3.23E-06	0.02130792	1.70E-05
1020	3499954	1		0.046404092	0.008798959	6.33E-06
158	3501363	9	COL4A2	0.011533849	0.018104363	2.52E-05
1408	3502223	9	ATP11A	0.002212029	0.006829333	5.34E-06
913	3506074	6		3.18E-06	0.016317744	1.38E-05
1569	3507963	2	KATNAL1	0.015967819	0.010333182	8.40E-06
1929	3510072	9	POSTN	0.002951948	0.010200983	8.04E-06
1568	3510096	9	POSTN	6.49E-06	0.008737308	7.60E-06
1777	3510099	9	POSTN	0.000751323	0.008159496	4.59E-06
1332	3510150	4	TRPC4	1.22E-05	0.008844699	3.51E-06
519	3511633	5	TNFSF11	0.000595218	0.012364946	6.51E-06
463	3512032	4	ENOX1	0.033960096	0.007007489	5.15E-06
1613	3513641	1		7.74E-06	0.009463004	4.74E-06
1123	3517038	1		0.012450296	0.006662742	3.90E-06
786	3517930	4	KLF12	0.00059375	0.008249929	2.90E-06
191	3521655	5	HS6ST3	0.031823166	0.016338133	2.03E-05
428	3523505	7	ITGBL1;RP11-397O8.4	0.006310467	0.014771455	1.26E-05
1471	3524517	1		0.006129156	0.007067951	6.11E-06
1570	3525217	1		0.000794501	0.008468936	4.75E-06
799	3525316	2	COL4A1	0.00034347	0.014745656	1.67E-05

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282	3525317	2	COL4A1	6.70E-07	0.02435786	2.92E-05
120	3525318	2	COL4A1	9.07E-07	0.029855107	3.15E-05
1702	3525346	9	COL4A1	0.017555038	0.007078593	7.84E-06
1572	3525347	9	COL4A1	0.002951948	0.008002999	5.89E-06
2002	3525376	9	COL4A1	0.00140662	0.008255721	7.04E-06
1138	3527440	9	PARP2	0.000417578	0.009113313	4.95E-06
1135	3527672	2	RNASE6	0.000909538	0.012047043	1.21E-05
1084	3527990	6		3.69E-05	0.017132822	1.65E-05
999	3528533	4	AE000661.2 8	0.005348101	0.006614602	5.62E-06
1208	3529692	4	RNF31	0.035044469	0.007877746	3.05E-06
980	3529894	4	LTB4R	0.045706551	0.007831994	3.62E-06
1869	3531193	4	COCH	0.030285522	0.006501799	5.60E-06
642	3532227	7	SNX6	4.38E-05	0.010058046	7.03E-06
1850	3533039	1		0.002187152	0.007213692	5.97E-06
327	3535010	1		0.002182207	0.013765072	9.95E-06
1102	3536724	4	LGALS3;A L139316.1	0.011264381	0.007864671	3.99E-06
1162	3537877	7	C14orf37	0.039082309	0.007619176	4.86E-06
766	3540148	2	HSPA2	0.014622507	0.007412038	3.46E-06
927	3540771	1		3.85E-06	0.010896849	6.72E-06
1630	3542092	2	SLC39A9	8.12E-06	0.010138736	5.76E-06
2031	3542093	2	SLC39A9	1.71E-05	0.008672443	6.82E-06
1583	3543814	8	C14orf43	0.047987301	0.006772589	5.92E-06
1412	3544272	9	YLP1M1	0.003965967	0.006997005	4.50E-06
750	3544533	4	FOS	0.004800285	0.008329058	7.28E-06
181	3544721	4	TTLL5	0.008619147	0.018014742	1.83E-05
2075	3545532	6		0.003188906	0.007127484	3.35E-06
1376	3546925	4	FLRT2	0.013721065	0.007711219	4.82E-06
1105	3549156	5	ITPK1	0.00247563	0.007281351	2.35E-06
298	3549159	5	ITPK1	0.000122396	0.011814315	4.49E-06
410	3550007	7	CLMN	0.024191116	0.007528968	1.46E-06
1182	3550126	1		0.019902689	0.006509539	3.04E-06
1307	3550432	9	PAPOLA	0.002543079	0.008731933	6.43E-06
1152	3550451	2	PAPOLA	1.66E-05	0.015015134	8.97E-06
620	3551602	4	EVL	0.001526056	0.010602987	6.67E-06
1243	3552386	1		0.000731459	0.00793614	3.48E-06
515	3553052	4	WDR20	8.57E-07	0.018753834	1.95E-05
1912	3553727	9	MARK3	0.00041969	0.007515649	5.85E-06
134	3553758	2	MARK3	0.000265615	0.022135548	2.26E-05
166	3553838	9	C14orf153; RP11- 73M18.2;A L139300.1	9.17E-05	0.018661694	2.19E-05
1681	3554544	7	CDCA4	0.001054975	0.010173309	7.36E-06
1287	3554623	2	PACS2	0.009193693	0.006617289	5.66E-06
1932	3554841	2	CRIP2	9.17E-05	0.007654287	3.52E-06
351	3556347	9	SUPT16H	1.29E-06	0.02158001	2.25E-05
568	3557916	9	TM9SF1;RP 11-468E2.1	6.72E-05	0.01010437	7.35E-06

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243	3557960	4	TM9SF1;RP11-468E2.1;AL096870.1;C HMP4A	0.000191608	0.016704805	1.10E-05
960	3560007	8	AKAP6	0.009417954	0.009483293	6.50E-06
637	3560223	5	NPAS3	0.006389661	0.009451309	7.54E-06
937	3560438	2	EGLN3	0.001877871	0.009109859	6.72E-06
1960	3561338	9	MBIP	0.001877871	0.00715965	1.92E-06
220	3561724	1		5.66E-05	0.02169482	2.54E-05
124	3561767	8	CTD-2058B24.1	0.000146145	0.013827712	1.59E-05
2008	3562015	9	TRAPPC6B	9.90E-05	0.007586042	5.75E-06
1774	3562032	6		1.42E-05	0.009799503	2.98E-06
1589	3562055	5	CTAGE5	0.03244577	0.007294252	6.93E-06
1543	3562729	9	FKBP3	0.000158328	0.012294869	8.50E-06
1394	3565024	9	DDHD1	0.014650635	0.00854315	5.67E-06
144	3565594	9	WDHD1	3.92E-06	0.029618511	3.19E-05
1320	3565810	1		0.039419514	0.006735638	4.08E-06
1803	3565943	1		0.009323916	0.006563171	4.38E-06
898	3566362	1		2.38E-06	0.01176147	1.04E-05
733	3570152	7	SLC39A9	8.43E-06	0.017920236	1.69E-05
676	3570164	1		0.000742232	0.007613108	4.51E-06
729	3571068	4	DPF3	0.003217076	0.00842338	9.64E-06
1293	3571928	2	NPC2	1.42E-05	0.014150671	1.02E-05
1756	3572106	5	YLPM1	0.001143679	0.008301208	6.42E-06
1167	3572167	2	RPS6KL1	0.011762838	0.006906632	3.92E-06
978	3575711	1		0.046404092	0.008276865	7.07E-06
755	3576107	1		0.000579253	0.007787951	3.24E-06
1275	3576442	2	CCDC88C	0.000894351	0.006736738	4.90E-06
1580	3576864	4	TRIP11	0.002951948	0.006832084	5.69E-06
1828	3577079	2	LGMN	2.67E-05	0.009777743	6.33E-06
941	3577685	2	SERPINA9	0.047746878	0.009206783	9.30E-06
1818	3579555	9	WARS	0.004639335	0.006620066	5.48E-06
1710	3580123	6		0.000674778	0.008482164	4.73E-06
514	3580457	8	TRAF3	0.002404431	0.00816779	3.06E-06
208	3581157	9	AKT1	9.72E-07	0.017106987	1.81E-05
1846	3584519	4	SNRPN;SNORD108	0.005336831	0.006734131	8.20E-06
1894	3587051	6		0.000483071	0.006821996	2.71E-06
1853	3588099	2	TMEM85	0.000587911	0.00910916	9.28E-06
493	3590406	9	NUSAP1	5.35E-07	0.018890824	2.23E-05
1073	3590434	9	RTF1	0.002874523	0.01035944	1.38E-05
1272	3591735	4	WDR76	6.02E-05	0.010372129	5.14E-06
141	3594180	1		0.020503158	0.019553702	2.88E-05
471	3595274	3	AC016525.1	0.006090929	0.010571349	1.04E-05
1106	3595459	9	GCOM1;AC090651.1;G RINL1A	0.000540412	0.00953604	8.67E-06
2083	3596392	6		0.00360478	0.006859042	4.20E-06

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1128	3597927	4	SNX22	0.005236373	0.009698804	7.02E-06
771	3598798	9	SMAD6	0.0079631	0.013209737	1.11E-05
950	3598809	4	SMAD6	7.32E-06	0.013268823	5.23E-06
658	3600663	5	PKM2	6.11E-05	0.006935628	3.53E-06
691	3600707	7	CELF6	0.005817181	0.008292249	4.96E-06
1265	3602135	9	C15orf39	0.000348767	0.008774654	6.01E-06
300	3602538	9	FBXO22	0.000271873	0.010327297	4.23E-06
2024	3605298	6		0.000516748	0.007297057	4.19E-06
531	3606365	9	AKAP13	0.011925564	0.014048446	1.47E-05
789	3606371	4	AKAP13	0.000562297	0.008998609	4.54E-06
689	3606507	8	KLHL25	0.001268815	0.008091689	3.62E-06
1567	3607176	1		0.03244577	0.006957836	8.45E-06
1962	3607875	4	ZNF710	0.002887295	0.00824511	3.71E-06
1122	3608291	9	CRTC3	7.71E-05	0.006560753	1.92E-06
1051	3608380	1		1.52E-05	0.014679978	1.04E-05
171	3608542	9	AC068831.1 ;UNC45A	0.024147101	0.014062914	1.15E-05
308	3609034	1		0.00809385	0.008166242	6.40E-06
1409	3610580	1		0.018126	0.008073478	3.34E-06
461	3610850	4	IGF1R	0.000115329	0.011783696	6.89E-06
1480	3613297	5	CYFIP1	0.000338249	0.007322941	3.43E-06
433	3615994	9	MTMR10	0.032789863	0.012174049	9.65E-06
472	3619652	9	DNAJC17	0.020051318	0.007567661	2.83E-06
1335	3619970	5	TYRO3	0.024995647	0.007527987	5.58E-06
408	3622256	9	DUOXA1	0.001111606	0.013225165	8.44E-06
1685	3623298	6		0.001201893	0.008487235	4.64E-06
1201	3624150	9	DMXL2	0.000113163	0.008737126	3.53E-06
603	3625209	1		0.000909538	0.009521061	6.84E-06
1355	3626324	9	ALDH1A2	0.006363163	0.006967527	5.37E-06
329	3626947	4	MYO1E	0.000165213	0.012396011	8.86E-06
1297	3629800	5	SLC24A1	0.00241526	0.007108487	5.22E-06
1649	3630807	4	ITGA11	0.043006584	0.007070619	3.20E-06
800	3631715	5	THSD4	0.002350957	0.008460984	5.38E-06
1881	3631998	9	PKM2	1.77E-05	0.008339926	7.97E-06
1707	3633108	7	CSK	0.00010346	0.006803205	1.99E-06
281	3633239	2	RPP25	0.004749446	0.011305801	9.00E-06
701	3633468	2	PTPN9	8.24E-05	0.01263796	9.39E-06
342	3633789	1		0.031655198	0.010760075	1.29E-05
1785	3635006	1		0.007013144	0.007732766	5.49E-06
506	3636219	1		0.000487927	0.011230631	7.37E-06
530	3636467	3	C15orf40	3.19E-05	0.012446094	6.72E-06
320	3636521	5	TM6SF1	7.74E-05	0.013827425	7.45E-06
1927	3636531	6		4.46E-05	0.006967514	2.72E-06
1955	3636534	9	AC024270.1	6.74E-06	0.008661601	7.98E-06
522	3639047	9	PRC1	0.000293755	0.021280706	1.95E-05
123	3639054	9	PRC1	0.010100664	0.025201383	3.68E-05
1923	3642244	4	PCSK6	0.00076237	0.006698636	2.18E-06
1486	3642303	9	PCSK6	0.011398396	0.006563752	4.97E-06
935	3644067	4	MAPK8IP3	0.014482591	0.006785207	4.01E-06

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1142	3644647	9	E4F1	0.012043037	0.009620411	8.84E-06
70	3645319	1		0.009940781	0.024791572	2.57E-05
306	3645476	2	KREMEN2	0.025777155	0.009389094	7.22E-06
341	3645652	1		0.022361426	0.016525847	1.46E-05
552	3646448	9	UBN1	0.000120755	0.016425661	1.61E-05
1680	3646802	4	RBFOX1	0.023281585	0.00682901	3.36E-06
1155	3649263	4	BFAR	5.94E-05	0.009644722	5.18E-06
2068	3650718	7	ARL6IP1	0.000408197	0.008537529	6.97E-06
491	3650720	7	ARL6IP1	0.000397001	0.017872044	1.57E-05
2049	3650850	2	ITPRIPL2	0.000563692	0.006746985	5.10E-06
1336	3656881	1		3.67E-05	0.007684195	2.95E-06
1276	3658909	5	SHCBP1	0.000483071	0.010824915	7.91E-06
1482	3659265	1		0.024995647	0.006856396	6.12E-06
1133	3659928	1		0.000457168	0.012434795	1.58E-05
1205	3662100	4	MT3	0.000203565	0.007595331	6.87E-07
705	3663746	1		0.040170313	0.010447485	7.74E-06
252	3665867	4	NUTF2	0.002293409	0.012252329	1.43E-05
1120	3667448	5	HYDIN	0.00051035	0.007418618	2.56E-06
1623	3667557	1		0.003781407	0.006522573	2.35E-06
159	3668335	1		0.006389661	0.018264551	2.24E-05
1177	3668759	5	FA2H	0.000165213	0.009488445	5.47E-06
1924	3671836	7	COTL1	2.19E-05	0.009188463	4.39E-06
46	3672375	1		9.32E-08	0.068293918	8.00E-05
153	3672652	9	FOXC2	0.010386073	0.014074276	1.46E-05
1506	3672970	2	JPH3	0.004521888	0.007853911	3.53E-06
78	3673319	6		0.011533849	0.025675715	3.77E-05
917	3675052	3	AXIN1	0.046795588	0.007478615	2.60E-06
406	3676115	2	NME3	0.000203565	0.011839051	7.55E-06
1315	3676601	4	CASKIN1	0.001168298	0.007803578	3.44E-06
299	3677917	2	ADCY9	4.55E-05	0.019273282	1.32E-05
974	3680474	7	SNN	0.001283816	0.008241237	7.03E-06
2015	3680538	9	ZC3H7A	6.62E-06	0.008429013	5.75E-06
1898	3681408	4	PARN	0.000110135	0.006617645	5.82E-06
1242	3685365	1		0.030555206	0.008234817	1.17E-05
1091	3685648	9	ARHGAP17	0.005416181	0.009485484	9.37E-06
1253	3685774	1		0.01415169	0.011101576	7.70E-06
1422	3685788	1		0.002080741	0.008376621	5.65E-06
331	3686345	4	XPO6	0.002571681	0.009429634	1.25E-06
1324	3686981	8	RUNDC2C	0.000751323	0.010013645	2.70E-06
1100	3687400	1		2.99E-05	0.009900281	3.48E-06
435	3687775	5	ZNF48	0.009627872	0.010281022	1.32E-05
244	3687981	3	C16orf93	3.74E-05	0.012026254	7.79E-06
207	3688068	3	CTF2P	3.07E-06	0.018860953	1.72E-05
2044	3689930	2	VPS35	0.000319739	0.007906231	5.17E-06
1660	3689951	9	VPS35	6.38E-06	0.00913068	8.04E-06
1364	3690072	5	GPT2	0.001561876	0.010540522	6.53E-06
1989	3694664	2	CDH11	0.00207602	0.008120261	7.70E-06
1250	3694693	9	CDH11	4.31E-05	0.008270469	7.34E-06
928	3695096	9	AC132186.2	0.008619147	0.011094646	1.11E-05

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1423	3695391	7	CES4A	0.0038061	0.006571526	5.20E-06
586	3696274	1		0.001689593	0.009564298	6.29E-06
1247	3699295	5	ZNRF1	0.000873066	0.008486615	4.04E-06
1690	3699734	9	ADAT1	0.000712087	0.006749163	2.51E-06
685	3699913	1		1.41E-06	0.013152305	1.07E-05
295	3703547	1		0.000221959	0.015552834	1.72E-05
1715	3704487	4	FAM38A	0.022526284	0.006567648	3.55E-06
640	3704496	1		0.012720391	0.009555613	5.12E-06
1995	3707126	2	ARRB2	0.001628328	0.006507684	4.21E-06
1610	3708862	9	CD68	0.00071035	0.010528404	1.33E-05
541	3711048	6		0.000996275	0.008838354	6.05E-06
1493	3711987	9	PIGL	0.013379902	0.008147589	7.37E-06
1454	3717119	9	NF1	2.26E-05	0.009405833	4.88E-06
561	3718005	5	ACCN1	0.033664154	0.007046032	5.45E-06
1112	3718104	5	ACCN1	9.72E-05	0.009822418	5.26E-06
665	3718684	4	AP2B1	0.000742232	0.008729072	4.07E-06
1314	3719372	9	AATF	0.000461778	0.007820628	6.09E-06
847	3719860	1		0.019317948	0.007902788	4.29E-06
1387	3719966	4	PSMB3	0.000155402	0.008781182	3.21E-06
762	3720001	2	LASP1	0.000136311	0.015837481	1.21E-05
59	3720978	5	TOP2A	1.72E-06	0.047128916	4.13E-05
44	3720986	5	TOP2A	6.24E-07	0.096289981	0.000148557
1557	3720988	5	TOP2A	0.000229029	0.01011419	8.45E-06
51	3720992	5	TOP2A	2.14E-08	0.063588907	7.19E-05
877	3721456	9	FKBP10	7.36E-05	0.009162263	6.97E-06
1512	3726146	1		2.49E-05	0.007143351	5.19E-06
1941	3726285	7	COL1A1	2.08E-05	0.010400379	8.52E-06
397	3726287	5	COL1A1	5.98E-06	0.021237214	1.83E-05
833	3726289	5	COL1A1	2.23E-05	0.016265471	1.43E-05
688	3726379	9	EME1	0.000474683	0.00860949	8.22E-06
1144	3728550	1		0.000862602	0.011254423	5.64E-06
615	3728572	1		0.00028925	0.009148564	6.03E-06
1305	3728970	9	PRR11	2.42E-05	0.013089929	7.09E-06
99	3729181	9	CLTC	6.11E-08	0.03000392	3.82E-05
1068	3730880	5	STRADA	3.45E-05	0.008004559	4.75E-06
1655	3731133	1		0.001204733	0.00994669	1.39E-05
1674	3731143	6		8.09E-05	0.006870019	2.73E-06
1254	3732739	6		6.32E-05	0.009173345	7.10E-06
569	3734860	9	KIAA0195	0.000712087	0.010991321	6.89E-06
1110	3735014	2	MYO15B	0.000203031	0.0074482	3.26E-06
773	3735349	9	C17orf106	0.012043037	0.009510322	6.39E-06
844	3735745	1		0.004194748	0.007501714	3.37E-06
938	3737994	4	RP13-766D20.2	6.62E-06	0.009372956	8.59E-06
940	3740825	3	MIR132	0.006674036	0.007581392	2.03E-06
225	3742407	4	PFN1	0.000909538	0.012421274	8.61E-06
223	3743231	1		4.19E-05	0.015381152	5.64E-06
599	3743292	3	MIR497HG	0.001098492	0.009759828	2.84E-06
1788	3745080	1		0.000126422	0.008893994	4.71E-06

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870	3748225	9	FLII	0.025777155	0.009133044	8.23E-06
608	3748820	7	RNF112	0.001543869	0.008899881	2.96E-06
344	3749011	2	ULK2	1.52E-05	0.014790792	6.57E-06
1388	3749061	9	ULK2	0.000310049	0.006756375	6.24E-06
1539	3749447	6		0.003773209	0.006991449	6.66E-06
1391	3750115	1		0.013302264	0.009082288	7.05E-06
2004	3750596	7	TMEM97	4.69E-05	0.010906008	6.44E-06
1071	3751077	4	C17orf63	0.000645623	0.008905467	3.00E-06
1286	3752264	9	EVI2B	2.99E-05	0.012105796	6.65E-06
1519	3752342	5	RAB11FIP4	0.00401772	0.006569666	5.67E-07
66	3755466	5	LASP1	4.43E-06	0.036109365	2.80E-05
65	3755470	6		4.15E-06	0.044191091	5.33E-05
1013	3755539	9	PLXDC1	0.001501439	0.007489452	3.31E-06
1863	3755856	2	IKZF3	0.00016045	0.007545863	2.81E-06
1375	3756091	1		0.006167603	0.00745408	3.32E-06
268	3756105	7	MSL1	1.95E-05	0.015854797	1.50E-05
151	3756196	9	TOP2A	1.82E-06	0.028647724	1.83E-05
1556	3756197	9	TOP2A	0.008619147	0.0072412	3.45E-06
54	3756230	9	TOP2A	8.74E-07	0.053313237	6.05E-05
1206	3756234	2	TOP2A	0.003465953	0.010570624	8.22E-06
63	3756235	2	TOP2A	3.94E-06	0.043172399	4.70E-05
1434	3757088	9	KRT15	0.008028233	0.00842142	6.04E-06
1203	3757100	9	KRT15	0.000689814	0.009508723	9.53E-06
577	3757573	4	ZNF385C	0.00240984	0.008390462	4.38E-06
196	3757645	9	KAT2A	7.65E-07	0.020633913	2.39E-05
214	3757985	9	PSMC3IP	0.006245159	0.015412602	1.46E-05
464	3758792	2	TMEM101	0.002047903	0.009826673	1.07E-05
1998	3758943	2	ATXN7L3	0.002162534	0.007948762	3.78E-06
1178	3759233	4	GPATCH8	1.09E-05	0.00904615	6.29E-06
872	3760226	1		0.032732293	0.00868694	6.90E-06
178	3761459	2	HOXB7;HOXB9	0.023754148	0.016255176	1.79E-05
75	3762200	2	COL1A1	0.000102339	0.036754271	4.77E-05
438	3762201	2	COL1A1	1.26E-06	0.020791186	1.69E-05
67	3762203	2	COL1A1	0.000124394	0.038573659	5.08E-05
76	3762204	9	COL1A1	2.02E-05	0.035560963	4.53E-05
1456	3762206	9	COL1A1	4.39E-05	0.014078043	9.84E-06
324	3762208	9	COL1A1	1.53E-05	0.025263426	1.75E-05
746	3762212	9	COL1A1	3.75E-05	0.013541175	1.07E-05
80	3762238	9	COL1A1	5.32E-05	0.027867168	2.65E-05
1224	3762257	9	COL1A1	0.000120755	0.013331704	1.14E-05
686	3762258	9	COL1A1	9.74E-05	0.014149484	1.04E-05
703	3762268	9	COL1A1	5.08E-05	0.018236337	1.83E-05
2076	3764125	2	SRSF1	0.000628393	0.007325163	4.57E-06
1510	3764880	5	CLTC	0.000142667	0.010897302	5.34E-06
1369	3765948	5	TLK2	5.31E-05	0.009267069	3.83E-06
1240	3766160	1		0.000402054	0.009821347	6.87E-06
1283	3766835	6		0.015281883	0.006658549	3.35E-06
860	3767533	1		0.000306094	0.006888914	3.37E-06

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326	3768673	9	ABCA8	0.00659163	0.009956292	7.56E-06
458	3769694	4	AC007639.1	0.000547163	0.009413625	2.22E-06
1170	3770533	4	C17orf28	0.000357766	0.007280479	2.38E-06
197	3770609	9	HN1	0.002303775	0.025254776	2.62E-05
142	3770610	9	HN1	2.02E-05	0.021529189	1.88E-05
402	3770724	2	SLC25A19	0.000228432	0.011282404	7.12E-06
1014	3772175	5	AFMID	0.007582294	0.006943524	2.20E-06
1763	3772574	4	CYTH1	2.15E-05	0.008498103	5.41E-06
1351	3772842	9	RBFOX3	0.004426107	0.006930221	4.64E-06
1862	3775861	9	TYMS	0.003071703	0.008057605	3.71E-06
1836	3775862	9	TYMS	1.38E-05	0.009694831	4.94E-06
1754	3778001	9	KIAA0802	2.89E-05	0.0068828	3.01E-06
1295	3778069	9	KIAA0802	0.000663296	0.006827917	4.67E-06
1540	3779045	5	FAM38B	8.85E-06	0.006719053	3.01E-06
661	3782809	1		0.020732462	0.009591141	7.34E-06
1061	3784854	4	FHOD3	0.00010346	0.009326947	5.90E-06
1665	3784859	9	FHOD3	0.024456705	0.007280018	5.36E-06
1740	3787462	8	ZBTB7C	0.002951948	0.006763521	4.40E-07
986	3787934	6		0.001628328	0.015025107	1.58E-05
314	3788043	1		0.001628328	0.011501453	7.55E-06
1431	3788695	9	DCC	0.000802243	0.007942304	3.46E-06
709	3790001	4	NEDD4L	0.002951948	0.008086304	6.49E-06
623	3791665	5	BCL2	0.007675909	0.012378141	1.24E-05
260	3794316	5	ZNF516	1.63E-06	0.017848595	1.49E-05
1612	3794399	1		5.57E-05	0.007036327	2.08E-06
918	3795871	5	TYMS	0.000413384	0.009451406	6.52E-06
666	3797622	9	LAMA1	0.000132342	0.012744611	1.54E-05
1521	3798448	7	RAB31	0.017588173	0.01180553	1.14E-05
274	3799752	8	C18orf1	0.022526284	0.009387286	1.00E-05
1844	3799904	5	C18orf1	1.71E-05	0.007083003	2.77E-06
1664	3800020	5	C18orf1	0.035784134	0.007025272	3.31E-06
1187	3802335	1		0.002298587	0.007497642	2.52E-06
659	3803102	1		9.78E-06	0.012949041	5.98E-06
657	3803770	5	DTNA	0.000264928	0.011040738	1.09E-05
1159	3809977	5	NEDD4L	0.004913892	0.007014438	2.16E-06
527	3810024	5	NEDD4L	0.000151311	0.010952355	3.58E-06
462	3810026	5	NEDD4L	0.002571681	0.008565392	4.49E-06
328	3810046	5	NEDD4L	0.001233477	0.010318079	8.37E-06
249	3810508	1		0.024859934	0.011192154	5.93E-06
538	3811176	7	KIAA1468	6.13E-05	0.012391652	3.65E-06
1296	3816342	9	SF3A2	0.002514771	0.007861145	2.79E-06
605	3816537	5	AC092068.1 ;GNG7	0.001119544	0.006736721	5.36E-06
1513	3817492	7	SH3GL1	0.002242228	0.008418791	8.39E-06
1494	3818943	9	PNPLA6	4.60E-05	0.008429176	4.84E-06
1088	3819244	5	AC010336.1	0.0207709	0.007382382	4.02E-06
1614	3819416	4	LASS4	0.002453518	0.006618225	3.85E-06
1515	3819433	9	LASS4	0.000142286	0.007928883	2.25E-06
631	3820347	9	PPAN-	0.004924341	0.010289222	1.17E-05

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			P2RY11;PP AN			
1677	3821267	2	CNN1	0.00140662	0.006567496	3.81E-06
681	3822704	9	CD97	2.74E-06	0.013772023	4.92E-06
1328	3823462	4	AC020911.1	0.032789863	0.006785128	6.44E-06
998	3824263	7	PLVAP	2.71E-05	0.013076432	1.57E-05
1874	3824338	2	FAM125A	0.000385118	0.007035401	1.60E-06
1292	3824841	2	PIK3R2	0.005543059	0.007453355	8.22E-06
652	3824886	2	IFI30	4.52E-06	0.017855887	1.23E-05
1377	3824888	2	IFI30	0.003684101	0.010168272	1.04E-05
1671	3825896	5	PBX4	4.91E-05	0.007660187	5.03E-06
1200	3829042	7	ANKRD27	0.000124059	0.007752649	1.97E-06
1212	3830127	5	AC020907.3	0.03121109	0.010360673	8.51E-06
896	3832101	8	ZNF573	0.009627872	0.008241546	3.50E-06
393	3832546	9	RYR1	1.49E-05	0.011890674	7.57E-06
1876	3832722	2	ACTN4	3.39E-05	0.008349225	6.66E-06
968	3832980	4	ZFP36	0.004114217	0.010049579	4.54E-06
1284	3833496	7	BLVRB	0.03685538	0.006962699	6.88E-06
443	3833552	9	SPTBN4	0.005040635	0.011004892	3.37E-06
853	3834543	9	ARHGEF1	0.018924879	0.0080258	3.50E-06
1943	3835890	2	APOE	0.000524526	0.007074782	5.65E-06
1832	3837064	2	GRLF1	0.002080741	0.007511443	5.05E-06
600	3837159	9	SAE1	0.004749446	0.010789705	3.01E-06
310	3837244	1		5.29E-05	0.013243168	9.18E-06
610	3837791	2	GRIN2D	0.001921299	0.009458325	6.40E-06
1271	3837819	1		0.030881616	0.00909433	3.40E-06
995	3840810	2	ZNF765	2.12E-05	0.009499038	5.84E-06
188	3841985	4	EPS8L1	0.007398176	0.018336943	1.47E-05
1352	3843632	1		0.012019459	0.006787939	6.05E-06
1789	3844578	4	SHC2	0.002420691	0.006584521	3.73E-06
852	3844980	9	SBNO2	0.009627872	0.008088964	6.05E-06
564	3847993	4	CD70	0.019681587	0.007379819	3.29E-07
1373	3850013	9	COL5A3	0.034258318	0.006866394	6.03E-06
1935	3850053	4	EIF3G	3.34E-05	0.006523882	3.13E-06
1641	3850436	9	KRI1	6.18E-06	0.009498748	5.51E-06
523	3850559	4	TMED1	0.001219026	0.011207839	1.11E-05
785	3851376	1		0.008812862	0.010323631	5.63E-06
1416	3851726	9	HOOK2	4.98E-05	0.008114691	5.42E-06
105	3852452	9	RFX1	0.000124394	0.017123737	1.54E-05
819	3852796	4	DNAJB1	0.002849134	0.00888026	4.00E-06
1933	3852890	9	EMR2	0.029699585	0.006995595	3.97E-06
483	3853114	2	NOTCH3	0.000126422	0.016671556	1.24E-05
1729	3853116	2	NOTCH3	0.003872676	0.007830713	5.66E-06
1282	3854920	2	LSM4	0.020465161	0.008117307	7.33E-06
1165	3855225	9	COMP	0.010785085	0.009827647	9.87E-06
562	3855231	9	COMP	0.000103742	0.016123279	1.50E-05
636	3855232	9	COMP	0.000674778	0.012020397	1.25E-05
1089	3855522	4	TMEM161 A	0.027951183	0.008592818	4.08E-06

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247	3856015	2	AC104523.1	8.64E-05	0.01488092	6.53E-06
808	3856288	6		0.002024742	0.010085361	9.23E-06
782	3857807	1		0.002293409	0.007008648	1.30E-06
1348	3857937	1		4.98E-05	0.008955614	5.35E-06
1095	3859962	7	C19orf55	2.42E-05	0.00991284	3.70E-06
2020	3860139	2	TYROBP	0.003716277	0.008084936	7.41E-06
1533	3861561	9	LGALS4	0.012305161	0.008083965	4.75E-06
1288	3862193	9	FCGBP	0.020351547	0.00902822	8.96E-06
1687	3865345	2	PPP1R13L	0.000579253	0.007965781	2.31E-06
956	3867149	4	LMTK3	4.32E-05	0.008497033	5.08E-06
1370	3867534	5	FTL	0.000617654	0.006556618	4.97E-06
1579	3867772	9	SLC6A16	0.0015655	0.007315823	5.70E-06
977	3868126	2	PNKP	0.001843787	0.007146769	4.84E-06
1714	3868195	9	IL4I1	0.041003559	0.007474114	2.69E-06
1067	3868892	3	KLK14	0.018331444	0.008434542	8.81E-06
1063	3868997	2	CLDN2	0.000998659	0.006686711	1.02E-06
648	3869569	6		0.005648885	0.007042573	6.92E-06
854	3869641	6		0.008706715	0.008642584	1.06E-05
981	3870896	2	CDC42EP5	0.001409908	0.012765074	9.25E-06
1795	3871283	9	PPP6R1	0.000982084	0.006611289	4.50E-06
1919	3872856	9	A1BG;ZNF497	0.000570716	0.007014539	5.81E-06
1967	3873181	2	TRIB3	9.59E-05	0.006721722	2.86E-06
400	3876447	5	JAG1	5.48E-06	0.017523697	1.48E-05
1934	3878250	6		0.002600581	0.007315515	4.90E-06
394	3879946	7	NCRNA00261	0.001670221	0.009304477	7.16E-06
1786	3880845	2	GINS1	0.000570716	0.007449206	4.29E-06
1322	3881457	9	TPX2	1.47E-05	0.011597387	5.87E-06
1223	3881458	9	TPX2	0.003181899	0.011954527	9.58E-06
165	3882316	1		2.10E-06	0.027157072	2.16E-05
1904	3884900	4	FAM83D	0.000483071	0.007216721	4.26E-06
1546	3886774	2	SEMG1	0.005890702	0.009568906	6.81E-06
1826	3887717	7	SULF2	0.006618995	0.007122866	2.39E-06
1668	3889268	4	RP4-723E3.1	0.004322902	0.006987245	4.02E-06
1070	3890589	2	RAE1	0.002811439	0.009946063	9.48E-06
1059	3890610	4	RBM38	0.033605237	0.007490625	3.98E-06
338	3891323	5	CTS2	1.03E-06	0.019701911	1.99E-05
1717	3893625	4	ZGPAT	0.004976894	0.007043225	5.36E-06
865	3894010	9	MYT1	0.031823166	0.007346013	6.25E-06
1092	3895779	4	RP11-119B16.2	0.000152935	0.007248562	4.58E-06
1277	3896023	2	PRNT	0.018126	0.007004643	4.38E-06
1078	3896401	4	GPCPD1	0.000192114	0.009048337	5.25E-06
1963	3899419	4	OVOL2	0.003024609	0.006721937	3.45E-06
1563	3899905	5	RIN2	8.88E-05	0.008535517	1.66E-06
305	3901183	5	GZF1	0.006537209	0.011649055	8.10E-06
1588	3901363	2	CST1	0.000435853	0.006853365	3.36E-06
2028	3902753	7	ASXL1	2.67E-05	0.006638061	3.60E-06

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2030	3903852	3	EDEM2;MT IP3	0.000532413	0.007106081	6.51E-06
1731	3904090	9	FER1L4;AL 389875.1	5.05E-05	0.007249279	5.01E-06
871	3904560	2	NDRG3	0.017888918	0.009731465	6.23E-06
901	3907235	2	SDC4	9.59E-05	0.014513443	9.93E-06
232	3908635	2	PREX1	0.000518037	0.014616305	1.08E-05
1083	3910198	5	TSHZ2	0.000637737	0.007642783	4.14E-06
2005	3910788	2	AURKA	0.002303775	0.008034016	6.32E-06
1776	3911737	5	GNAS	1.65E-05	0.006751443	4.63E-06
655	3911768	2	CTSZ	0.000126082	0.017035647	1.84E-05
715	3911769	9	CTSZ	8.58E-06	0.016324218	1.44E-05
769	3912527	5	CDH4	0.004061321	0.009439512	1.15E-05
892	3913561	4	DIDO1	0.001283816	0.008853705	3.51E-06
962	3913575	9	DIDO1	2.25E-05	0.010752142	1.01E-05
1542	3913577	4	DIDO1	0.002951948	0.00662747	1.65E-06
1804	3913713	2	YTHDF1	0.000722593	0.007517051	5.77E-06
1875	3917818	8	TIAM1	0.000272577	0.006979198	6.08E-06
1220	3918161	4	C21orf63	0.04726916	0.008466627	6.54E-06
1638	3918604	2	IFNAR1	0.000200907	0.007891488	3.40E-06
453	3919218	7	RCAN1	0.001643447	0.006886772	3.36E-06
1437	3920026	9	CHAF1B	0.000197761	0.007853932	4.30E-06
1044	3921056	1		0.003428273	0.009262185	5.83E-06
206	3922319	1		0.044564191	0.014070978	1.58E-05
1659	3923366	4	AGPAT3	0.000462937	0.006632473	3.14E-06
1766	3923935	7	SUMO3	0.000873066	0.009282175	6.64E-06
1396	3925911	8	C21orf34	0.044263782	0.007994666	5.95E-06
1772	3927606	1		0.002641545	0.006502541	3.15E-06
2073	3929666	2	TMEM50B; AP000300.3	0.000525832	0.007247528	2.97E-06
2006	3930023	5	MRPS6;AP 000318.2	0.000153753	0.007677257	6.18E-06
1207	3932278	3	HMGNI	0.00195225	0.009766647	7.74E-06
1398	3932707	4	DSCAM	0.014179003	0.007108958	2.59E-06
1673	3934672	9	SUMO3	0.007946892	0.009316771	7.21E-06
1298	3936105	7	CECR1	0.002629781	0.007226038	4.30E-06
670	3936779	3	DGCR5	0.006297356	0.007821734	5.43E-06
882	3937768	9	SNAP29	0.000509079	0.008037211	5.22E-06
1735	3937798	2	CRKL	0.000113778	0.011359599	1.07E-05
653	3939344	1		0.012377537	0.006710491	7.82E-06
1725	3939351	1		0.002481187	0.007874982	3.76E-06
1175	3939354	1		0.0264846	0.007324555	6.75E-06
707	3939358	1		0.00040614	0.010891317	8.74E-06
576	3939495	2	MMP11	0.001268815	0.014070716	9.94E-06
726	3940746	4	ADRBK2	0.003965967	0.011477167	1.06E-05
1069	3942014	9	RFPL1	4.10E-05	0.006778254	3.28E-06
233	3942071	9	NF2	1.05E-06	0.019752284	1.31E-05
1946	3942670	3	MTMR3;TU G1	0.000153344	0.009669208	9.02E-06
930	3943191	1		0.000468776	0.010341943	7.19E-06

SEQ ID NO	Aff P-ID	A	B	C	D	E
1451	3943222	2	YWHAH	0.00021566	0.013533518	1.67E-05
1252	3943311	3	RP1-90G24.10	8.73E-05	0.007568258	3.79E-06
1851	3944661	2	KCTD17	0.023538302	0.007190772	5.18E-06
359	3944775	1		0.000800301	0.009903548	4.44E-06
966	3944939	9	NOL12;TRI OBP	0.002849134	0.008944874	4.95E-06
601	3945520	2	APOBEC3A	8.40E-07	0.014765996	1.11E-05
356	3947246	9	SEPT3	0.004699102	0.013660068	1.15E-05
1428	3947350	6		0.000372622	0.006796499	3.83E-06
380	3948681	9	FBLN1	0.006969913	0.009183224	6.72E-06
101	3949198	9	GRAMD4	3.80E-05	0.021704647	1.73E-05
1075	3949566	1		0.000248937	0.007112984	2.14E-06
1751	3951205	6		0.000130223	0.007570276	4.56E-06
1603	3952519	9	DGCR14	0.015281883	0.008978517	1.28E-05
1899	3953861	7	CRKL	0.001504933	0.007170792	4.34E-06
1237	3954368	2	TOP3B	0.037498543	0.007241529	1.28E-06
2021	3956783	2	AP1B1	7.26E-05	0.007011229	3.96E-06
1700	3956841	1		0.00515944	0.006531317	3.49E-06
1235	3957024	9	ASCC2	0.015136312	0.007228397	3.59E-06
1339	3958074	7	YWHAH	6.02E-05	0.01323046	7.68E-06
885	3958175	9	SLC5A4	0.000873066	0.011103233	8.58E-06
422	3960135	9	CARD10	0.042066262	0.010130553	1.11E-05
289	3962111	7	SREBF2	0.000511623	0.017319589	1.35E-05
1113	3962470	6		0.003098917	0.007741604	4.41E-06
804	3962932	3	SCUBE1	0.000197241	0.010510173	4.00E-06
190	3965086	1		0.001219026	0.012512162	7.10E-06
103	3965316	2	BRD1	0.000113778	0.025245222	2.10E-05
287	3967872	1		0.01020177	0.012116789	1.25E-05
1473	3968670	8	MID1	0.006297356	0.007050988	1.23E-06
132	3968897	1		1.39E-05	0.017841672	1.98E-05
834	3971935	4	ZFX	0.040585072	0.007638758	3.94E-06
353	3973877	2	RP5-972B16.2;C YBB	8.88E-05	0.019334343	2.32E-05
1230	3974321	1		0.000103742	0.009748928	6.08E-06
748	3974602	3	RP11-169L17.2	7.28E-05	0.01454949	1.06E-05
1407	3975196	1		0.013854351	0.006635681	5.98E-06
1036	3976688	2	EBP	0.002157641	0.013487046	1.43E-05
1868	3977052	9	MAGIX	1.55E-05	0.00881525	6.38E-06
1505	3977310	4	CLCN5	0.023452452	0.007299256	7.03E-06
1303	3978435	2	TSR2	0.013747629	0.011233971	1.17E-05
2050	3979989	2	AR	0.00041969	0.007110435	2.61E-06
1347	3981275	4	NHSL2	0.001484083	0.007898961	8.62E-06
2029	3981889	1		0.001070147	0.007759571	5.95E-06
1389	3982824	4	SH3BGRL	0.000425014	0.007299911	3.97E-06
1996	3984554	9	CSTF2	0.01560657	0.006911261	6.59E-06
1379	3985558	2	NGFRAP1	1.89E-05	0.013521885	1.10E-05
863	3985758	9	PLP1	7.71E-05	0.010589385	6.72E-06

SEQ ID NO	Aff P-ID	A	B	C	D	E
890	3988764	4	RP5-113911.1	0.000246362	0.009691417	4.17E-06
737	3990584	9	UTP14A	0.000438052	0.011094743	5.44E-06
744	3990660	9	BCORL1	0.013881148	0.008292344	8.84E-06
588	3991537	5	GPC3	0.032963108	0.009771426	5.77E-06
946	3991667	4	PHF6	7.84E-05	0.009377693	4.41E-06
1987	3991676	9	PHF6	0.00022254	0.007170117	5.77E-06
1691	3991722	2	HPRT1	0.000125743	0.008299216	5.16E-06
1618	4001867	2	SH3KBP1	0.000155817	0.008800731	7.41E-06
390	4001936	9	SH3KBP1	2.85E-05	0.018253605	1.50E-05
1800	4004831	9	DYNLT3	3.14E-05	0.007135752	4.30E-06
263	4005034	5	RP5-972B16.2;TSPAN7	6.09E-05	0.014111468	1.22E-05
1402	4005967	4	CASK	0.001561876	0.007092994	4.08E-06
1761	4007481	5	EBP	0.000111942	0.009912108	5.20E-06
837	4007956	9	CACNA1F	0.030881616	0.008004059	3.19E-06
1736	4009008	6		6.02E-05	0.008854541	6.11E-06
212	4011774	2	SNX12	3.98E-05	0.017028115	1.23E-05
500	4011923	2	ZMYM3	0.004052566	0.008667107	6.03E-06
1399	4015424	1		6.21E-05	0.007349564	1.18E-06
1103	4019335	9	RP13-347D8.6;RP13-347D8.5	0.000982084	0.007331499	2.59E-06
1002	4021793	9	IGSF1	0.010262873	0.007382385	5.45E-06
1698	4023960	4	FGF13	0.000102061	0.006988413	4.80E-06
1625	4024213	4	ATP11C	0.000292246	0.00706917	3.99E-06
86	4025394	6		3.32E-07	0.027696162	2.93E-05
765	4025854	6		0.001587412	0.013914483	1.16E-05
288	4027060	9	MECP2	2.41E-05	0.01789865	1.05E-05
1667	4030249	1		0.002577437	0.007582739	2.71E-06
1675	4030633	1		0.000126422	0.008284604	3.42E-06
352	4033522	6		0.000972729	0.011250995	1.11E-05
294	4037889	1		0.004841315	0.00915344	6.80E-06
1056	4040209	6		0.00587839	0.008940693	5.30E-06
156	4041204	6		0.008812862	0.014698895	1.37E-05
1765	4044236	6		0.005170366	0.007435892	4.42E-06
621	4046788	1		0.000460621	0.011139661	8.65E-06
285	4053554	9	AGRN	0.005853836	0.006573388	4.59E-06
1487	4053582	9	AGRN	0.000183201	0.00684421	3.08E-06
508	4053813	4	RILPL1	0.03724011	0.010183757	7.18E-06

Example 14: Validation of the 22-marker Prostate cancer Genomic Classifier in multiple cohorts of varying clinical risk.

Previously, we have reported the development and independent validation of a 22-marker genomic classifier (GC) that predicts rapid metastatic disease progression post Radical

Prostatectomy (RP). This classifier was initially developed and independently validated in a cohort of patients that underwent RP between 1987 and 2001 with high-risk clinical and pathological characteristics, and later further validated in an independent high-risk cohort of patients from the same institution that underwent RP between 2000 and 2006. In those studies, it was demonstrated that GC was able to best predict metastatic disease progression (Met) among patients with clinically high-risk features. Increasing risk based on the GC scores correlated with poorer outcome based on extensive follow-up data on the patients that comprised these cohorts. Furthermore, clinical utility of GC has been demonstrated by a third study on the physician decision-impact of GC on treatment (Tx) recommendations (Example 10). In this project, we have further assessed the association of GC with poor outcome across four independent cohorts of prostate cancer patients from multiple institutions. Results for the previously reported discovery and validation cohorts are also presented for comparison. In cohorts where the metastatic outcome is available (the primary endpoint for which GC was developed), we assessed the ability of GC to classify patients based on their predicted probability of metastasis at 5 years. For cohorts where there is limited outcome data including when patients eventually developed metastatic disease we used surrogate pathological endpoints to correlate these to the predicted probability of metastasis based on the tumor biology.

Methods

The validations pursued in this study were based on the following datasets:

1) Institute of Cancer Research – UK (ICR): 28 primary frozen tissue samples obtained from patients that underwent RP. Clinical characteristics and details on tissue preparation, RNA extraction, amplification and hybridization can be found in the corresponding study (Jhavar et al, BJU Int, vol. 103, no. 9, pp. 1256–69, 2009) and in the Gene Expression Omnibus (GEO) deposited dataset GSE12378. Endpoints used for this study are: Biochemical Recurrence (BCR), Gleason Score and Pathological Stage.

2) Memorial Sloan Kettering Cancer Centre – USA (MSKCC): 131 primary and 19 metastatic fresh frozen tissue samples obtained from 150 patients post RP. Clinical characteristics and details on tissue preparation, RNA extraction, amplification and hybridization can be found in the corresponding study (Taylor et al, Cancer Cell, vol. 18, no. 1, pp. 11–22, 2010) and in the GEO deposited dataset GSE21034. Clinical variables and

endpoints used for this study are: Age, BCR, Development of metastasis, Gleason Score and Pathological Stage.

3) Fundació Institut Mar d'Investigacions Mèdiques – Spain (FIMIM): 18 primary frozen tissue samples obtained from 18 patients post RP. Clinical characteristics and details on tissue preparation, RNA extraction, amplification and hybridization can be found in the corresponding study (Agell et al, *Am J Pathol*, vol. 181, no. 5, pp. 1585–94, 2012) and in the GEO deposited dataset GSE30521. Endpoints used for this study are: Gleason Score and Pathological Stage.

4) Erasmus Medical Center – Netherlands (EMC): 48 primary frozen tissue samples obtained from 48 patients post RP. Clinical characteristics and details on tissue preparation, RNA extraction, amplification and hybridization can be found in the corresponding study (Boormans et al, *Int J Cancer*. 133(2):335-45; Jul 15 2013) and in the GEO deposited dataset GSE41408. Clinical variables and endpoints used for this study are: BCR, development of metastasis, Gleason Score and Pathological Stage.

The samples from these four cohorts were preprocessed using frozen Robust Multiarray Average (fRMA), with quantile normalization and robust weighted average summarization.

5) Mayo Clinic – Training and First Independent Validation (Mayo Clinic I and II): 359 and 186 primary formalin-fixed paraffin-embedded (FFPE) tissue samples, respectively. Clinical characteristics and details on tissue preparation, RNA extraction, amplification, hybridization and preprocessing can be found in Example 1. Clinical variables and endpoints used for this study are: BCR, development of metastasis, Gleason Score and Pathological Stage.

6) Mayo Clinic – Second Independent Validation (Mayo Clinic III): 219 primary FFPE tissue samples. Study inclusion criteria, clinical characteristics and details on tissue preparation, RNA extraction, amplification, hybridization and preprocessing can be found in Example 1. Clinical variables and endpoints used for this study are: BCR, development of metastasis, Gleason Score and Pathological Stage. This cohort is based on a case-cohort design, which allows assessment of survival using the Barlow method (Barlow et al *J Clin Epidemiol*, vol. 52, no. 12, pp. 1165–72, 1999).

For each cohort, the associated expression values for the 22 markers in GC were extracted from the Affymetrix Human Exon Arrays available for each patient and the GC score was computed. A prediction curve using Cox regression modeling to convert the oligonucleotide microarray 22-marker GC score into a patient probability of clinical metastasis at 5 years post RP was used (hereinafter referred to as GC probability). The curve was modeled using a population of 1,010 high-risk men treated for prostate cancer with RP (Example 1), for the endpoint of clinical metastasis at 5-year post RP. A function is created that translates GC scores into 5-year clinical metastasis event probabilities, and the resulting line of best fit is used for future predictions for novel patients. This probability is reported as a percentage probability at 5 years post RP. The risk probability of metastasis at five years was computed for each of the patients. Risk probabilities were further dichotomized around the 6% average risk of metastasis at 5 years that was observed in the prospectively-designed blinded validation study of a high risk population treated at Mayo Clinic (Example 1). Negative predictive value (NPV) and positive predictive value (PPV) were calculated to reflect a population prevalence of 4.5% (Solo et al, ASCO Annual Meeting, vol. 29. Journal of Clinical Oncology, p. abstr 4637). When a study cohort had the data for survival analysis, all metrics used to assess performance of GC, such as area under the receiver-operating characteristic curve, accuracy, sensitivity and specificity were calculated using methods suitable for censored survival data and described in (Heagerty et al, Biometrics, vol. 56, no. 2, pp. 337–44, 2000).

Results

The 1008 samples assessed in this study correspond to formalin-fixed paraffin-embedded (FFPE) or fresh frozen tissue obtained post Radical Prostatectomy (RP) and present varying risk levels as determined by clinical guidelines and based on patient clinical and pathological characteristics. Of the 7 cohorts assessed in this study, five of them (MSKCC, EMC, and Mayo Clinic I, II and III) corresponding to 962 unique patients had metastasis outcome data, the primary endpoint for which GC was developed. Across these 962 patients, 46% were patients > 65 years at RP and over 60% were defined by NCCN guidelines as high-risk and candidates for postoperative radiation therapy (Table 56). In order to quantify the prognostic ability of GC in these five cohorts, we have computed the Area Under the Receiver Operating Characteristic (ROC) curve (AUC) on the risk probabilities of metastasis obtained with the

assay. The AUC metric allows us to evaluate a prognostic tool across all thresholds of sensitivity and specificity represented in the ROC curve. Higher values, closer to 1 indicate a better performance. The AUC on these cohorts ranges from 0.76 (Mayo Clinic II) to 0.88 (MSKCC cohort), with the highest performance obtained of 0.90 in Mayo Clinic I, the training set used to develop GC (Table 56). GC risk probabilities were dichotomized around the 6% average risk of metastasis at 5 years that was observed in the prospectively-designed blinded validation study of a high risk population treated at Mayo Clinic (Example 1). Using this threshold, the overall accuracy varies between 70% (Erasmus Medical Center cohort) to 89% (MSKCC cohort) and the average sensitivity and specificity is 69% and 80% respectively, with an average negative predictive value (NPV) of 98.2%. This demonstrates strong performance by GC across these five cohorts based on the above-mentioned metrics. Gleason score, arguably the most prognostic pathological variable in prostate cancer, had an average accuracy, sensitivity and specificity, NPV and PPV of just 72%, 61%, 77%, 97.7%, 11.3% when dichotomized into patients with Gleason score ≥ 8 versus Gleason score < 8 . Other routine clinical and pathological factors had a much lower ability to prognosticate the development of metastasis in these cohorts (data not shown). As noted in our previous reports, GC provided independent prognostic information and is a better predictor of metastasis than clinical or pathological variables among men at risk of recurrence due to its significantly increased specificity. In fact, the addition of routine clinical and pathological factors including Gleason score to GC does not significantly improve its ability to predict 5-year metastasis probabilities. Furthermore, these results suggest that GC is a robust test for predicting the risk probability of metastasis at five years that can be reliably used across cohorts of varying clinical characteristics and practice settings, with a strong ability to correctly identify patients that are not at true risk of metastasizing due to the biological nature of their tumor, as evidenced by the high specificity and NPV. It is important to note that these performance statistics are confounded by the non-randomized assignment of postoperative adjuvant and salvage treatment, which can significantly delay and in some cases even prevent the development of metastasis (see below). Overall, within these five cohorts, those patients with no metastatic event have a median risk probability that falls below the 6% threshold (Figure 56). Accordingly, those patients that had metastasis have a median risk probability above the 6% threshold, with many of them presenting clear high risk tumor biology. While this observed trend is in agreement with the expected results, there are some patients that correspond to low risk probabilities with metastasis and to high risk probabilities without the

event. Several factors can explain these results. First, patients with a high predicted risk probability may not have metastasized due to early intervention and removal of the primary localized tumor with RP that proved curative. Second, insufficient follow-up data may result in an unrecorded metastasis event (the time to develop metastasis in prostate cancer can take 8-10 years after surgery). Last, post RP secondary treatment of patients (e.g., radiation or hormonal therapy) can significantly delay or suppress the progression to metastatic disease.

From the 7 cohorts with computed probabilities of metastasis at five years, metastasis outcome data was not available for 2 of them (ICR, FIMIM). Still, an assessment of the correlation between GC probabilities and clinical risk can be explored. The joint prevalence of biochemical recurrence (BCR), pT3 disease and high Gleason Score (GS) were used as guidelines to rank the 7 cohorts from lowest to highest risk (Figure 57). As expected, the proportion of patients classified as low risk based on GC probabilities decreases as the clinical risk of the cohort increases. Accordingly, the proportion of patients assessed as high-risk by GC increases as clinical risk increases. For example, in the lowest risk populations (ICR, MSKCC), GC did not overestimate risk as less than 6.7% of patients had high probabilities. In contrast, in the Mayo cohorts, over 23% of patients had the highest GC probabilities (with a probability of metastasis at 5 years greater than 13%). This analysis shows in 1008 patients that the distribution of GC probabilities, as one would expect, reflects the underlying biological risk for metastatic disease progression in diverse patient populations. Whereas the metastasis event is the most direct endpoint that can be used to evaluate the performance of GC, other features available for most cohorts described here can also prove useful to understand its ability to properly predict the probability of metastasis.

An established pathological feature that is used among clinicians for treatment decisions (alone or in combination with other clinical variables) is the Gleason Score (GS). While this is a subjective metric that is based on interpretation of histology, when conducted by an expert genitourinary pathologist it has been shown to be the top performing prognostic feature in prostate cancer. However, the majority of prostate cancer patients are classified as GS7, which as a group that has proved to be highly heterogeneous in terms of clinical outcomes. Overall, higher GS values are indicative of altered tissue architecture and correlates with poor outcome. Hence, the distribution of predicted risk probabilities of metastasis at five

years by GC should be such that it increases across higher GS. The distribution of the predicted risk probabilities of metastasis across 997 patients from 7 cohorts with available GS shows that this trend is confirmed (Figure 58), with an increasing median value of this risk probability as GS increases. Furthermore, GC proves accurate when categorizing metastatic events within GS groups (Figure 58). As expected, the widest variation of GC probability was observed in the GS7 group. Still, most of the GS7 samples that developed metastasis had high GC probabilities. These results highlight the potential joint role of GC with histopathology information for improving risk prediction.

In addition to GS, 414 patients within the 7 cohorts have information on BCR event. Whereas BCR has low specificity for the development of metastasis (Pound et al, JAMA, vol. 281, no. 17, pp. 1591–7, 1999) and hence assessment of correlation of GC probabilities with BCR might not be informative, for the set of patients for which BCR was not observed post RP the expected result of a test that has high specificity is that most patients would have a low risk probability of metastasis at five years. As expected, when focusing on patients that did not present with BCR post RP within these 7 cohorts, the median probability of metastasis is consistently found below the 6% threshold, corresponding to a low risk GC test result (Figure 59). Still, for a small fraction of the 414 patients the risk probability falls above the 6% threshold, which may be explained by several factors discussed above for the metastatic endpoint. For those patients from the Mayo clinic cohorts that were treated after RP (and before BCR, Figure 59) the proportion of patients treated within the low risk probability group is lower than the proportion of patients treated within the high risk probability group (Table 57). Interestingly, many of the patients with predicted probabilities above the 6% threshold were treated (likely as a consequence of other adverse pathological factors such as positive surgical margins), suggesting that for patients with high GC probabilities, intensification with secondary adjuvant therapy may delay or suppress BCR and subsequent metastatic disease for primary adenocarcinomas that presented initially with aggressive tumor biology.

GC has been evaluated in 7 independent cohorts totaling 1,008 prostate cancer patients who underwent RP for their primary tumor. The performance results of GC were consistent across all validation cohorts and did not overestimate metastasis in lower risk patients, showing an expected distribution of probabilities across diverse patient populations based on their

biological risk for metastatic disease progression. Overall, GC is an independent and better predictor of metastasis than clinical or pathological variables among men at risk of recurrence, and can also identify patients that are not at true risk of metastasizing, thereby sparing them additional morbid therapies. The robust specificity and negative predictive value of GC demonstrated in both retrospective and prospective studies establishes the clinical validity of the GC test.

Study	MSECC (N = 150)	EMC (N = 48)	Mayo I (N = 359)	Mayo II (N = 186)	Mayo III (N = 219)	Overall (N = 962)
Institution	Memorial Sloan Kettering	Erasmus Medical Center	Mayo Clinic	Mayo Clinic ¹	Mayo Clinic ²	
% Metastasis (Prevalence in Cohort)	19%	19%	40%	37%	8%	19%
% Patients > 65 years old	17%	-	57%	55%	33%	46%
% NCCN High Risk	43%	67%	63%	58%	74%	61%
% pT3	31%	54%	47%	46%	43%	44%
% Gleason 8+	16%	19%	39%	38%	37%	35%
AUC	0.88	0.82	0.90	0.76	0.79	0.82
Overall Accuracy	89%	71%	82%	70%	70%	77%
Sensitivity	61%	73%	67%	72%	78%	69%
Specificity	96%	69%	91%	69%	62%	80%
NPV ³	98.1%	98.3%	98.3%	98.1%	98.4%	98.2%
PPV ³	41.8%	10.6%	36.0%	9.9%	8.8%	14.0%

Study characteristics of 5 cohorts with Metastasis information available and Decipher performance in predicting Metastasis. Overall accuracy, sensitivity and specificity reflect 6% Metastatic probability cutoff. NCCN high risk as defined by either pathologic tumor stage pT3 or positive surgical margins (SM).

Table 56

Study	Mayo I	Mayo II	Mayo III
Below cutoff	25%	35%	45%
Above cutoff	55%	44%	53%

Table 57

Example 15: Performance of a 22-marker Genomic Classifier that Predicts Metastasis following Radical Prostatectomy in Patients Recommended for Secondary Therapy by AUA and NCCN Clinical Practice Guidelines

We have previously described a 22-marker genomic classifier (GC) that has much improved performance over standard clinicopathologic variables in detecting the potential for metastasis based on the genetic profile of a primary tumor at RP. Here we examine whether prostate cancer patients designated as high risk by AUA or NCCN criteria post-RP can be more accurately categorized based on their genomic profile (i.e. GC risk score), thereby

identifying men who may benefit from therapy intensification and those who may be spared from unnecessary treatment.

(a) Specimen Selection and Processing

This study focused on a cohort of patients from the Mayo Clinic tumor registry who underwent RP for prostatic adenocarcinoma from 2000-2006 (Example 1). This population was clinically high-risk for metastasis, as defined by pre-operative prostate-specific antigen (PSA) levels >20ng/mL, pathological Gleason score ≥ 8 , SVI, or GPSM (Gleason score; pre-operative PSA; SVI; SM) score ≥ 10 (Thompson et al, *The Journal of urology*. 2007;178(2):459–63). We designed a case-cohort study that randomly sampled ~20% of the cohort and added the metastatic patients to the dataset who were not selected in the random sampling. After exclusion for tissue unavailability and quality control, 159 patients were identified from this population (48 with metastasis and 111 without) who had pathologically confirmed pT3N0M0 disease, or pT2N0M0 disease with positive surgical margins; patients with these features are recommended for adjuvant radiotherapy per AUA and NCCN guidelines (Rosenfeld S. NCCN Clinical Practice Guidelines in Oncology (NCCN Guidelines®) Prostate Cancer. 2013; Thompson et al, Adjuvant and Salvage Radiotherapy After Prostatectomy: AUA/ASTRO Guideline. *J Urol*.)

Following histopathological review of the above cases, formalin-fixed paraffin embedded (FFPE) primary prostatic adenocarcinoma tissues were macrodissected as described previously. Total RNA was then extracted and purified using RNeasy FFPE nucleic acid extraction kit (Qiagen Inc., Valencia, CA), and subjected to whole-transcriptome amplification using the WT-Ovation FFPE system (NuGen, San Carlos, CA). Amplified products were fragmented, labeled, and hybridized to Human Exon 1.0 ST GeneChips (Affymetrix, Santa Clara, CA). Following microarray quality control using the Affymetrix Power Tools packages (Lockstone, *Briefings in bioinformatics*. 2011;12(6):634–44) probeset summarization and normalization was performed by frozen robust multi-array analysis, which is available through Bioconductor (McCall et al, *Biostatistics (Oxford, England)*. 2010;11(2):242–53). The expression of the 22 features in the array that compose GC (Example 3) were used as input to compute the score for each of the 159 high-risk patients.

(b) Statistical Analysis

Graphical diagnostic, receiver operating characteristic (ROC)-based, and censored data methods were used to determine a tentative GC score cutoff for NCCN group with a higher risk of metastasis comparing to the original validation dataset (Example 1). GC was

compared to standard clinicopathologic variables for predicting the primary endpoint of metastasis. The Concordance Summary index (c-index), an extension of area under the ROC curve (AUC) for censored survival data was used to compare classifier performance to predict metastasis. Survival ROC curves (Heagerty et al, *Biometrics*. 2000;56(2):337–44) were evaluated for prediction of metastasis within 5 years post-RP. For the survival ROC function, the nearest-neighbors estimator was used with $\lambda=0.002$ to approximate survival function density.

A weighted Cox proportional hazards analysis was used to test for associations with the metastatic endpoint for a case-cohort study design (Lin and Ying, *Journal of the American Statistical Association*. 88(424):1341–1349; Barlow et al, *Journal of clinical epidemiology*. 1999;52(12):1165–72). Proportional hazards assumptions of the Cox model were confirmed by evaluating the scaled Schoenfeld residuals (Grambsch PM, Therneau TM. Proportional Hazards Tests and Diagnostics Based on Weighted Residuals. 2013;81(3):515–526). GC was used as a continuous variable (step size=0.1); pathological Gleason score was dichotomized into <8 and ≥ 8 ; pre-operative PSA values were log transformed due to their skewed distribution; SVI, SM, ECE and adjuvant hormone therapy administration were used as binary variables. Cumulative incidence curves were constructed using Fine-Gray competing risks analysis to accommodate censoring due to death and other events (Fine et al, *Journal of the American Statistical Association*. 94(446):496–509). Time-dependent analyses were performed by weighting patients without metastasis as suggested by Barlow (Barlow WE. Robust Variance Estimation for the Case-Cohort Design. 2013;50(4):1064–1072). Net clinical benefit was estimated using an extension of decision curve analysis for survival data (Vickers et al, *BMC medical informatics and decision making*. 2008;8:53).

All statistical analyses were performed in R v2.14.1. All tests were two-sided with a type I error probability of 5%.

RESULTS

This study identified 159 patients who met the AUA and NCCN criteria for consideration of adjuvant radiation therapy. Total of 57 (35.8%) men had pT2N0M0 with positive surgical margins, and 102 (64.2%) men had pT3N0M0 or higher disease from a case-cohort of high-risk prostate cancer patients (Table 58). A total of 83 (52.2%) patients experienced biochemical recurrence (BCR), 48 (30.2%) developed metastatic disease as evidenced by bone and/or CT scans, and 18 (11.3%) died of disease at last follow-up.

To understand the prognostic ability of the 22–marker classifier, GC, within this group of patients, survival ROC curves at 5 years for the metastasis endpoint were built for this classifier as well as for established clinicopathologic variables evaluated at RP (Figure 60). GC exhibited an AUC of 0.82 while the most significant clinicopathologic variable was the pathological Gleason score (pGS) with an AUC of 0.67. Furthermore, the lower bound for the associated 95% confidence interval (CI) for GC did not overlap with the upper bound for any clinicopathologic variables other than pGS, suggesting that GC significantly outperforms most established variables. The AUC of GC was also higher than that of several previously reported prognostic genes for prostate cancer (Figure 61). GC was also compared to other standardized clinical nomograms, which included the Stephenson nomogram (Stephenson et al, Postoperative Nomogram Predicting the 10-Year Probability of Prostate Cancer Recurrence After Radical Prostatectomy. 2008;23(28):7005–7012) and CAPRA-S (Cooperberg et al, *Cancer*. 2011;117(22):5039–46.) (Figure 62). GC outperformed both established nomograms (AUC of 0.82, 0.76 and 0.71, respectively) for prediction of metastasis at 5 years following RP.

To consider the potential prognostic role of clinicopathologic variables in combination, a clinical-only (CC; including pGS, pre-op PSA, ECE, SVI, SM) classifier was constructed for this cohort of patients, and was then combined with GC to produce a genomic-clinical classifier (GCC). While the AUC of CC (0.73) was comparable to the other clinical-only nomograms, its combination with GC (as GCC) increased its AUC to 0.86. However, the overlap in the 95% CIs for GCC and GC indicated that their performances were statistically comparable. The combination of GC with the Stephenson nomogram, the best performing clinical-only classifier in this cohort, increased the AUC to 0.84, although the 95% CIs still indicated that its performance was comparable to that of GC alone.

Decision curves were then used to compare the net clinical benefit (i.e., clinical implication of false positives) of genomic-based classifiers with clinicopathologic factors and clinical-only models. When compared to clinicopathologic variables, GC showed a far higher net benefit (Figure 63A). When compared to clinical-only risk models, genomic-based classifiers (i.e. GC and GCC) had comparably higher net benefit, thereby suggesting that GC models have increased specificity (i.e., lower false positives), without sacrificing sensitivity (Figure 63B).

The performance of GC within this set of patients was further assessed by univariable and multivariable survival analysis. Univariable analysis showed that GC was significantly

prognostic for the metastasis endpoint ($p < 0.001$; Table 59A). Pathological GS ($p < 0.001$) and ECE ($p = 0.02$) were also significant predictors of metastasis with wider 95% CIs.

Multivariable analysis showed that the prognostic ability of GC was retained, after adjusting for clinicopathologic variables and adjuvant hormone treatment ($HR = 1.59$, 95% $CI = [1.33, 1.90]$, $p < 0.001$), most clinicopathologic variables with the exception of pre-op PSA ($p = 0.009$) became statistically insignificant (Table 59B). These observations persisted even when primary and secondary pathological Gleason grades were considered separately (Table 60). While univariable analysis also showed that clinical-only nomograms including CC, Stephenson nomogram and CAPRA-S were significantly prognostic for the metastasis endpoint (all $p < 0.001$; Table 61A), paired multivariable analysis of GC with each clinical-only nomogram showed that GC independently carried the most prognostic potential ($p < 0.001$) with the highest hazard ratio (Table 61B).

The GC scores associated with patients in this high-risk cohort ranged from 0.0086 to 0.9906 with a median of 0.35 (IQR: 0.21, 0.604). The patients associated with lower scores may represent (i) false negative cases, or (ii) those with a lower risk than that estimated by AUA and NCCN guidelines. To address this observation, an optimal threshold that maximizes sensitivity and specificity for the GC score was first derived at 0.4. Patients were then categorized to GC-low risk ($GC < 0.4$) and GC-high risk ($GC \geq 0.4$) groups based on their GC scores. As shown in Figure 64, only 13 of 88 (14.8%) patients in the GC-low risk group had a metastatic event compared to 49.3% of cases in the GC-high risk group. This difference in the number of metastatic events suggests that GC low scores within this cohort correspond to patients that might need re-assessment of their risk levels. The proportion of men who metastasized based on this grouping of their GC scores was comparable even after excluding patients who received adjuvant treatments (Figure 65).

To further assess the distribution of GC scores described above, cumulative incidence plots depicting the frequency of development of metastasis over time were generated for GC-low and GC-high risk groups (Figure 66). The cumulative incidence probabilities of developing metastasis were significantly different between the two risk groups based on GC scores ($p < 0.001$), with a 2% incidence at 5 years (5% at 10 years) for the GC-low risk group compared to a 14% incidence at 5 years (25% at 10 years) for the GC-high risk group. The reclassification and cumulative incidence results suggest that there are a significant number of patients in the GC-high risk group that could benefit from treatment, whereas patients in

the GC-low risk group may not be at high risk of progressing to metastasis and hence not need intensified treatment.

We have previously shown that a multivariable GC composed of 22 markers has independent prognostic value for detecting metastatic prostate cancer compared to established clinicopathologic variables in the post RP setting. While GC is prognostic for high-risk disease after prostatectomy, clinical decisions regarding treatment intensification with adjuvant radiation are currently guided by presence of high-risk features including T3 disease (pT3N0M0) or T2 disease with positive margins (pT2N0M0, SM+). The results presented in this study detail the ability of GC to predict metastatic disease in such patients post RP.

Table 58

	Total	Cases	Controls
Clinicopathologic Factors	n	n (row %)	n (row %)
Study Cohort	159	48(30.0)	111 (70.0)
Pathological Stage			
pT2N0M0	57	8(14.0)	49(86.0)
pT3/4N0M0	102	40(39.2)	62(60.8)
Pathological Gleason Score (path GS)			
≤6	10	0 (0.0)	10 (100.0)
7	95	22(23.2)	73 (76.8)
≥8	54	26(48.1)	28 (51.9)
Pre-operative Prostate-specific Antigen (pre-op PSA)			
<10 ng/mL	97	26 (26.8)	71 (73.2)
10-20 ng/mL	42	14 (33.3)	28 (66.7)
>20 ng/mL	20	8 (40.0)	12 (60.0)
Seminal Vesicle Invasion (SVI)	63	24 (38.1)	39 (61.9)
Surgical Margin Status (SM)	105	28 (26.7)	77 (73.3)
Extra-capsular Extension (ECE)	74	30 (40.5)	44 (59.5)
Biochemical recurrence (BCR)	83	48 (57.8)	35 (42.2)

Prostate Cancer-specific Mortality (PCSM)	18	18 (100.0)	0 (0.0)
Adjuvant Radiation Therapy	22	9 (40.9)	13 (59.1)
Adjuvant Androgen Deprivation Therapy	42	16 (38.1)	26 (61.9)
Salvage Radiation Therapy	56	23 (41.1)	33 (58.9)
Salvage Androgen Deprivation Therapy	65	45 (69.2)	20 (30.8)

Table 59A

Clinicopathologic Factors	Total	Cases	Controls
	n	n (row %)	n (row %)
Study Cohort	159	48(30.0)	111 (70.0)
Pathological Stage			
pT2N0M0	57	8(14.0)	49(86.0)
pT3/4N0M0	102	40(39.2)	62(60.8)
Pathological Gleason Score (path GS)			
≤6	10	0 (0.0)	10 (100.0)
7	95	22(23.2)	73 (76.8)
≥8	54	26(48.1)	28 (51.9)
Pre-operative Prostate-specific Antigen (pre-op PSA)			
<10 ng/mL	97	26 (26.8)	71 (73.2)
10-20 ng/mL	42	14 (33.3)	28 (66.7)
>20 ng/mL	20	8 (40.0)	12 (60.0)
Seminal Vesicle Invasion (SVI)	63	24 (38.1)	39 (61.9)
Surgical Margin Status (SM)	105	28 (26.7)	77 (73.3)
Extra-capsular Extension (ECE)	74	30 (40.5)	44 (59.5)
Biochemical recurrence (BCR)	83	48 (57.8)	35 (42.2)
Prostate Cancer-specific Mortality (PCSM)	18	18 (100.0)	0 (0.0)
Adjuvant Radiation Therapy	22	9 (40.9)	13 (59.1)
Adjuvant Androgen Deprivation Therapy	42	16 (38.1)	26 (61.9)
Salvage Radiation Therapy	56	23 (41.1)	33 (58.9)
Salvage Androgen Deprivation Therapy	65	45 (69.2)	20 (30.8)

¹ Hazard ratio reported for 0.1 unit increments of raw score.² Hazard ratio reported for 1.0 unit increments of log-transformed level.

Table 59B

Genomic and Clinicopathologic Factors	Hazard Ratio (95% CI)	P
GC ¹	1.59(1.33-1.91)	< 0.001
Pathological Gleason Score ≥8	1.82 (0.78-4.22)	0.16
Pre-operative Prostate-specific Antigen ²	1.78(1.16-2.73)	0.009
Extracapsular Extension	1.15 (0.49-2.67)	0.75

¹ Hazard ratio reported for 0.1 unit increments of raw score.

² Hazard ratio reported for 1.0 unit increments of log-transformed level.

Table 60A

Genomic and Clinicopathologic Factors	Hazard Ratio (95% CI)	P
GC ¹	1.61 (1.37-1.89)	< 0.001
Pathological Gleason Grade primary	3.07 (1.77-5.32)	< 0.001
Pathological Gleason Grade secondary	1.47 (0.83-2.61)	0.19
Pre-operative Prostate-specific Antigen ²	1.41 (0.96-2.05)	0.08
Seminal Vesicle Invasion	1.75 (0.90-3.39)	0.10
Positive Surgical Margin	0.66 (0.33-1.29)	0.22
Extracapsular Extension	2.25 (1.14-4.46)	0.02
Adjuvant Hormone Therapy	1.53 (0.74-3.15)	0.25
Adjuvant Radiation Therapy	1.51 (0.62-3.67)	0.36

¹ Hazard ratio reported for 0.1 unit increments of raw score.

² Hazard ratio reported for 1.0 unit increments of log-transformed level.

Table 60B

Genomic and Clinicopathologic Factors	Hazard Ratio (95% CI)	P
GC ¹	1.60 (1.35-1.90)	< 0.001
Pathological Gleason Graded primary	2.73 (1.48-5.05)	0.001
Pre-operative Prostate-specific Antigen ²	1.85 (1.22-2.82)	0.004
Extracapsular Extension	0.91 (0.42-1.99)	0.82

¹ Hazard ratio reported for 0.1 unit increments of raw score.

² Hazard ratio reported for 1.0 unit increments of log-transformed level.

Table 61A

Genomic and Clinicopathologic Factors	Hazard Ratio (95% CI)	P
GC ¹	1.61 (1.37-1.89)	< 0.001
CC ¹	1.41(1.19-1.67)	< 0.001
GCC ¹	1.47 (1.27-1.69)	< 0.001
Stephenson 5-year ¹	1.41 (1.23-1.62)	< 0.001
CAPRA-S	1.50 (1.28-1.75)	< 0.001

¹ Hazard ratio reported for 0.1 unit increments of raw score.

Table 61B

Genomic and Clinicopathologic Factors	Hazard Ratio* (95% CI)	P
GC ¹	1.56 (1.32-1.84)	< 0.001
CC ¹	1.20 (0.96-1.51)	0.12
GC ¹	1.52 (1.27-1.82)	< 0.001
Stephenson 5-year ¹	1.35 (1.10-1.66)	0.005
GC ¹	1.56 (1.32-1.85)	< 0.001
CAPRA-S	1.45 (1.17-1.79)	< 0.001

¹ Hazard ratio reported for 0.1 unit increments of raw score.

*Adjusted for Adjuvant Hormone and Radiation Therapy

Example 16: Evaluation of a 22-marker genomic classifier for improved risk stratification in prostate cancer patients with specific adverse pathologies after surgery.

The presence of adverse pathological features (APFs) such as seminal vesicle invasion (SVI), extra capsular extension (ECE), surgical margins (SM) or Gleason score (GS) ≥ 7 , in radical prostatectomy (RP) specimens are considered risk factors for metastatic disease progression. The majority of patients that have APFs post-RP, however, will not develop metastatic disease and die of prostate cancer in their lifetime. Here, we evaluate the ability of a genomic classifier (GC, Example 3) to predict metastatic disease progression post-RP in SVI+, ECE+, SM+ or GS ≥ 7 APF patient subsets.

Methods

Patient cohort of previously described genomic prostate cancer studies from Mayo Clinic (high risk, Example 1) and Memorial Sloan Kettering Cancer Center (a.k.a. MSKCC, low-intermediate risk, Example 14) were combined. Details on these two cohorts can be found in Example 1 and Example 14, respectively.

Patients with lymph node involvement, missing APF information or non-primary tumor specimens were excluded. Clinical and genomic information was available for 285 patients to generate GC scores (Table 62).

Expression data for the 22 markers for each patient retrieved from the Affymetrix Human Exon Array and the combination of these into GC (Random Forest Algorithm) was used to obtain a patient score from 0 to 1. GC scores for each patient were calculated. GC scores range from 0 (low metastatic potential) to 1 (high metastatic potential).

Statistical Analysis

Subsets of the patients were selected from the final combined cohort according to the corresponding adverse pathology feature (SM+, ECE+, SVI+ or GS ≥ 7).

Standard ROC analysis in the overall cohort and the subsets was performed. Odds ratios were calculated by a multivariable logistic regression model and included GC scores with all relevant APFs. Variable provided independent and statistically significant in $p < 0.05$.

GC scores were dichotomized into high (GC ≥ 0.4) and low risk. Reclassification of APF subgroups by GC risk categories, was assessed.

Results

Across both patient cohorts, the c-index of GC was 0.79 and significantly higher than any individual APF (range 0.54-0.72) for predicting metastatic disease post-RP (Figure 67). The c-indices of GC in the APF subset analysis for SVI+, ECE+, SM+ and $GS \geq 7$ subsets were 0.83, 0.79, 0.86 and 0.77, respectively (Figures 68-71). Multivariable analysis revealed that GC was the most significant predictor of metastatic disease progression across both cohorts (Table 63) and within all APF subsets with odds ratios (for 0.1 unit increments) of 1.87, 1.56, 1.86 and 1.58 in SVI+, ECE+, SM+ and $GS \geq 7$ subsets, respectively (all $p < 0.001$) (Table 64). Reclassification analysis revealed that most prostate cancer-specific deaths occurred in patients with high GC score ($GC \geq 0.4$) (Table 65).

This subset analysis suggests that a genomic classifier approach provides additional prognostic information to pathological variables and maintains consistent performance for predicting metastasis among subsets of patients with specific APF.

Throughout this specification, unless the context requires otherwise, the word "comprise", or variations such as "comprises" or "comprising", will be understood to imply the inclusion of a stated step or element or integer or group of steps or elements or integers but not the exclusion of any other step or element or integer or group of elements or integers.

Any discussion of documents, acts, materials, devices, articles or the like which has been included in the present specification is not to be taken as an admission that any or all of form part of the prior art base or were common general knowledge in the field relevant to the present disclosure as it existed before the priority date of each of the appended claims.

Table 62

Clinical Variable	Pathological Factors/ End Points	Study (%)
Patients	-	285
Follow up	Median, yrs (range)	5.66 (0.15-12.4)
Pre-operative PSA	<10 ng/ml	187
	10-20 ng/ml	62
	>20 ng/ml	36
Pathological Gleason Score	≤6	42
	7	159
	≥ 8	84
Adverse Pathology Features	Positive surgical margins	126
	Extracapsular Extension	139
	Seminal Vesicle Invasion	72
	Pathologic Gleason ≥ 7	243
Biochemical Recurrence	Event	109
Metastatic disease	Event	60
PCSM	Event	20

Table 63

MVA in overall patient cohort (N=285)			
	OR	95% CI	p-value
GC ¹	1.54	1.31 – 1.81	<0.0001
SM+	1.00	0.50 – 2.00	0.99
ECE	1.54	0.78 – 3.07	0.22
SVI	1.87	0.92 – 3.82	0.08
Path GS ²	2.92	1.47 – 5.77	0.002
pPSA ³	1.25	0.92 – 1.69	0.16

Table 64

SVI+ patients				ECE+ patients			
	OR	95% CI	p-value		OR	95% CI	p-value
GC	1.87	1.37 – 2.55	0.0001	GC	1.56	1.24 – 1.96	0.0001
SM+	4.03	0.92 – 17.63	0.06	SM+	1.01	0.39 – 2.56	0.99
ECE	0.37	0.08 – 1.65	0.19	SVI	1.11	0.44 – 2.82	0.82
Path GS	1.62	0.46 – 5.65	0.45	Path GS	2.33	0.94 – 5.80	0.07
pPSA	1.07	0.65 – 1.77	0.78	pPSA	1.32	0.89 – 1.95	0.17
SVI- patients				GS≥7 patients			
	OR	95% CI	p-value		OR	95% CI	p-value
GC	1.86	1.43 – 2.42	<0.0001	GC	1.58	1.35 – 1.84	<0.0001
ECE	1.34	0.39 – 4.55	0.64	SM+	0.88	0.45 – 1.73	0.70
SVI	3.74	1.07 – 13.06	0.04	ECE	1.48	0.75 – 2.91	0.25
Path GS	1.65	0.55 – 4.96	0.38	SVI	1.60	0.79 – 3.24	0.19
pPSA	1.21	0.78 – 1.86	0.39	pPSA	1.21	0.89 – 1.65	0.22

CLAIMS

1. A method of prognosing prostate cancer in a subject, comprising:
 - (a) assaying an expression level in a sample from the subject for a plurality of targets, wherein the plurality of targets comprises at least five targets selected from IQGAP3, ANO7, ZWILCH, CAMK2N1, RABGAP1, EPPK1, GLYATL1P4/PCAT-80, LASP1, MYBPC1, NFIB, NUSAP1, PBX1, PCAT-32, PCDH7, S1PR4, THBS2, TNFRSF19, C6orf10, UBE2C, SENP7, ANLN, C10orf116, PPP6R3, PDS5B, TOP2A, IL1RAP, CENPE, GALNT8, KCNQ1, C6orf155, LUZP2, HEATR3, TMEM1, CFBXXbacBPG116M5.17, ECHDC2, ARNTL or SEQ ID NOs. 1-43; and
 - (b) prognosing prostate cancer in a subject based on the expression levels of the plurality of targets.
2. The method of claim 1, wherein the plurality of targets comprises a coding target.
3. The method of claim 2, wherein the coding target is an exonic sequence.
4. The method of any one of claims 1 to 3, wherein the plurality of targets comprises a non-coding target.
5. The method of claim 4, wherein the non-coding target comprises an intronic sequence or partially overlaps an intronic sequence.
6. The method of claim 4, wherein the non-coding target comprises a sequence within the UTR or partially overlaps with a UTR sequence.
7. The method of any one of claims 1 to 6, wherein the target comprises a nucleic acid sequence.
8. The method of claim 7, wherein the nucleic acid sequence is a DNA sequence.
9. The method of claim 7, wherein the nucleic acid sequence is an RNA sequence.
10. The method of any one of claims 1 to 9, wherein the plurality of targets comprises at least 5, 10, 15 or 20 targets selected from IQGAP3, ANO7, ZWILCH,

CAMK2N1, RABGAP1, EPPK1, GLYATL1P4/PCAT-80, LASP1, MYBPC1, NFIB, NUSAP1, PBX1, PCAT-32, PCDH7, S1PR4, THBS2, TNFRSF19, C6orf10, UBE2C, or SEQ ID NOs. 1 to 22.

11. The method of any one of claims 1 to 9, wherein the plurality of targets comprises at least 10 targets selected from IQGAP3, ANO7, ZWILCH, CAMK2N1, RABGAP1, EPPK1, GLYATL1P4/PCAT-80, LASP1, MYBPC1, NFIB, NUSAP1, PBX1, PCAT-32, PCDH7, S1PR4, THBS2, TNFRSF19, C6orf10, UBE2C, SENP7, ANLN, C10orf116, PPP6R3, PDS5B, TOP2A, IL1RAP, CENPE, GALNT8, KCNQ1, C6orf155, LUZP2, HEATR3, TMEM1, CFBXXbacBPG116M5.17, ECHDC2, ARNTL or SEQ ID NOs. 1-43.

12. The method of any one of claims 1 to 9, wherein the plurality of targets comprises at least 15 targets selected from IQGAP3, ANO7, ZWILCH, CAMK2N1, RABGAP1, EPPK1, GLYATL1P4/PCAT-80, LASP1, MYBPC1, NFIB, NUSAP1, PBX1, PCAT-32, PCDH7, S1PR4, THBS2, TNFRSF19, C6orf10, UBE2C, SENP7, ANLN, C10orf116, PPP6R3, PDS5B, TOP2A, IL1RAP, CENPE, GALNT8, KCNQ1, C6orf155, LUZP2, HEATR3, TMEM1, CFBXXbacBPG116M5.17, ECHDC2, ARNTL or SEQ ID NOs. 1-43.

13. The method of any one of claims 1 to 9, wherein the plurality of targets comprises at least 20 targets selected from IQGAP3, ANO7, ZWILCH, CAMK2N1, RABGAP1, EPPK1, GLYATL1P4/PCAT-80, LASP1, MYBPC1, NFIB, NUSAP1, PBX1, PCAT-32, PCDH7, S1PR4, THBS2, TNFRSF19, C6orf10, UBE2C, SENP7, ANLN, C10orf116, PPP6R3, PDS5B, TOP2A, IL1RAP, CENPE, GALNT8, KCNQ1, C6orf155, LUZP2, HEATR3, TMEM1, CFBXXbacBPG116M5.17, ECHDC2, ARNTL or SEQ ID NOs. 1-43.

14. The method of any one of claims 1 to 13, wherein the prognosing includes determining the malignancy of the prostate cancer.

15. The method of any one of claims 1 to 13, wherein the prognosing includes determining the stage of the prostate cancer.

16. The method of any one of claims 1 to 13, wherein the prognosing includes assessing the risk of prostate cancer recurrence.

17. The method of any one of claims 1 to 16, further comprising sequencing the plurality of targets.
18. The method of any one of claims 1 to 17, further comprising hybridizing the plurality of targets to a solid support.
19. The method of any one of claims 1 to 18, wherein the plurality of targets comprises the 19 genes: IQGAP3, ANO7, ZWILCH, CAMK2N1, RABGAP1, EPPK1, GLYATL1P4, LASP1, MYBPC1, NFIB, NUSAP1, PBX1, PCAT-32, PCDH7, S1PR4, TSBP, THBS2, TNFRSF19, UBE2C.
20. The method of claim 2, wherein the coding target is a coding antisense sequence.
21. The method of claim 4, wherein the non-coding target comprises an intergenic sequence.
22. The method of claim 1, wherein the plurality of targets consist of SEQ ID NOs: 1-22.
23. The method of claim 18, wherein the solid support is a bead or array.
24. The method of claim 10, wherein the plurality of targets comprises a coding target or a non-coding target.
25. The method of claim 24, wherein the coding target is a coding antisense sequence or an exonic sequence.
26. The method of claim 24, wherein the non-coding target comprises an intronic sequence, partially overlaps an intronic sequence, an intergenic sequence, a UTR or partially overlaps with a UTR sequence.
27. The method of claim 10, wherein the plurality of targets comprises a nucleic acid sequence.

28. The method of claim 27, wherein the nucleic acid sequence is selected from the group consisting of a DNA sequence and a RNA sequence.
29. The method of claim 1, wherein the plurality of targets consist of SEQ ID NOs: 1-43.
30. The method of claim 10, wherein the plurality of targets consist of SEQ ID NOs: 1-22.
31. The method of claim 10, further comprising sequencing the plurality of targets.

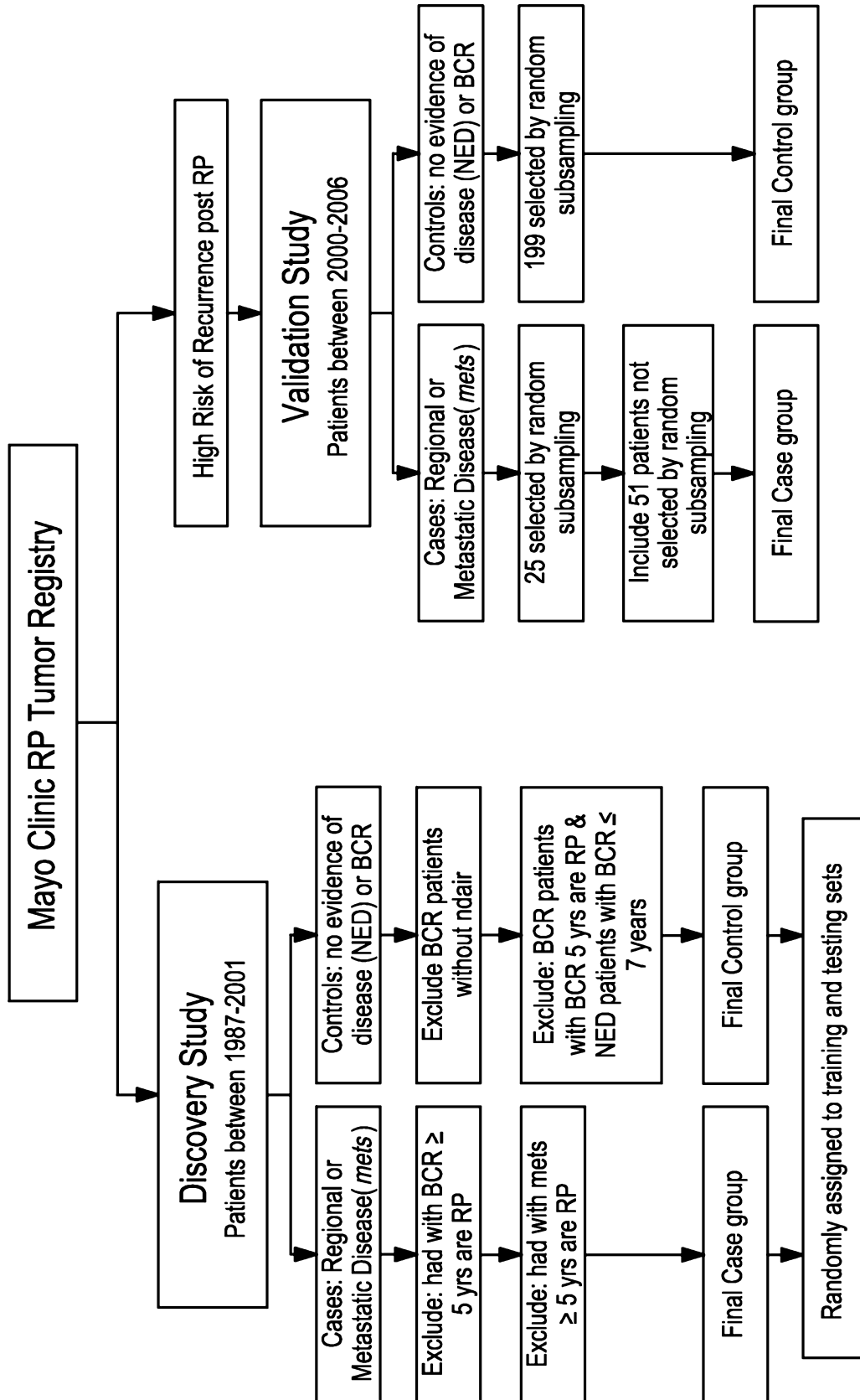
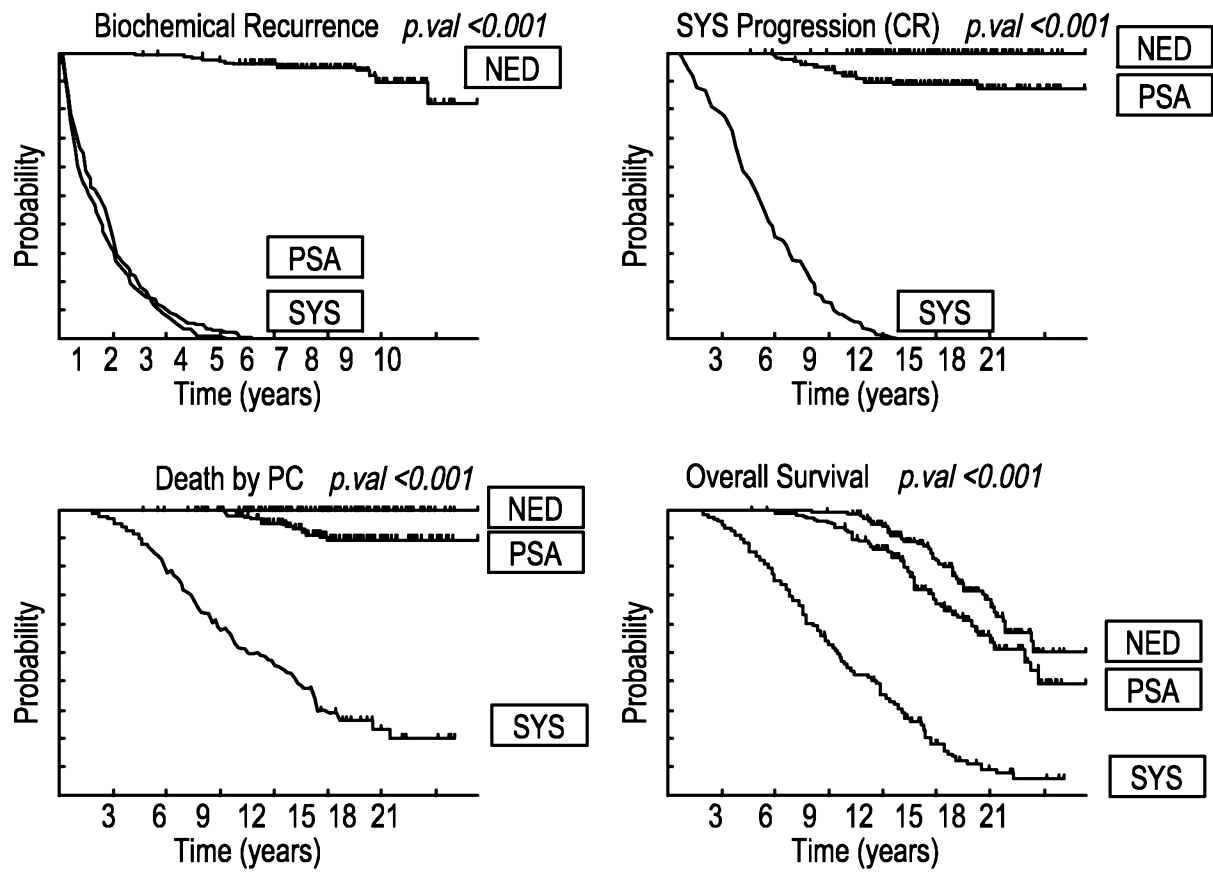


FIG. 1

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**FIG. 2**

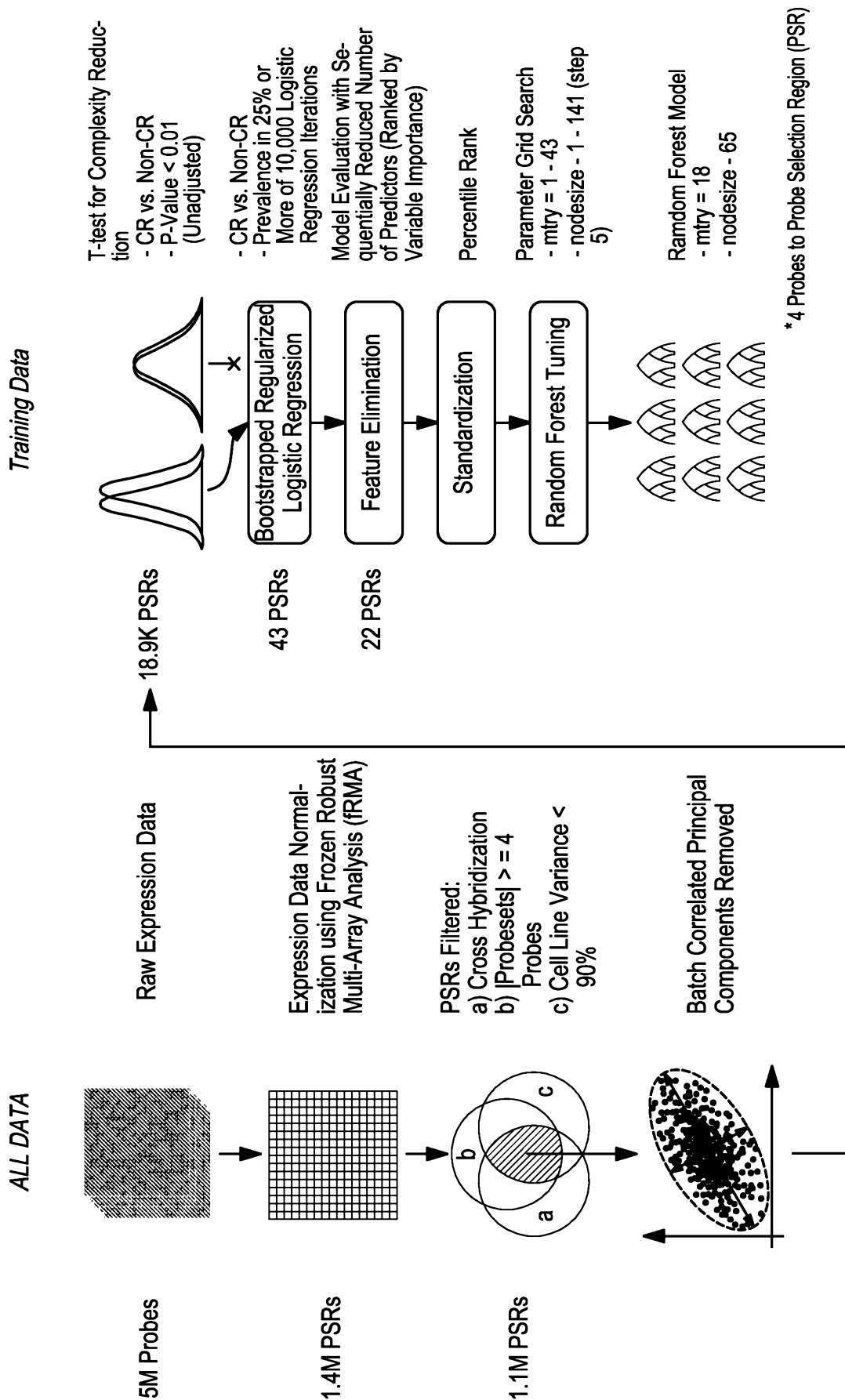


FIG. 3

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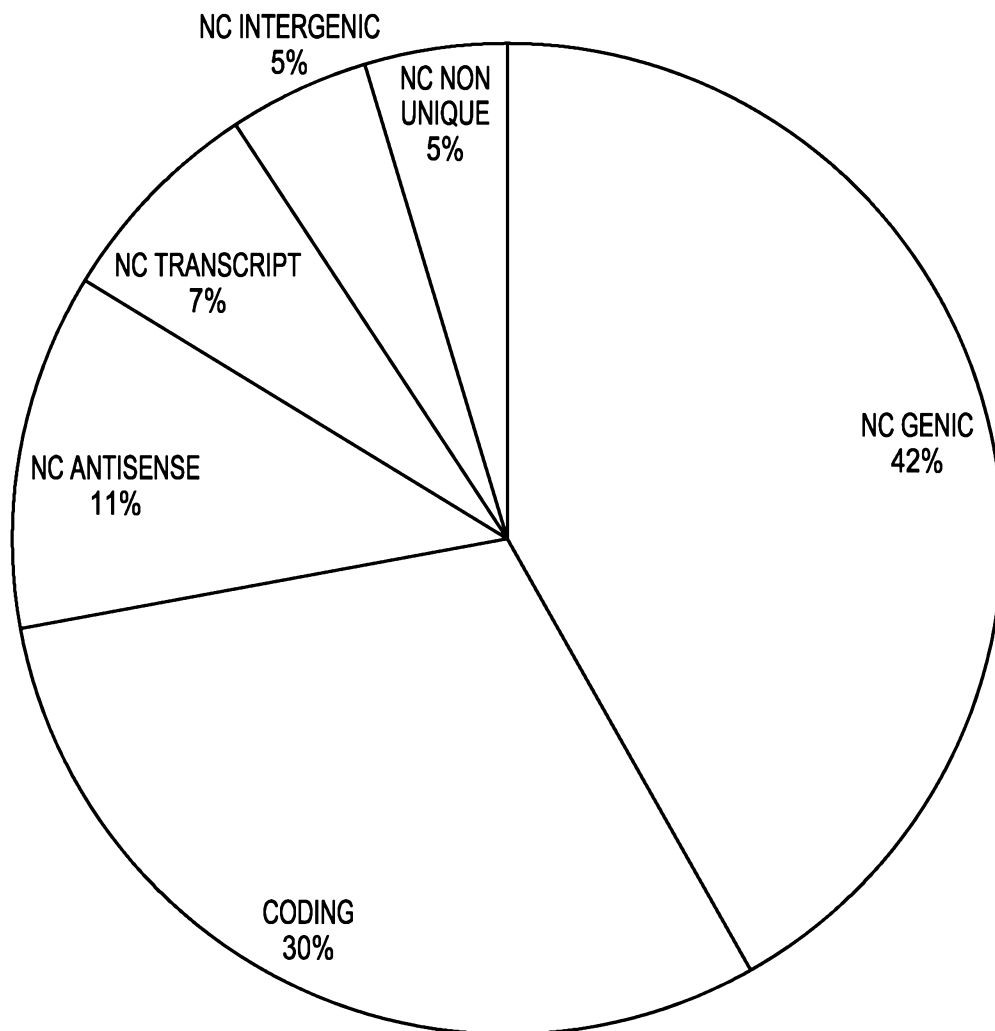
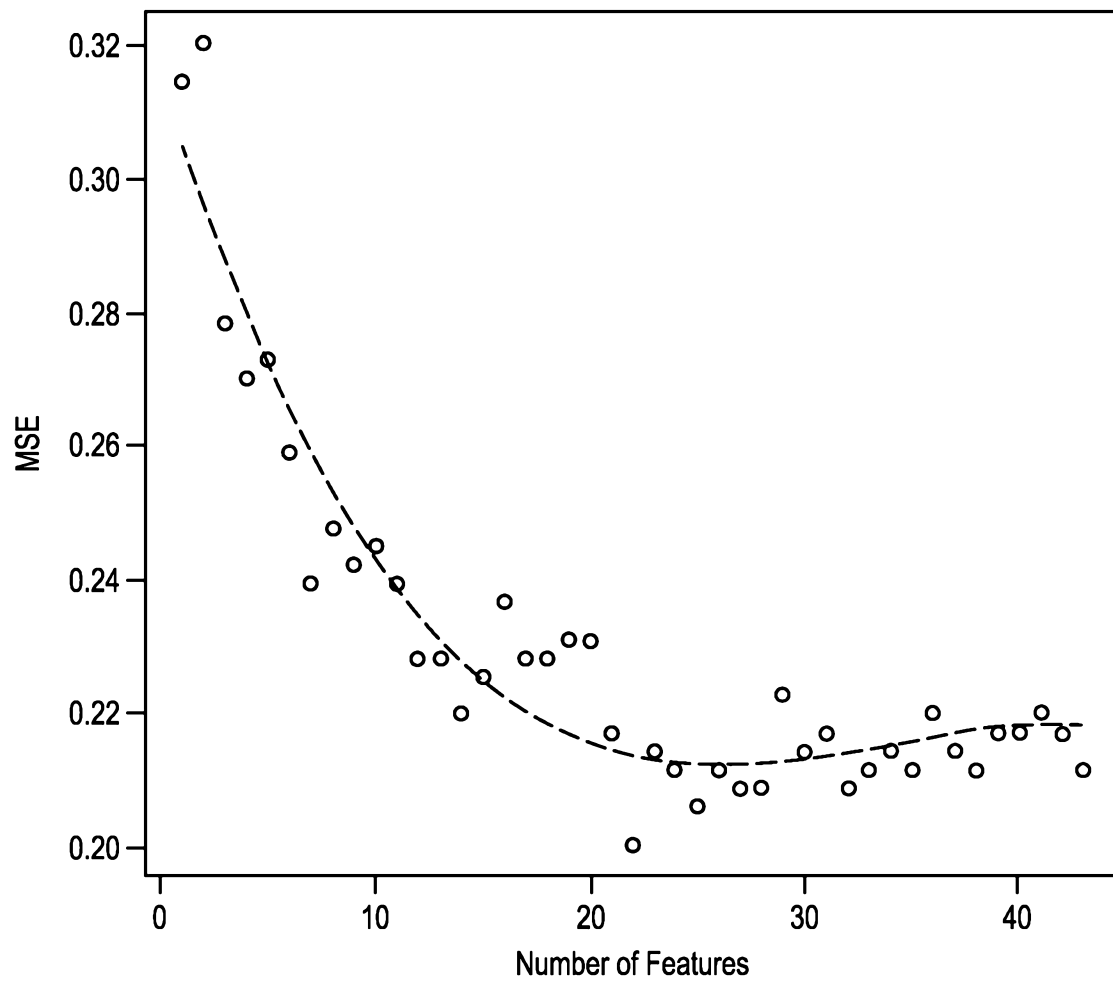
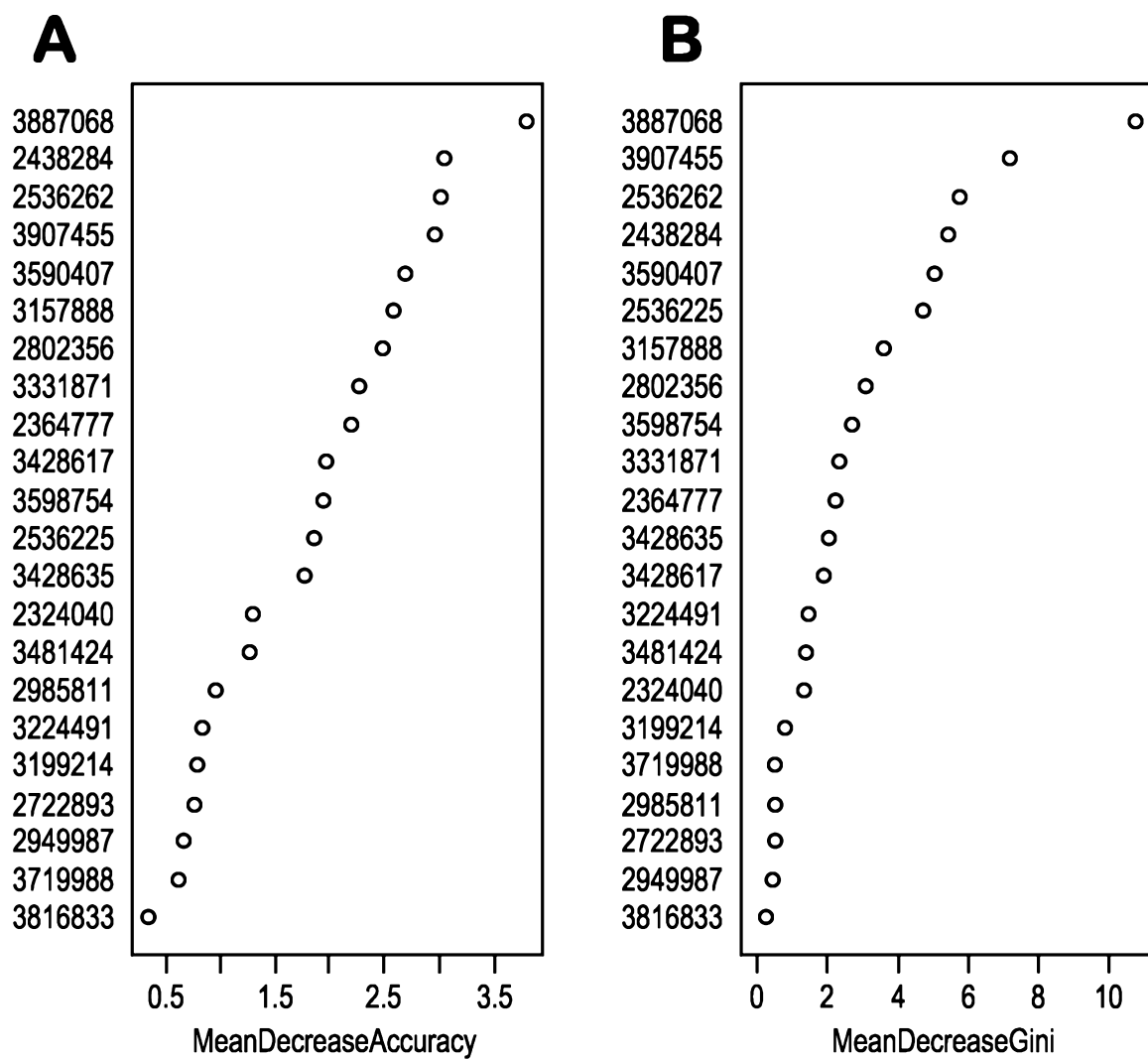


FIG. 4

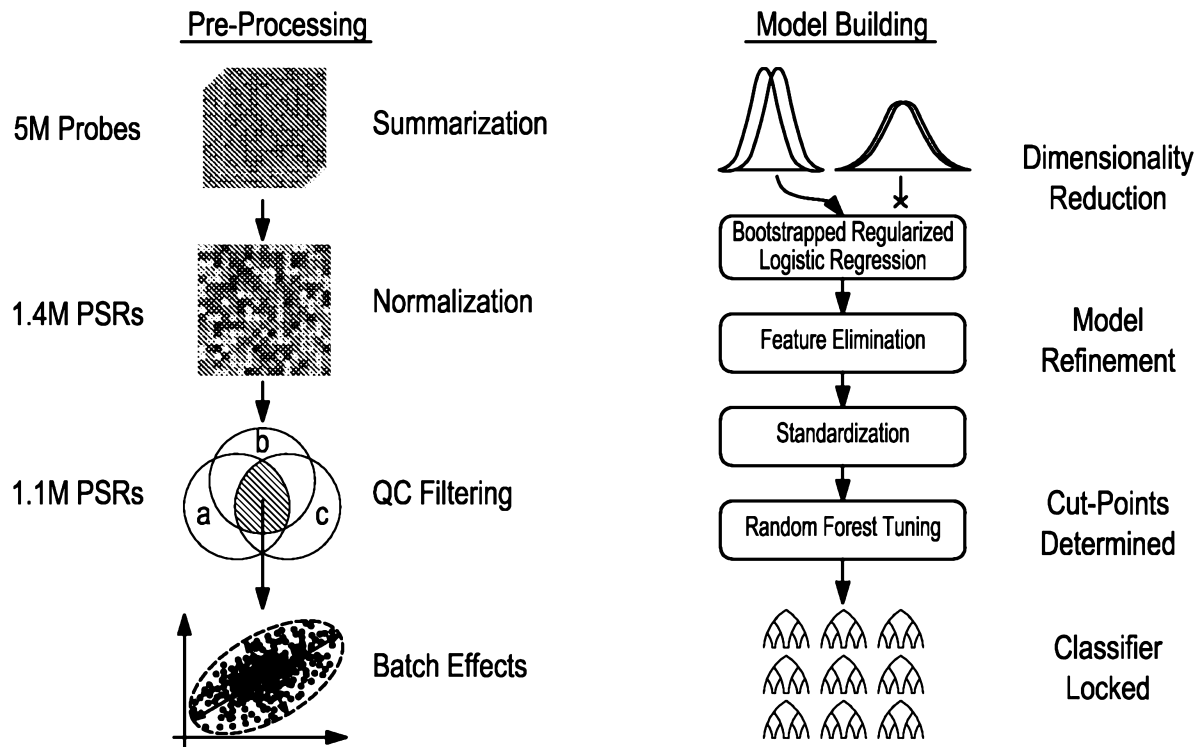
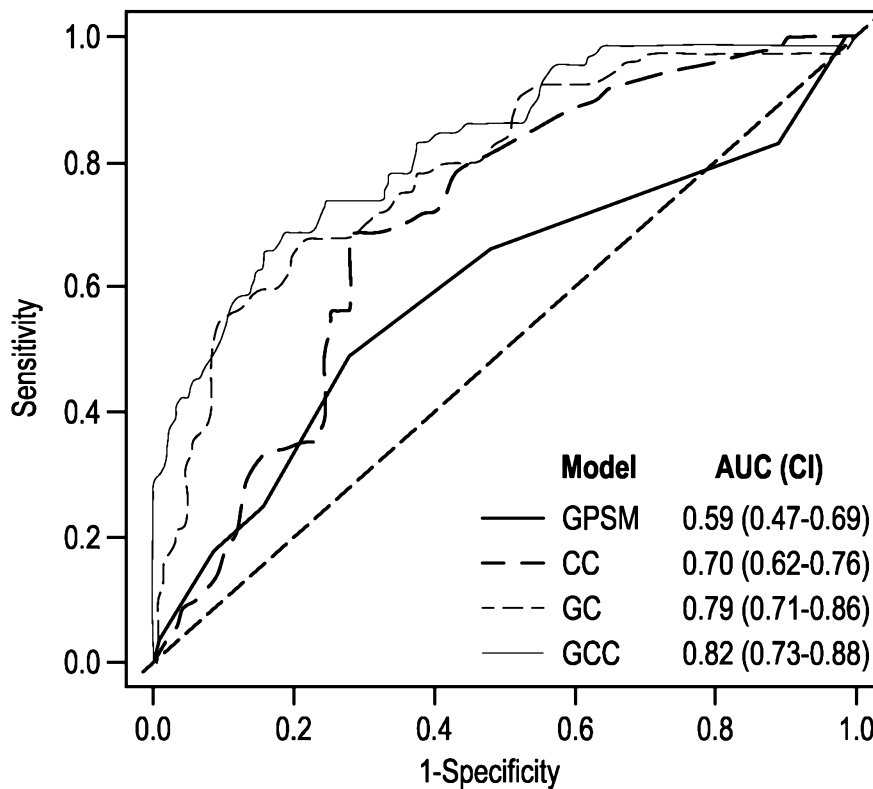
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**FIG. 5**

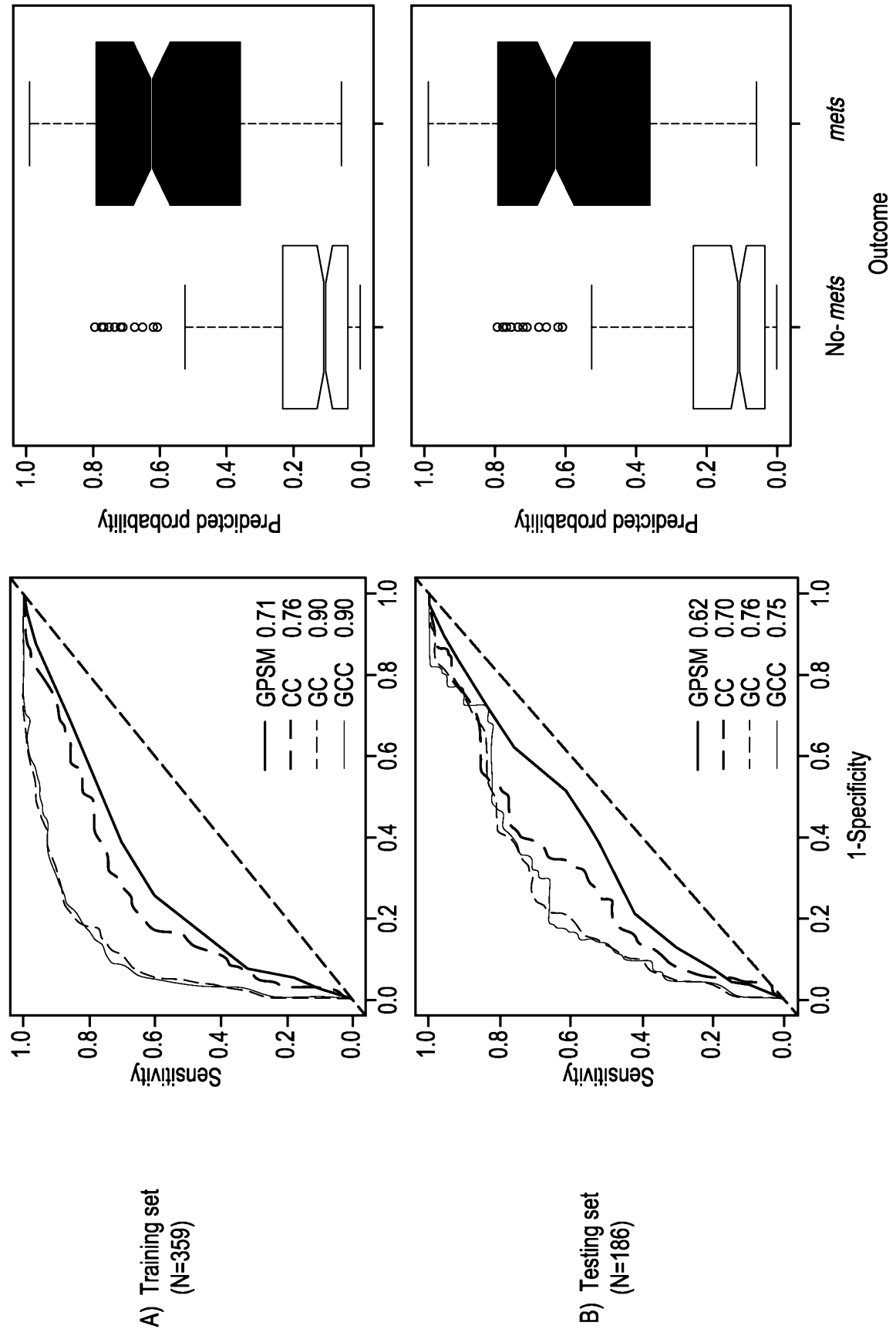
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**FIG. 6**

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**FIG. 7****FIG. 8**

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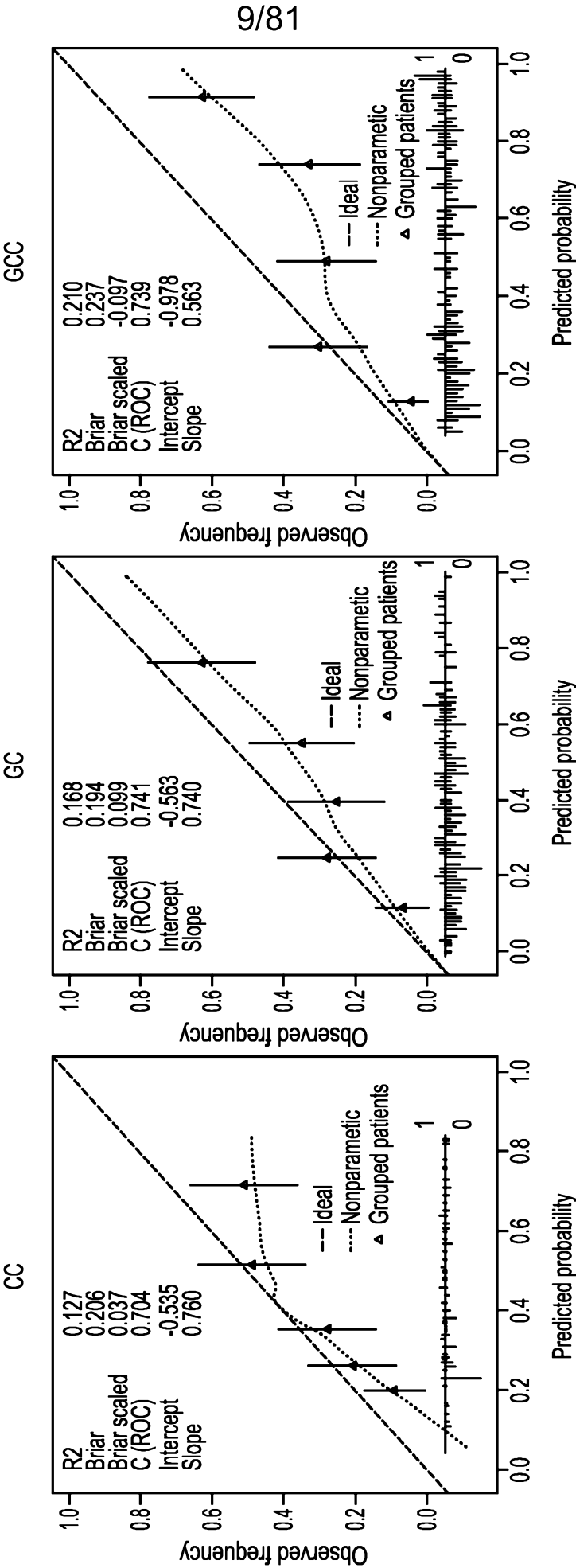
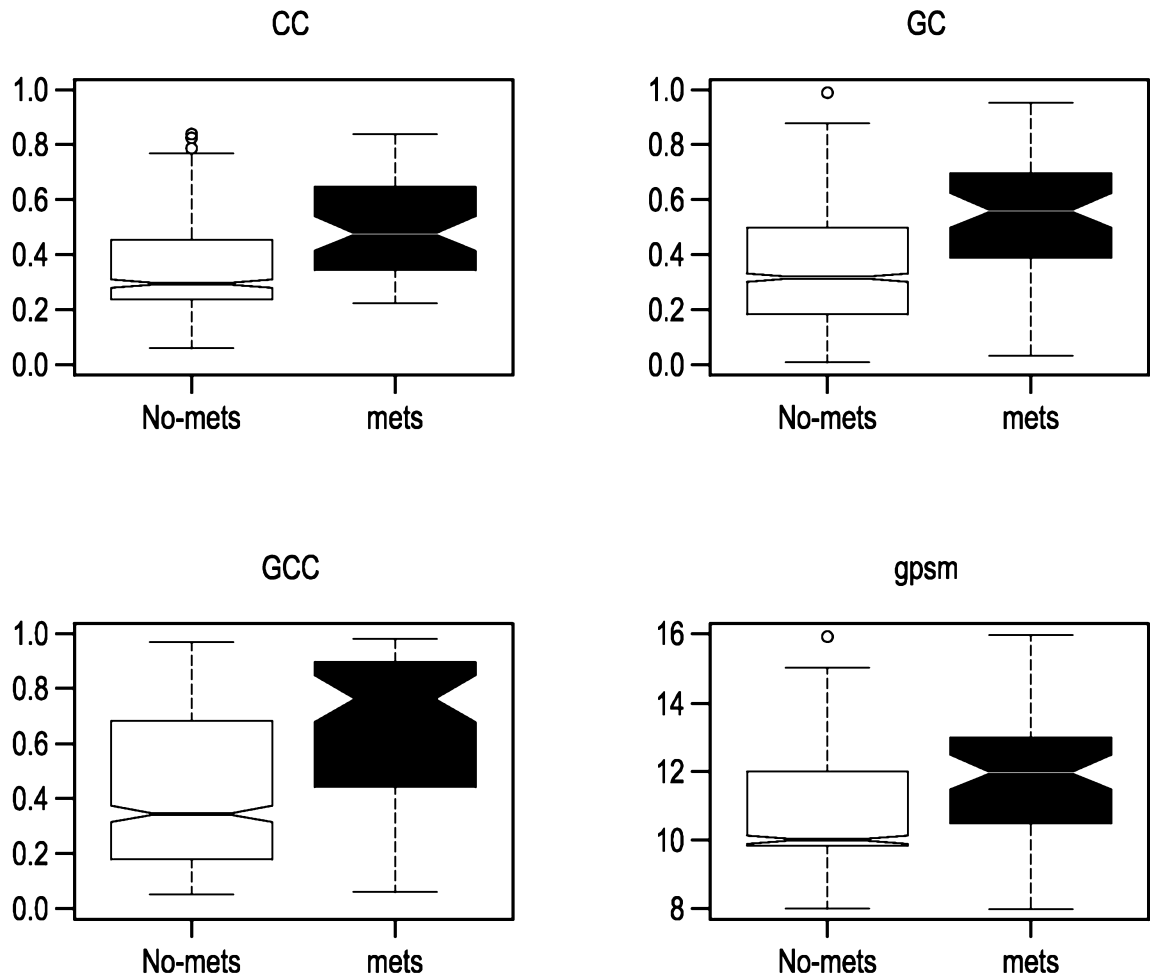
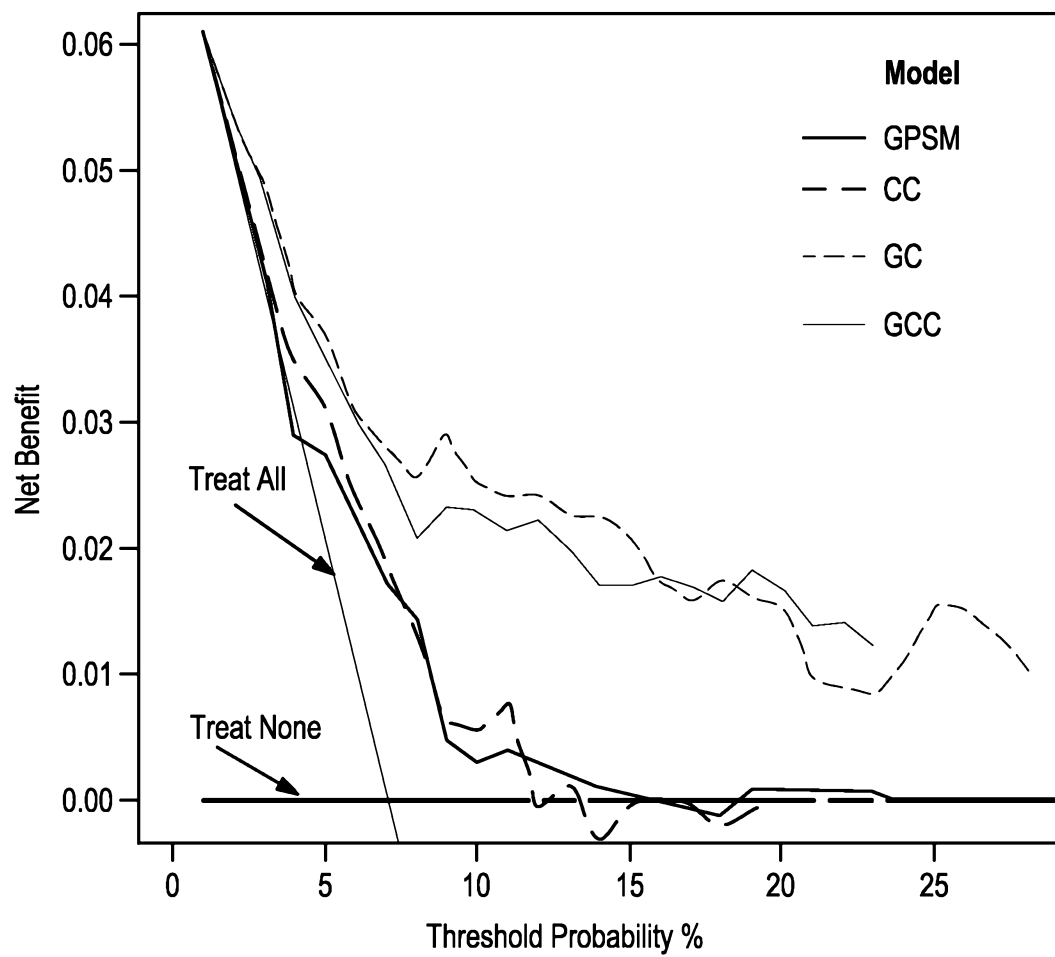


FIG. 10

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**FIG. 11**

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**FIG. 12**

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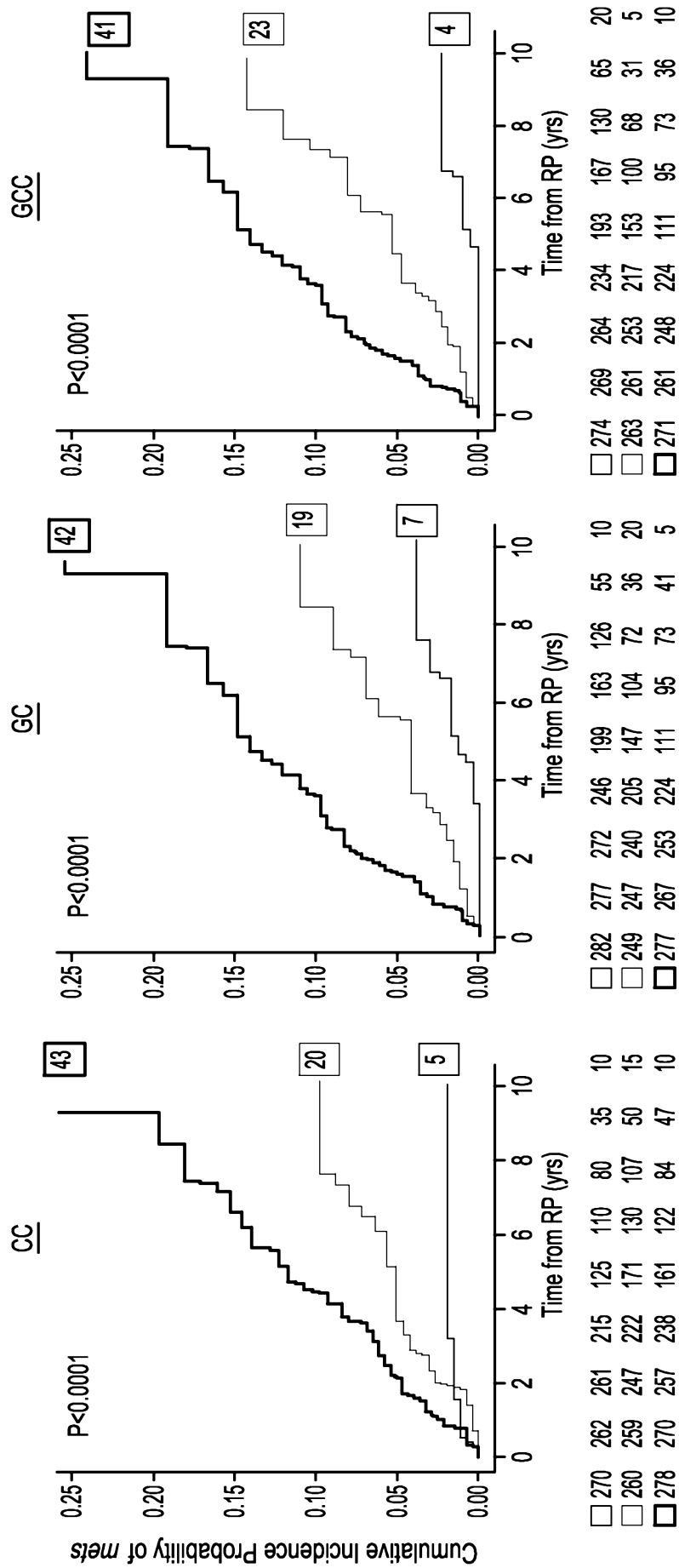


FIG. 13

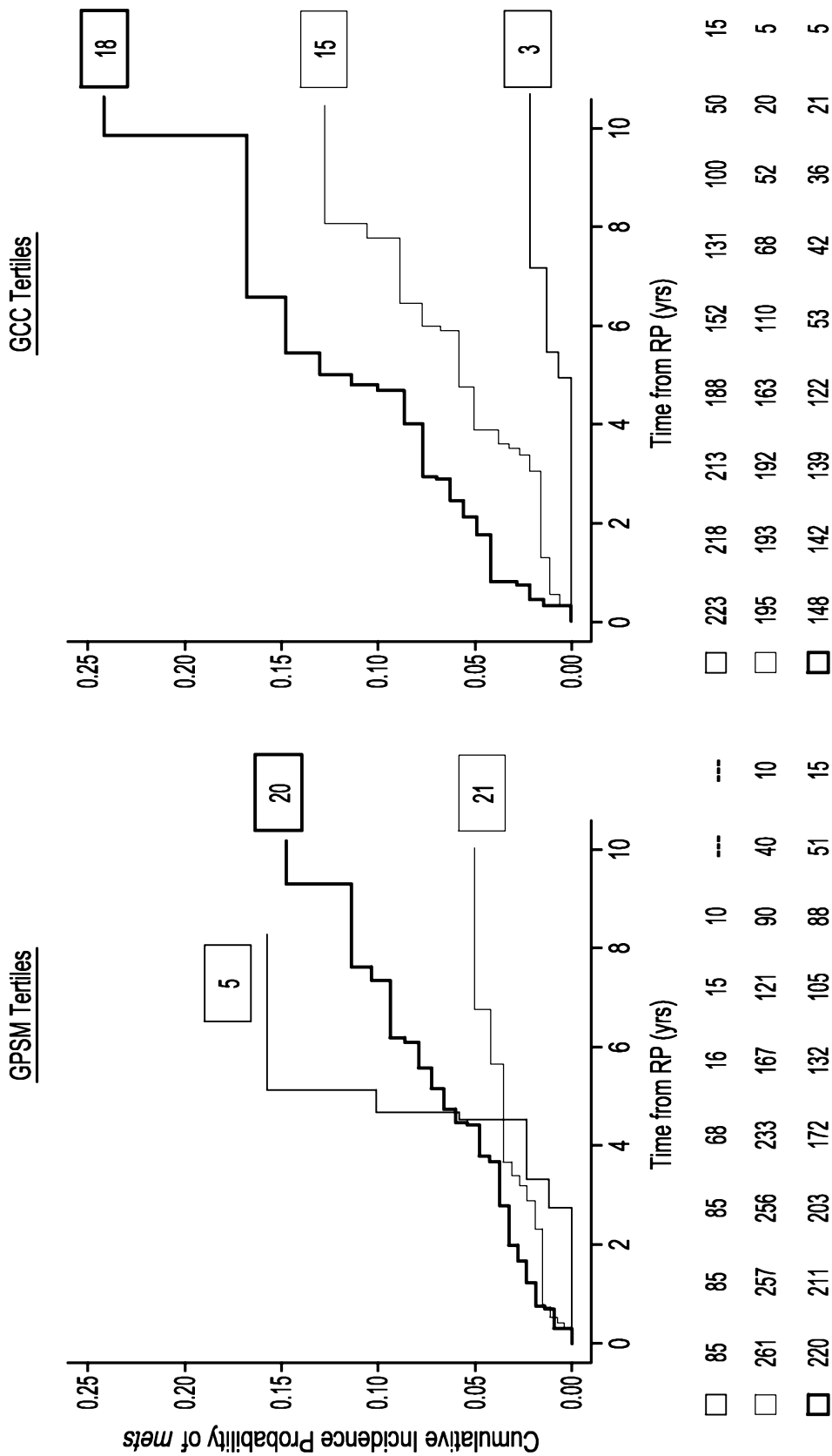


FIG. 14

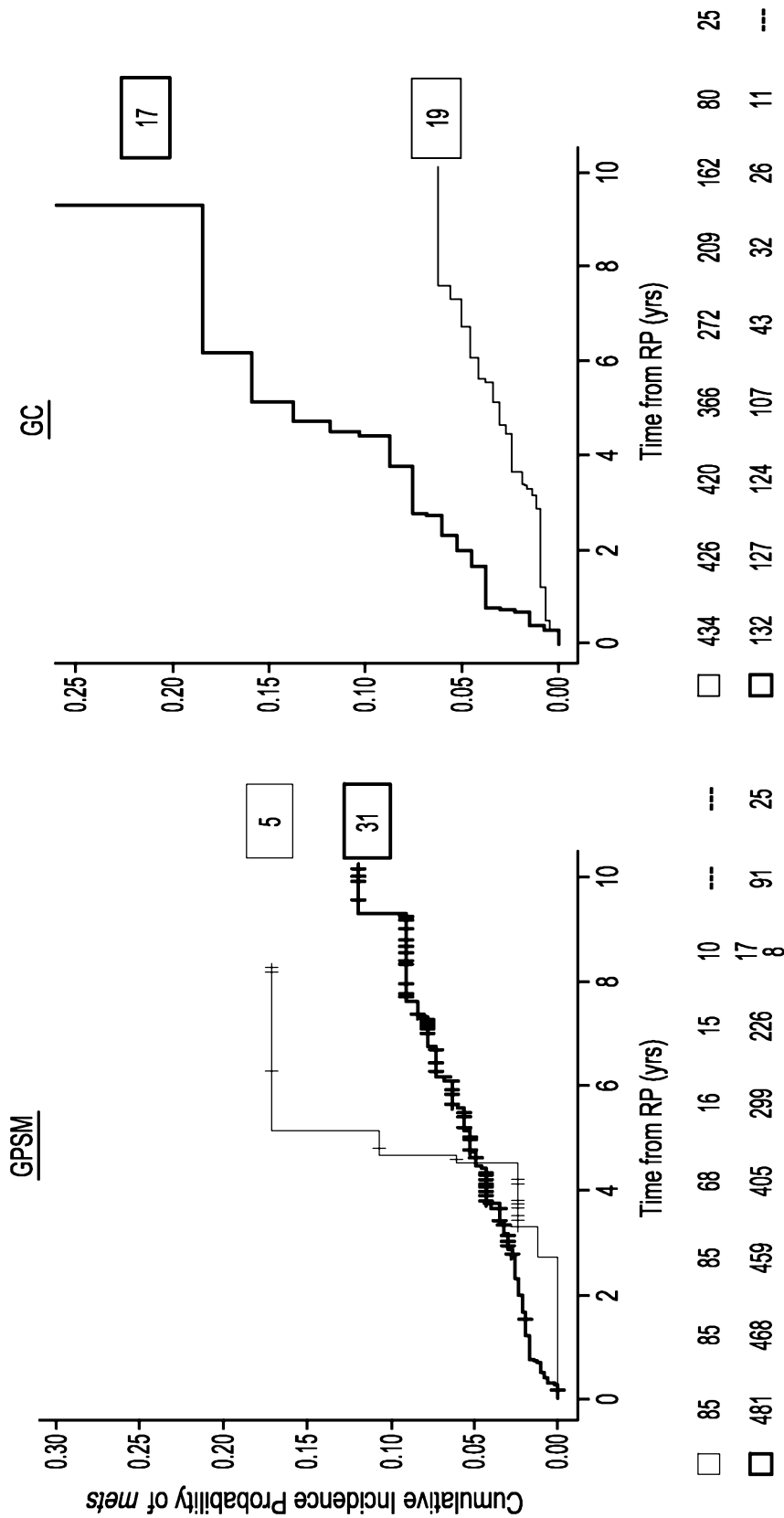


FIG. 15

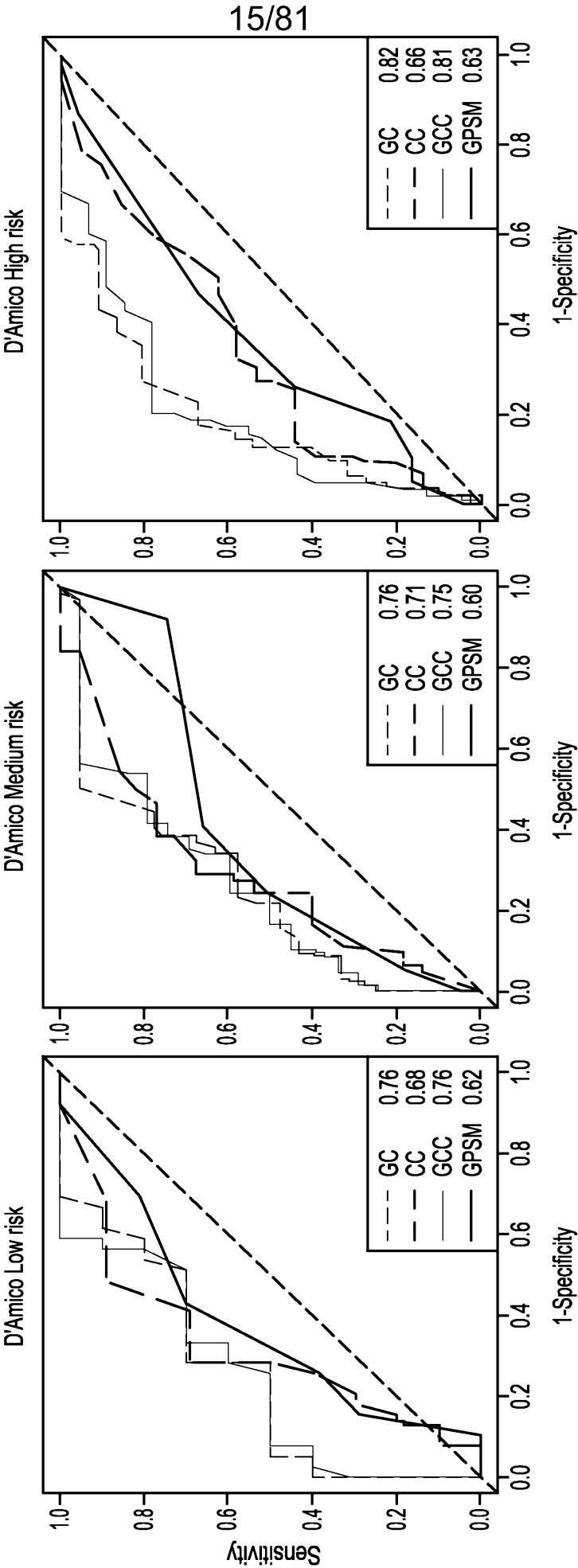


FIG. 16

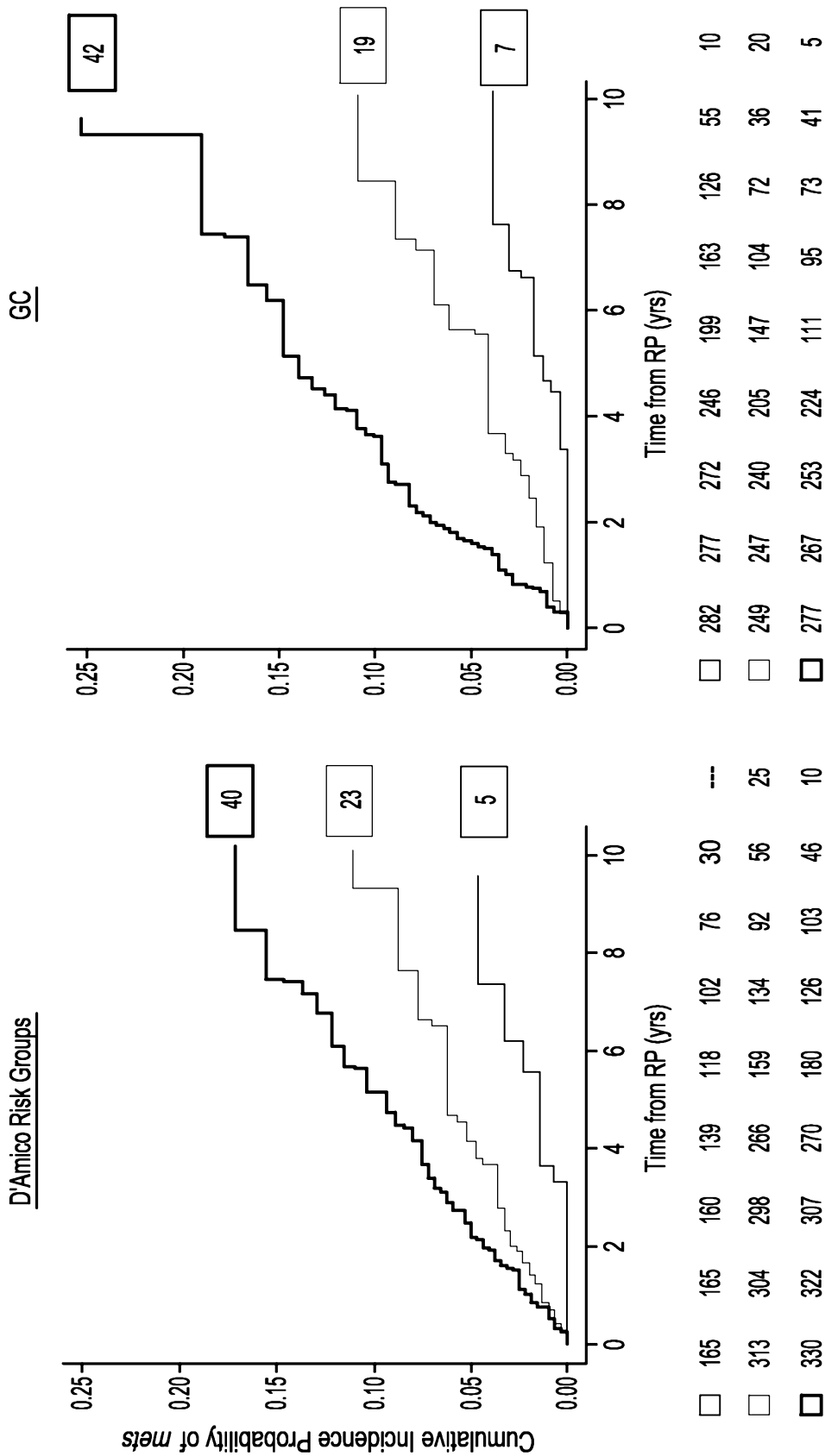
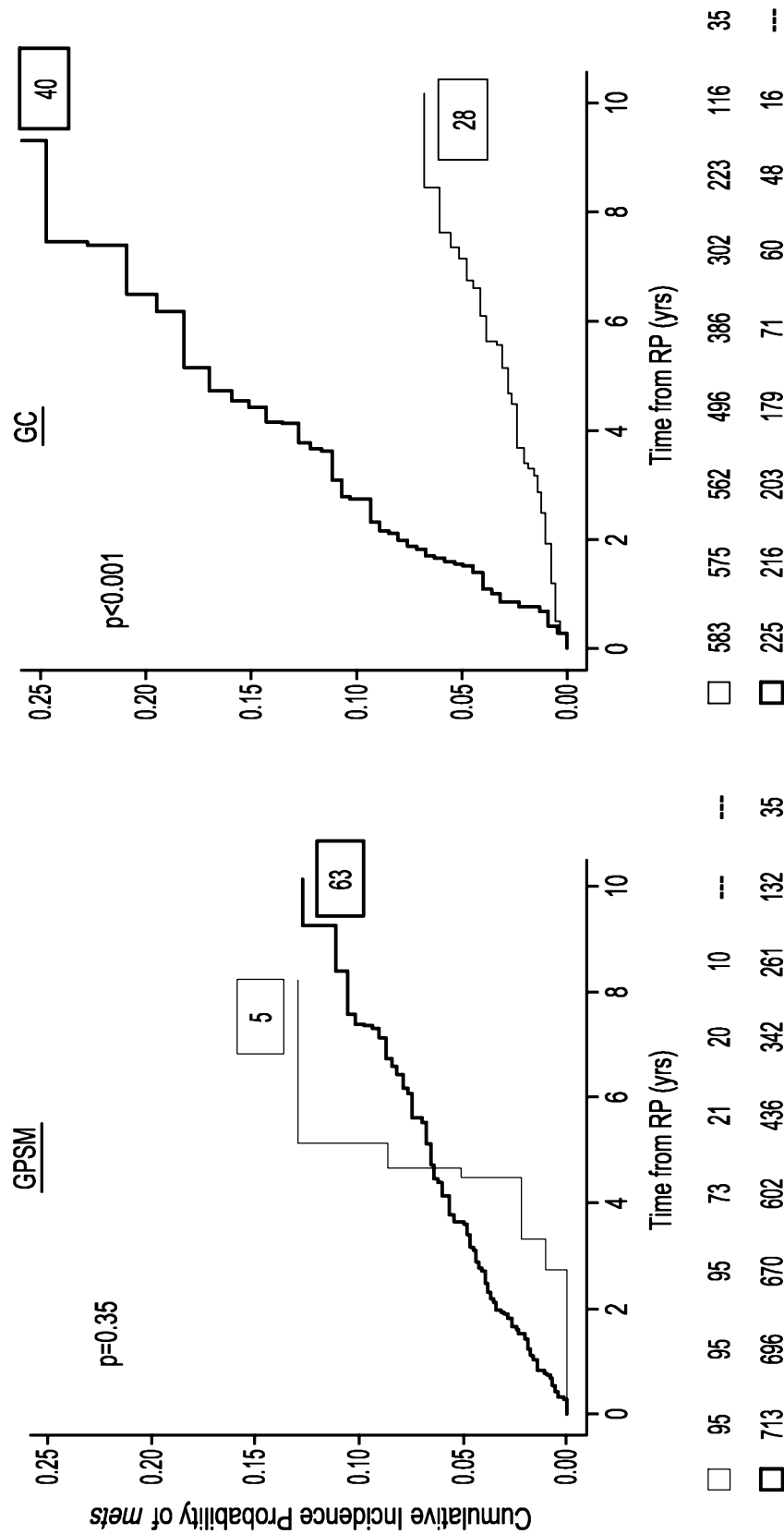
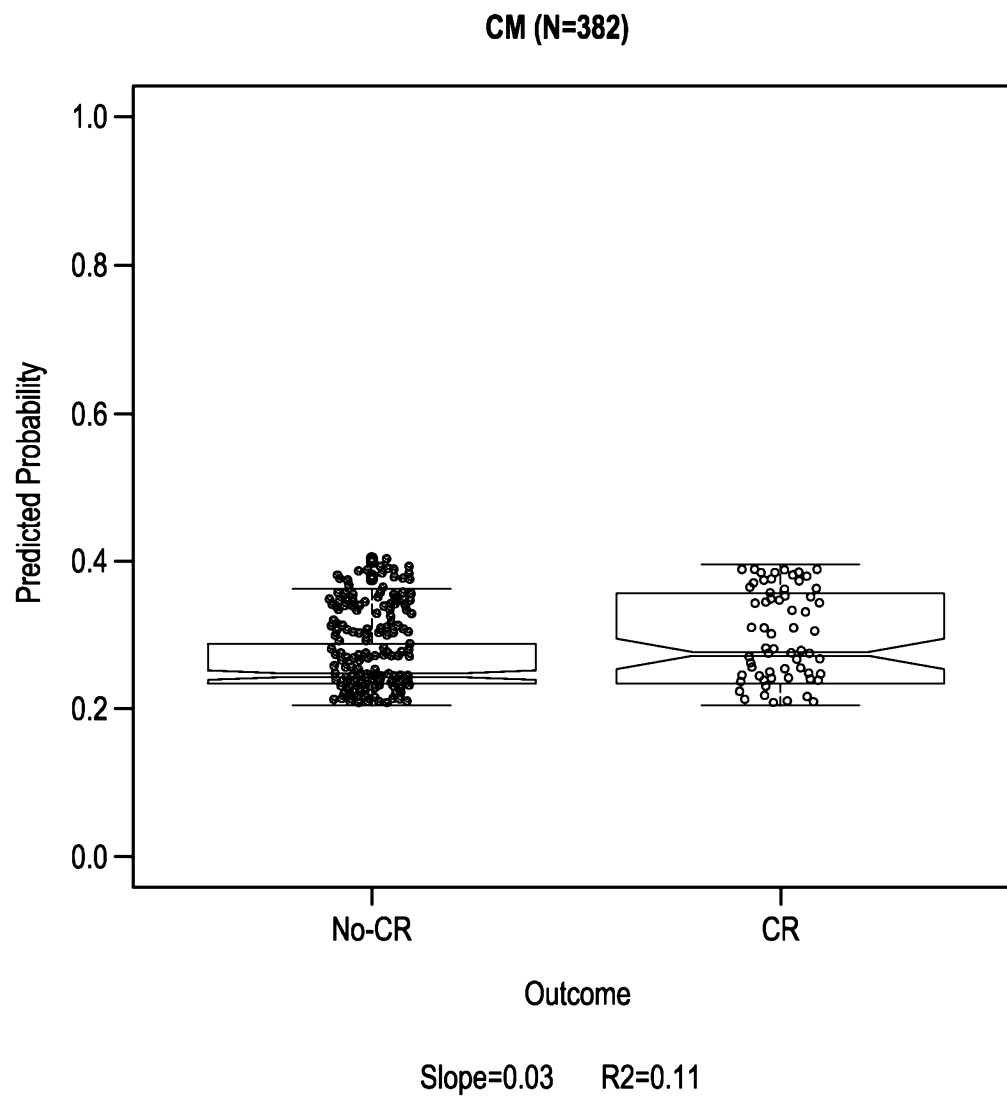


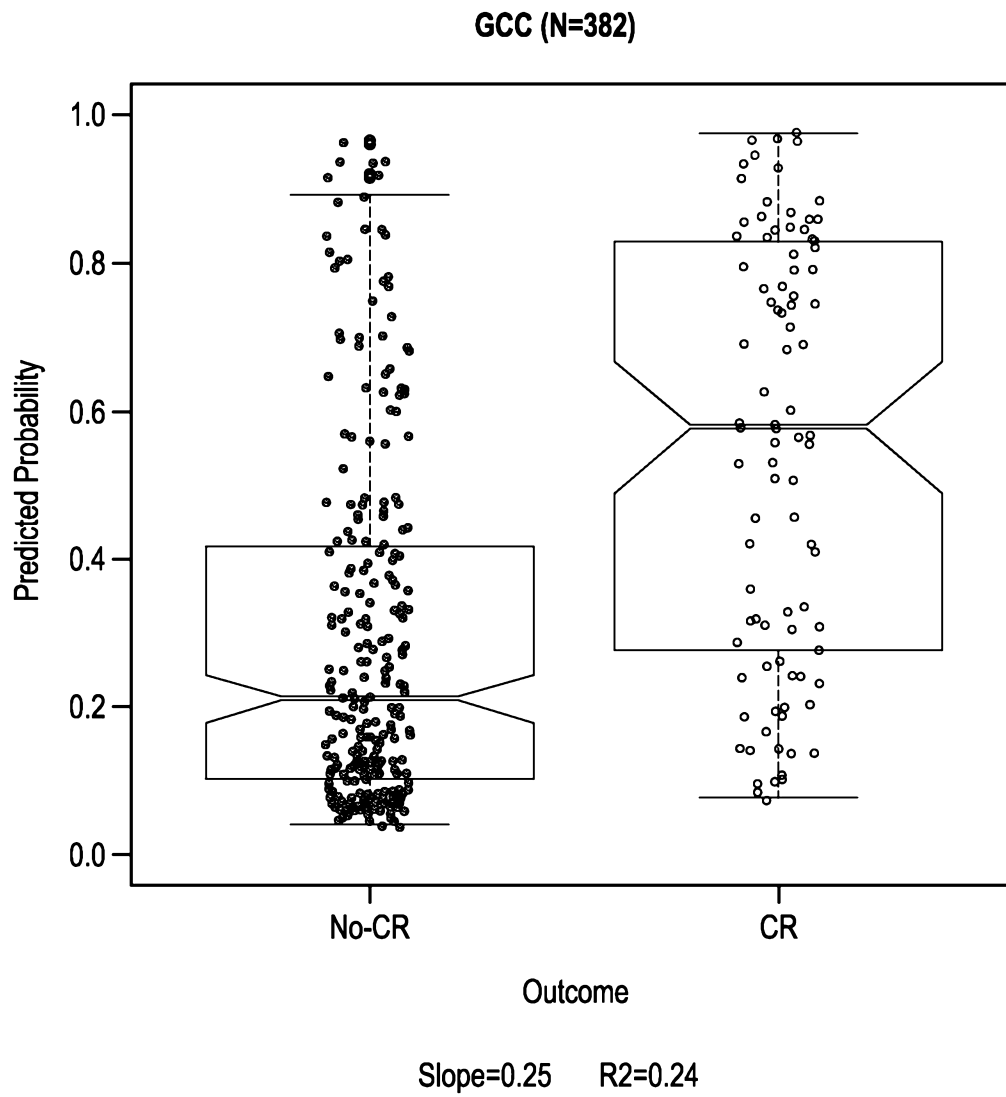
FIG. 17



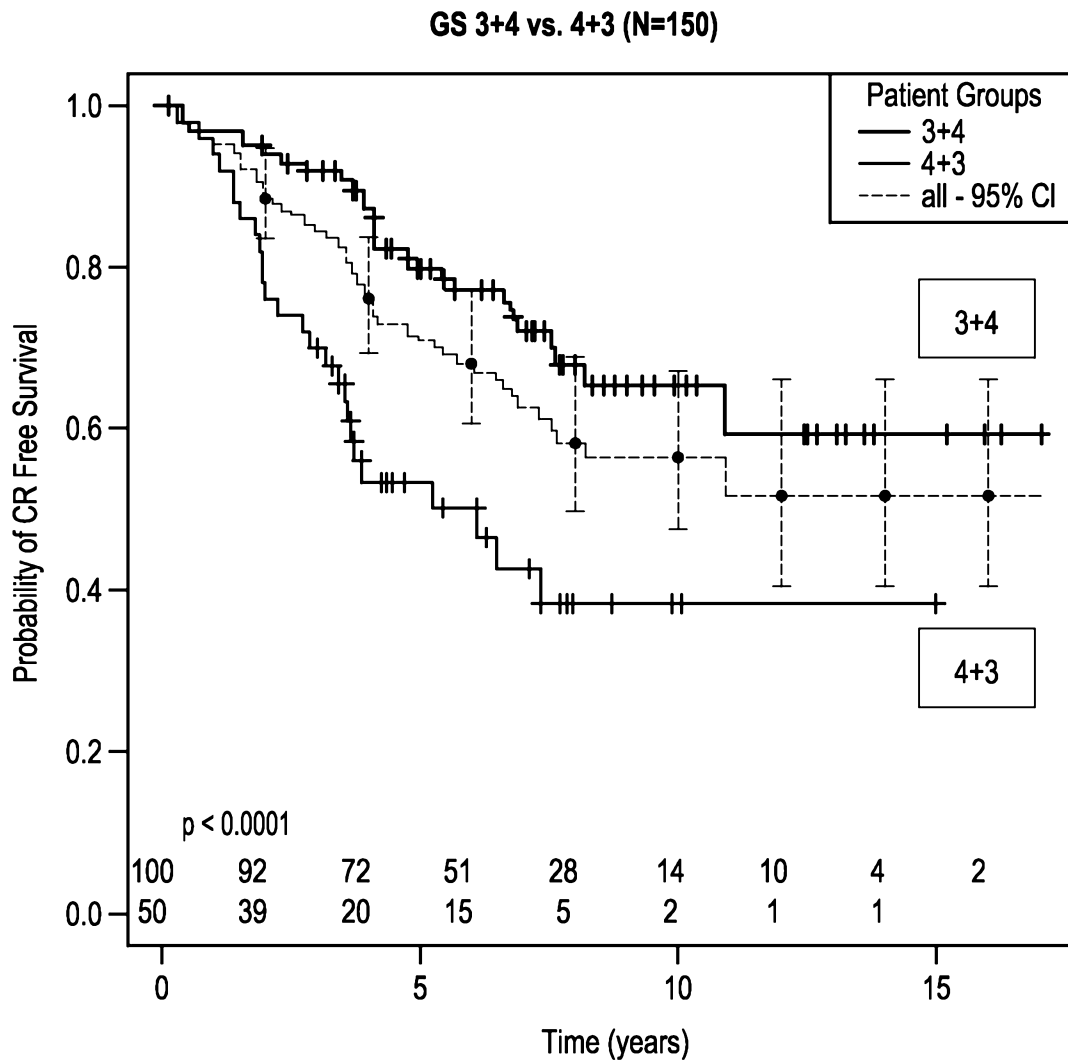
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**FIG. 19A**

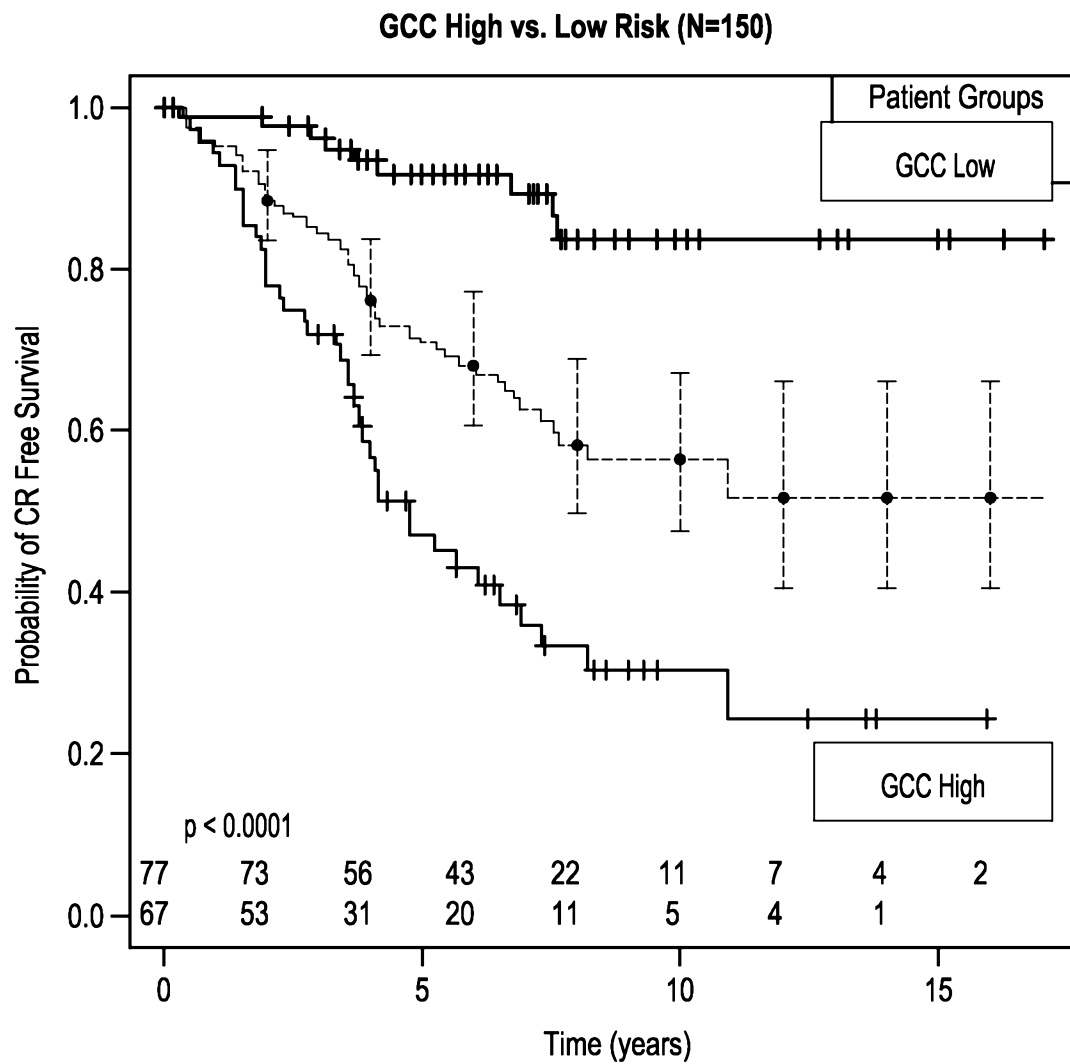
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**FIG. 19B**

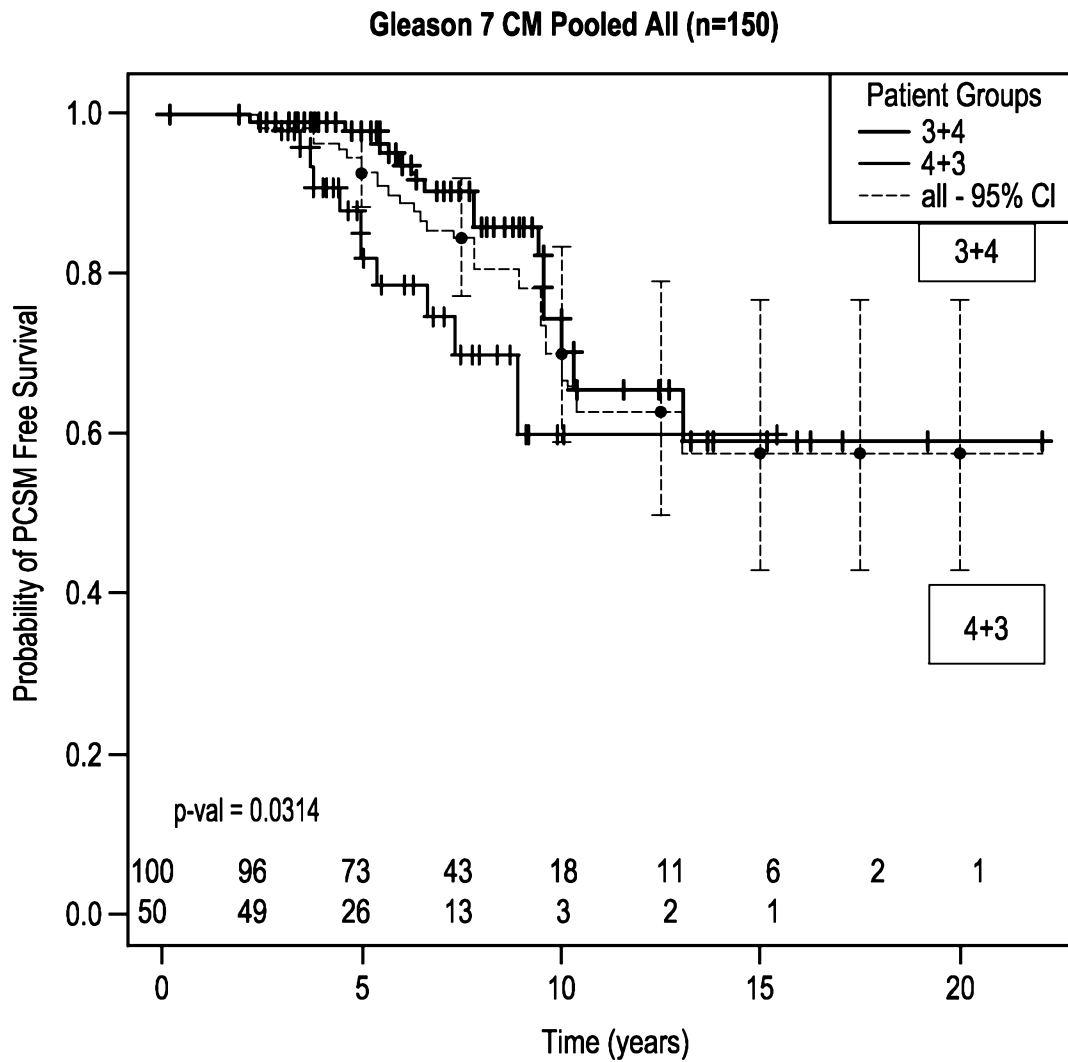
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**FIG. 20A**

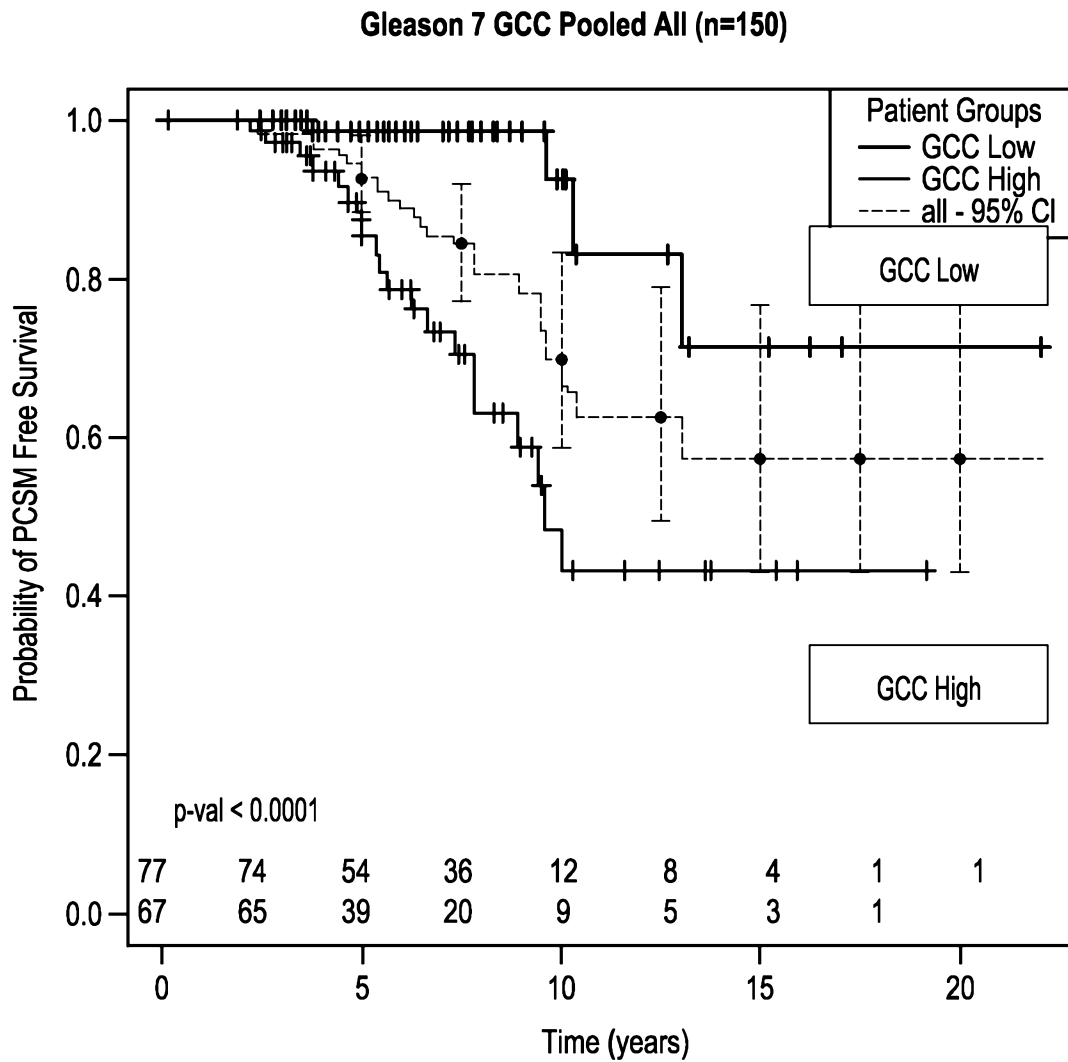
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**FIG. 20B**

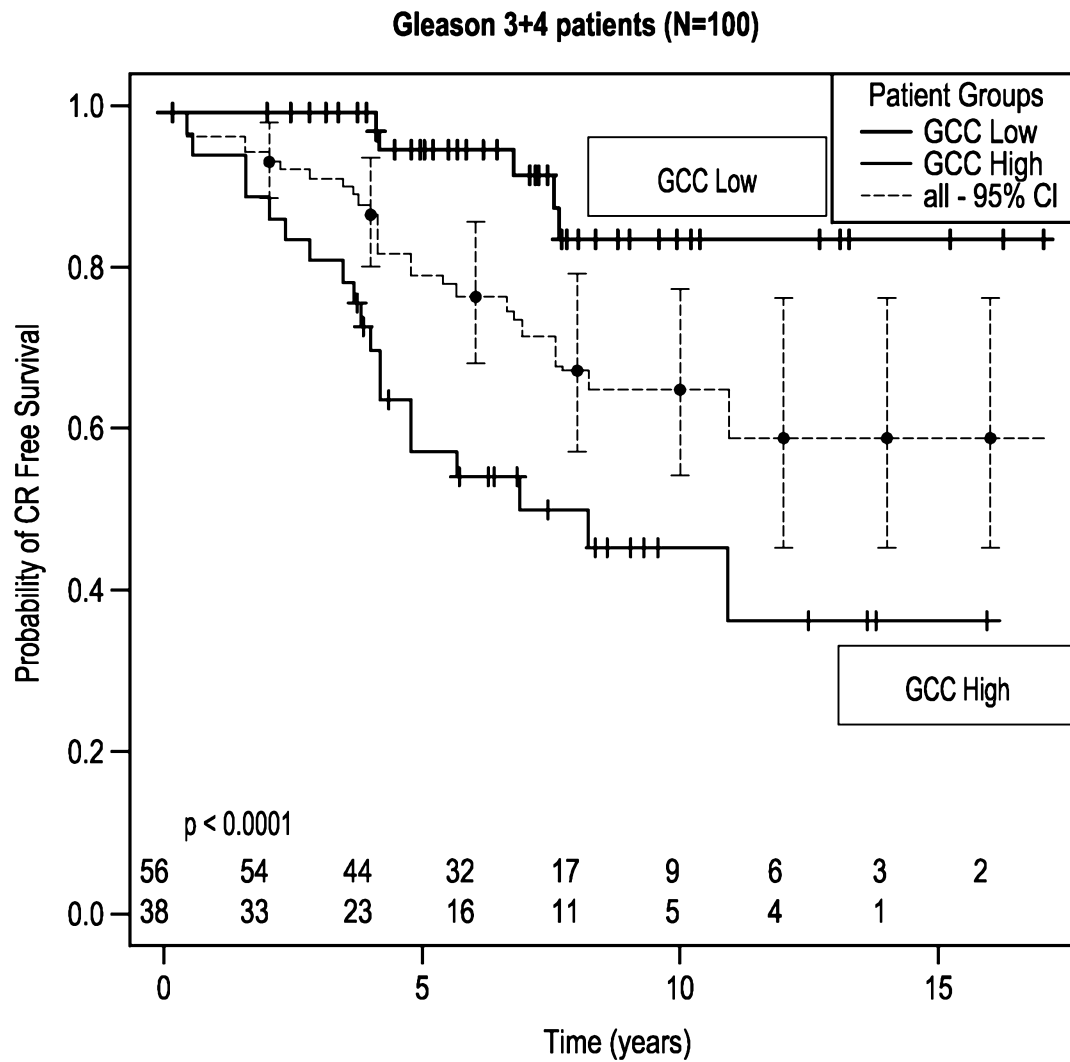
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**FIG. 21A**

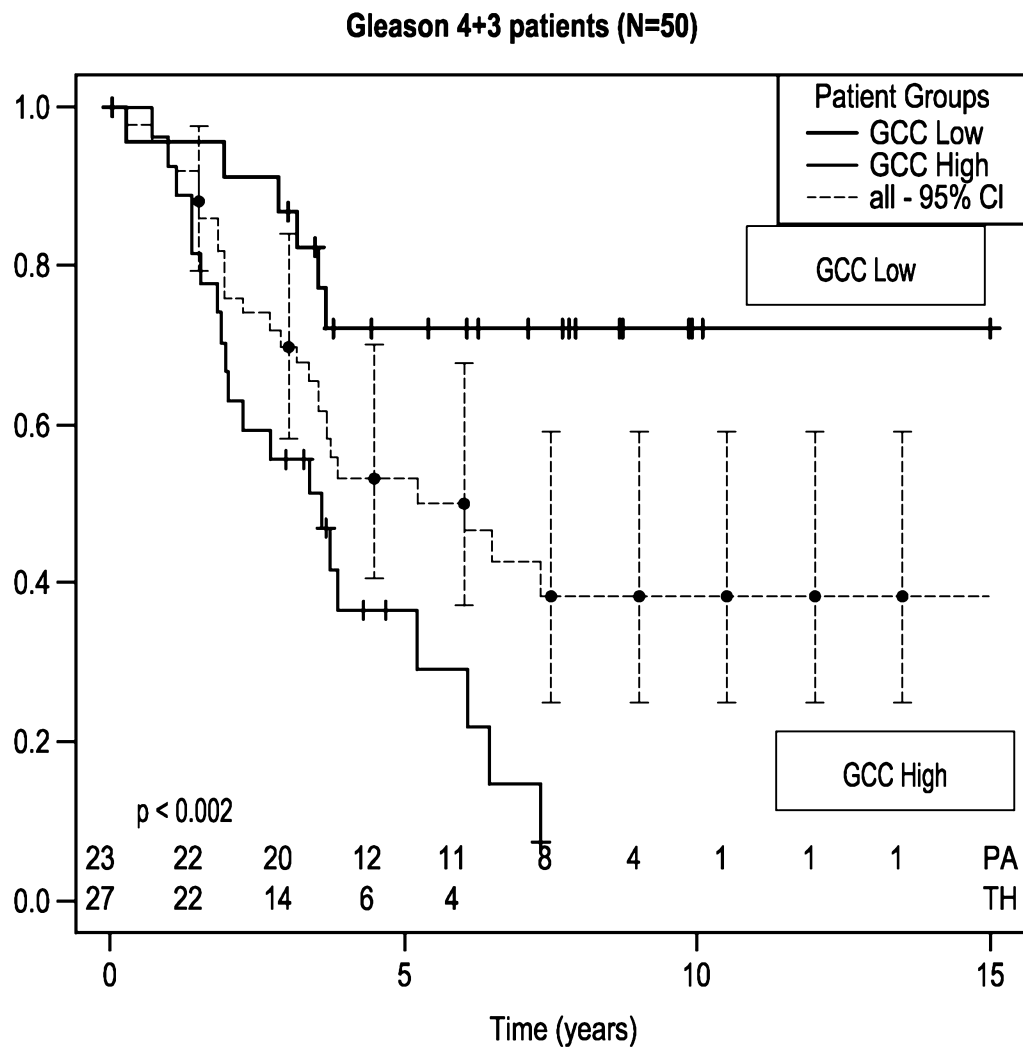
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**FIG. 21B**

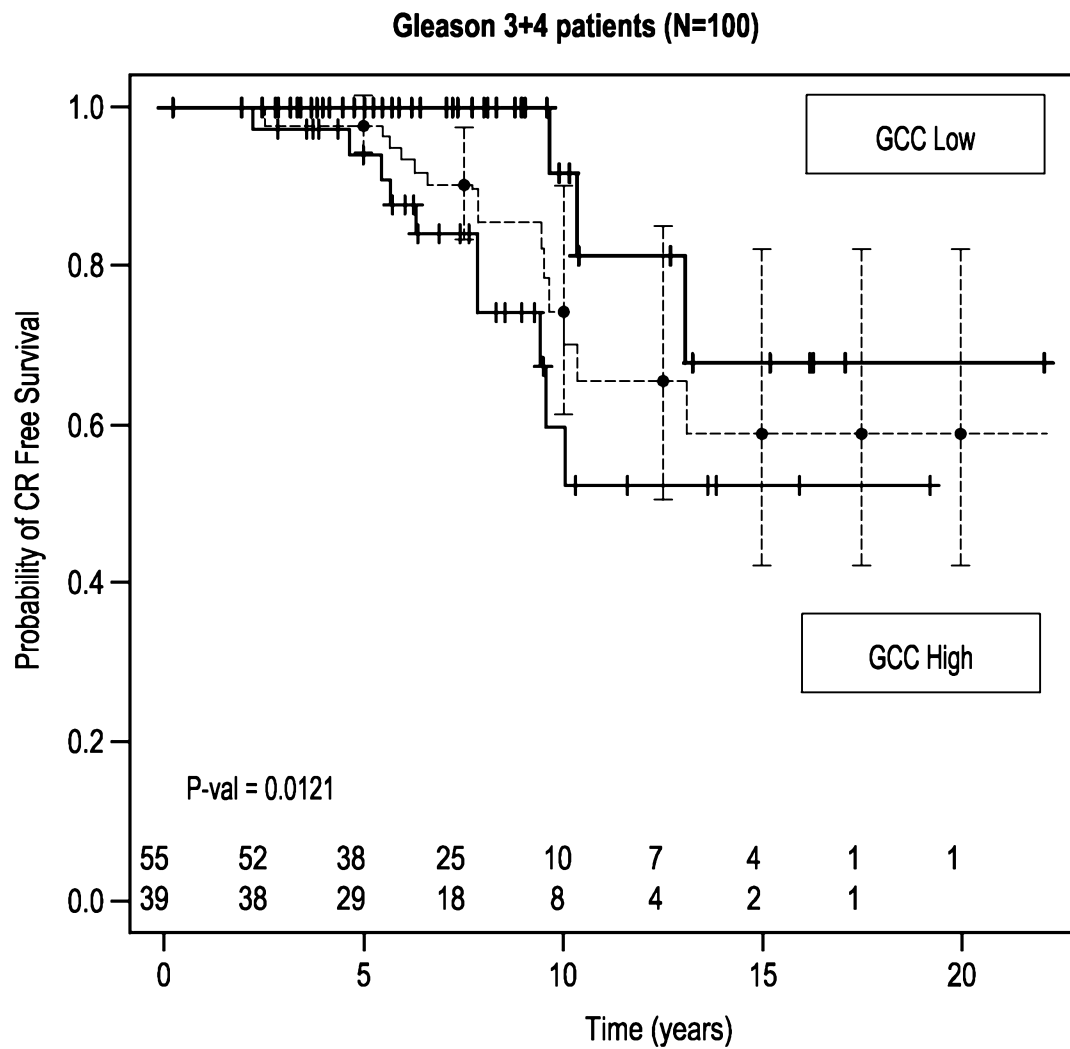
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**FIG. 22A**

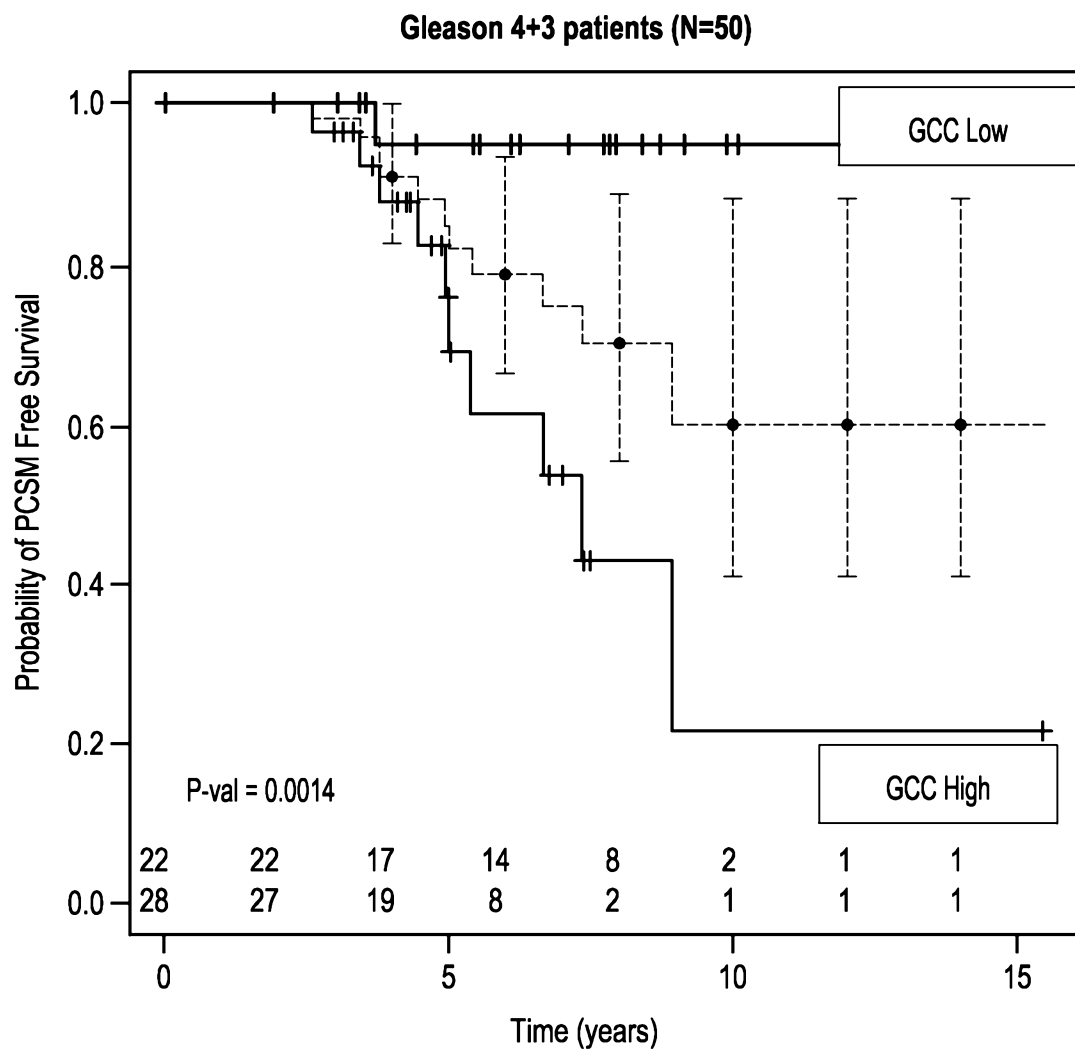
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**FIG. 22B**

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**FIG. 23A**

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**FIG. 23B**

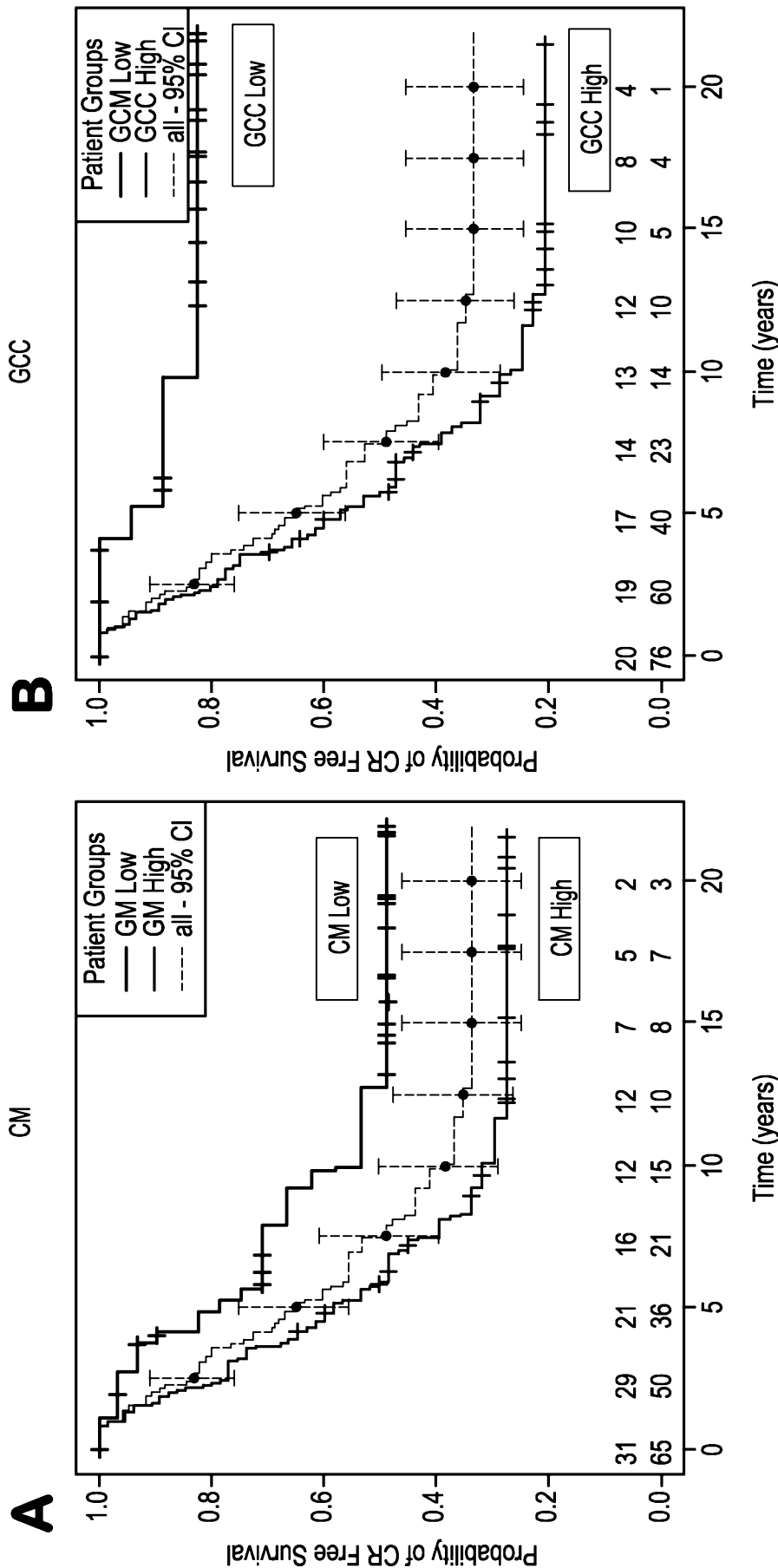
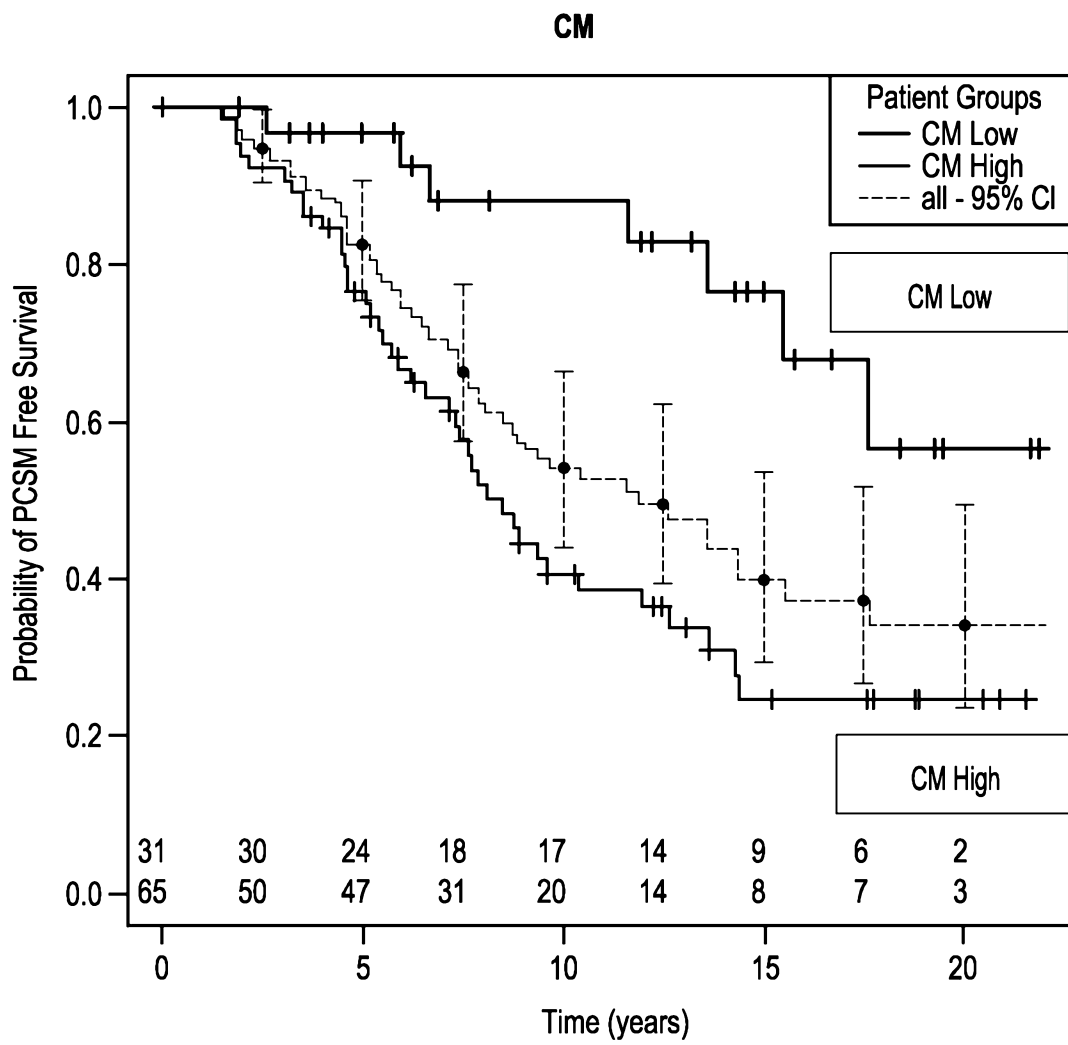
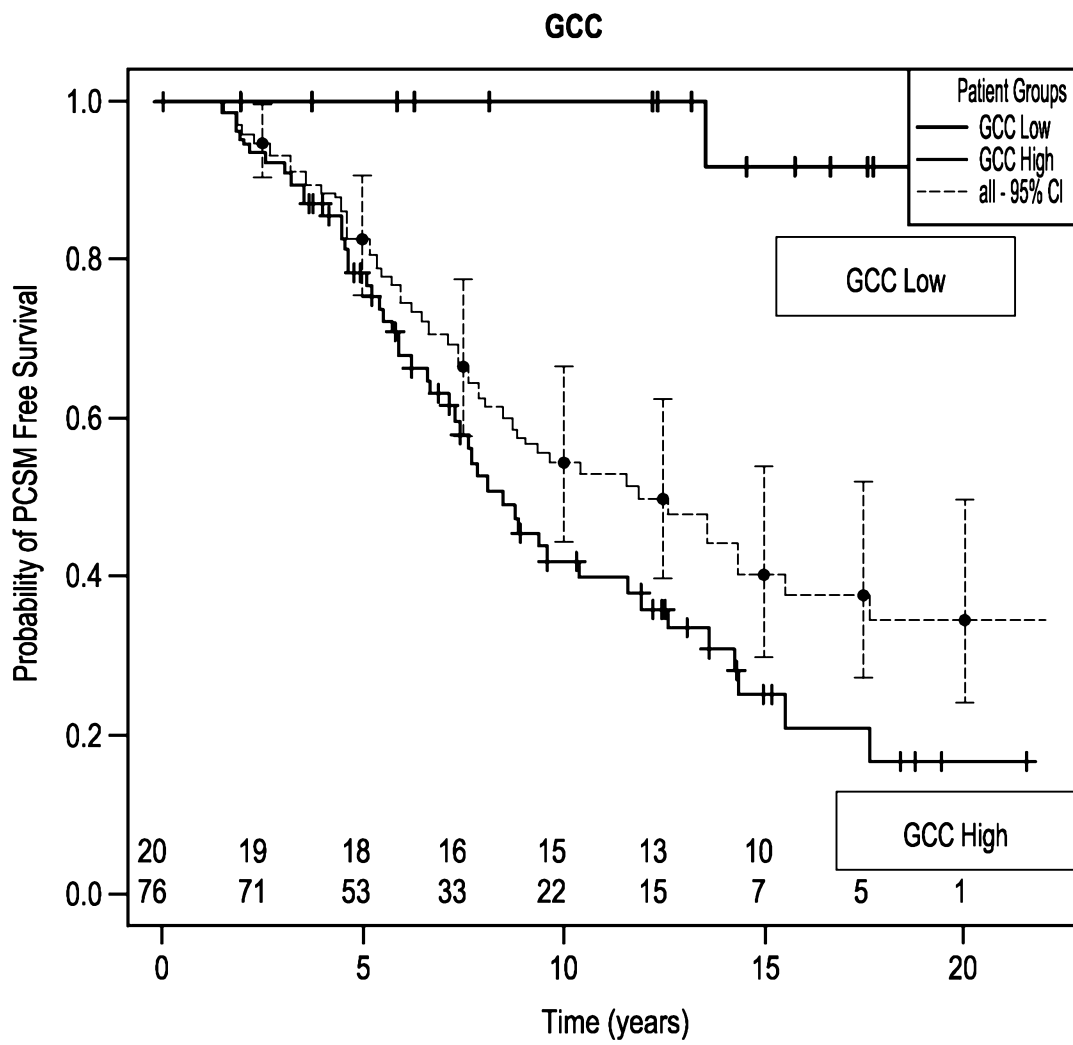


FIG. 24

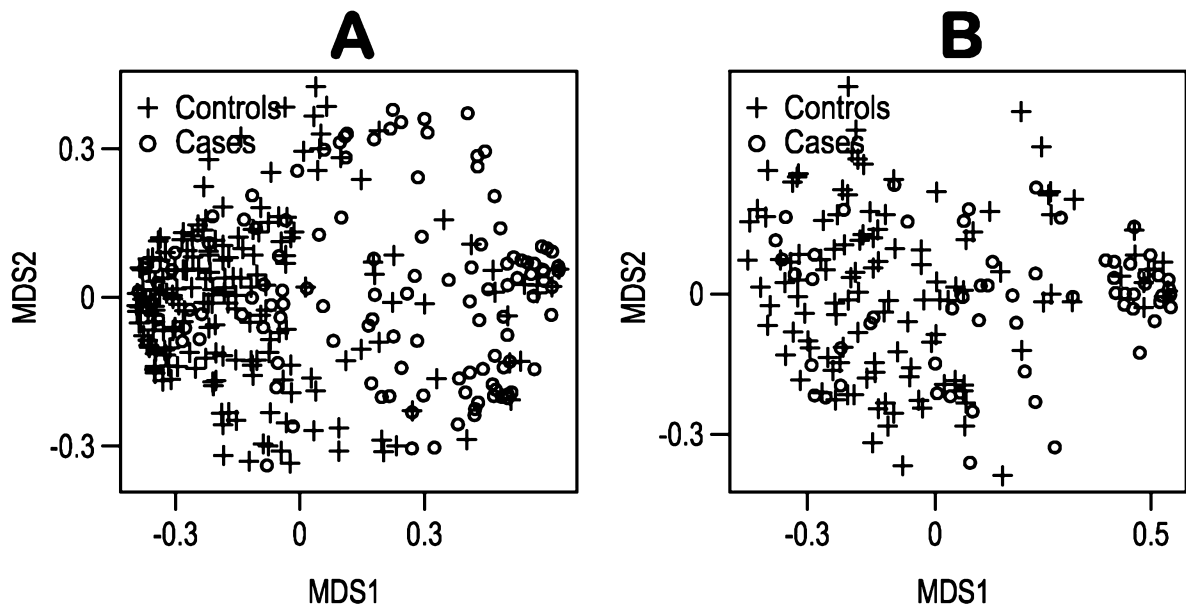
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**FIG. 25A**

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**FIG. 25B**

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**FIG. 26**

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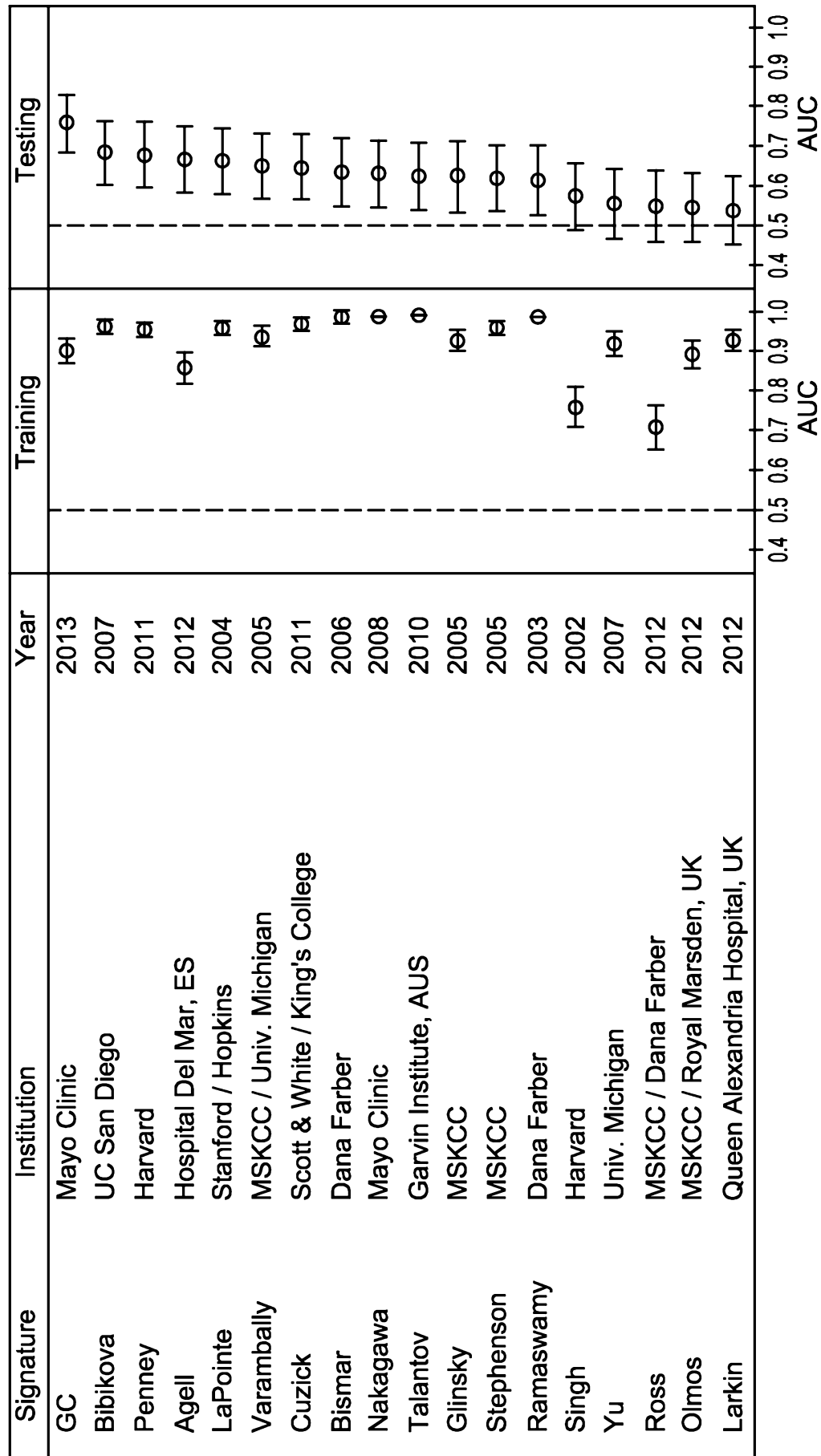
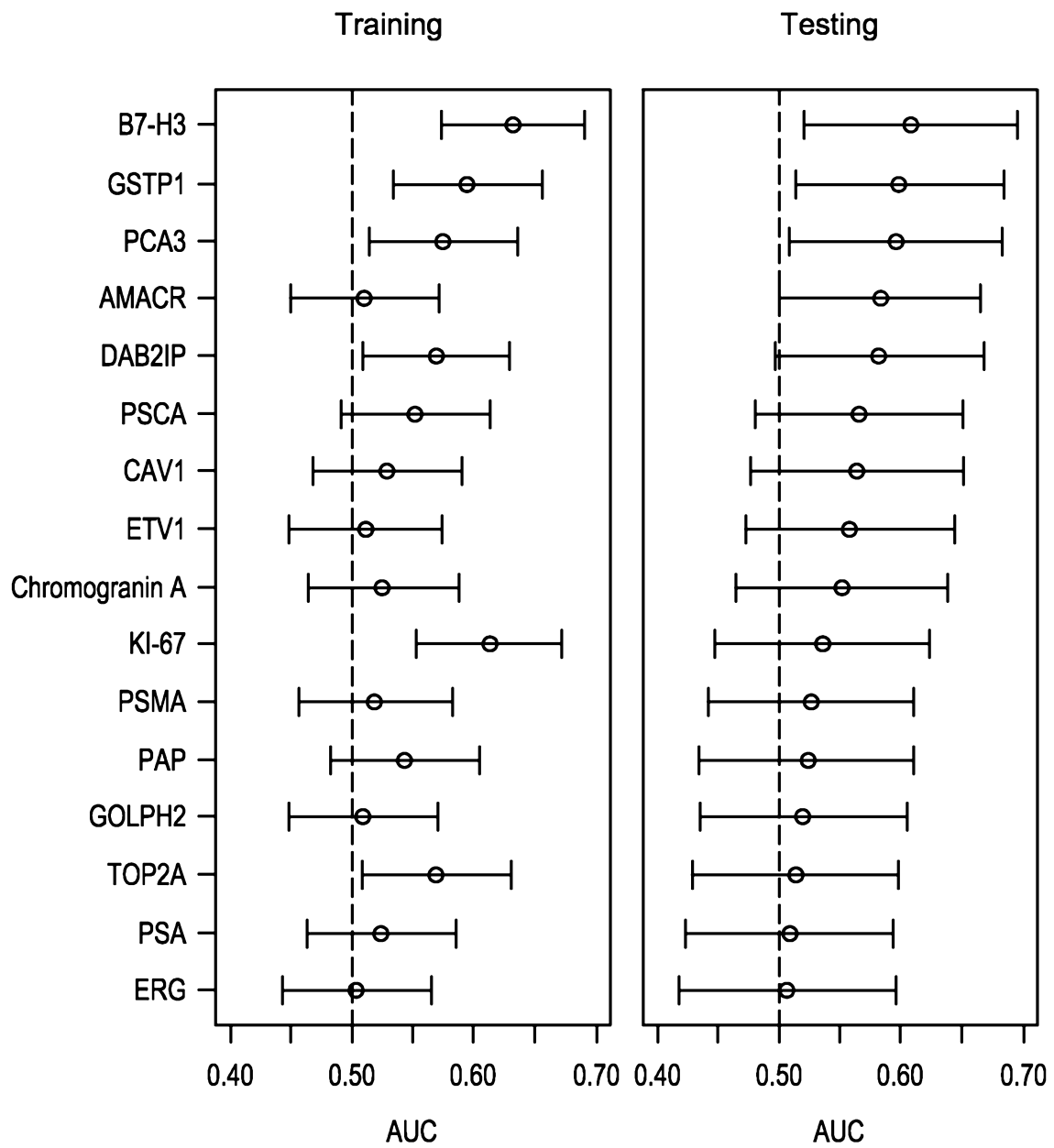


FIG. 27

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**FIG. 28**

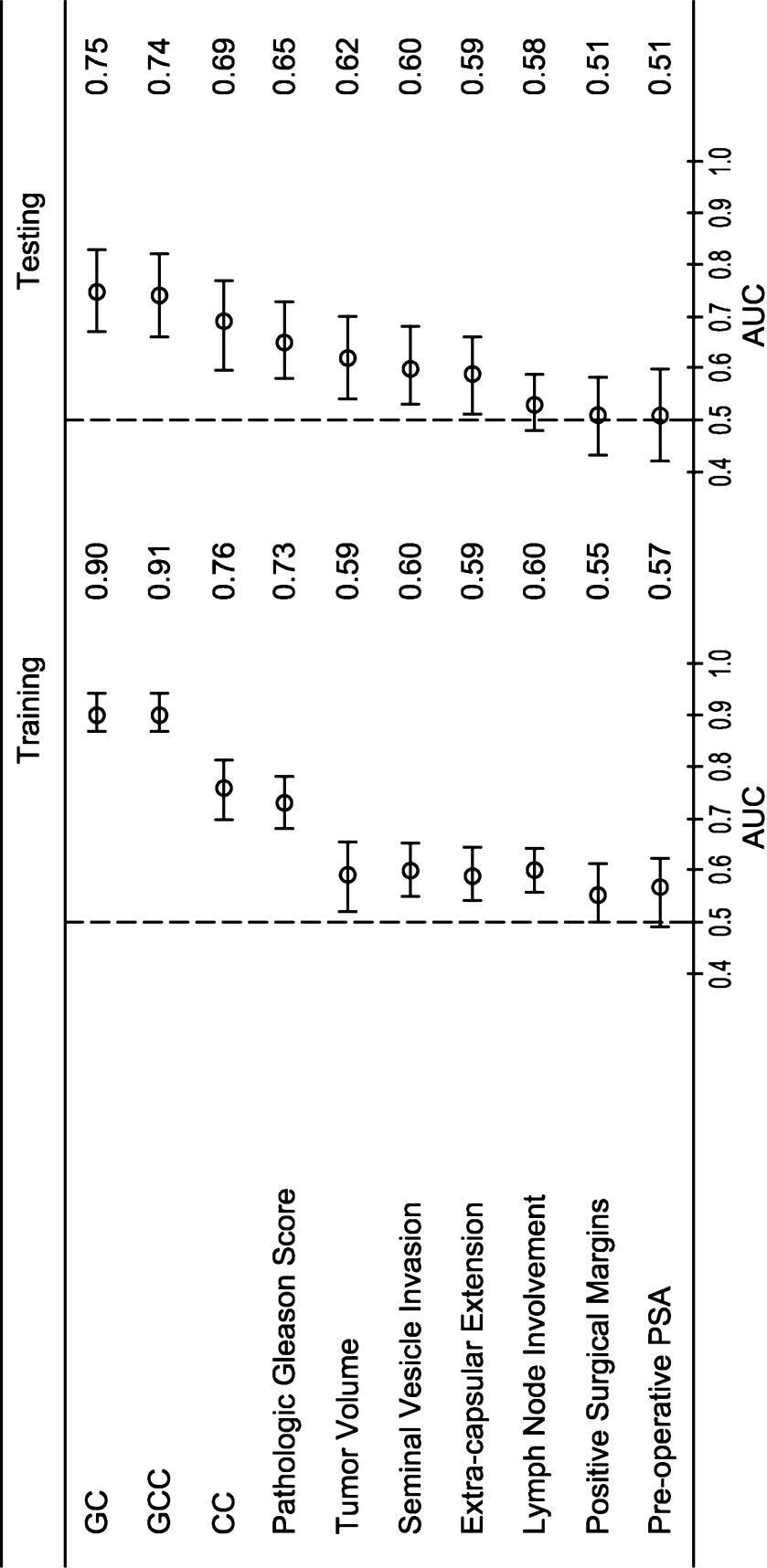
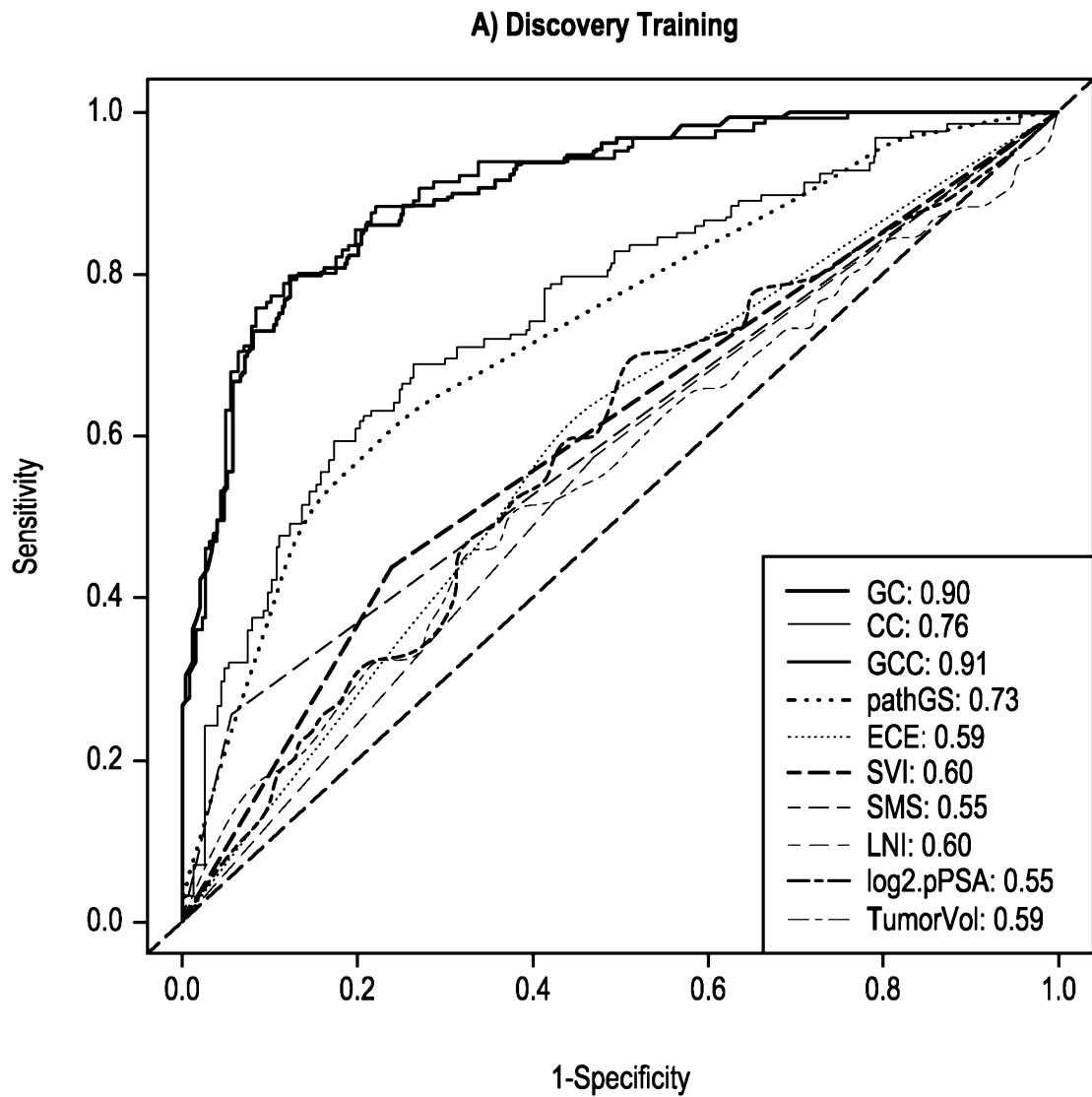
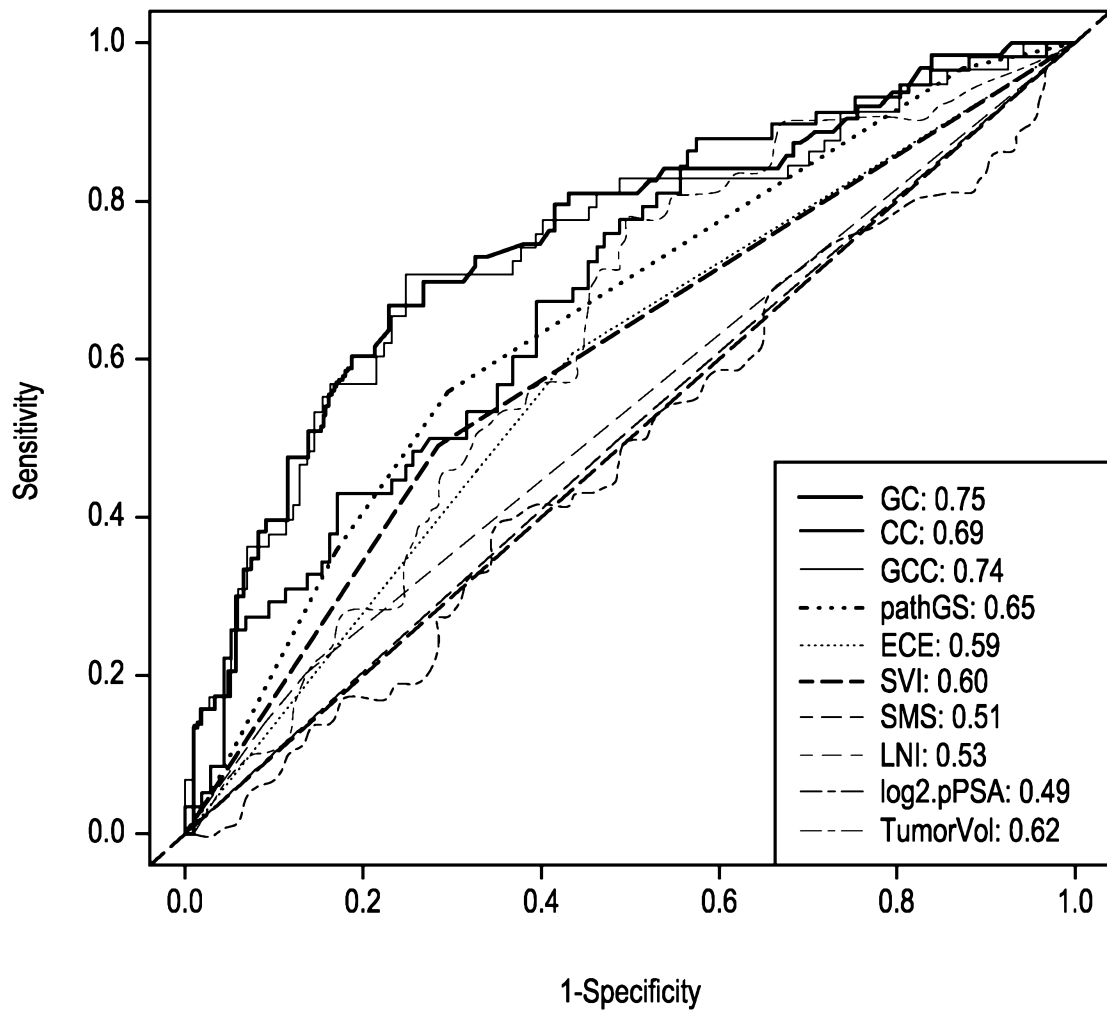


FIG. 29

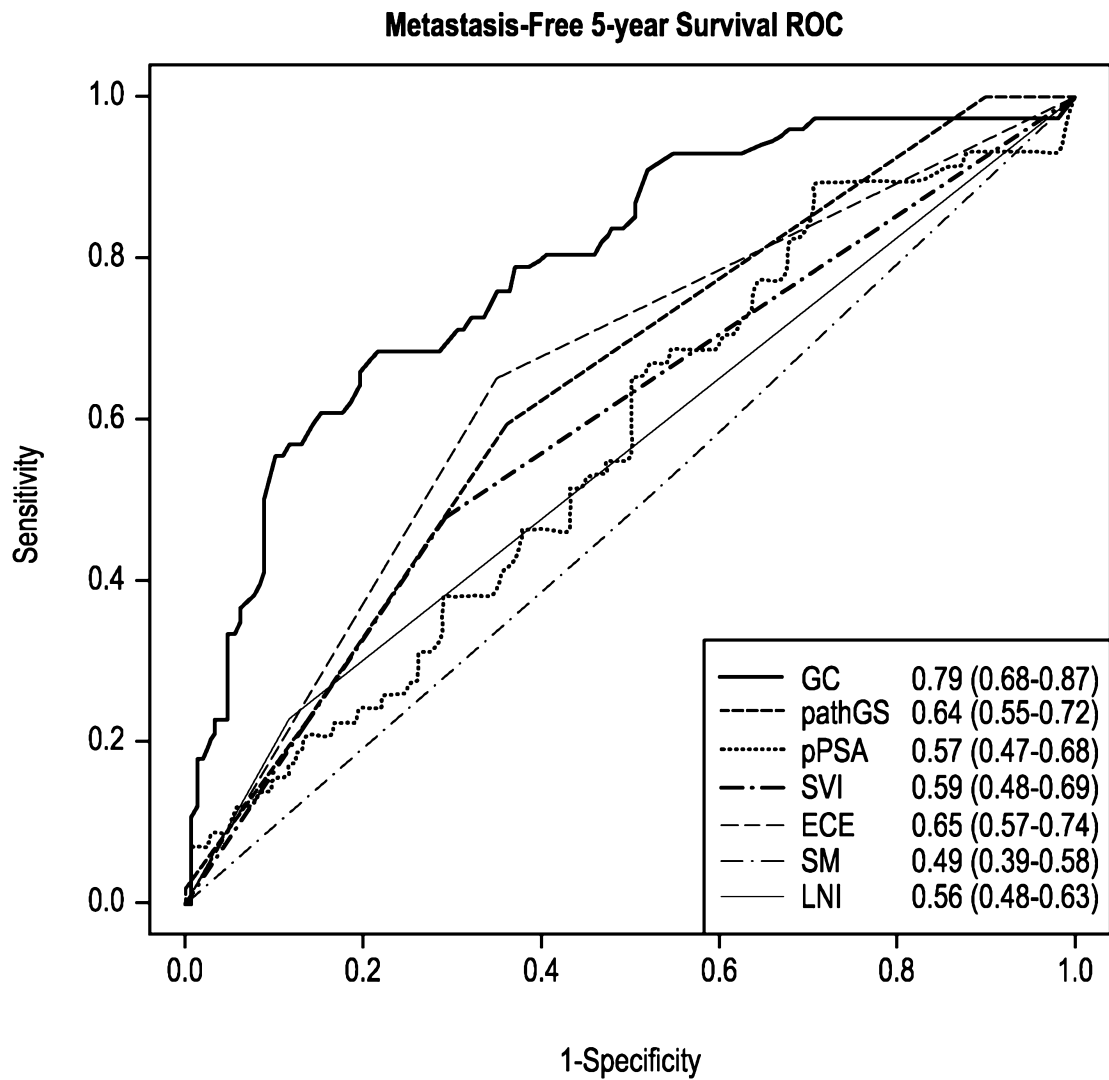
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**FIG. 30A**

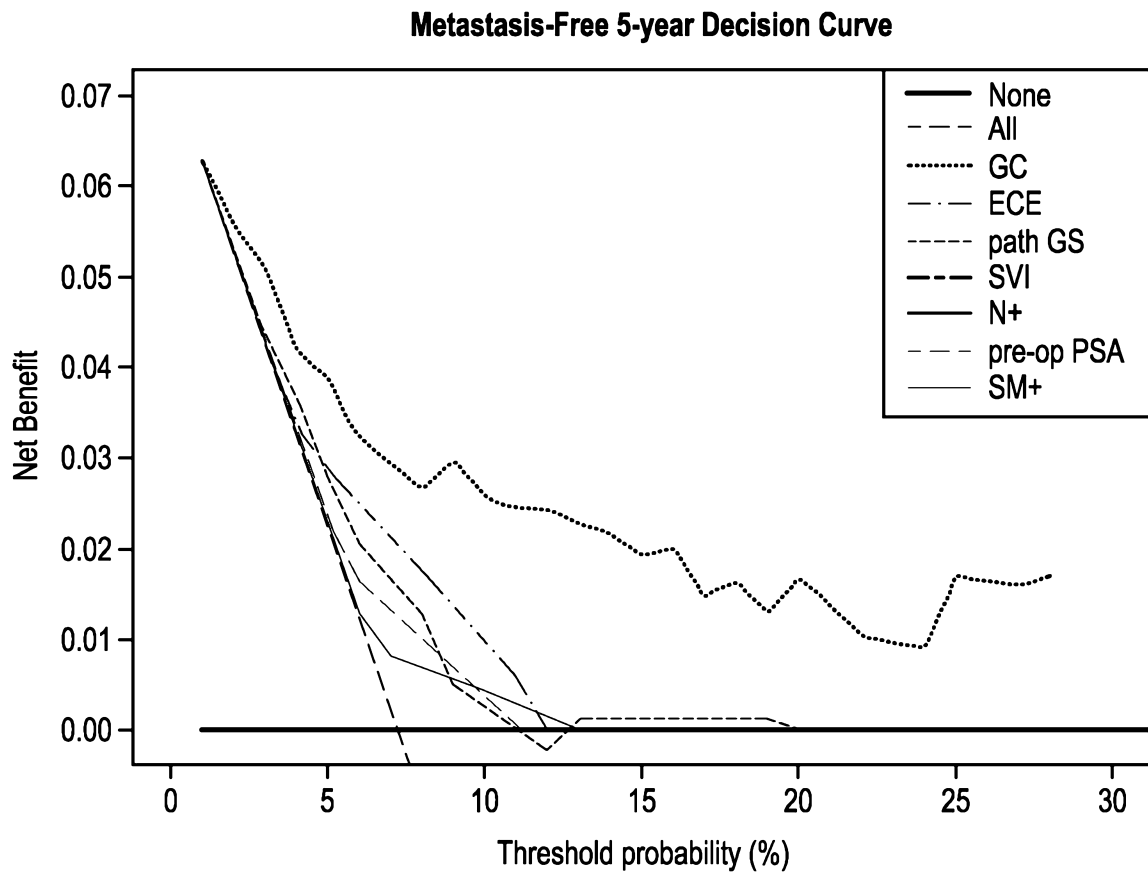
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B) Discovery Testing**FIG. 30B**

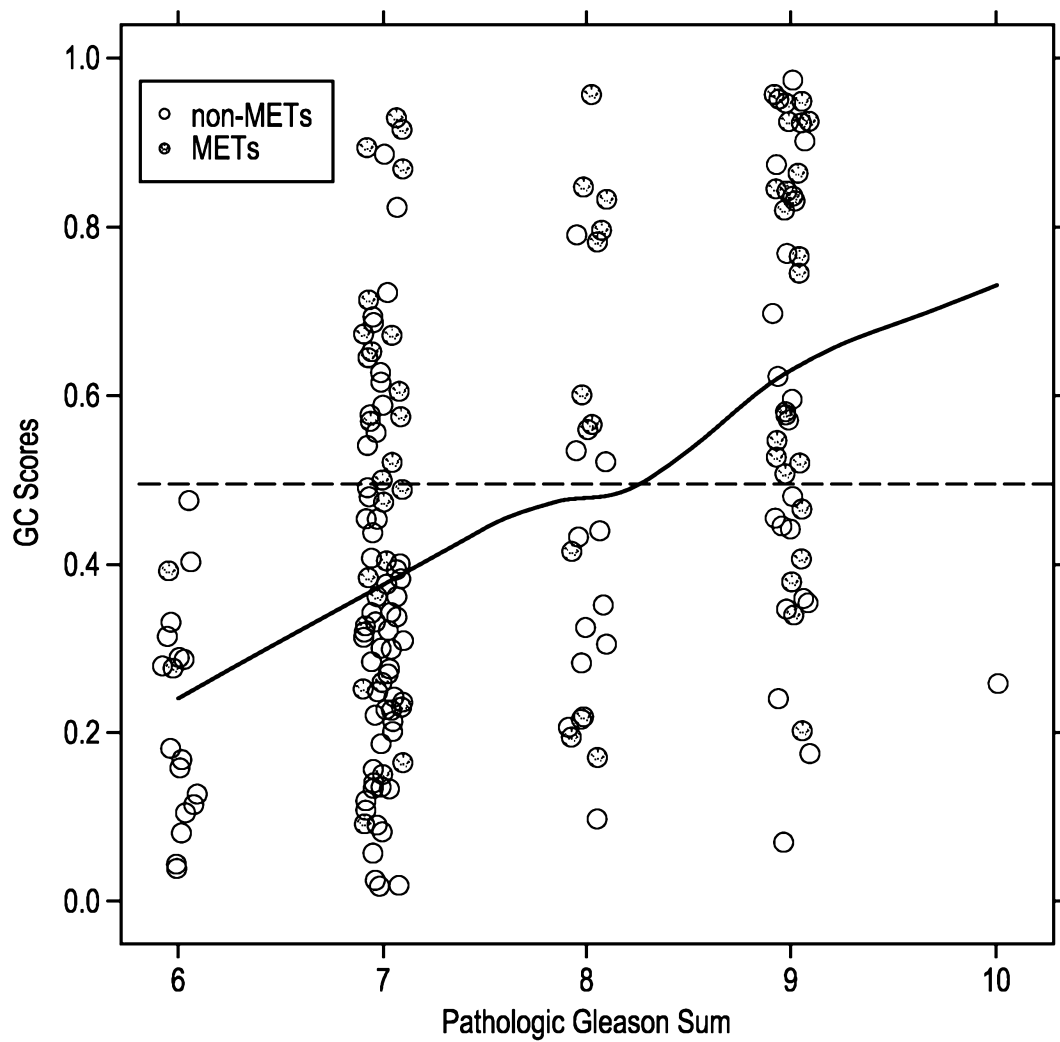
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**FIG. 31**

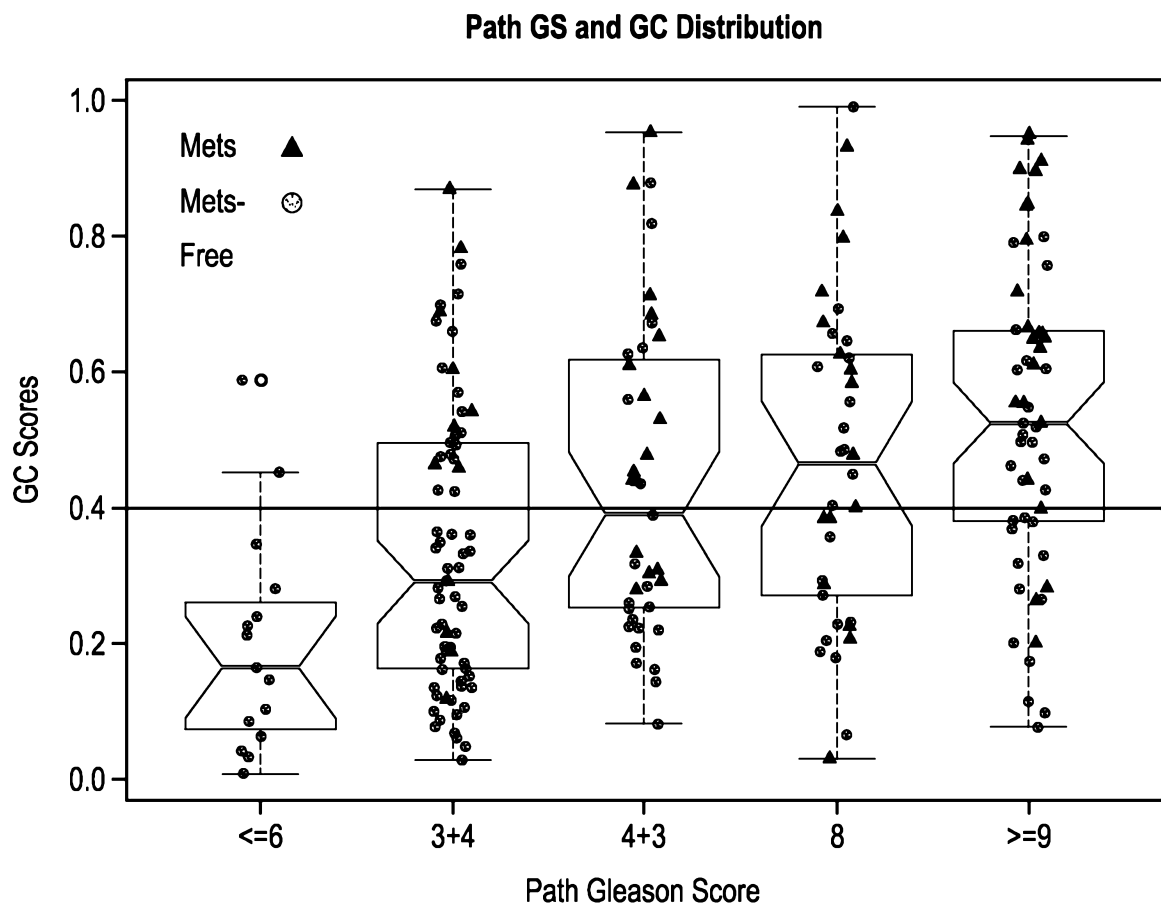
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**FIG. 32**

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**FIG. 33**

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**FIG. 34**

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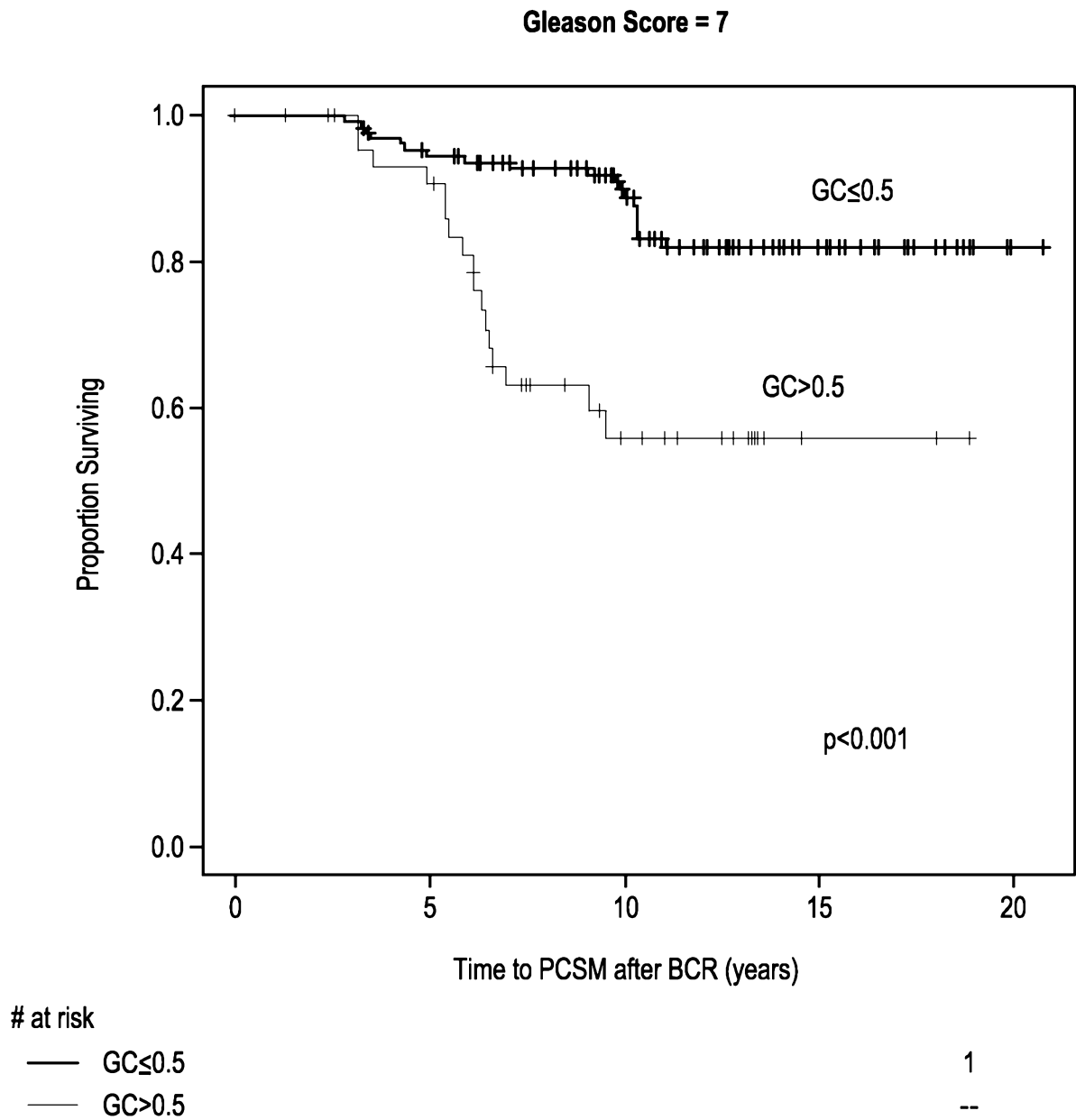


FIG. 35A

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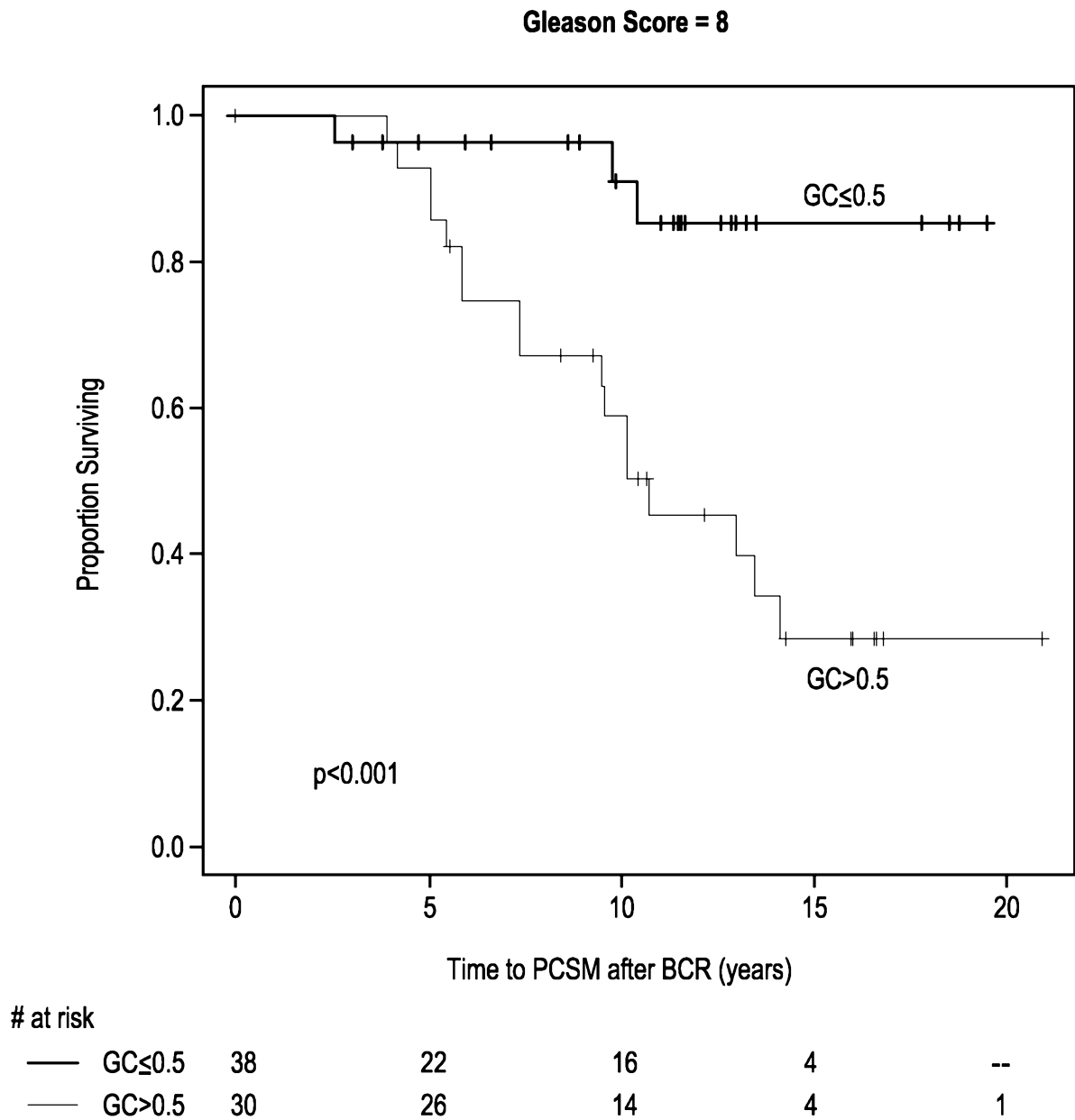


FIG. 35B

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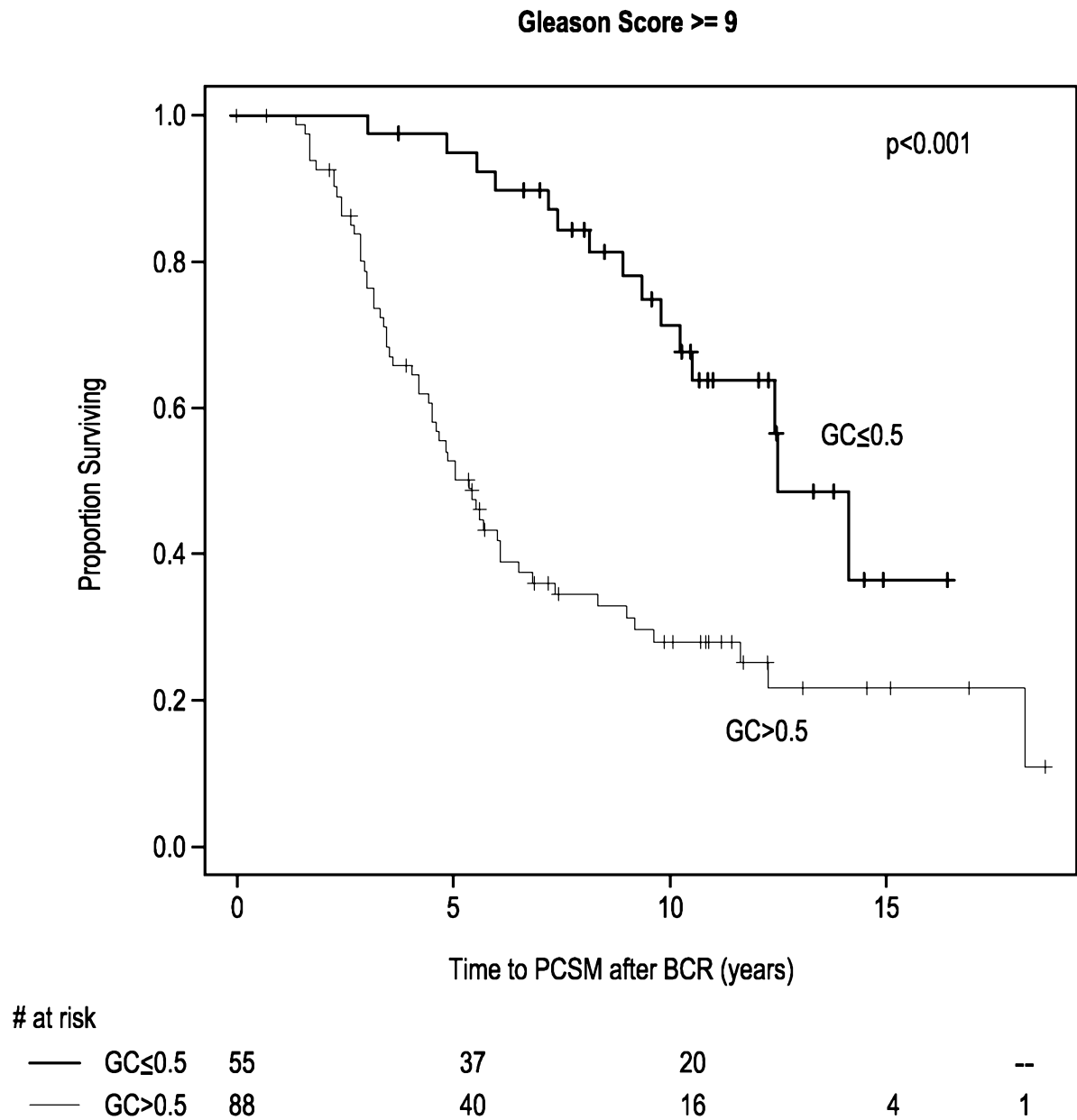


FIG. 35C

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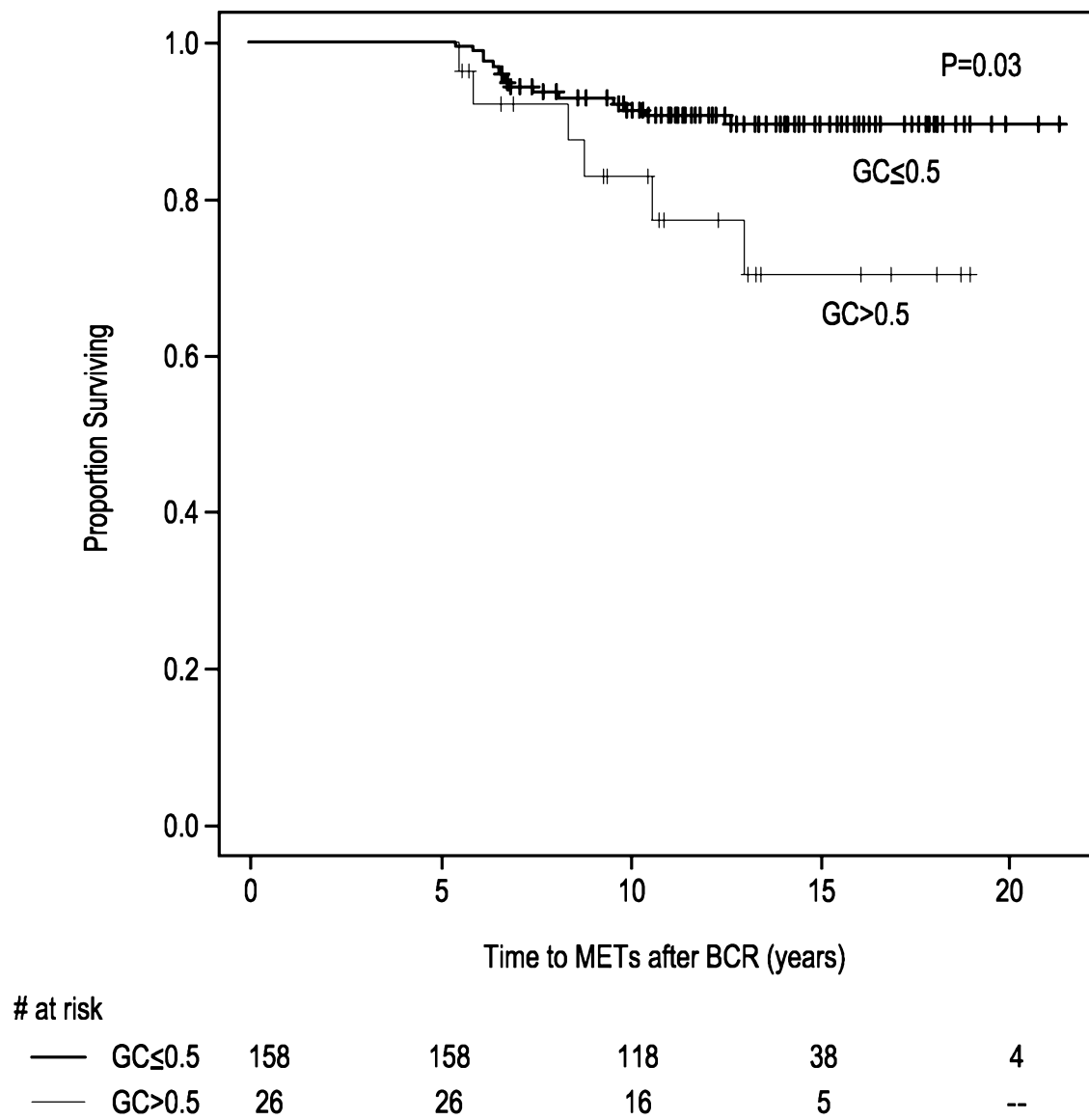
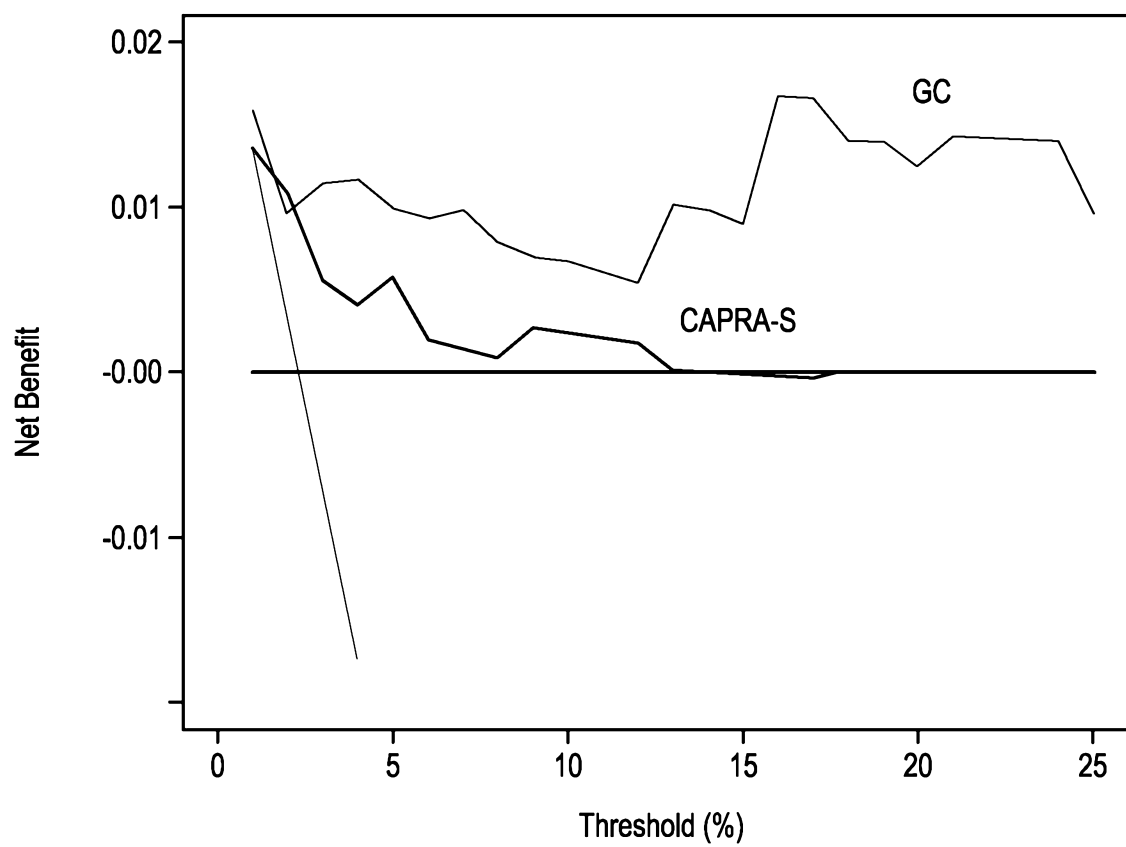
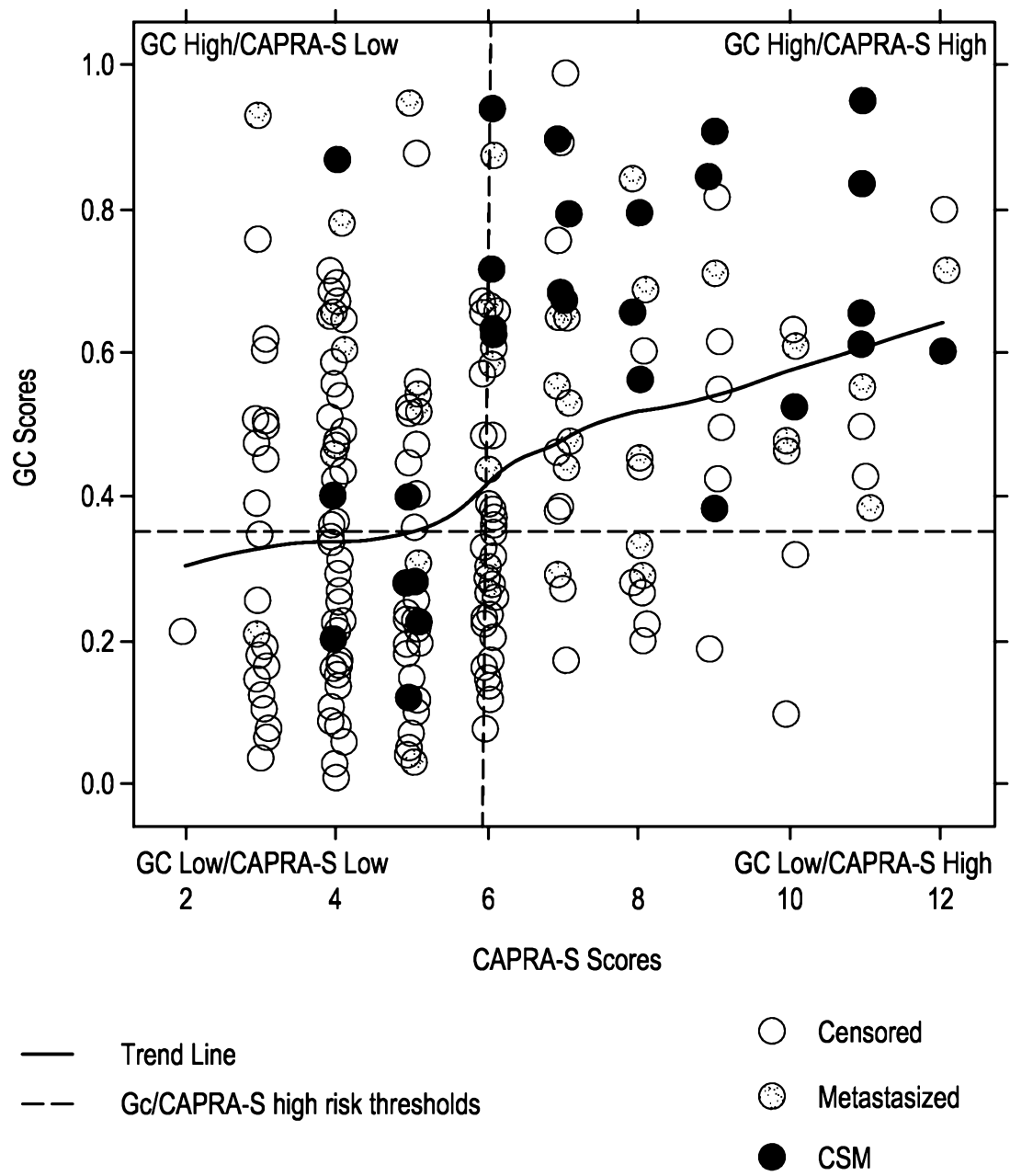


FIG. 36

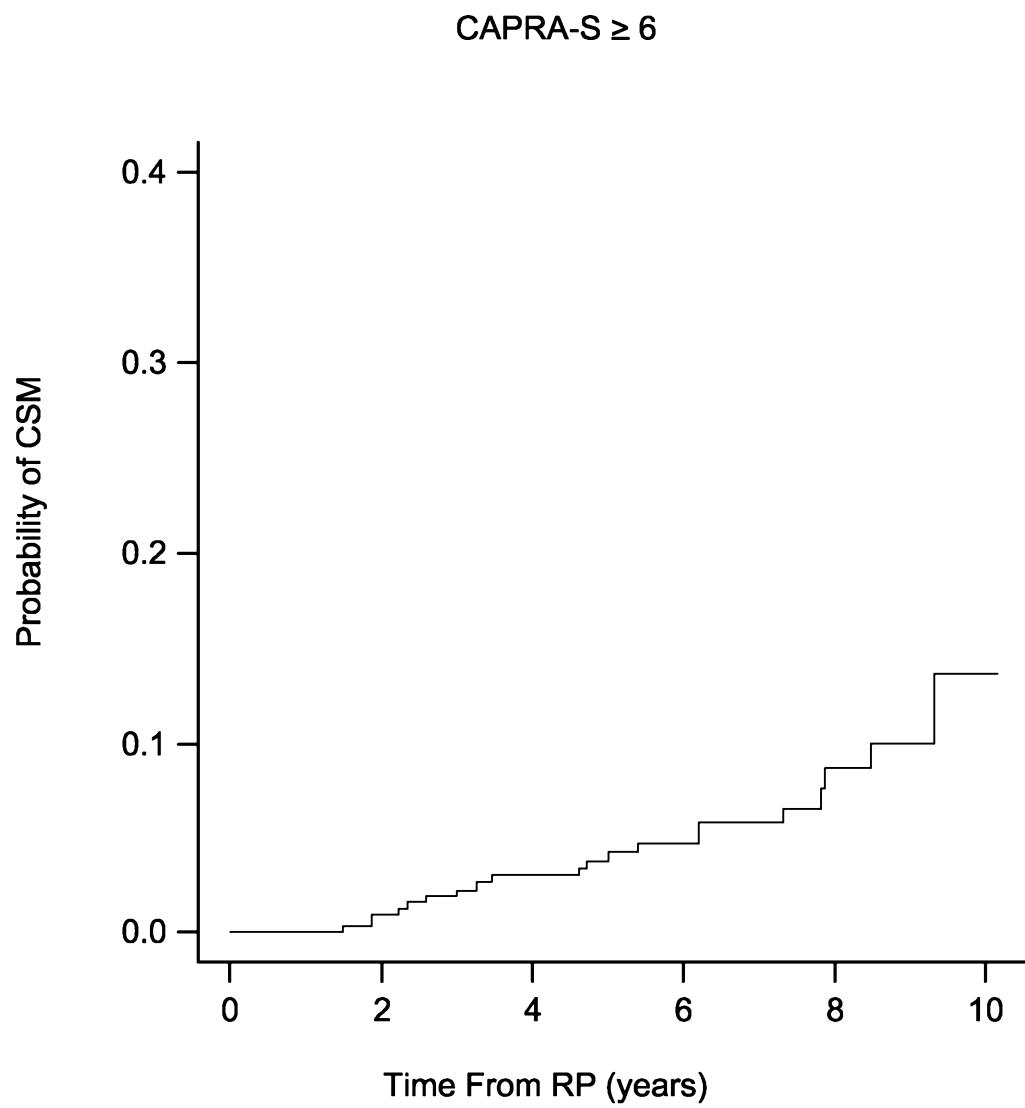
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**FIG. 37**

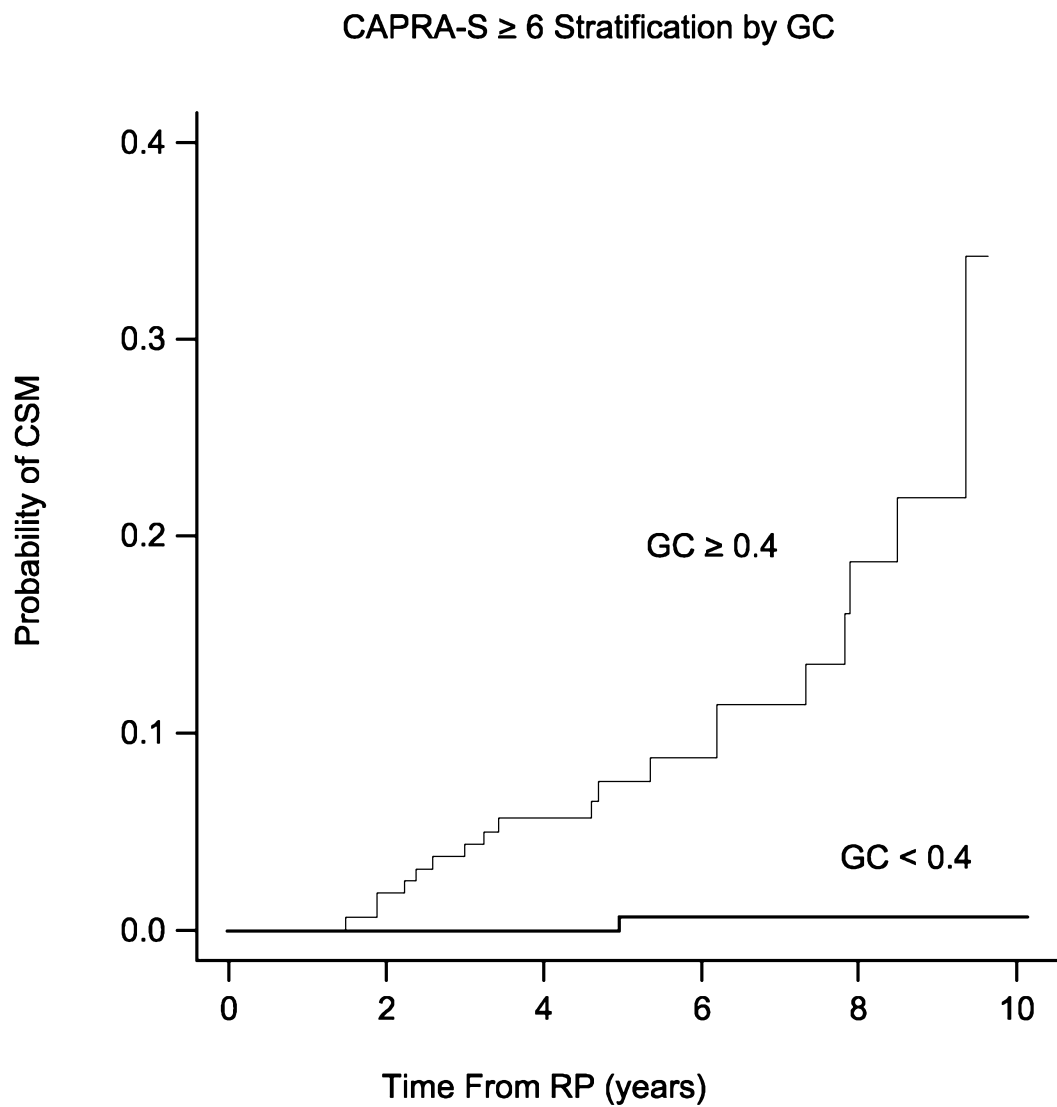
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**FIG. 38**

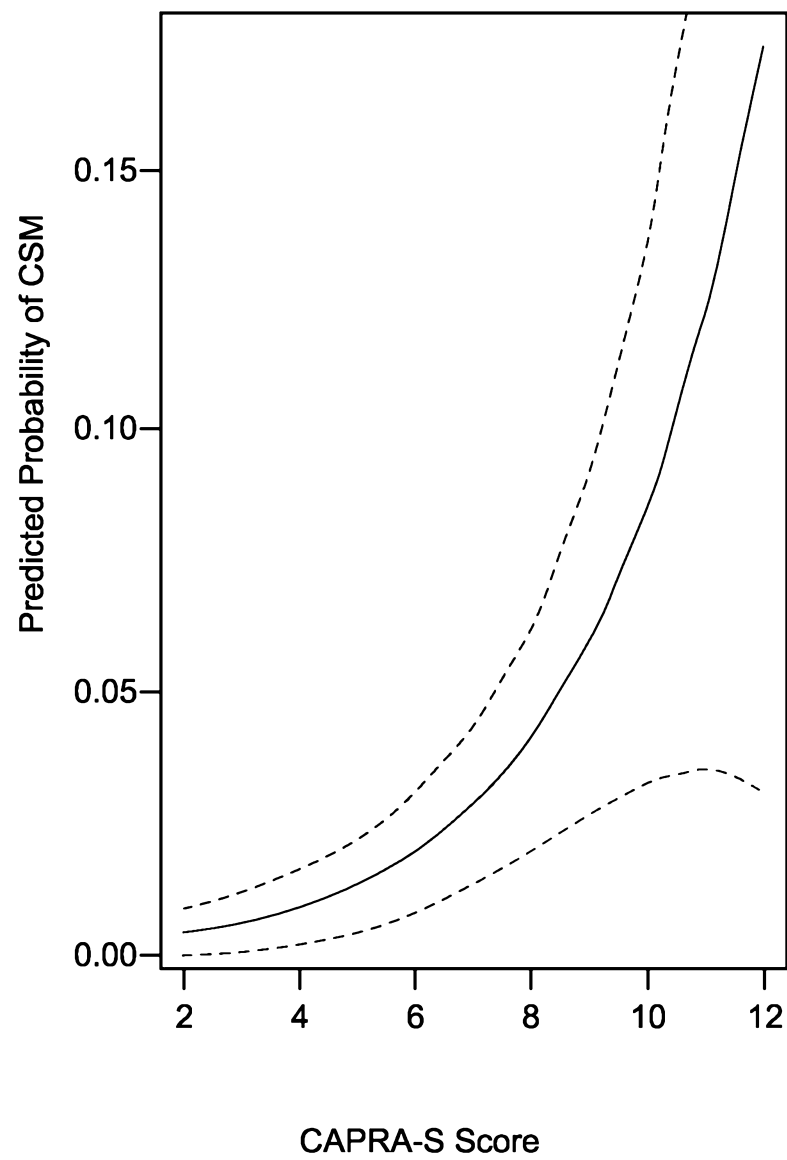
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**FIG. 39A**

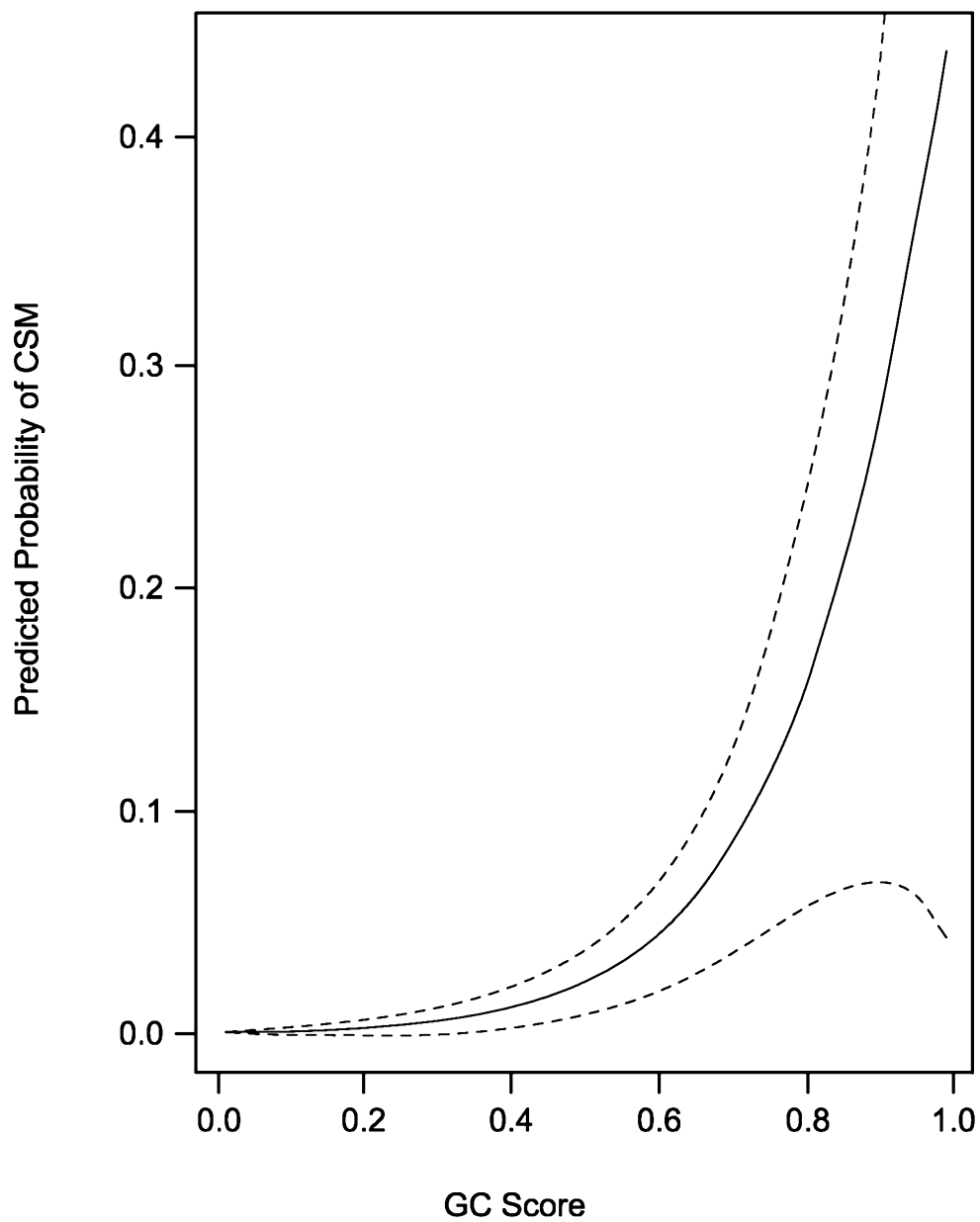
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**FIG. 39B**

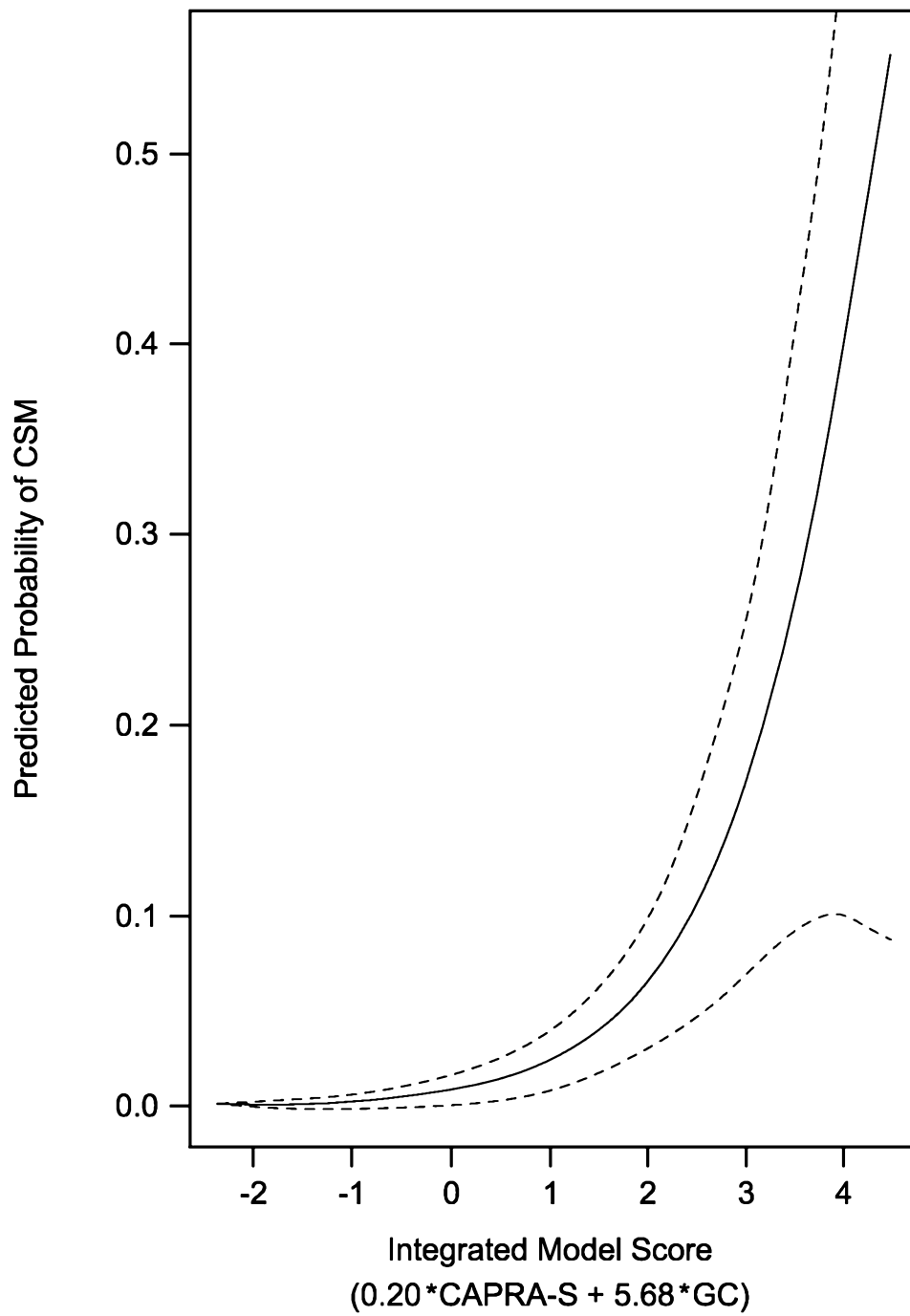
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**FIG. 40A**

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**FIG. 40B**

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**FIG. 40C**

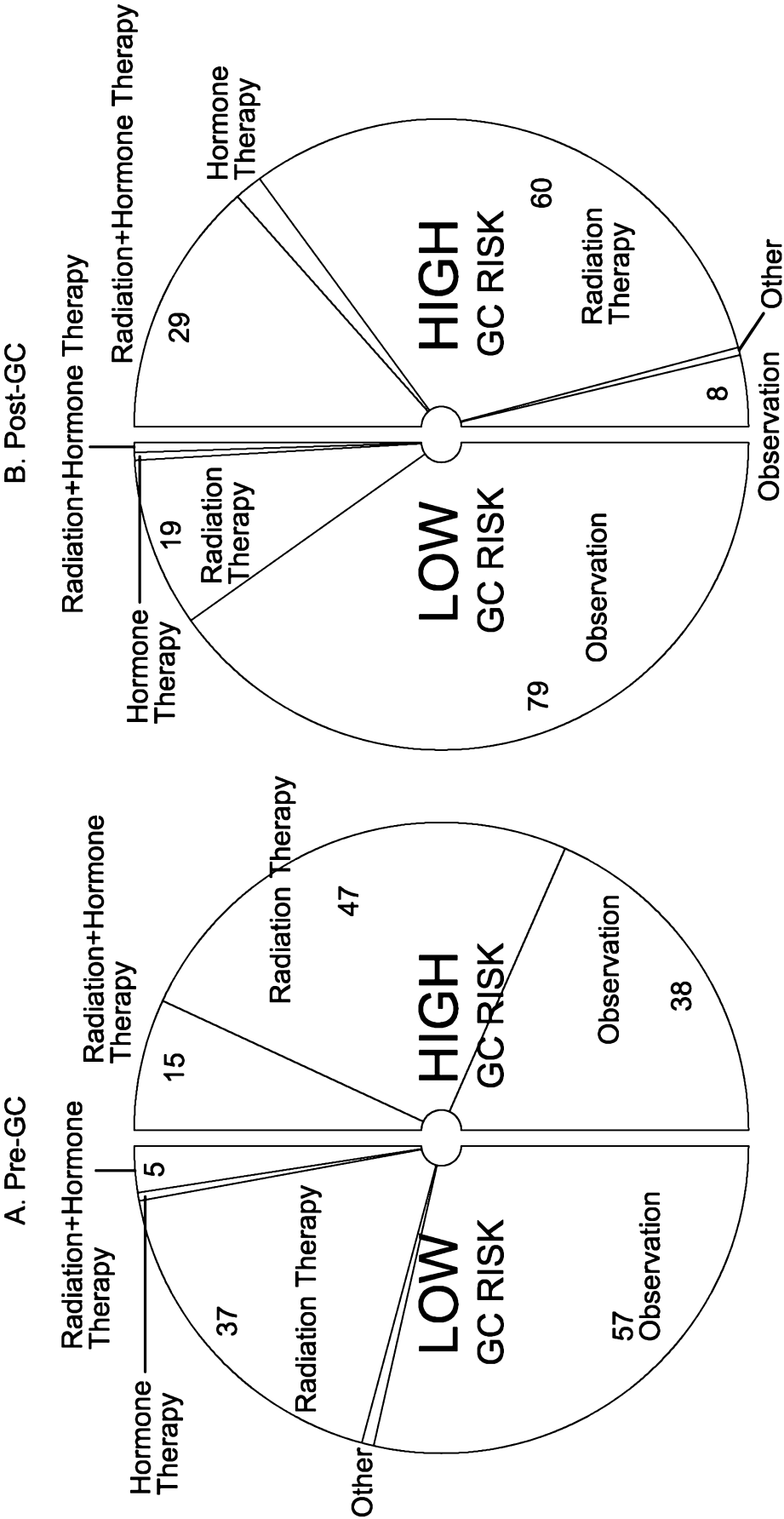
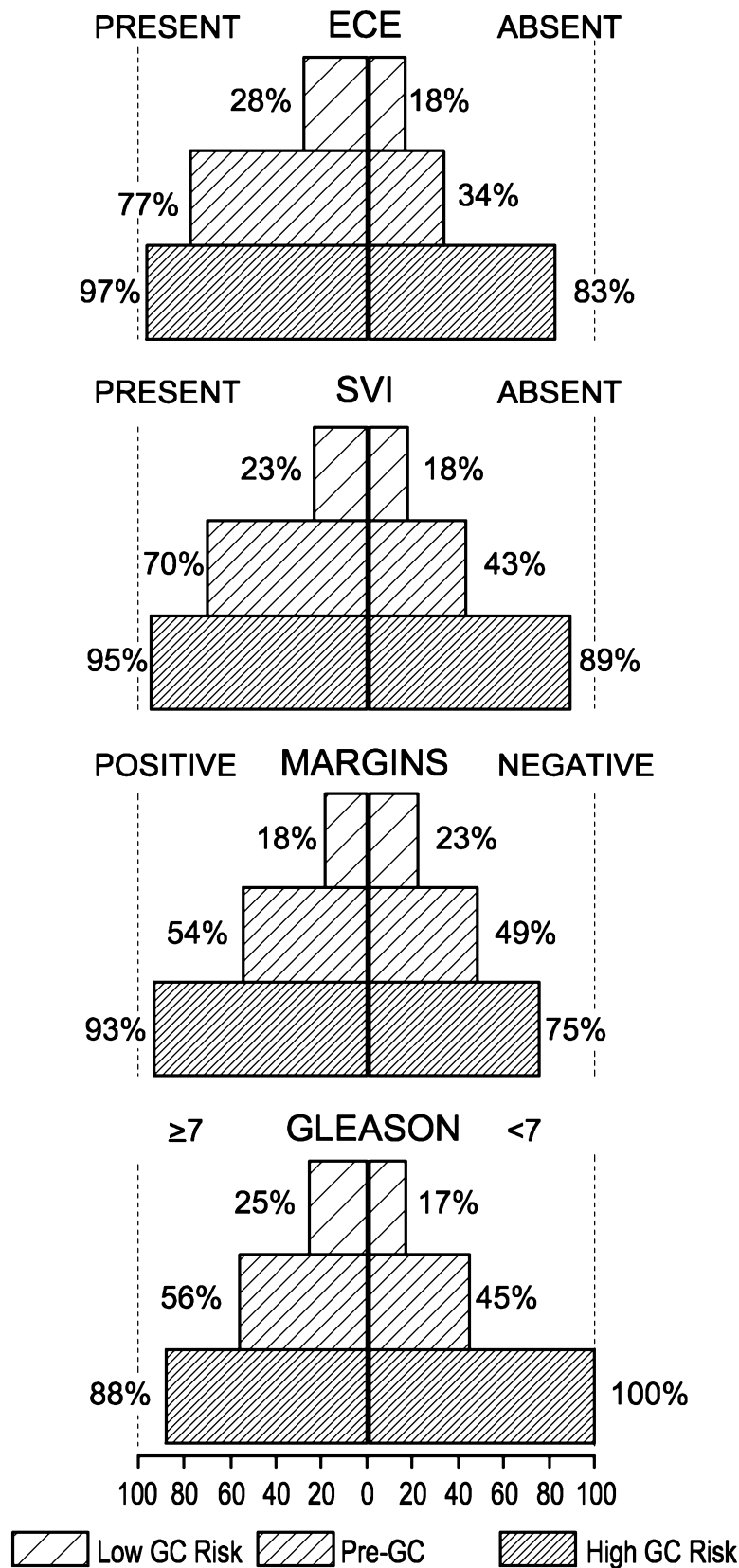


FIG. 41

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**FIG. 42**

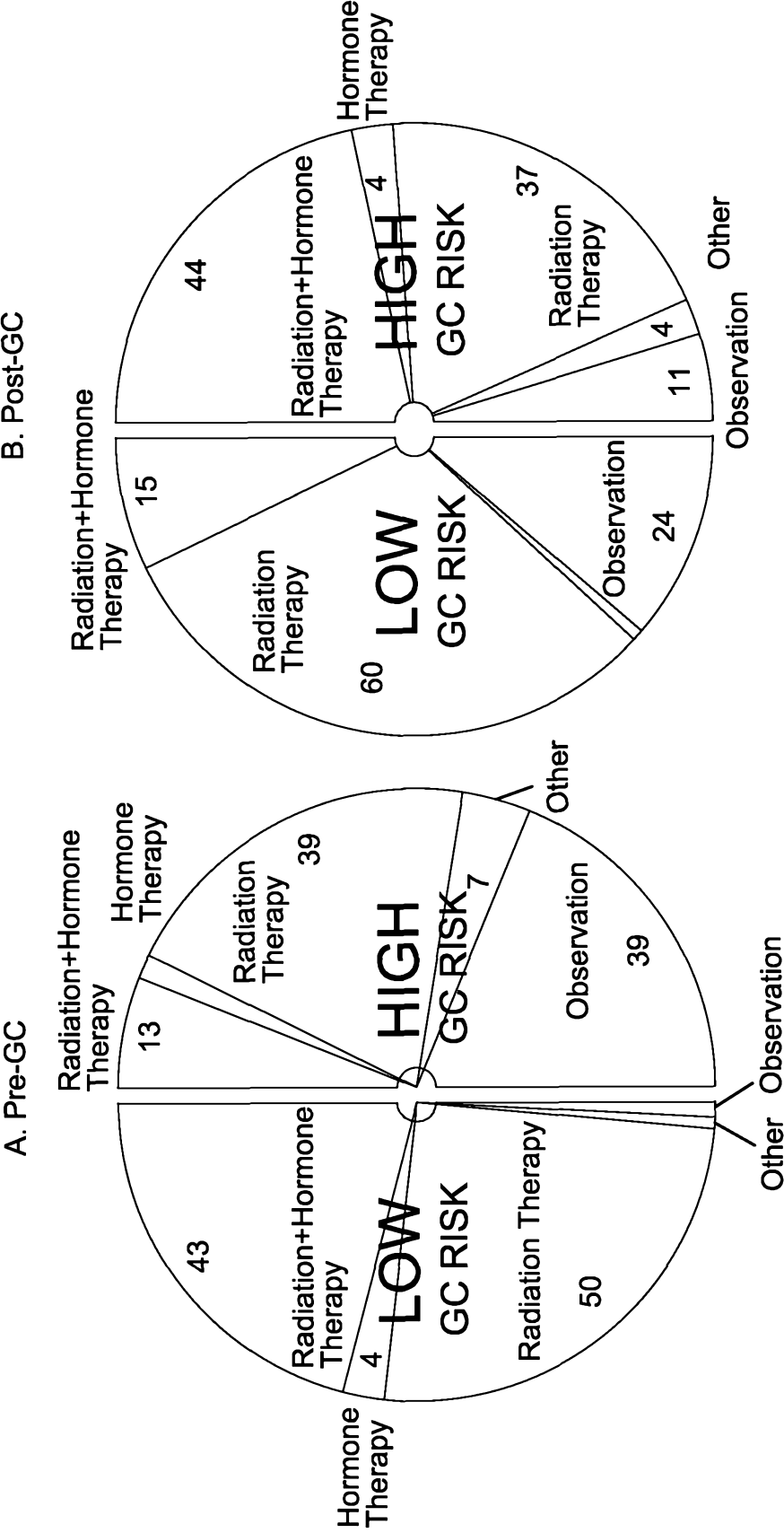
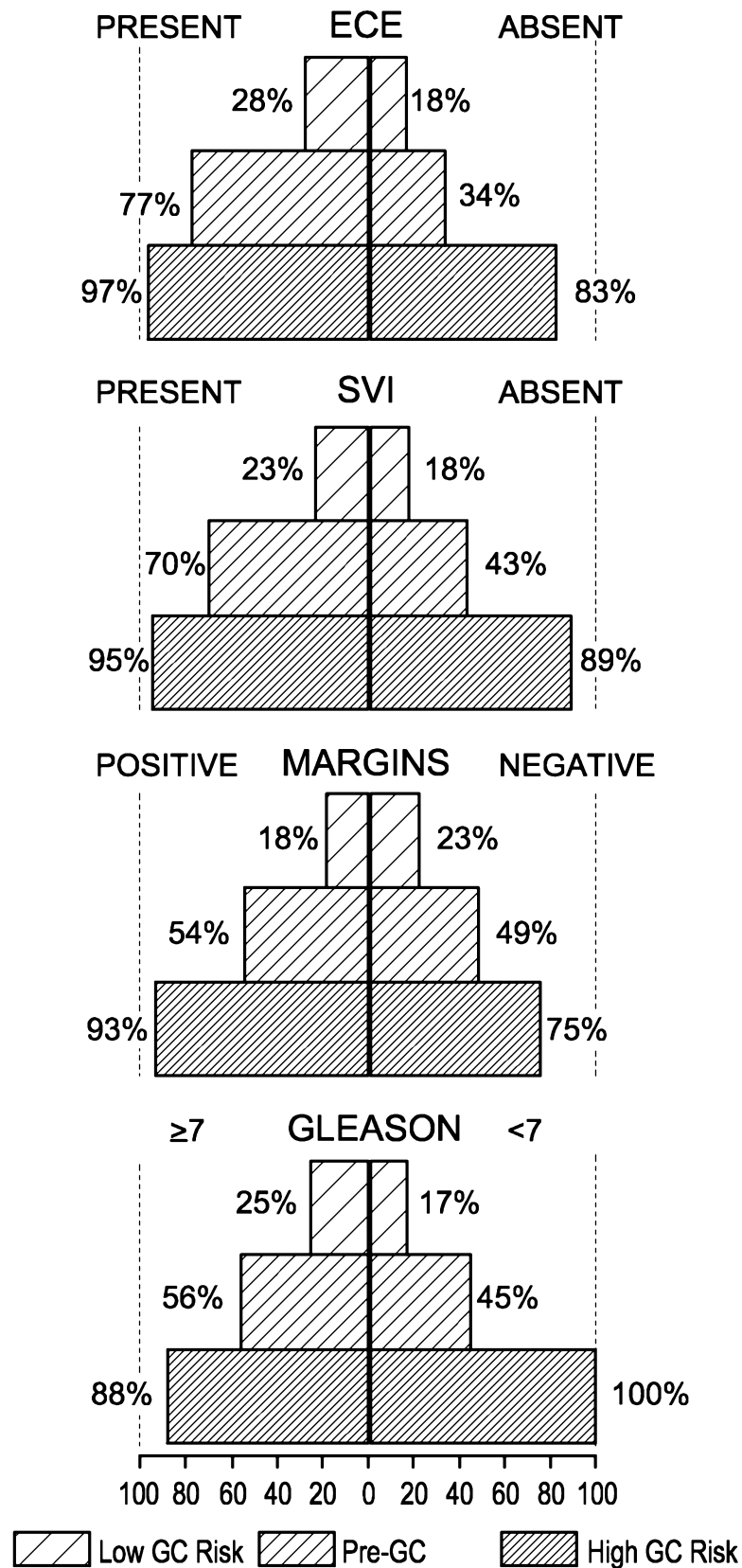
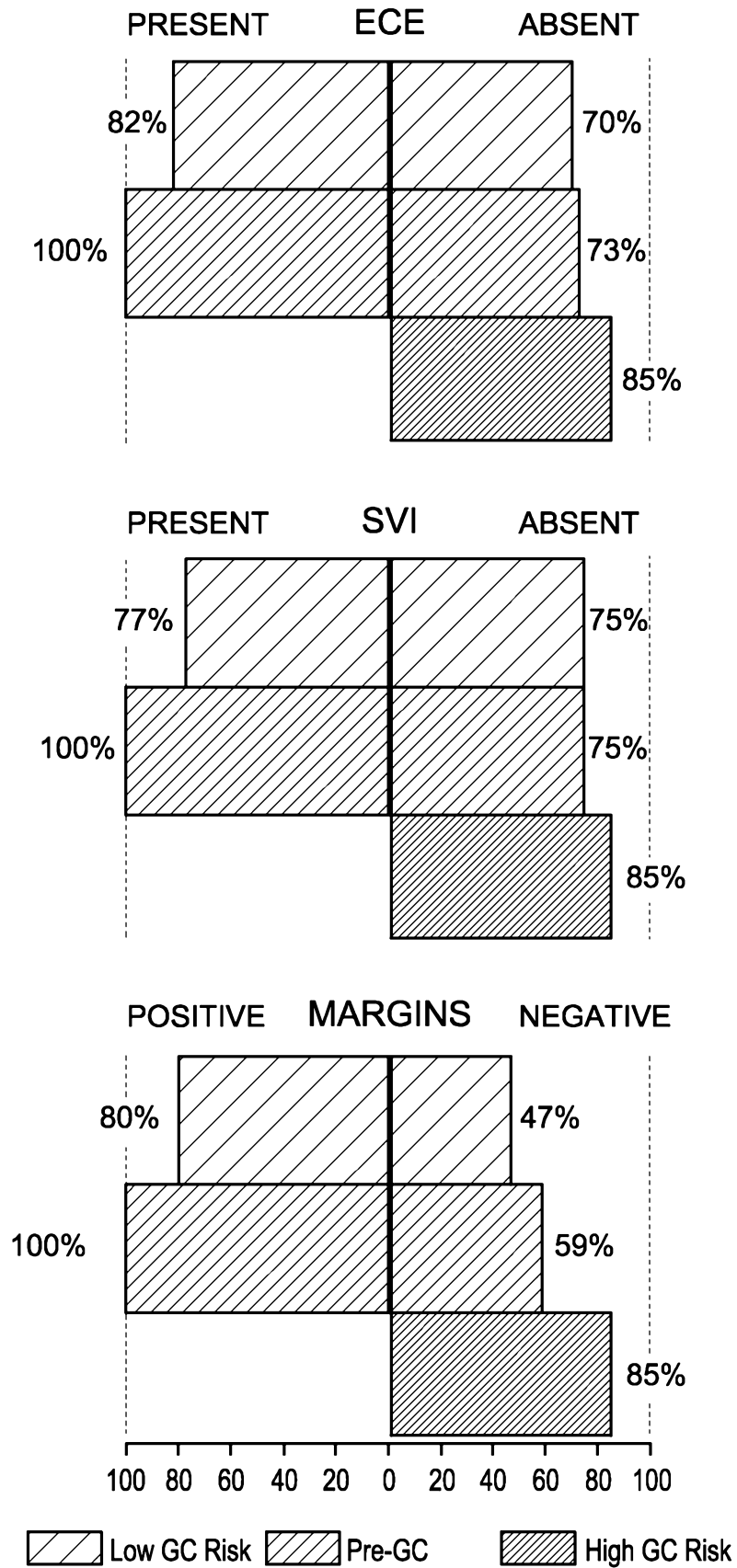


FIG. 43

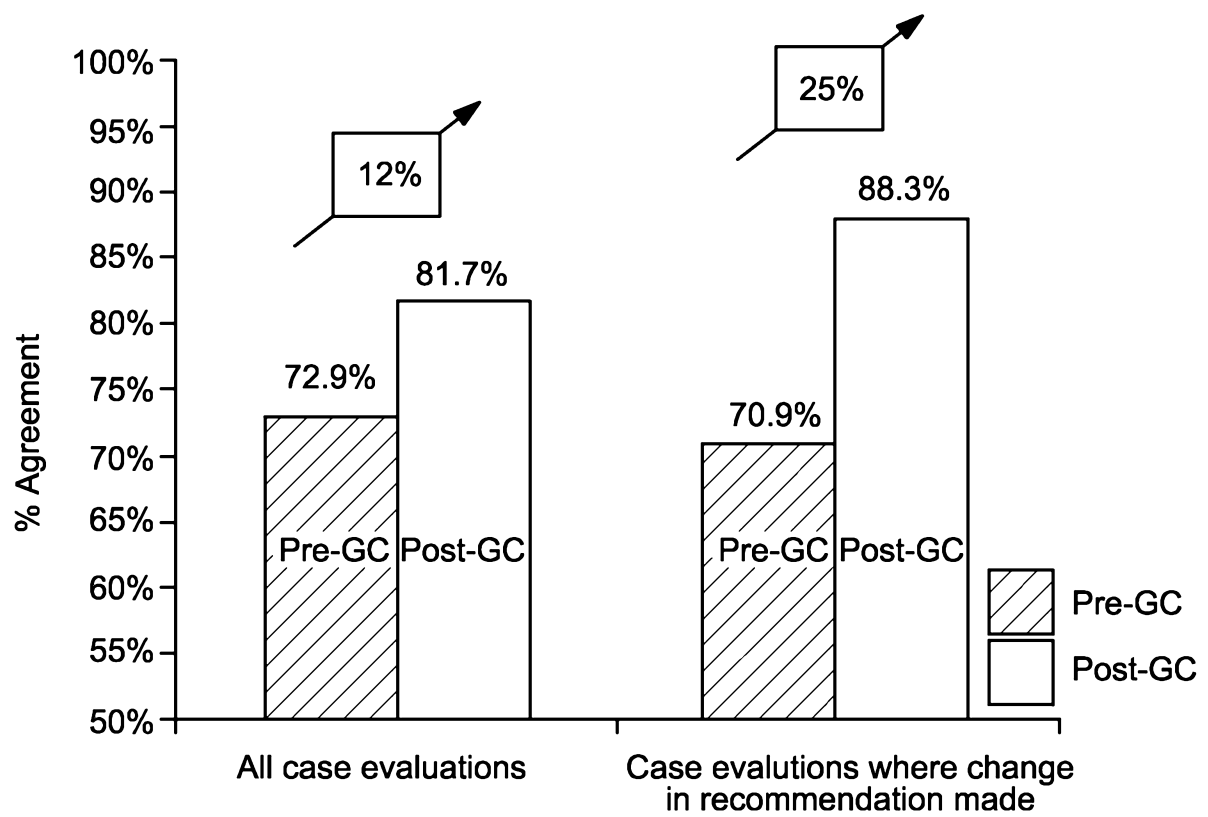
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**FIG. 44A**

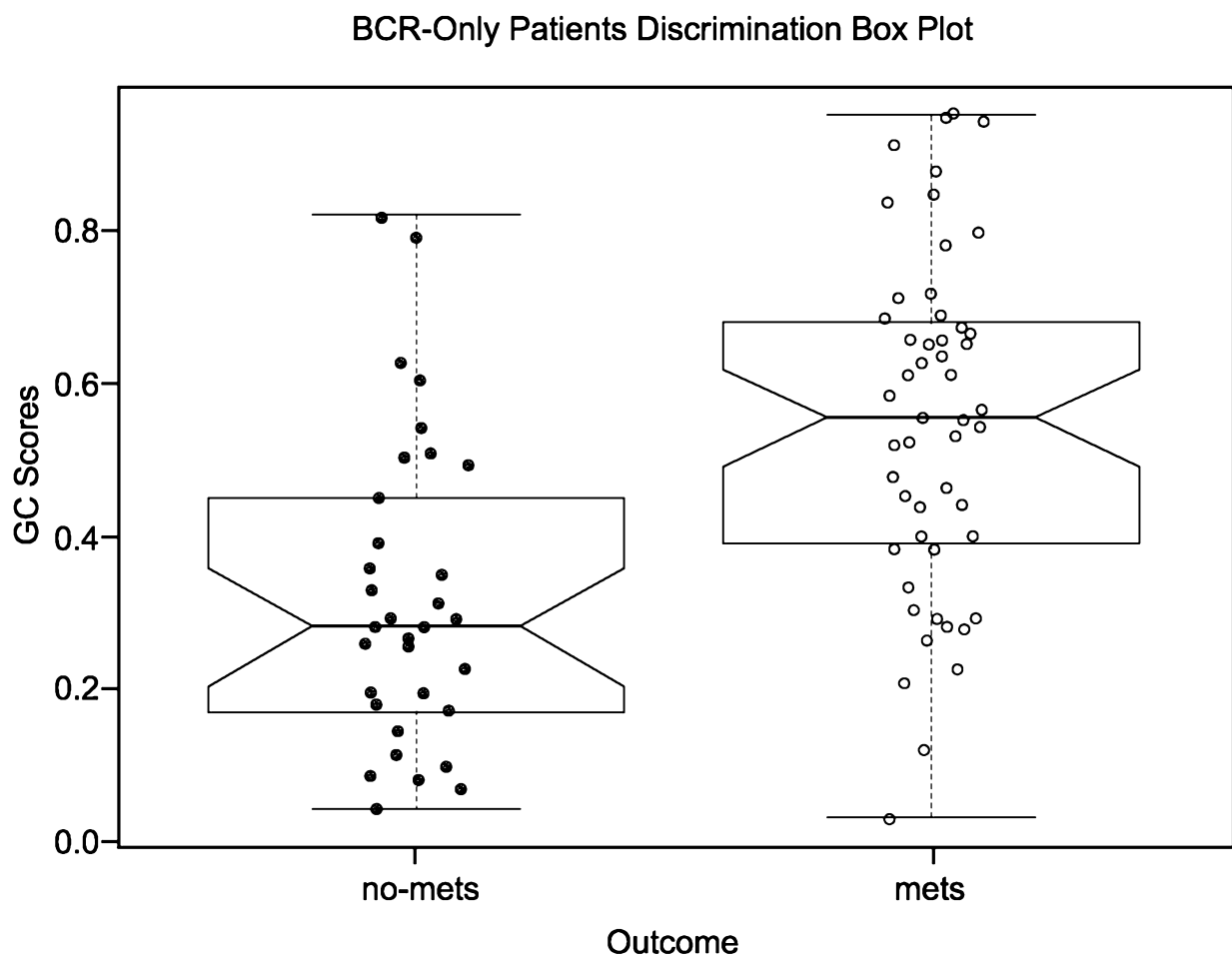
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**FIG. 44B**

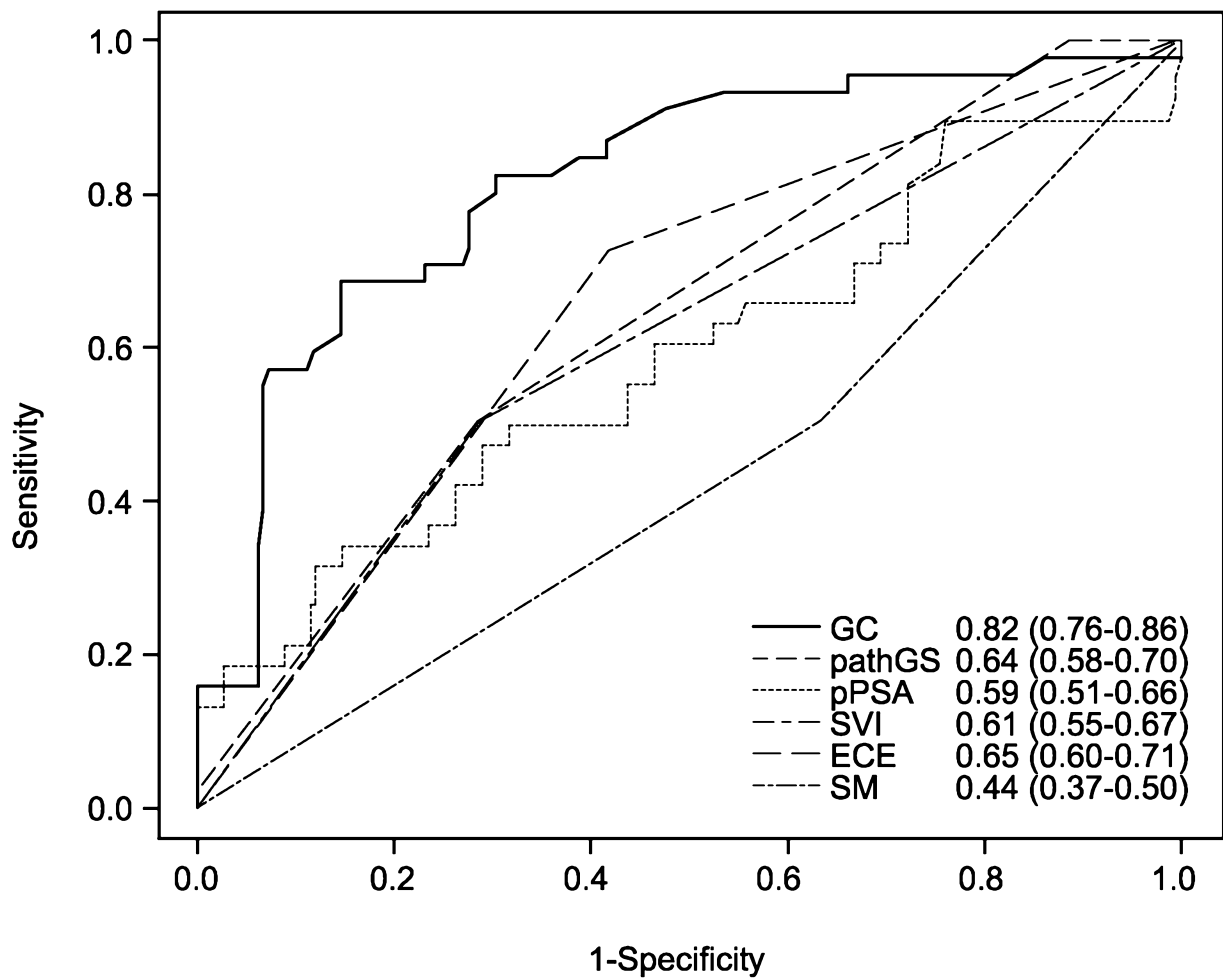
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**FIG. 45**

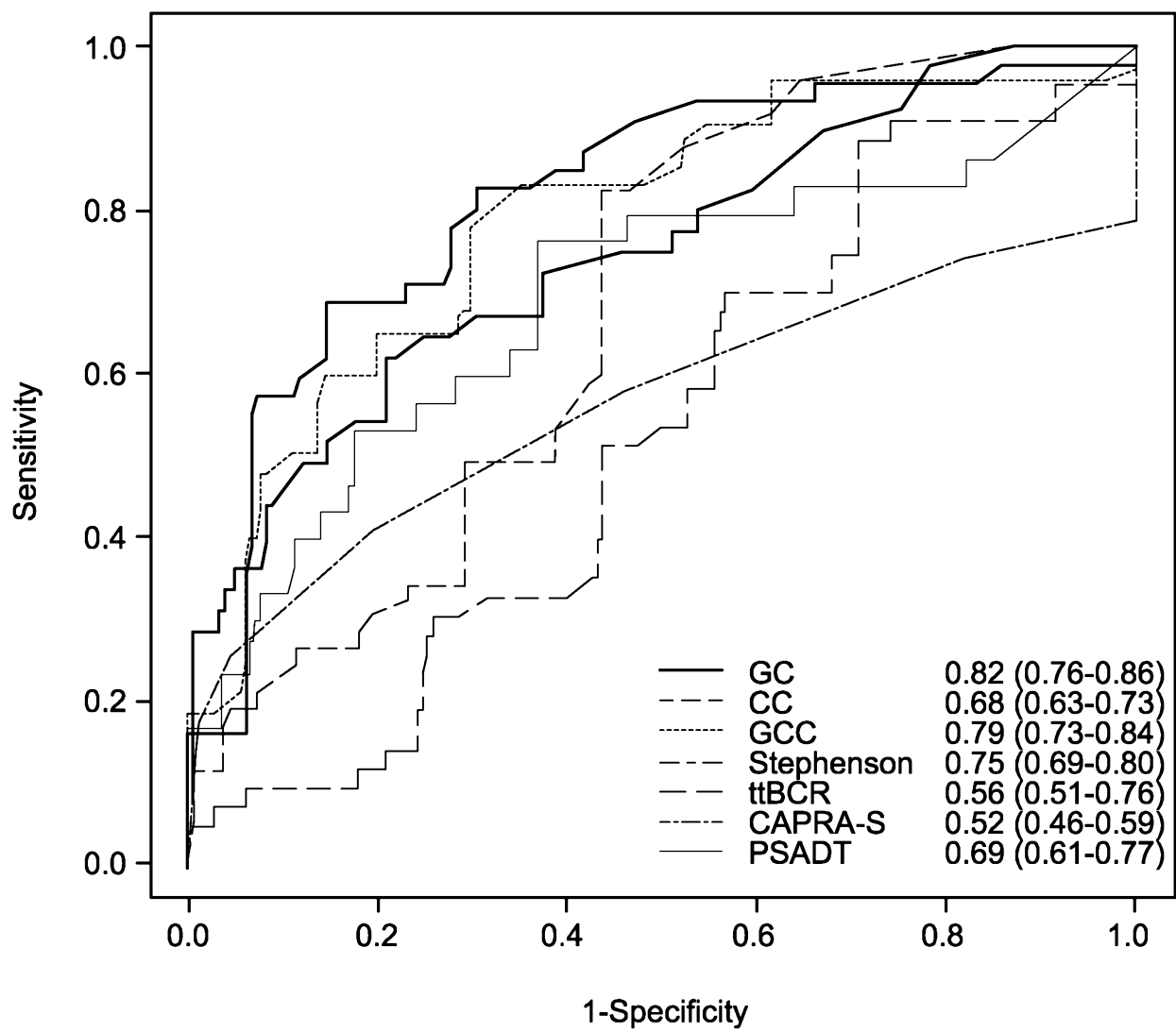
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**FIG. 46**

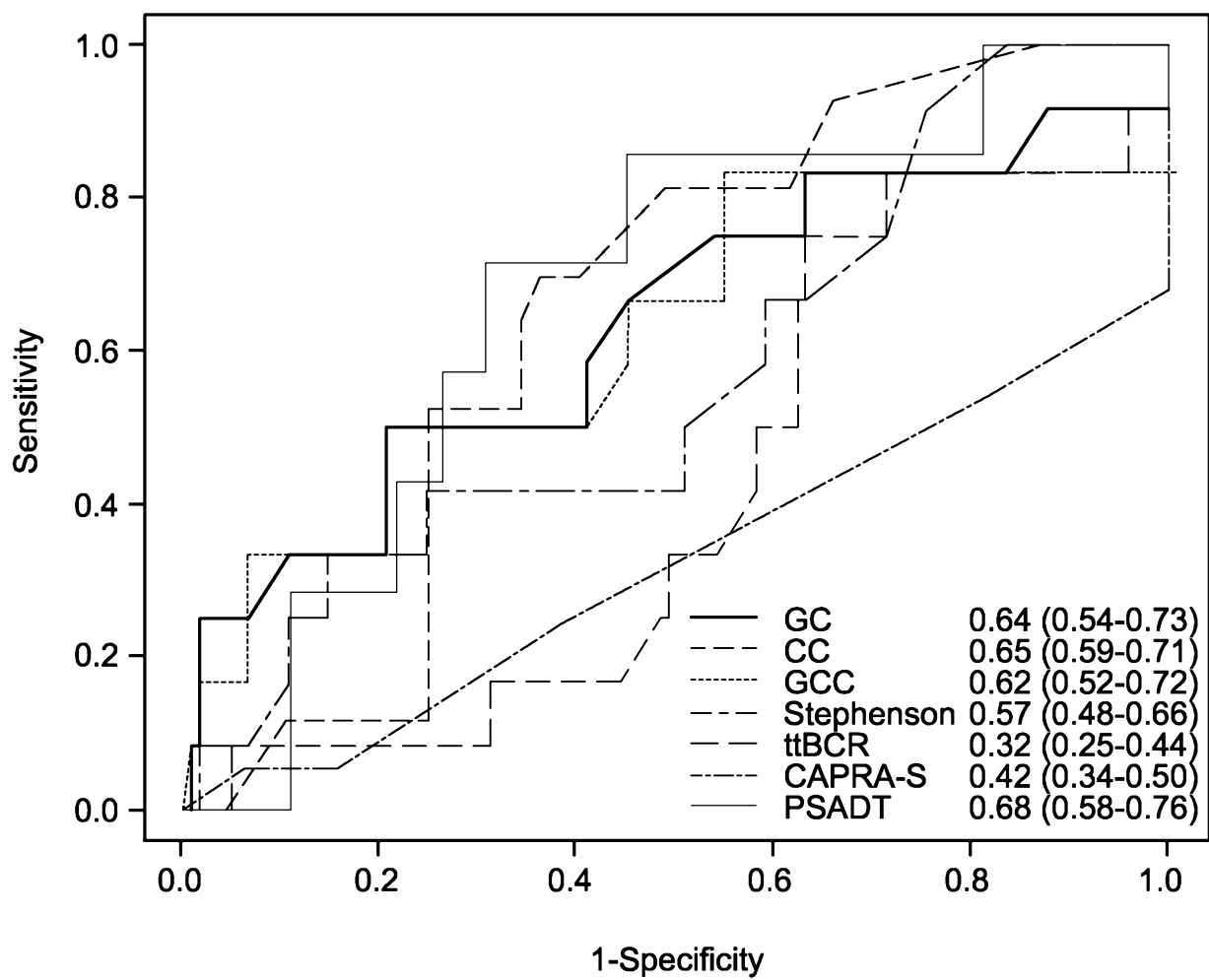
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**FIG. 47**

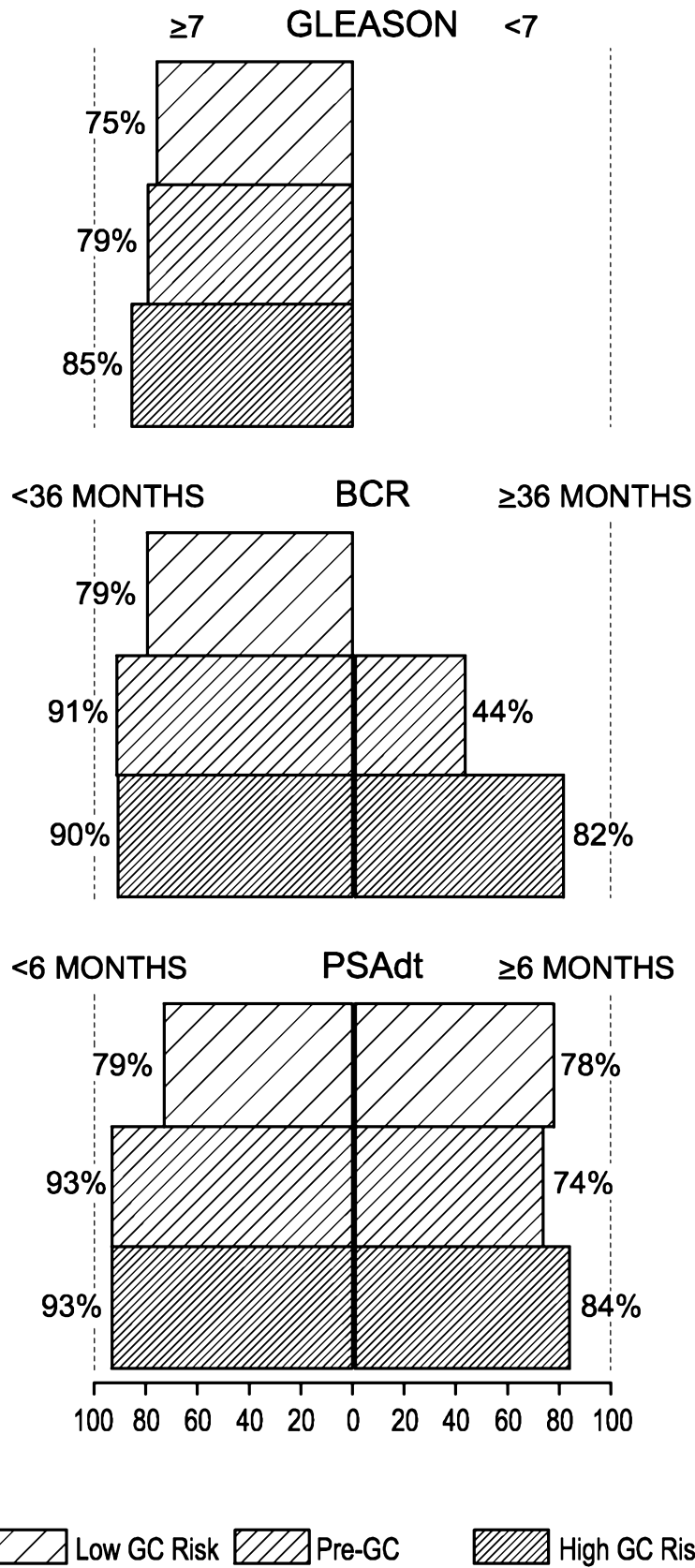
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**FIG. 48**

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**FIG. 49**

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**FIG. 50**

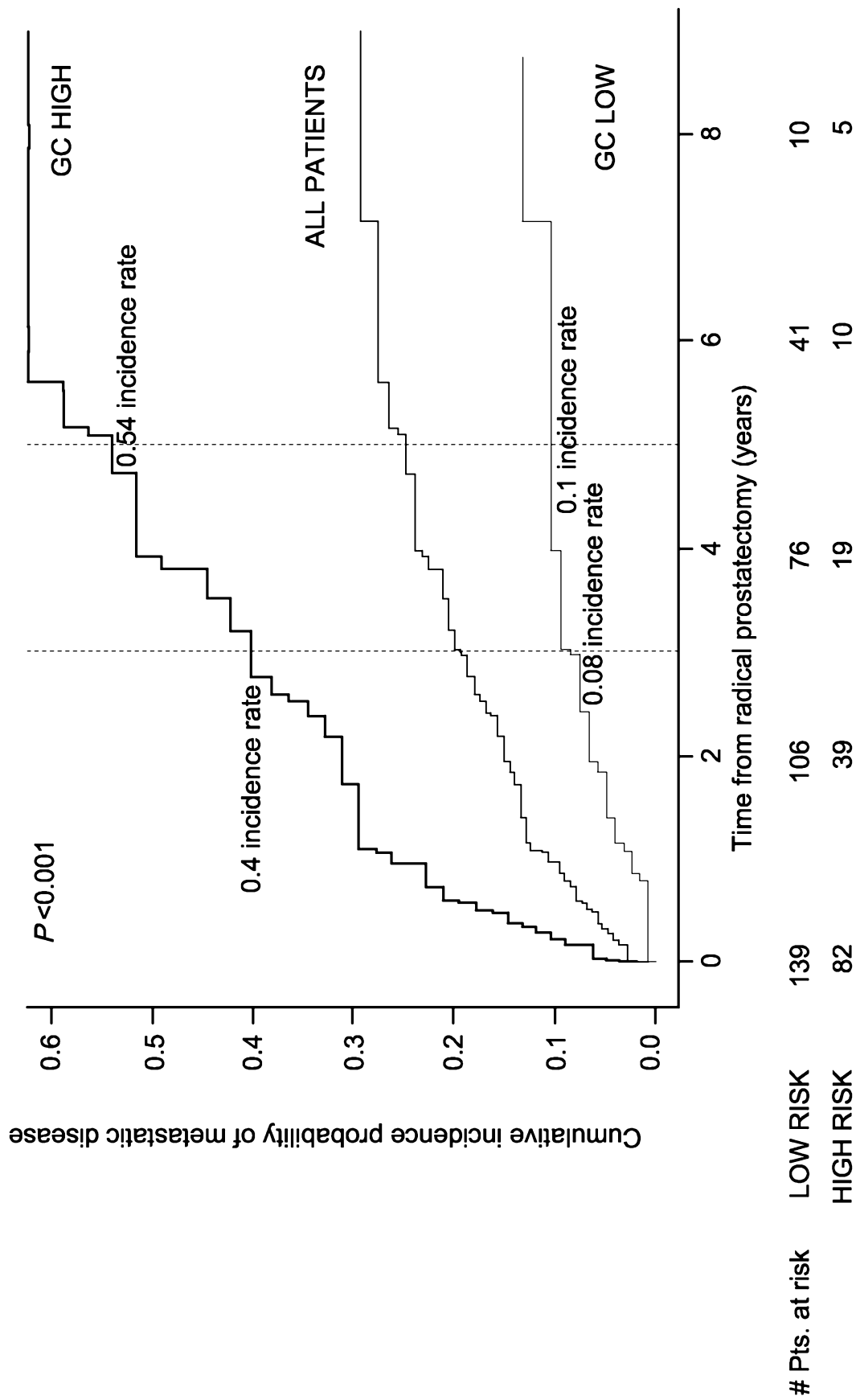


FIG. 51

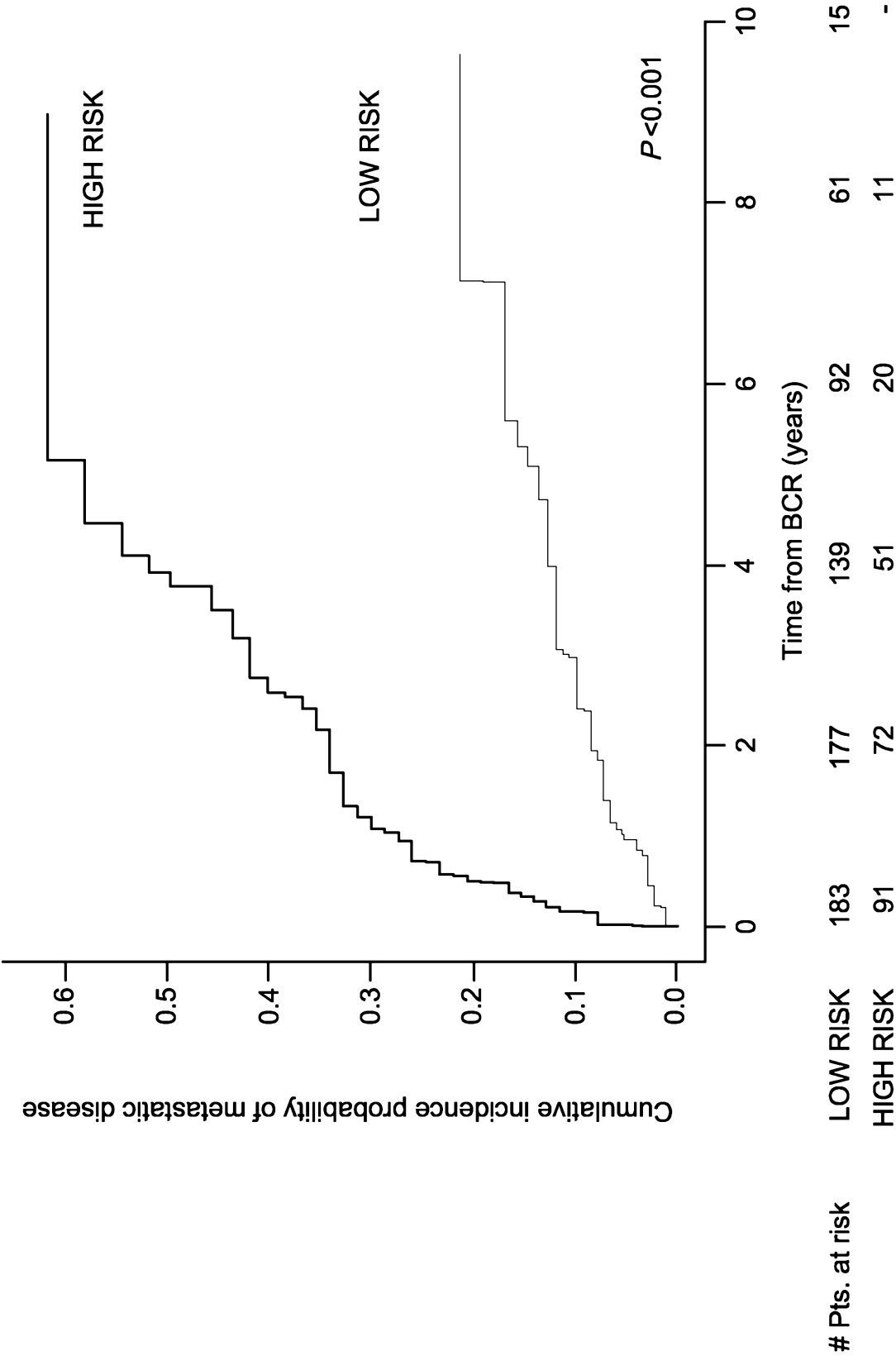


FIG. 52

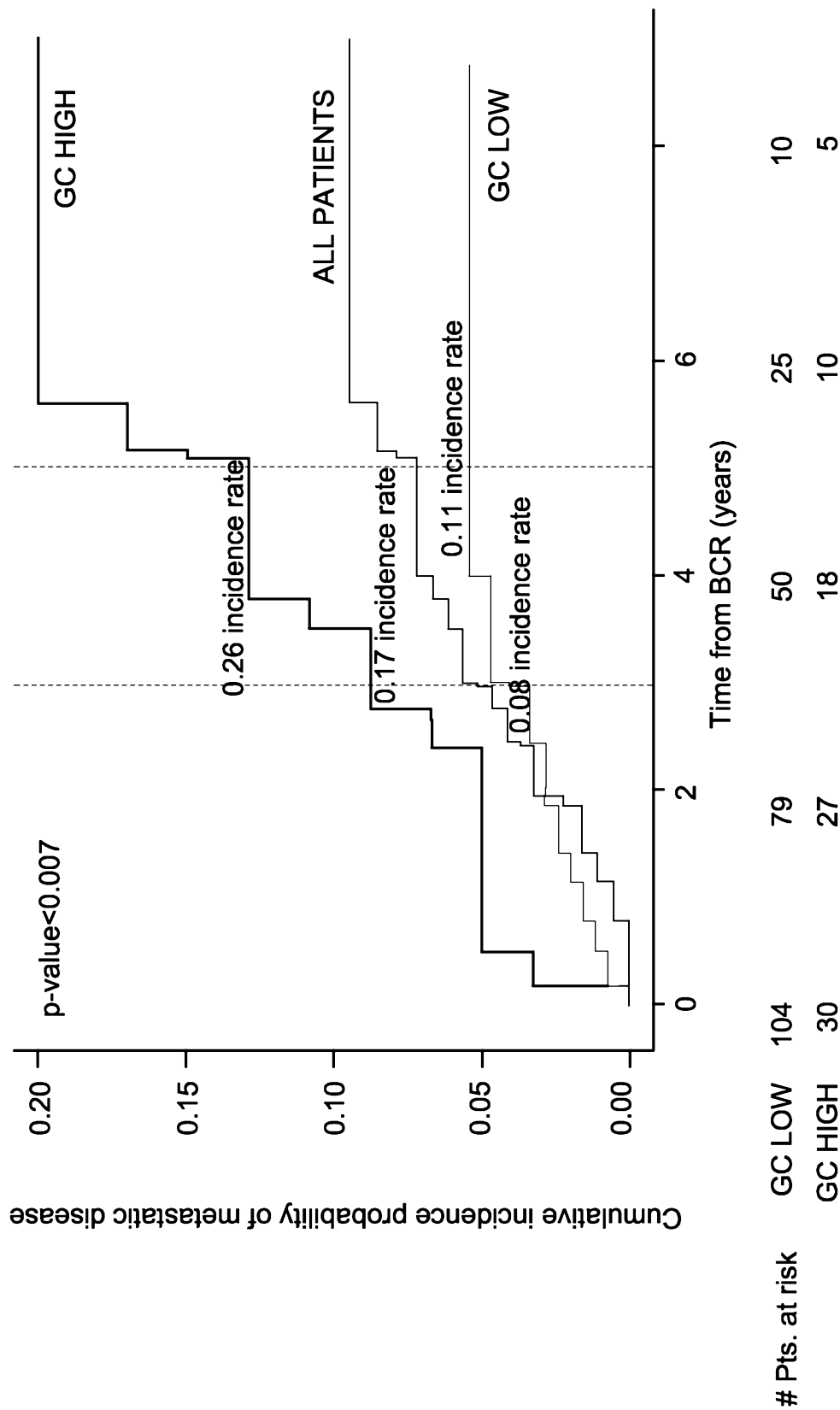
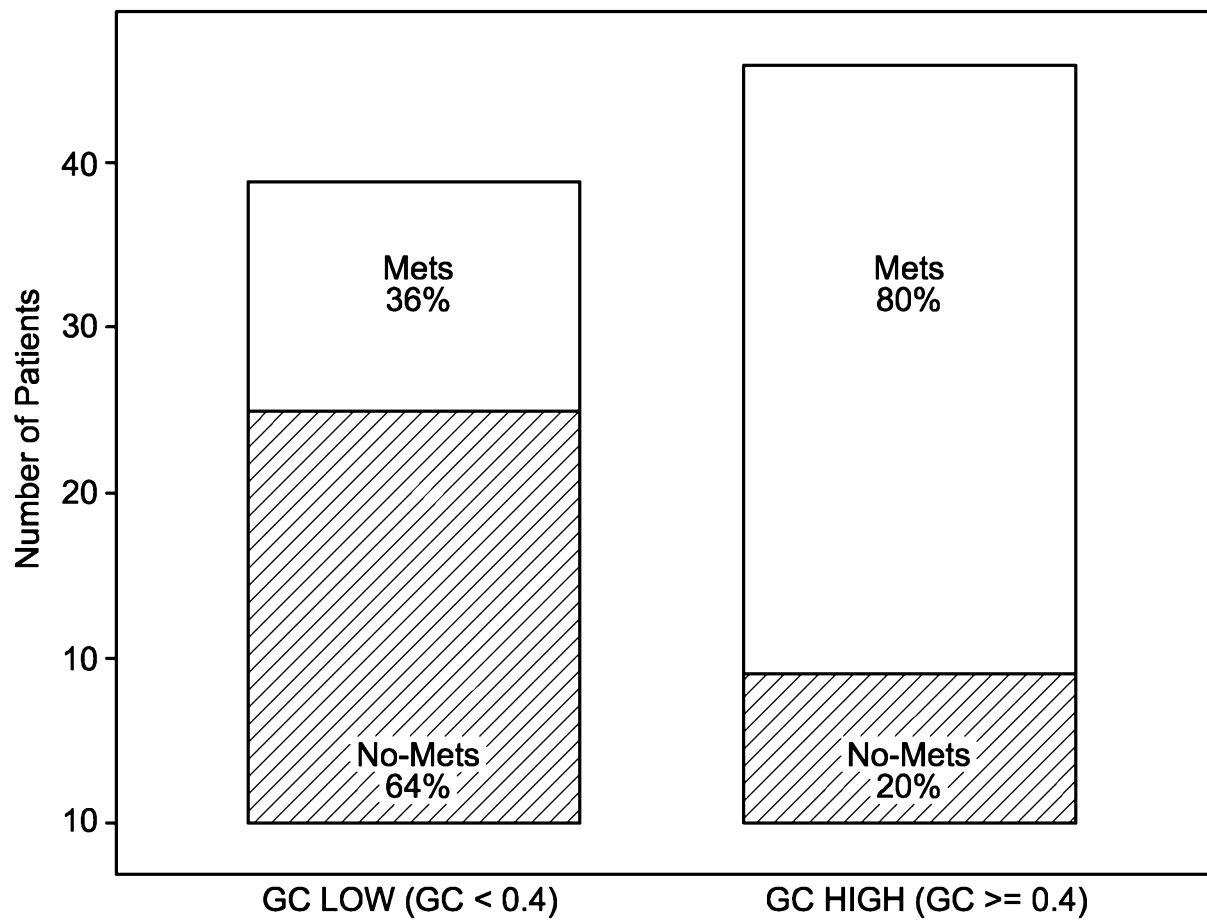
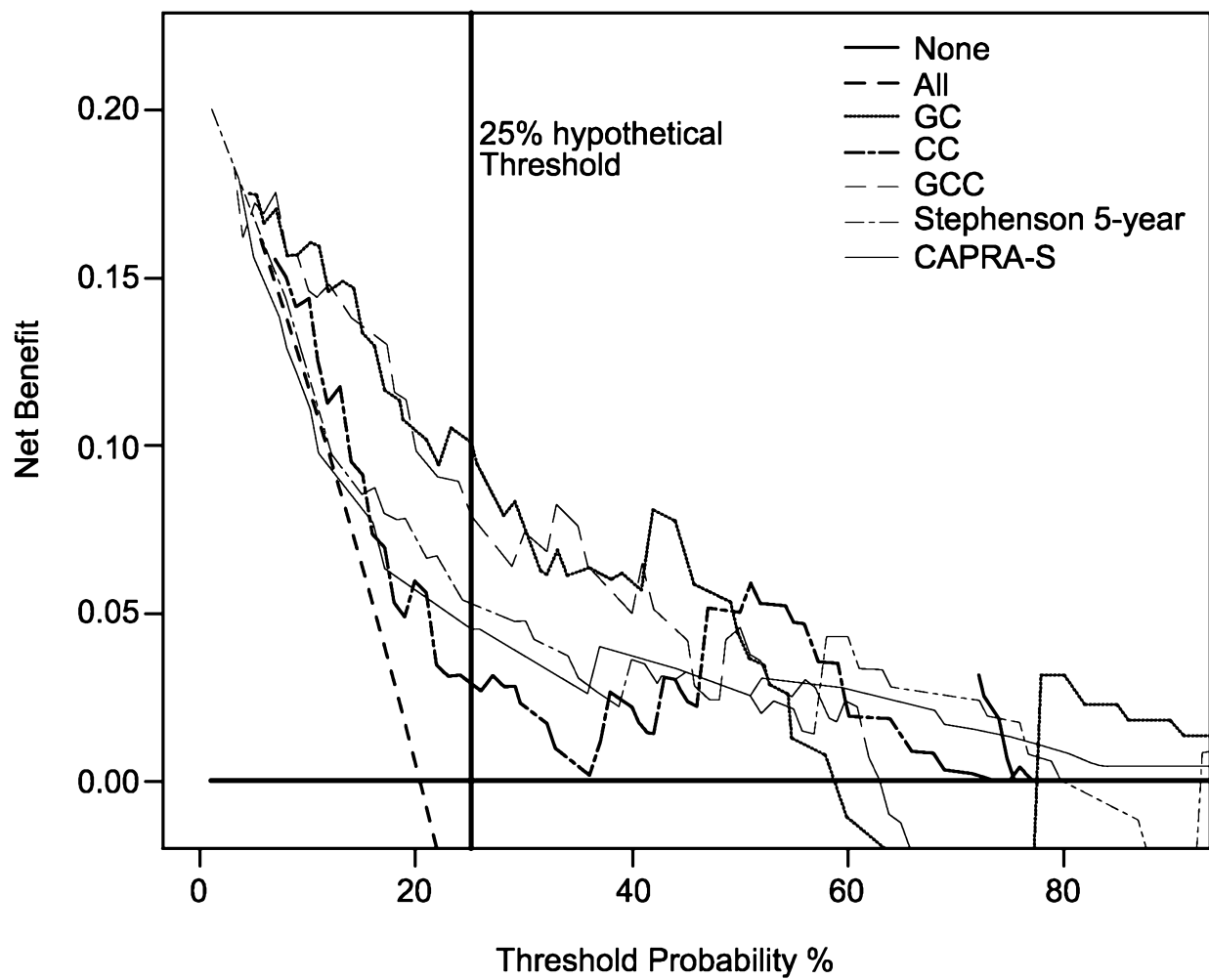


FIG. 53

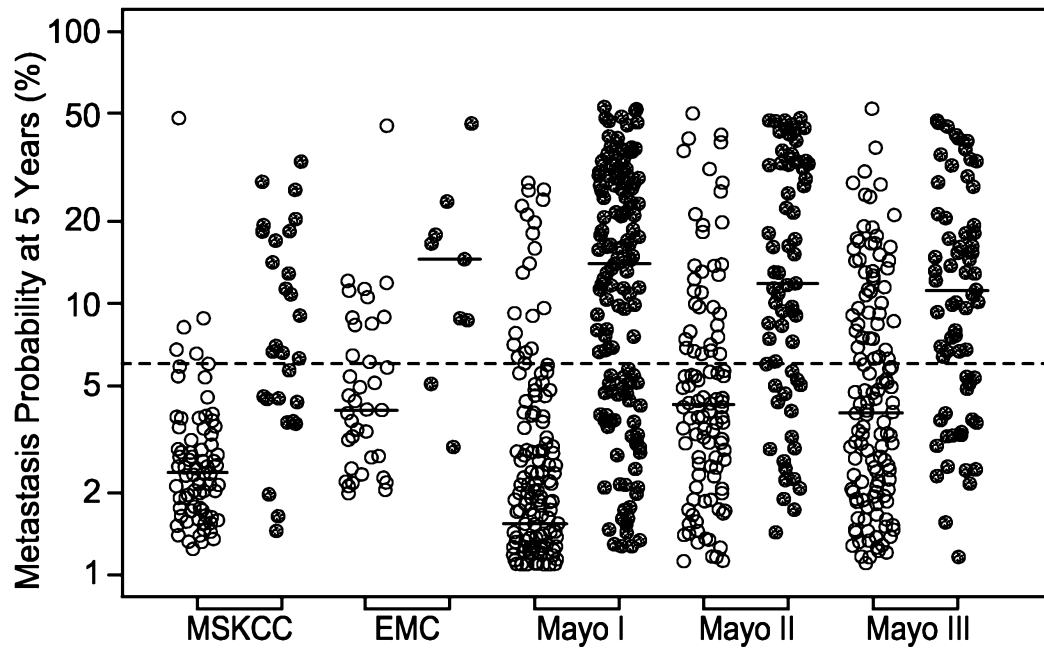
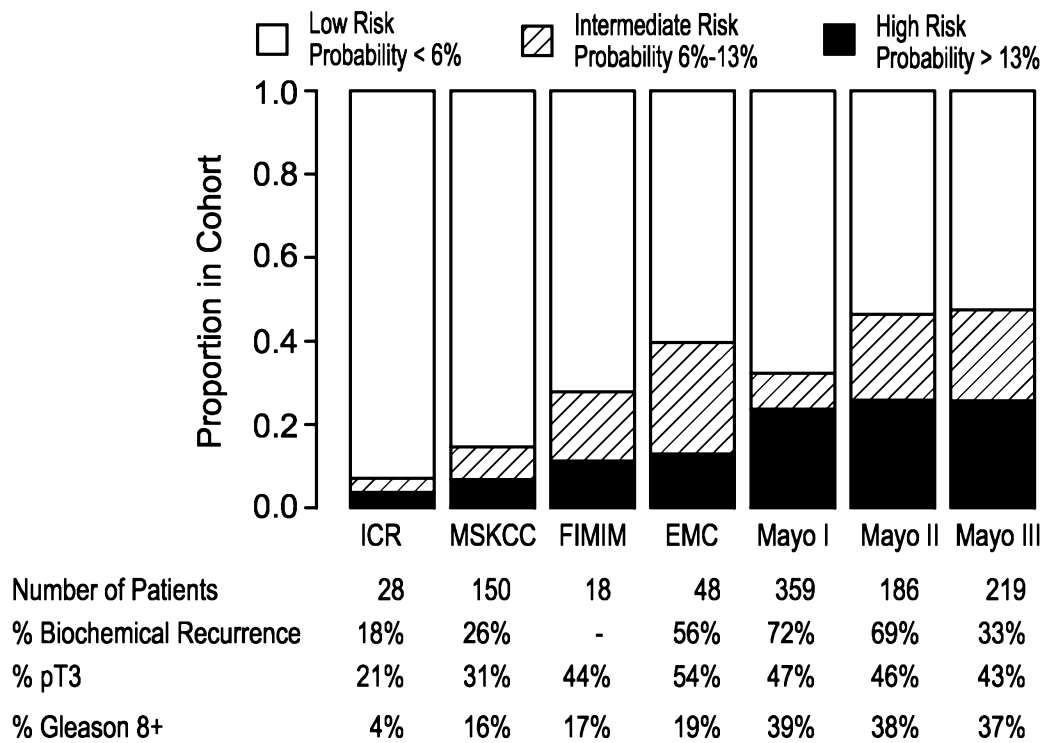
66/81

**FIG. 54**

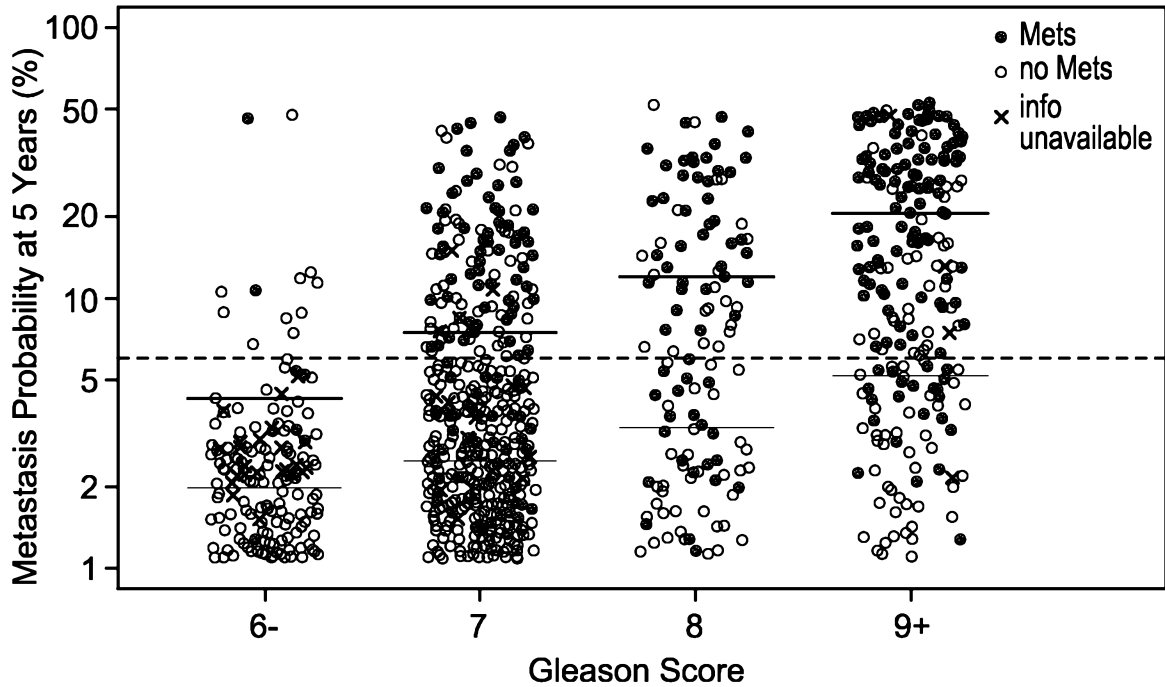
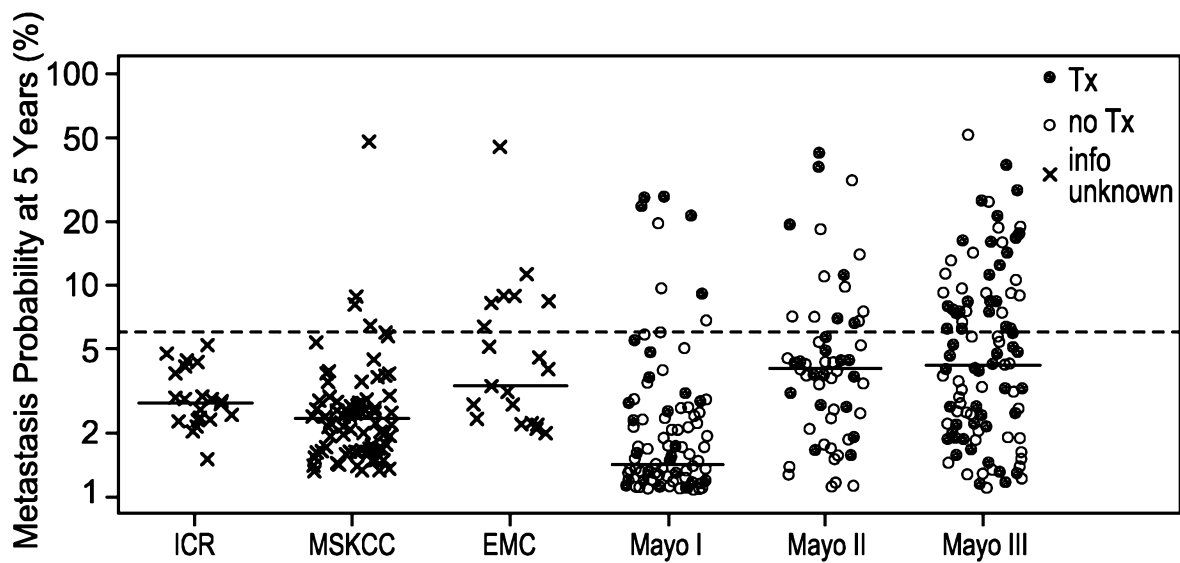
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**FIG. 55**

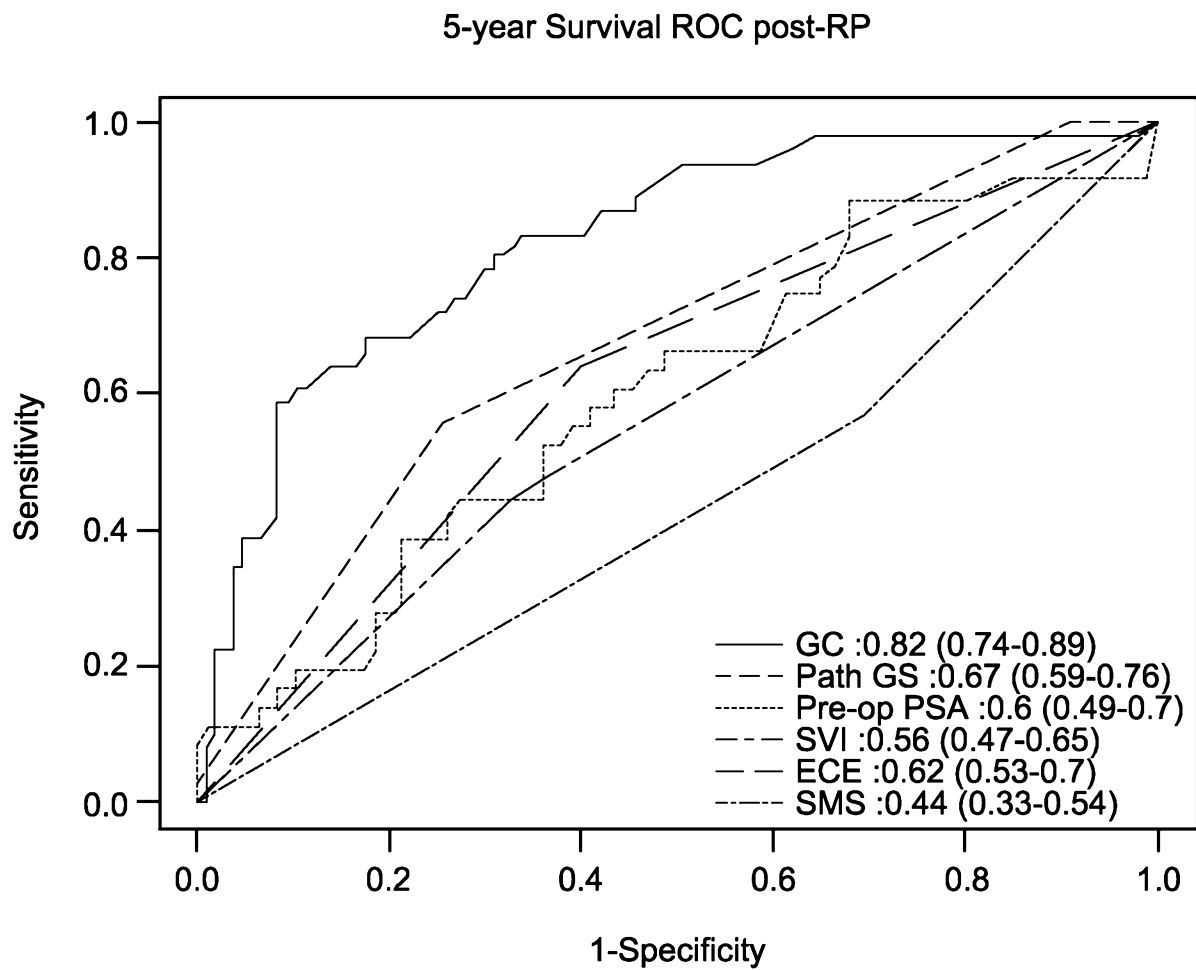
68/81

**FIG. 56****FIG. 57**

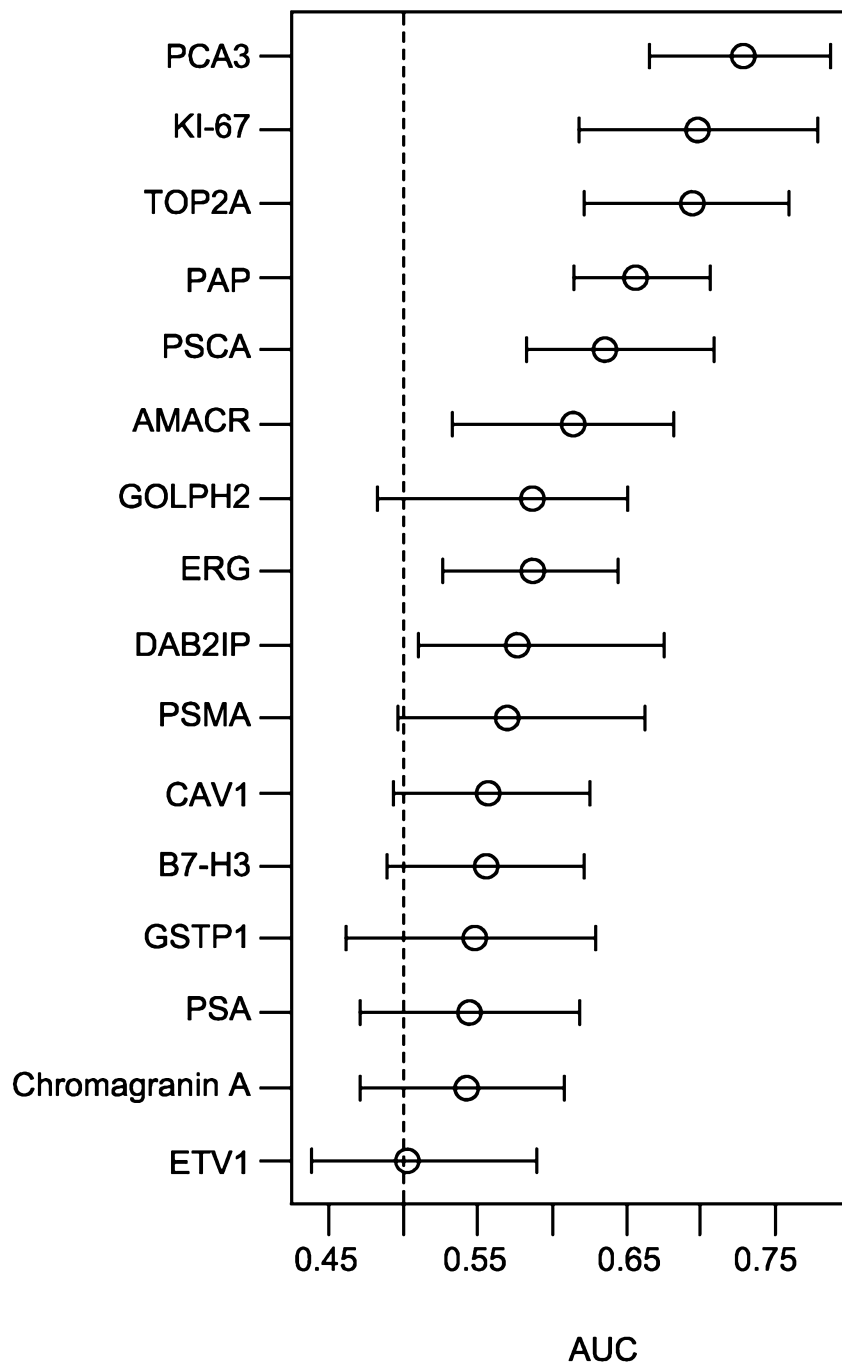
69/81

**FIG. 58****FIG. 59**

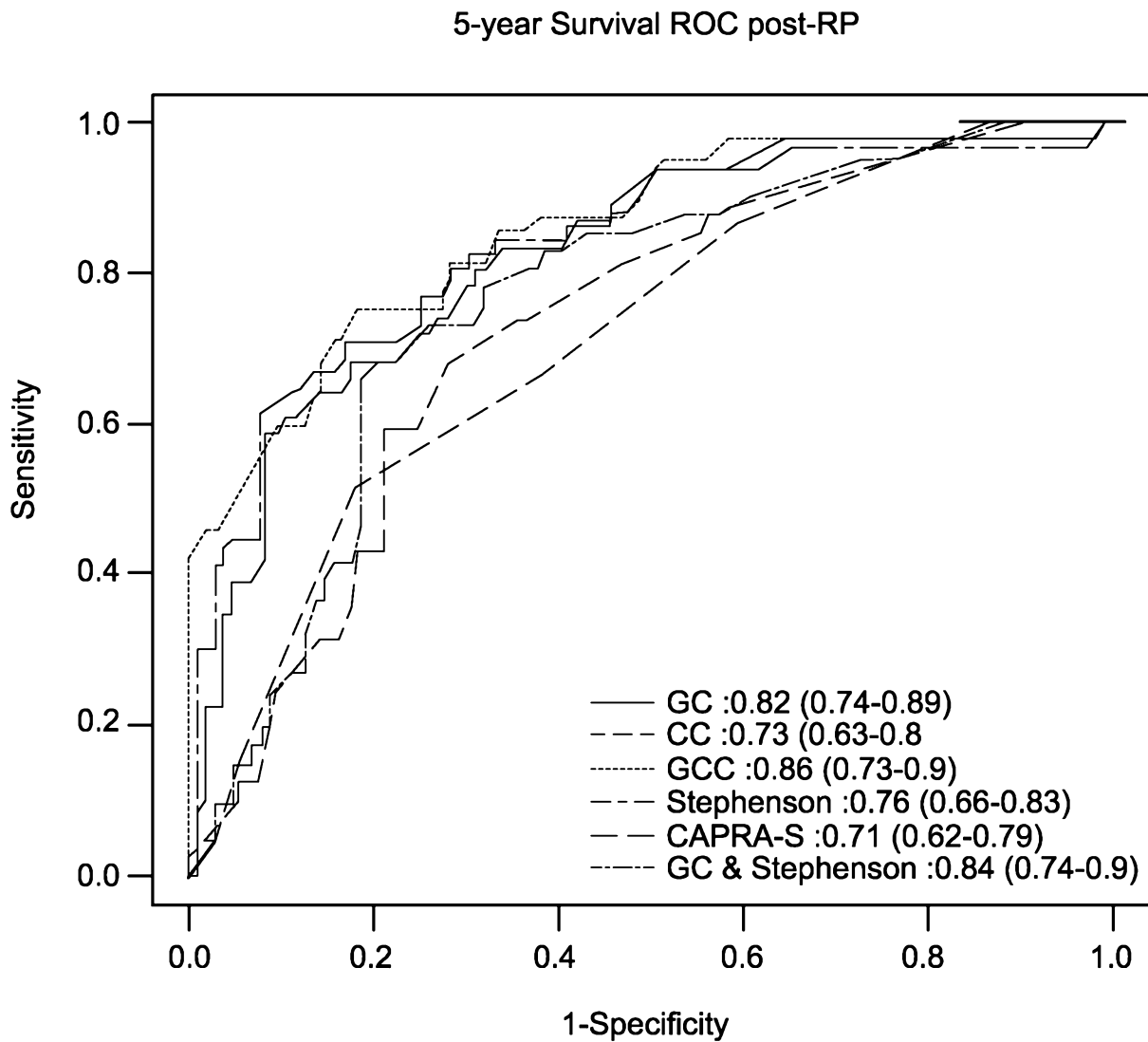
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**FIG. 60**

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**FIG. 61**

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**FIG. 62**

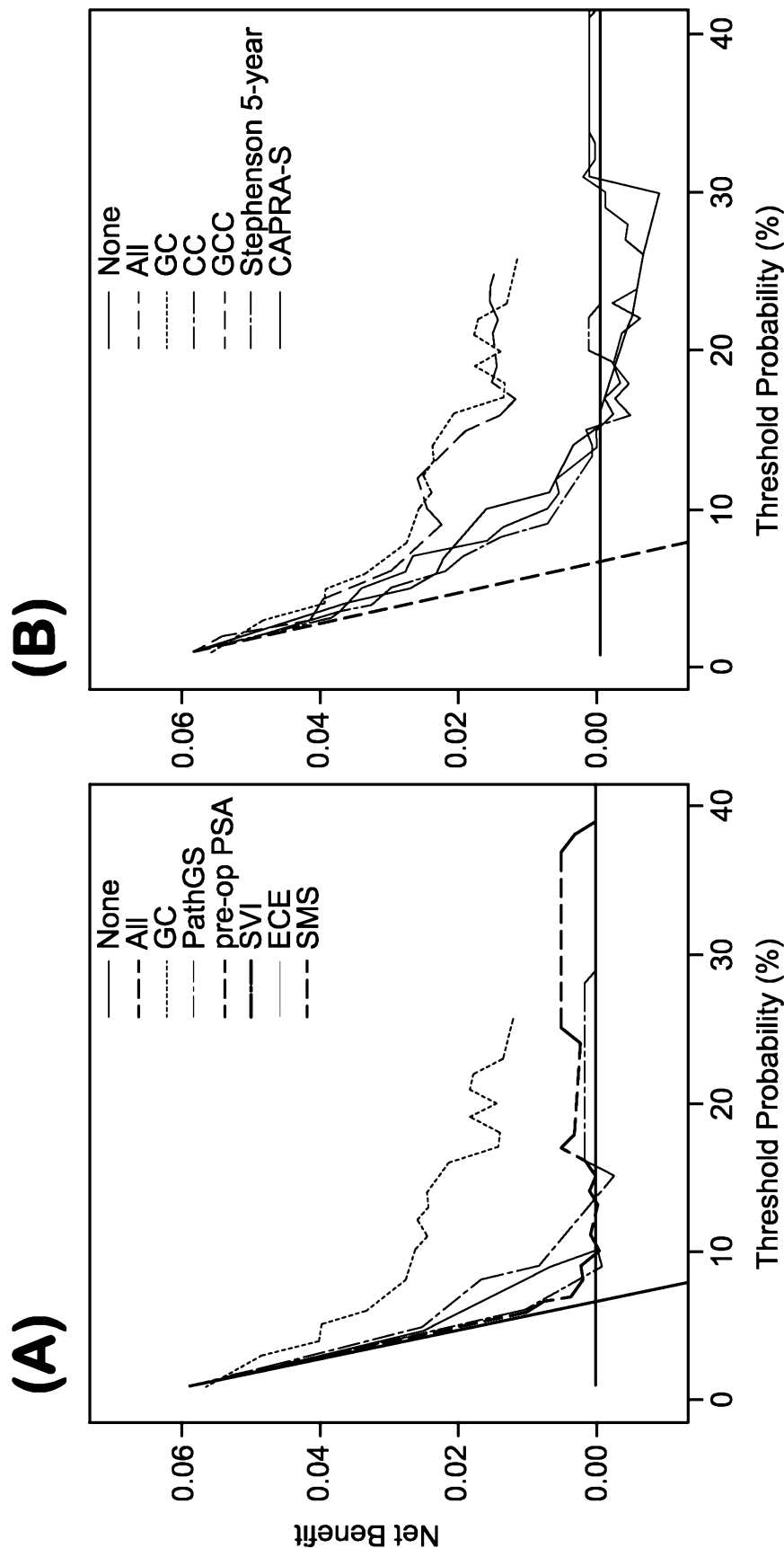
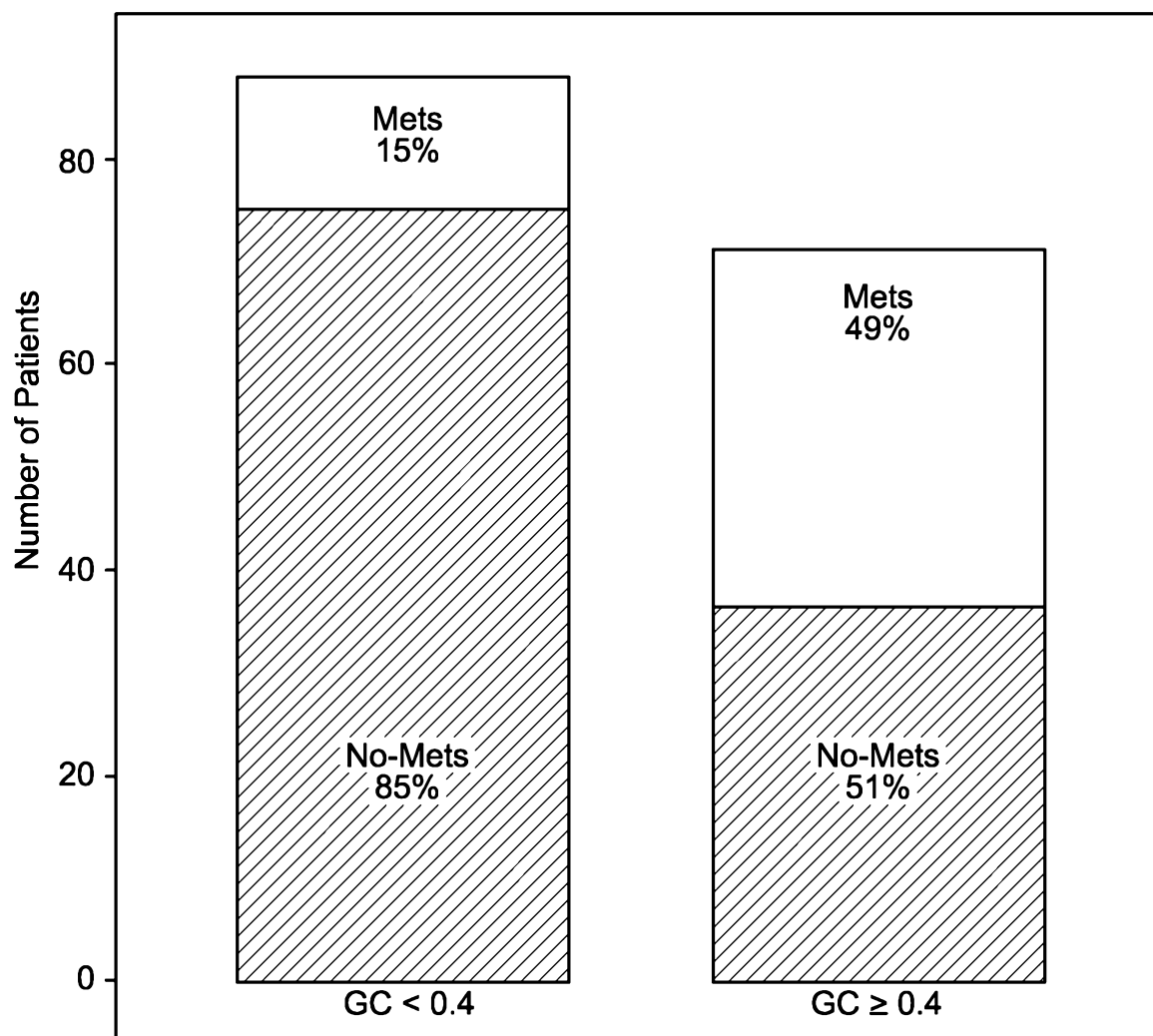
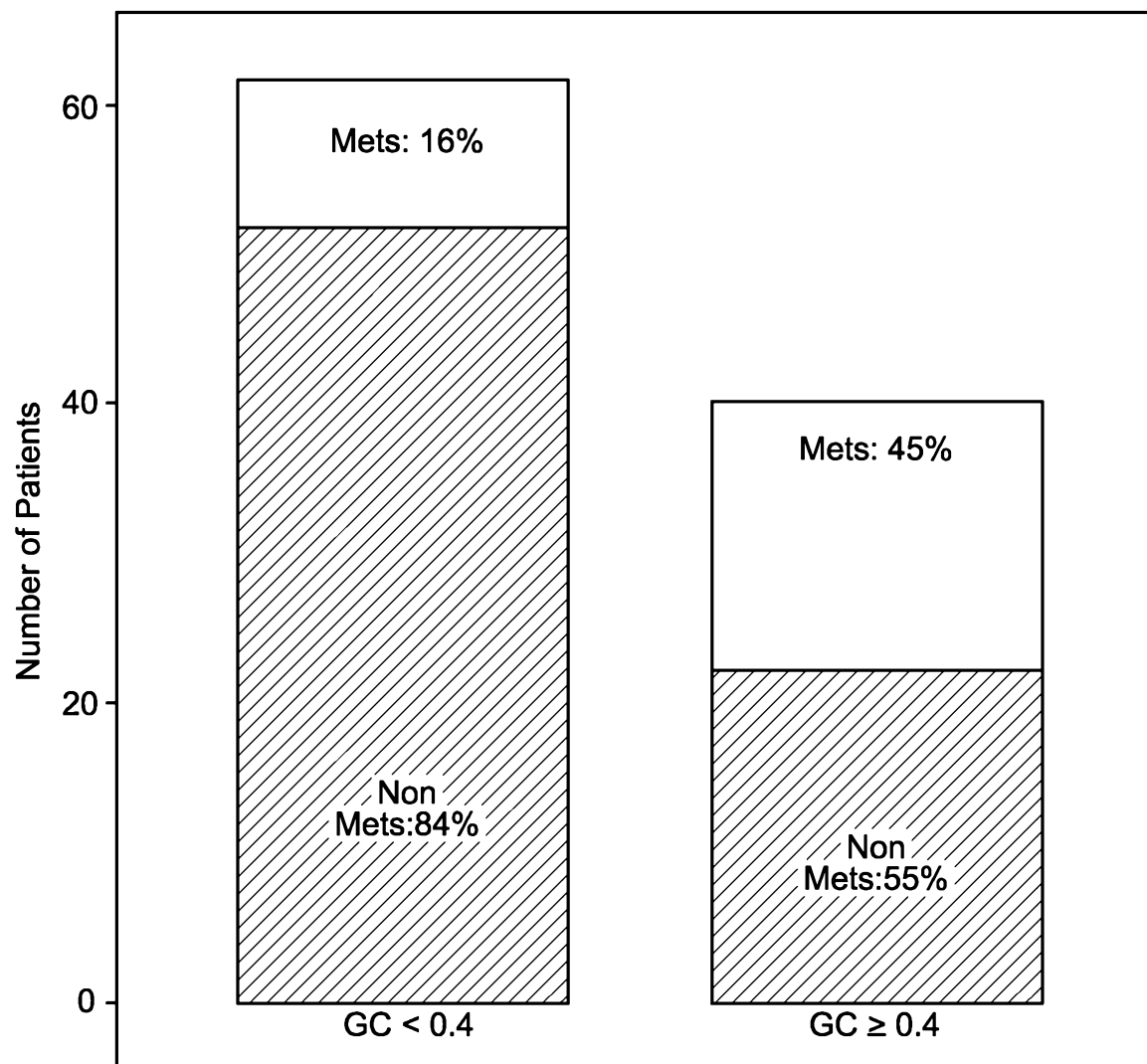


FIG. 63

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**FIG. 64**

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**FIG. 65**

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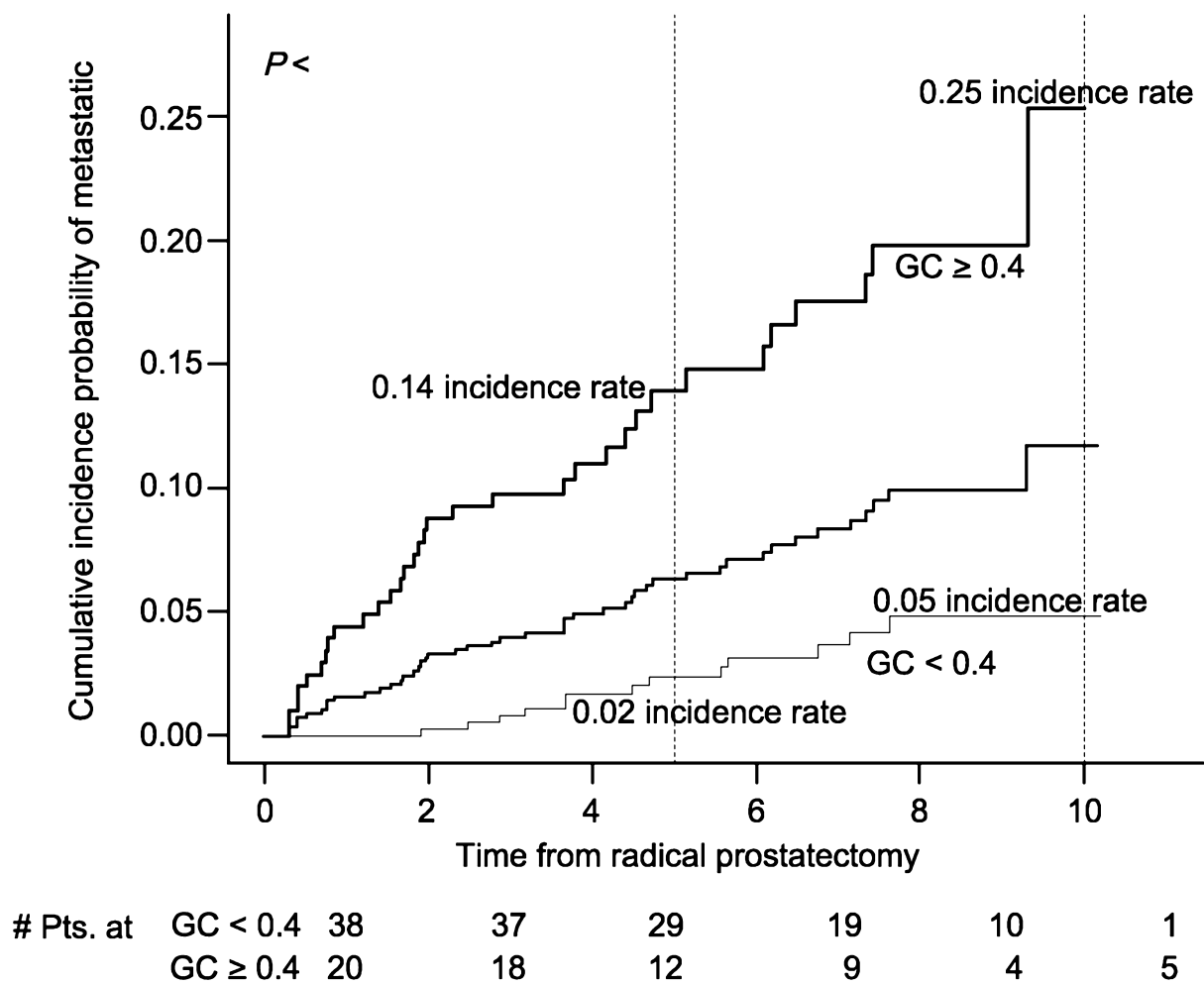
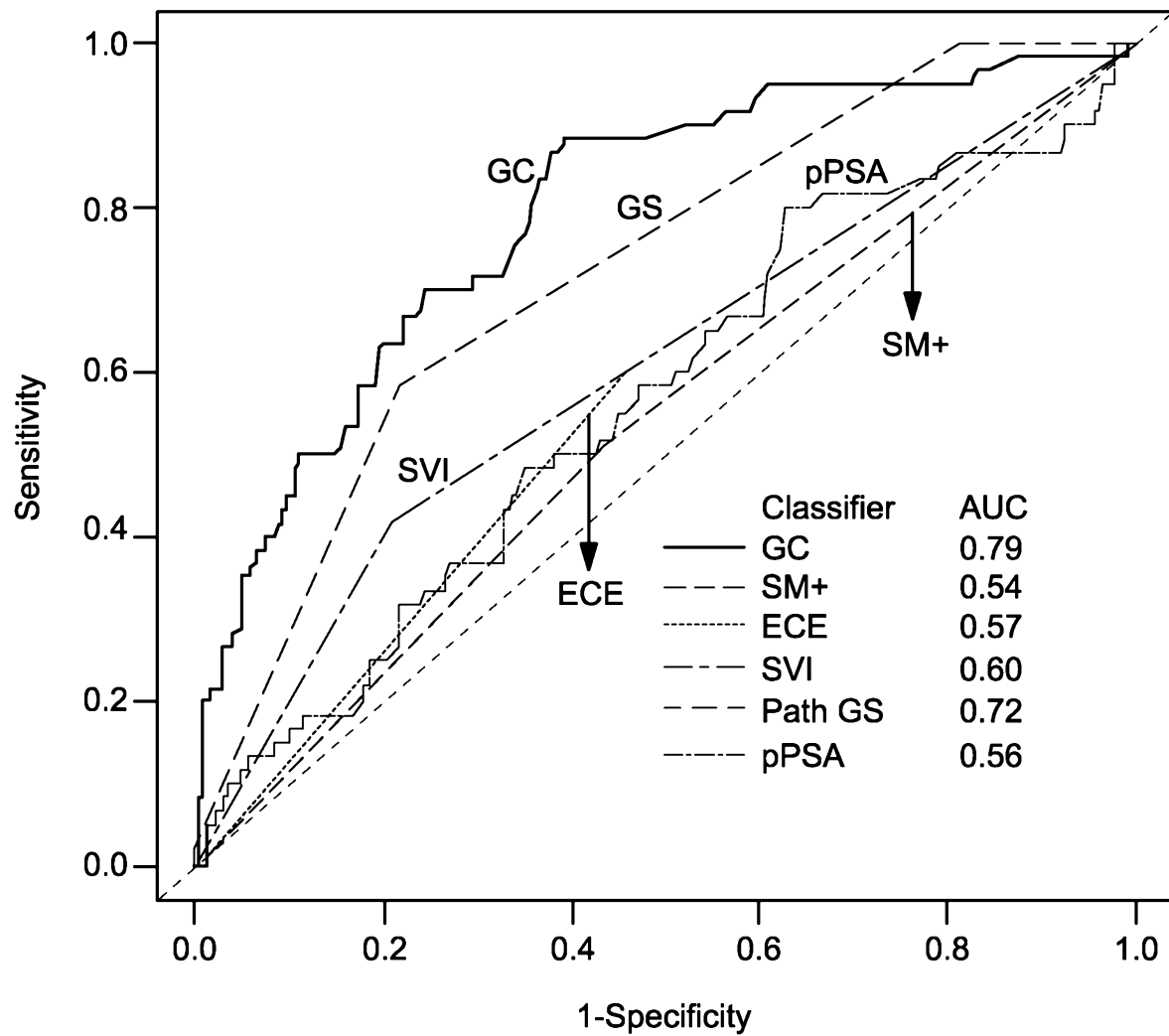
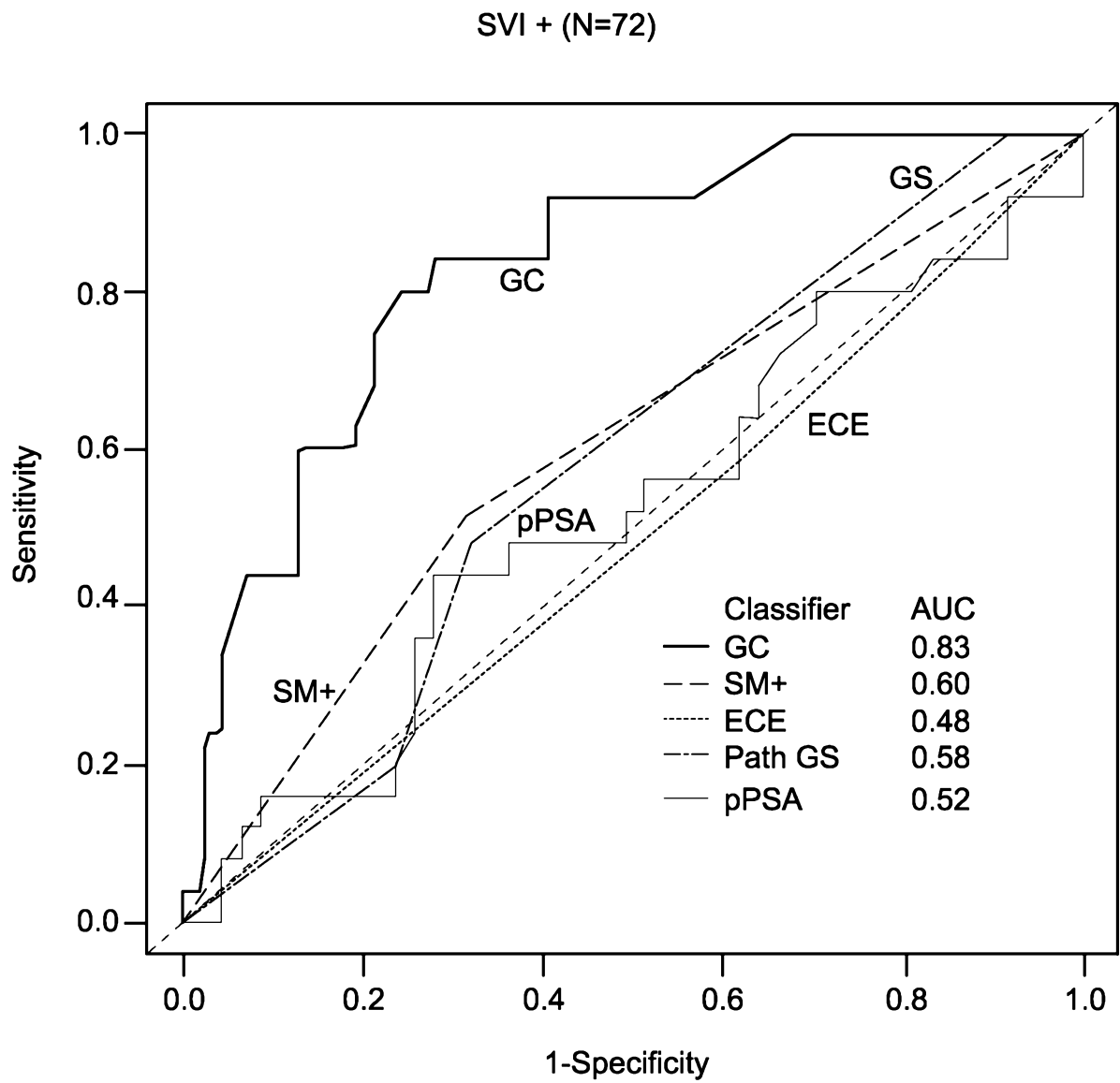


FIG. 66

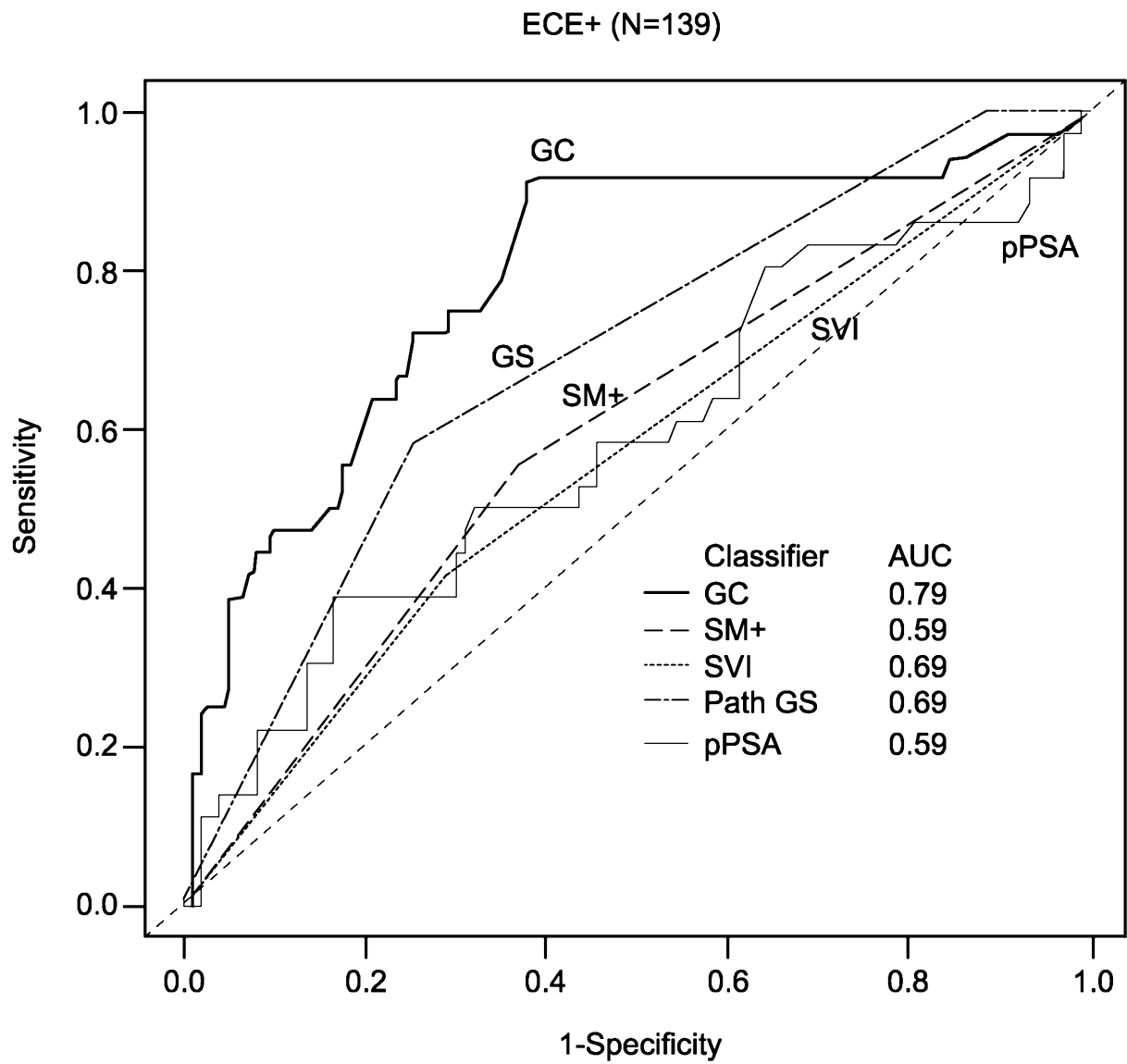
77/81

**FIG. 67**

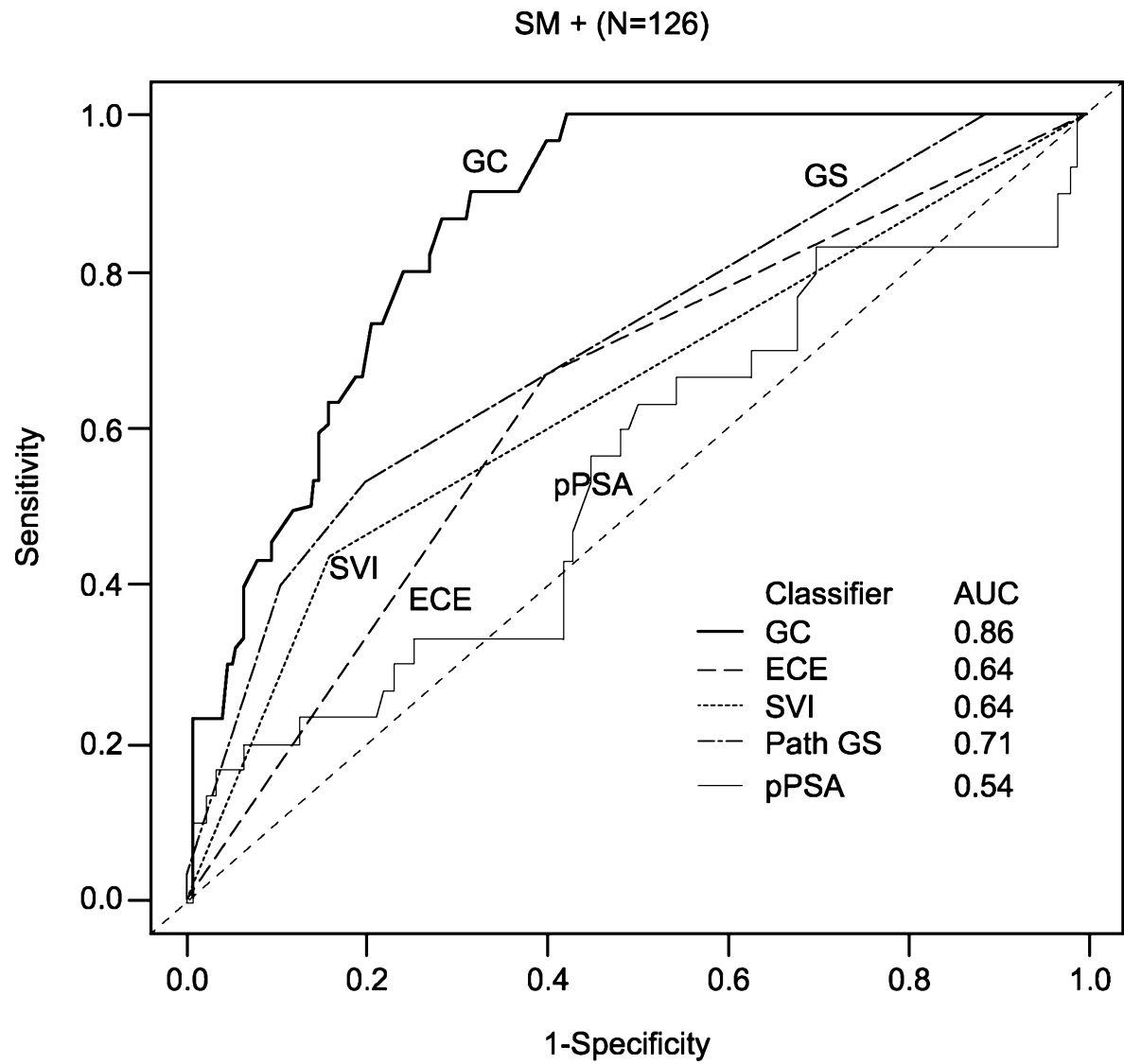
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**FIG. 68**

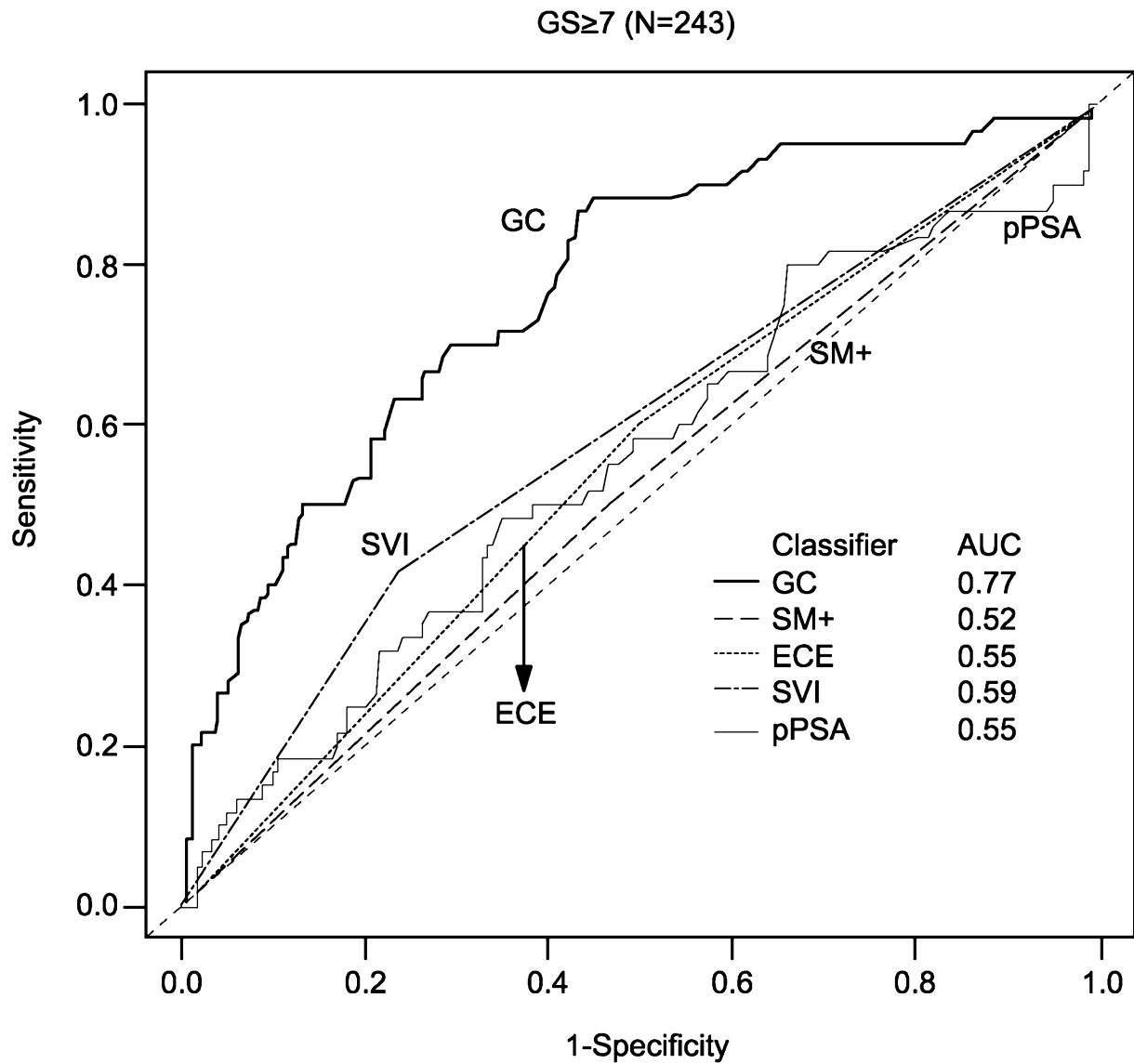
79/81

**FIG. 69**

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**FIG. 70**

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**FIG. 71**

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MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH
BUERKI, Christine
CRISAN, Anamaria
DAVICIONI, Elai
ERHO, Nicholas George
GHADESSI, Mercedeh
JENKINS, Robert B.
VERGARA CORREA, Ismael A.

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 <213> Homo sapiens

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cgaa                                          124

<210> 13
<211> 28
<212> DNA
<213> Homo sapiens

<400> 13
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ggagctcact atataattat aaagggctaa ttcatcaaga ggatataaaa attataagta      240
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<213> Homo sapiens

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<400> 37
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<400> 38
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<210> 39
<211> 164
<212> DNA
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<400> 39
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<213> Homo sapiens

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<213> Homo sapiens

<400> 41
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<210> 42
<211> 186
<212> DNA
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<400> 42
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acctga 186

<210> 43
<211> 40
<212> DNA
<213> Homo sapiens

<400> 43
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<210> 44
<211> 108
<212> DNA
<213> Homo sapiens

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<210> 48
 <211> 73
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 <213> Homo sapiens

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 <211> 150
 <212> DNA
 <213> Homo sapiens

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<210> 50
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 <210> 51
 <211> 118
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 <210> 52
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 <212> DNA
 <213> Homo sapiens

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 <210> 53
 <211> 155
 <212> DNA
 <213> Homo sapiens

 <400> 53
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 <210> 54
 <211> 63
 <212> DNA
 <213> Homo sapiens

 <400> 54
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 <210> 55
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 <212> DNA
 <213> Homo sapiens

 <400> 55
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 <210> 56
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 <212> DNA
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gggaaaaaaa cacttgaggg cagcaataca tggagctcag ttatgattac tttgttcct 240
tcatactcac ctcatcacta tcaaactcat tatcatttga aacaagccga aagtctc 297

<210> 57
<211> 109
<212> DNA
<213> Homo sapiens

<400> 57
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gttcagactc catgacattc cttgggtgta taccctccaa tccatttga 109

<210> 58
<211> 63
<212> DNA
<213> Homo sapiens

<400> 58
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<210> 59
<211> 110
<212> DNA
<213> Homo sapiens

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<211> 208
<212> DNA
<213> Homo sapiens

<400> 60
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tcttaaacad gagtgagaat ctgttgcccc aacctaaggt gactttaaat ccaaggtaaa 180
aaacacggca tgggtattag tttgaata 208

<210> 61
<211> 70
<212> DNA
<213> Homo sapiens

<400> 61
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ccccttgagg 70

<210> 62
 <211> 105
 <212> DNA
 <213> Homo sapiens

<400> 62
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 ccacagccac agtacactga ggggtccatgc gtcacgtccc tctgt 105

<210> 63
 <211> 94
 <212> DNA
 <213> Homo sapiens

<400> 63
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 tctcgtgggg tcctgcctgt ttagtcgctt tcag 94

<210> 64
 <211> 290
 <212> DNA
 <213> Homo sapiens

<400> 64
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 cgagttccg cagatctgca gatttgaaga ggtattttatt ctcatttctg ccttcccagt 180
 ccagcagaag ttctaatttg tggacggcag ctttggtaat taacaaagtg tgttctgtga 240
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 <212> DNA
 <213> Homo sapiens

<400> 65
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 caaccccata taaaaagatg aactggcggc ttcacac 157

<210> 66
 <211> 212
 <212> DNA
 <213> Homo sapiens

<400> 66
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<210> 67
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 <212> DNA
 <213> Homo sapiens

<400> 67
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 gtttttatct ttgaccaacc gaacatgacc aaaaaccaa agtgcattca acct 114

<210> 68
 <211> 113
 <212> DNA
 <213> Homo sapiens

<400> 68
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<210> 69
 <211> 210
 <212> DNA
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<400> 69
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 caaactctga actgtctgaa ttctgtggaa gcagaatata ttgaggtcct gaccacggtg 180
 tccagccctg ctgtagaact atgtggatca 210

<210> 70
 <211> 246
 <212> DNA
 <213> Homo sapiens

<400> 70
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 agagagcata tctactgggtt caaaccccag ctctaccgg caaagcccgg ggcctccacc 120
 tgggtgttcc catccatgaa gcgggggatac acagtgtgga gcccttgagg ggttggggag 180
 tgtgcctgcc ctcaccgagc atcagctcat aaatacaaca acagttgcct tcacgtgctg 240
 atgctc 246

<210> 71
 <211> 213
 <212> DNA
 <213> Homo sapiens

<400> 71
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 gctgctgtcc agaggcggag gtaaacttg atccctcctg cacactcagc tctctcatgg 180

aagtcggagc cctcagggtc acctgaaaac tct 213

<210> 72
 <211> 115
 <212> DNA
 <213> Homo sapiens

<400> 72
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 gaaccagcag gctgtgtgga tgcaaggccc agtgctcccc tgttctctga ggagg 115

<210> 73
 <211> 31
 <212> DNA
 <213> Homo sapiens

<400> 73
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<210> 74
 <211> 448
 <212> DNA
 <213> Homo sapiens

<400> 74
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 aattgaacat gagtccgcac gctgttttct ttcaaaaggc atcaaaacgg aaagcctctc 420
 taaggggaag acctttcaac tccattca 448

<210> 75
 <211> 31
 <212> DNA
 <213> Homo sapiens

<400> 75
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<210> 76
 <211> 129
 <212> DNA
 <213> Homo sapiens

<400> 76
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 gacgttggc 129

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 <212> DNA
 <213> Homo sapiens

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 cccagcaatc attcccaggt gatcggccag tggtttttta ggctcactcg tctgggtctgg 180
 tctgattcca agattccctg gaaacacaga gaatgcttat gacctctgca gttcttgcct 240
 aaagagactg caaaagatca ctgacattcc ttaggactcc caggaggcac gtccagctaa 300
 gggactgtct gcaccatttt aagc 324

<210> 78
 <211> 129
 <212> DNA
 <213> Homo sapiens

<400> 78
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 aagcgtctct ggagctggga taggccactg tgtaagatgc aaggctggag agtgggtatc 120
 tgccaaccc 129

<210> 79
 <211> 39
 <212> DNA
 <213> Homo sapiens

<400> 79
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<210> 80
 <211> 29
 <212> DNA
 <213> Homo sapiens

<400> 80
 tgggattccc tggacctaaa ggtgctgct 29

<210> 81
 <211> 343
 <212> DNA
 <213> Homo sapiens

<400> 81
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 caccgttggt tgcccccttc cggaccctgt gctctctctt ccgattcaga ttcaaaagca 180
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 acttttaaag ttgcaggctt tgtaactgct cttagcagag gcaggttctg ctttagaaag 300
 tttgcatacc atcatTTTTT tcttggttct taatcagcga atc 343

GBX1170_3WO_ST25.txt

<210> 82
 <211> 420
 <212> DNA
 <213> Homo sapiens

<400> 82
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 tggagggcat taagagttga aaaggcttat atggttaact accttagact atatctacag 180
 cagggctctgg tttgccagaa caagtttaaa gtggctgttt attaagtttg ctattttcag 240
 aattgaaact ataagaccgc catttgacac tgaaacttgc gtgaatccta aattgcatca 300
 attatctatt tgataaaagc ttattctaatt ttaaaacctt atagagtaag agactgatat 360
 atatagcagt cttaaagatc acgtcatctg ctttacatta gtccagtcac gtgcttcgta 420

<210> 83
 <211> 110
 <212> DNA
 <213> Homo sapiens

<400> 83
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 gccccatgct gccagacctg atcgcagaca gccactgttc ccattccttg 110

<210> 84
 <211> 279
 <212> DNA
 <213> Homo sapiens

<400> 84
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 tataggaaat tcaggagatt gaggaacaaa ttaagtgatg tcattaggaa aaagtcagac 180
 aattaaaaaa tgtaggtgag gcactctaaa gcaactagct tggactcttc aaaaaattgt 240
 catgggaaat tagaatggta ccgccaactc tggaaaaca 279

<210> 85
 <211> 250
 <212> DNA
 <213> Homo sapiens

<400> 85
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 atgtgccaag agccagagca ggtgaagaca cctacagatg ctgcctcctc tggacactgc 180
 ctctgggtgc ctgagctctg caccagagg gatgcaaaag agatccccgc agcacacttt 240
 gagatggcta 250

GBX1170_3WO_ST25.txt

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<210> 86
<211> 170
<212> DNA
<213> Homo sapiens

<400> 86
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actcaccact gtctgttctc tgagttttca tttccaggca tccgccctgc ctggatctcc      120
tcacctgcca ggaacttctc ctccacaagc cggccatccc agcaaaagtt      170

<210> 87
<211> 39
<212> DNA
<213> Homo sapiens

<400> 87
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<210> 88
<211> 37
<212> DNA
<213> Homo sapiens

<400> 88
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<210> 89
<211> 381
<212> DNA
<213> Homo sapiens

<400> 89
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gtcacagatc tcaccagct tccatgcaat ccaaagggcc gttctcactc ccaatgtgcc      120
cccggacca acagcactga gtctgtttcc aggcagtggg taagcagggc tgagaacttt      180
ccccaggcaa tctgcttccc agctgtgaaa gcaaatatgg ctttccttct tccccacct      240
gtggagactg cacaccgat tcacgccctt ccctgagttc tggccaggag tgttctcaat      300
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<210> 90
<211> 51
<212> DNA
<213> Homo sapiens

<400> 90
tggtttttca gtacagccag acagattgga attgggtaaa cctgataata a      51

<210> 91
<211> 94
<212> DNA
<213> Homo sapiens

<400> 91
aagcattgaa tggagcacct acctgcccc agtcagaaca tccccatctc gactggtgat      60

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gagtcaaatg cagggatcac agtgcattggg gaga 94

<210> 92
 <211> 74
 <212> DNA
 <213> Homo sapiens

<400> 92
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 cttagggagt tttt 74

<210> 93
 <211> 36
 <212> DNA
 <213> Homo sapiens

<400> 93
 ggaagggact cggagaaagc tacaagctgg ggccct 36

<210> 94
 <211> 116
 <212> DNA
 <213> Homo sapiens

<400> 94
 aagataggac atgtctgaga gctttggaga aaatcaagat tcagttagaa aaaggaaata 60
 aagaatttgg tgaccaagct gaagcagcac aggatgccac cttgactaca actact 116

<210> 95
 <211> 104
 <212> DNA
 <213> Homo sapiens

<400> 95
 cagagattaa ggaaccgagg agagagagac cgggaaaggg agagagaaag ggaaatgagg 60
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<210> 96
 <211> 30
 <212> DNA
 <213> Homo sapiens

<400> 96
 agcagttcag cttgaatcag agtagagtgg 30

<210> 97
 <211> 41
 <212> DNA
 <213> Homo sapiens

<400> 97
 ggagagaata agaacggcgg taacagttat tggcaaaaag c 41

<210> 98
 <211> 108
 <212> DNA
 <213> Homo sapiens

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<400> 98
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cgccagcaag aggagatcac acacctgcta tcgcaaatag ttgatttg 108

<210> 99
<211> 152
<212> DNA
<213> Homo sapiens

<400> 99
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ttgaaggaca tgcagctagc tttgcacagt ttaagatgga aggaaatgca gaagaatcaa 120
cgttattttg ttttgcagtt cggggccaag ct 152

<210> 100
<211> 99
<212> DNA
<213> Homo sapiens

<400> 100
ctgatcctcc agtggcaccg actgtgacag aggtgggaga tgactggtgt atcatgaact 60
gggagcctcc tgcctacgac ggaggctctc caatcctag 99

<210> 101
<211> 29
<212> DNA
<213> Homo sapiens

<400> 101
atacagtgga gcatcgtgcc cgaagtgtc 29

<210> 102
<211> 119
<212> DNA
<213> Homo sapiens

<400> 102
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ctgctggtgc attccaatca gagttgggat cagcagaaga cagaccatct aaaatttaa 119

<210> 103
<211> 708
<212> DNA
<213> Homo sapiens

<400> 103
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atttccaagt tttctaggaa cccatctccg tctgggcgct gtgagtgggg tgggcacgtc 180
cgggcagccc agtgcgtctg tcgcacgtcc ccaggccgtg ctgctggcgt cactttcttt 240
gatatgtagc tttttcttaa agacttttga atgtttaata attttgtaaa tcatgctctt 300
tacacagagt accacttatt taataagacg ggatgtaaat ttacaatgac aaatgtgtat 360

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tttaagaaaag aaaatgacat tattttgaat ggtactttgt ggaaagaggg gagaataaag	420
ttatgctgtg tacatcactt gcagatcacc aaaaacactc cgctgcccgt gaccgcccgt	480
gggtgtgtcc ccgctcccgt cgtcccgcgc acctcaaacc ccgcaggtgt gcctcccagc	540
ggattattta ttgtagaaag tgtattcatt tgctttataa tgaaaaatac atttgcaaag	600
gtatattgat atgcattttt atacaggcac ataaaaattc aacttggctt gggagcagaa	660
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<210> 104
 <211> 152
 <212> DNA
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cccagctccc ttgcctctca gtttgataa tc	152

<210> 105
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 <212> DNA
 <213> Homo sapiens

<400> 105 agccccaata tgtcaccgag ctgcagagcc cccagcccca ggcacagcca ccgggtggcc	60
agaagcagta cgtgacggag ctcccggctg tacc	94

<210> 106
 <211> 82
 <212> DNA
 <213> Homo sapiens

<400> 106 aaggcagaag tgactccga aattctcttt ctggactcag aaggaaacca aagcaattga	60
tgacaccgca tcccatacta aa	82

<210> 107
 <211> 74
 <212> DNA
 <213> Homo sapiens

<400> 107 gtttgagat tacgaagcat ttgtcattca gactgcccag gacatggaat cctggctgac	60
caaccgggaa caga	74

<210> 108
 <211> 147
 <212> DNA
 <213> Homo sapiens

<400> 108 catttccaag gggtaggtgc acaggtcaac agaactaaac tacagtgatc ttcccttaga	60

tccttttcta ctgaggtgaa tagctcaaaa gacaaggatg ccttttagtcc aggctaaccc 120
 ctgtagcctc tacgcaatta acacaga 147

<210> 109
 <211> 80
 <212> DNA
 <213> Homo sapiens

<400> 109
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 ctatgtatcc ctggcccacg 80

<210> 110
 <211> 82
 <212> DNA
 <213> Homo sapiens

<400> 110
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 aggctccttg ctccaacagt ca 82

<210> 111
 <211> 329
 <212> DNA
 <213> Homo sapiens

<400> 111
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 tggctccaac aagtcaccca agccctaatt ctagtaggtg gtcacatctg tctcttctct 180
 ttcatgttcc ttataactag tctgttacta agtcctgcca attctacctc agaatactcc 240
 ctttcagtcc ccctactgct gctctgttga gcattgaggc tctgcactta catcaggccc 300
 catctgcatc tctatgtcca gtgttactc 329

<210> 112
 <211> 172
 <212> DNA
 <213> Homo sapiens

<400> 112
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 caacagccag ccagccacta cccaaaaatg tctgcctgaa agcagctcca ggaggcaggc 120
 catggggagt ggaagtcggg gagaaactgg aagaggcgcc aagcagctgt ca 172

<210> 113
 <211> 148
 <212> DNA
 <213> Homo sapiens

<400> 113
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 gctccacctc gcgctcatgt gcacccaca gcgggcagtg cccctgtcgc ccaggagccc 120

ttggccgcca gtgcaacagc tgtgacag 148

<210> 114
 <211> 236
 <212> DNA
 <213> Homo sapiens

<400> 114
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 tgtcggagaa atcgtgattc tgaaagattt taaaatcaga agatttagaa atacattgtt 180
 tgttcccagt gccactatgg ccaggtaaatt ctcaggggct ttcttagccc agaagg 236

<210> 115
 <211> 103
 <212> DNA
 <213> Homo sapiens

<400> 115
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 tcctgcaggg cttctcctcc tctgtctttt ggagaaccag ggc 103

<210> 116
 <211> 222
 <212> DNA
 <213> Homo sapiens

<400> 116
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 aaagtaccac tactgcttta atgagacttc tgaaatccga tttgaaattg aagatgtcaa 120
 caataaaact gaatgtgaaa agcttatgga ggggaacaat acagagatca gatggaagaa 180
 cgtgaagatc aactttgaca atgttggggc aggatacctg gc 222

<210> 117
 <211> 30
 <212> DNA
 <213> Homo sapiens

<400> 117
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<210> 118
 <211> 58
 <212> DNA
 <213> Homo sapiens

<400> 118
 ggagacatcc acctgtgata ttgtccagtt tggtgcagaa tgtgacgaag atgccgag 58

<210> 119
 <211> 64
 <212> DNA
 <213> Homo sapiens

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<400> 119
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 aatc 64

<210> 120
 <211> 252
 <212> DNA
 <213> Homo sapiens

<400> 120
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 acccccagag ataaatgttt gtttatatca ctgtctagct gtttcaaaat ttaggtccct 120
 tggctctgtac aaataatagc aatgtaaaaa tggttttttg aacctccaaa tggaattaca 180
 gactcagtag ccatatcttc caacccccca gtataaattt ctgtctttct gctatgtgtg 240
 gtactttgca gc 252

<210> 121
 <211> 88
 <212> DNA
 <213> Homo sapiens

<400> 121
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 tcacctataa ggataagttt gacagctg 88

<210> 122
 <211> 342
 <212> DNA
 <213> Homo sapiens

<400> 122
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 ctagatagga agctaagcac agccatggtt gggaggctat atctaaagct catgaggggt 120
 gatccccggg ttaccagcct tcagcactcc ctctagcaac acccattct cttacctagc 180
 ggggatttgt acctttccac tgaggcctct ccatgtcctt tccctacctt tcatggcaat 240
 actttggcct gcctcttata ctggtactaa gttgaagtaa agctcaccct ttacttcctt 300
 acttgaaagt tctactctga gccttgactc ttagccacag tg 342

<210> 123
 <211> 104
 <212> DNA
 <213> Homo sapiens

<400> 123
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 aagagaagct gtggccacca ttatgtctgg gtcaaaggcc aagg 104

<210> 124
 <211> 101
 <212> DNA
 <213> Homo sapiens

GBX1170_3WO_ST25.txt

<400> 124
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aaccaggcac tctacctgca tcgctccagg aaactgctat g 101

<210> 125
<211> 104
<212> DNA
<213> Homo sapiens

<400> 125
aggaacaagt cctatttgat gaagatacct cagggagcct gggagcctat ggaaccaaca 60
gtgccctcga ctctgtcctt tccaggatgg ccactgcaca ctgc 104

<210> 126
<211> 114
<212> DNA
<213> Homo sapiens

<400> 126
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gattcacgaa tataaacgac agctcctcaa ctgcctccat gtcatcaccc tgta 114

<210> 127
<211> 130
<212> DNA
<213> Homo sapiens

<400> 127
taacagcatt gttcccatcc aggtagcaag gtcagccctt tccattgcct cacaggccct 60
tggagccctc acaagtgagg atctcatctg ttacccccac ctctcaactc aatctctggt 120
tcgctactag 130

<210> 128
<211> 284
<212> DNA
<213> Homo sapiens

<400> 128
cgcctcgggt acttacaatc cagtgcgat tataagttca gtttcaccgg gccggagcga 60
agggaagagg aggccgcaag gagccaagcg ggagagagcc gagcgtctcc ttgtcgtttc 120
cttaattctt cctgccgctt ggcagagtga tccactaccg attactgatg aaagggccccg 180
ggatgggcag cgcgaaatct tgccgagagg cgcagctcgc atcaccagac cccgcacctc 240
gccggccctc cgtccgggtc gcctaccag caaaaacgga agtg 284

<210> 129
<211> 207
<212> DNA
<213> Homo sapiens

<400> 129
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aggcctcaga gtccacagtg ggcagttgga accaggcccc agggaatctt tcagctgcat 120

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tccggctgtg atcggcgggc aacaggtaga ggtgctggag ggggatgagt cgtgattttc 180
agtgctctgtc atattcgatc aagtgtg 207

<210> 130
<211> 136
<212> DNA
<213> Homo sapiens

<400> 130
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tacatgttca caaattattg cataaacagc ataatcttca agacaagtgt ttgcaaacac 120
atgtccaatt caggaa 136

<210> 131
<211> 121
<212> DNA
<213> Homo sapiens

<400> 131
gtaccatcac tgaacgaagt tccccttcat tatttgaaac ctaatagttt tgtgaaattt 60
cggtgcatga ttcaggatat gtttgaccct gagttttaca tgggagttaa tgaaacgggt 120
a 121

<210> 132
<211> 158
<212> DNA
<213> Homo sapiens

<400> 132
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tgaatgaaac acatccaagg gccaccactt tgcaactcct gaaccaagca aaaccaactg 120
gtgtcctgtt gtagtgcgtg gttgtagagc tttaaagc 158

<210> 133
<211> 31
<212> DNA
<213> Homo sapiens

<400> 133
tcggttggtt acgcacgaaa ccagccagcc c 31

<210> 134
<211> 257
<212> DNA
<213> Homo sapiens

<400> 134
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tgagagtgga cggtatgtgt gtgaagtgggt gtatatggaa gcatctccct acactggcag 120
ccagtcatta ctagtacctc tgcgggagat catccggtgc taaaacatta cagttgccaa 180
ggaggaaaat actgaatgac tgctaagaat taaccttaag accagttcat agttaataca 240

ggtttacagt tcatgcc

257

<210> 135
 <211> 405
 <212> DNA
 <213> Homo sapiens

<400> 135
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 gctcacgcct gtaatctcag cactttggga ggctgaggca gctggatcac ttgaggtcag 120
 gagatcgaga ccagcctggc caacatggtg actccctgtc tccactaaaa atacaaaaat 180
 tagccaggtg tggtggcatg cacctgtagt cccagctact tgggaggctg agacaggaga 240
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 actgggcaac aaagttagac tatctcaaaa aaaaaaaaaag aaatctttct ttcaccgagc 360
 cctggtcatc atggtacgta tctcatgggt gtaaaggagt catta 405

<210> 136
 <211> 122
 <212> DNA
 <213> Homo sapiens

<400> 136
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 aggccaacaa ttgtccatga ccctcgaccc ccagaggaga tcctagctga tgaattgccca 120
 ca 122

<210> 137
 <211> 252
 <212> DNA
 <213> Homo sapiens

<400> 137
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 aaaatggaag cagtgaatcc aaaacagaca gaaaaatggt ctgaaaacga aaaaggagag 120
 aaaagtaaaa ccatatgaca catagacgac ccagaaaaca caccaaaaaa cttatgaaac 180
 acctcgatgg acaaaggaaa agtttctgtc acatgacaac ttaaaacggt ttccacagat 240
 aacgaatggg ta 252

<210> 138
 <211> 36
 <212> DNA
 <213> Homo sapiens

<400> 138
 tcttttccct aattgcgggc ctcaccattg catgca 36

<210> 139
 <211> 168
 <212> DNA
 <213> Homo sapiens

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<400> 139
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 ttaaaagtct atttatctac ttccttggtg gagaaggga ggagagtacc tgggaatcat 120
 tacgatccct agcagctcat cctgcccttt gaataccctc actttcca 168

<210> 140
 <211> 78
 <212> DNA
 <213> Homo sapiens

<400> 140
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 gcaacaccct tctcgag 78

<210> 141
 <211> 661
 <212> DNA
 <213> Homo sapiens

<400> 141
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 ccagcctgga ttatagatgg gtctgtatga tgtgctggta ccacatgaaa gagaacagct 180
 gcagtattca ctcacactca ctcaggggtg actgtgaagg gcagtgggtga aggagaatcc 240
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 cagacctaaa ttgattcatg gacagtcgct gatggtttag ctggatgggc agggccttaa 360
 aaagaacagg actggaagat tggtgacaag aaaatcttgg aaagagatat gtggctgaat 420
 ccctccgaat gggcagactg aagatatctg catctcacct gaatgccac caaagggcac 480
 ccactgcaga gaagaccctg aatcagatgg acagaattac atgctctgtg gctgtcagcc 540
 agcctctcta tgcagctgct gtggtgtctg ctcaacgggc cgatgaacaa agagctcttg 600
 gcagcaggga cagaggatat gtatgggtcc aacaacatgg aattctccct ccaaaggctg 660
 a 661

<210> 142
 <211> 92
 <212> DNA
 <213> Homo sapiens

<400> 142
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 tccccctggc ggcaagtcca gcctcgtctt gg 92

<210> 143
 <211> 77
 <212> DNA
 <213> Homo sapiens

<400> 143
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gcttcccaca tcacttc 77

<210> 144
 <211> 51
 <212> DNA
 <213> Homo sapiens

<400> 144
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<210> 145
 <211> 184
 <212> DNA
 <213> Homo sapiens

<400> 145
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 acccttcttt ttgctccttc tctgtagacc cataaatgcc cctgcatttg gagaccata 180
 aatc 184

<210> 146
 <211> 123
 <212> DNA
 <213> Homo sapiens

<400> 146
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 caaggggggt ttaaccgttt catgtgccct ggacaccctg ggcagtctgg taaagccgct 120
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<210> 147
 <211> 41
 <212> DNA
 <213> Homo sapiens

<400> 147
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<210> 148
 <211> 63
 <212> DNA
 <213> Homo sapiens

<400> 148
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 tga 63

<210> 149
 <211> 141
 <212> DNA
 <213> Homo sapiens

<400> 149
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gggagccttt tgagtggctt c 141

<210> 150
<211> 273
<212> DNA
<213> Homo sapiens

<400> 150
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tctggagctt ccctccctcc cctgcaaaag gggggtgggg atcaagtcca atcaagaaaa 180
agcccaccac gttttctcaa agagaaacaa aacgtaagca gtcccagtcc tgctcccctc 240
cgccccaga tctactcgtc agctcctccg att 273

<210> 151
<211> 85
<212> DNA
<213> Homo sapiens

<400> 151
caagggggag agtgatgact tccatatgga ctttgactca gctgtggctc ctcgggcaaa 60
atctgtacgg gcaaagaaac ctata 85

<210> 152
<211> 700
<212> DNA
<213> Homo sapiens

<400> 152
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tctttagaag ttatcaggaa tgtgttttaa acaagaagag aacttttcta aggaatgata 240
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acacacacac acacacacac acacgaaaaa caaagaaaaa aatgcttgag ctttttctaa 420
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caaaaggcat tttagtttct tttctctgtg ctctgagtcc acgtacagga atgcttgag 600
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<213> Homo sapiens

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 <213> Homo sapiens

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 ttctaacccc aaactcttac agatgttaga ca 92

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 <212> DNA
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<210> 156
 <211> 41
 <212> DNA
 <213> Homo sapiens

<400> 156
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<210> 157
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 <212> DNA
 <213> Homo sapiens

<400> 157
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 ttctcctgca tggcaaaact gcctattctg ctatttaaaa accctcaatg actttatttt 180
 ctactgccgc ctttttcatg tgcaaccaa 210

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 <212> DNA
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 gaccaccatt cccgagcaga 140

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<212> DNA
<213> Homo sapiens

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agtggtaggt ggacaatgtc atctactggc tgctaagaat gttatccctg tagtttgggg 180
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<210> 160
<211> 232
<212> DNA
<213> Homo sapiens

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tcaacacaaa gacatggaag attagagggt tgtcaacaca aagacacagg aagaatgggc 180
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<211> 90
<212> DNA
<213> Homo sapiens

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ccactttgag aaaggagtag agctagaagc 90

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<212> DNA
<213> Homo sapiens

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attaaactat ttttttgtga tttttttgaa caacaaaaaa tgtaaacaaat tgtaactgta 180
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 <212> DNA
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 aaccag 126

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 <212> DNA
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 cgagcctcag gccgatttgg acaggacttc agca 154

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 gcgctttgat tgcctgagtt tctgacactt cagggcccag aggtcctgcg aggggcagaa 180
 ctggaccccc atgccagtgc tgctgcagga gggcccatat actaggggtct gctgagctgt 240
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gtgcagcccc cagagagagg cccatgggct cagaccaggc tttgttgtcc tgctctgagt 780
atcctgagat ta 792

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<400> 169
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<210> 170
<211> 34
<212> DNA
<213> Homo sapiens

<400> 170
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<210> 171
<211> 100
<212> DNA
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acctcatgct ggcggtctg cgtacgctgg ttggcatttg 100

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<211> 138
<212> DNA
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tttgagccgc ctgagcga 138

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<212> DNA
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<400> 173
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<210> 174
<211> 83
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gcaagtccgc tcgctgcatg gag                                              83

<210> 175
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<213> Homo sapiens

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<211> 101
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<213> Homo sapiens

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cctctggtct accaggcccg gttcccaggt tgcagcaggg a                          101

<210> 178
<211> 137
<212> DNA
<213> Homo sapiens

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<210> 179
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<212> DNA
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<400> 179
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 <210> 181
 <211> 144
 <212> DNA
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 tctgtgttac tgatgtctct catc 144

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 <400> 182
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 <210> 183
 <211> 33
 <212> DNA
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 <210> 184
 <211> 108
 <212> DNA
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 <210> 185
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 <400> 185
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 aagggccgag gcagggccag accagagcat cctgggtaca ggcctgggct ctccagggcc 180
 tgggcctgat tcaggtgcag tgggcactcc tgaagggtca gagcggcatc tgccaggcag 240
 cccctctggc ttccgctgag gtggttgagc gcctggggca gagcctgggt ggtcagaggc 300

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<211> 90
<212> DNA
<213> Homo sapiens

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tccttgctca catctgtttc aatggaatga 90

<210> 188
<211> 128
<212> DNA
<213> Homo sapiens

<400> 188
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agcagagggg ctcagcaggg acagcgtgct gggagctgcc ggccccacac aggggggtgcc 120
gcggccct 128

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<212> DNA
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 aacccccacc cacctcccca ctgcccaccc actcacccat ctctttctgct ttcctttctcc 240
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 ccttgacacc tcctctgccc tttatcttcc tcctcctcct cctcacagcc tttccccctc 360
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 cttacagcct a 431

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 <212> DNA
 <213> Homo sapiens

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<210> 191
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 <212> DNA
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 tggaggttaag aagtccaaaa tcaagcaatc tacagagttg gtgcttctaa ggggtatgag 180
 agaacaattt atttcaggcc catctccctc tatgtgagtc tgtcttcaa 229

<210> 192
 <211> 46
 <212> DNA
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<400> 192
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<210> 193
 <211> 31
 <212> DNA
 <213> Homo sapiens

<400> 193
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<210> 194
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 <212> DNA
 <213> Homo sapiens

<400> 194

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ccctcgctgg gcagccaagt ttgccgcaac ctgccttttc acagacagct ctttgtgtgt	180
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<212> DNA	
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 <212> DNA
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 gct 63

<210> 208
 <211> 63
 <212> DNA
 <213> Homo sapiens

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 acccatg 367

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 aggataaaaa gtcattgcaa gccacaatt gttcctaata ctcacaaaat gctggagaaa 180
 ttaaatttat tctttattgc tcaaagtgtt acctaggtca ctgggcgatg ggaaaattgg 240
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 caaggcatct tagagtgttg tgggaacttg gttcagagca ttaacaccaa gacttttatt 360
 accccggatt tataataggc tgtgctg 387

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 gtgtgtggcc cgaggaagct ggacagcggc agtgggcctg ctgaggcctt ctcttgaggc 180
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 aagagacctt gg 252

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 <211> 199
 <212> DNA
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 ttacccgcgg tagggaagg catcaacact gtcttccttc cattctcctt tccccatcc 180
 catttagtgc tgccacagg 199

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 <212> DNA
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 cttttcagta tatgatgggt attta 145

<210> 214
 <211> 69
 <212> DNA
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 tttgcggat 69

<210> 215
 <211> 101
 <212> DNA
 <213> Homo sapiens

<400> 215
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<212> DNA
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ggggcct 127

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tgggaggcct cgtaccagcc aggatcccaa gcgtcccgtc ccttggaag ttcagccaga 240
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<212> DNA
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<210> 220
<211> 176
<212> DNA
<213> Homo sapiens

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aatattgtag aacatttagc tataatgtat tttaatgtga tccctcaatg tcaaca 176

<210> 221
 <211> 95
 <212> DNA
 <213> Homo sapiens

<400> 221
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 <211> 54
 <212> DNA
 <213> Homo sapiens

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 <211> 100
 <212> DNA
 <213> Homo sapiens

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 <212> DNA
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 <213> Homo sapiens

<400> 225
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<210> 226
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 <212> DNA
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<210> 232
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 <213> Homo sapiens

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<210> 234
 <211> 107
 <212> DNA
 <213> Homo sapiens

<400> 234	
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cctgtactga ctctaggaag ggctggagtt gttttgaatg ggcgccc 167

<210> 236
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<212> DNA
<213> Homo sapiens

<400> 236
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<210> 237
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<212> DNA
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<212> DNA
<213> Homo sapiens

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<211> 92
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 <213> Homo sapiens

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<210> 243
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 <212> DNA
 <213> Homo sapiens

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<210> 244
 <211> 50
 <212> DNA
 <213> Homo sapiens

<400> 244
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<210> 245
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 <213> Homo sapiens

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 <212> DNA
 <213> Homo sapiens

<400> 246
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<210> 247
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 <212> DNA
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tc 782

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<212> DNA
<213> Homo sapiens

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ttagaattta aacacaggca agcattaagt atgttta 97

<210> 249
<211> 100
<212> DNA
<213> Homo sapiens

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tcgcattaac agccccctca tcggggggtg ccttgagagac 100

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<211> 106
<212> DNA
<213> Homo sapiens

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<211> 69
<212> DNA
<213> Homo sapiens

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ctcgtctcc 69

<210> 252
<211> 113
<212> DNA
<213> Homo sapiens

<400> 252
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tcacctggcc tcggggaagt aaactgcccc catgagacta agggatcact tgc 113

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<211> 301
<212> DNA
<213> Homo sapiens

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ccttccagct atccccactg acatgcaaac caagcctcta gaccagcccg tccaccggcc	240
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 <212> DNA
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 <212> DNA
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cagtttctcc agaactgtta ggaaattaag ttgttaatgt gttactgagt ttgatcaggg	180
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 <213> Homo sapiens

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<212> DNA
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 <211> 33
 <212> DNA
 <213> Homo sapiens

 <400> 259
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 <210> 260
 <211> 129
 <212> DNA
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 <210> 261
 <211> 33
 <212> DNA
 <213> Homo sapiens

 <400> 261
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 <210> 262
 <211> 90
 <212> DNA
 <213> Homo sapiens

 <400> 262
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 GCTGAGACAA TGGCCAAAGG GTCAGCTGGA 90

 <210> 263
 <211> 80
 <212> DNA
 <213> Homo sapiens

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 GCCTAGTGTG TCACGGACCA 80

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<211> 73
<212> DNA
<213> Homo sapiens

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gtagccagta aca                                                                73

<210> 265
<211> 90
<212> DNA
<213> Homo sapiens

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cagaggcttc ccagcaattc tgtgcccagg                                          90

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<211> 203
<212> DNA
<213> Homo sapiens

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agagaatcag tggatgggta gaattttaag cagtaggtag ttaccaatg tagaacgagg      180
attagcttag acacctagtc tgg                                                203

<210> 267
<211> 111
<212> DNA
<213> Homo sapiens

<400> 267
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tgagaattaa gaaacactaa gtaaggaaag cacactctca ggtatgcggc a              111

<210> 268
<211> 614
<212> DNA
<213> Homo sapiens

<400> 268
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tgttctgaaa ctaaccatcc ccactttctt ttccaaagat tttggttttt gagcagtaaa      180
gaaattgtta tccattaact gaaaaaataa tcacagccaa acatcccttc ccacatgact      240
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cgatgtcttt tctactctgt gaagatggct tgcttcacgc cttcacttgt cattcctctt      360
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ccactataag gaggggtgtac caggggtgaga agagtgccat gcaggcacag ctctaaagga 480
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 gagagcccat ttcc 614

<210> 269
 <211> 829
 <212> DNA
 <213> Homo sapiens

<400> 269
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 <212> DNA
 <213> Homo sapiens

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 ca 62

<210> 271
 <211> 80
 <212> DNA
 <213> Homo sapiens

<400> 271
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<210> 272
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<212> DNA
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 <212> DNA
 <213> Homo sapiens

<400> 273
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<210> 274
 <211> 67
 <212> DNA
 <213> Homo sapiens

<400> 274
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 gcccatg 67

<210> 275
 <211> 182
 <212> DNA
 <213> Homo sapiens

<400> 275
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ca 182

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<212> DNA
<213> Homo sapiens

<400> 276
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<210> 277
<211> 88
<212> DNA
<213> Homo sapiens

<400> 277
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tgctggccgg ctctgtggtg atcgtggt 88

<210> 278
<211> 175
<212> DNA
<213> Homo sapiens

<400> 278
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tctcatttgg tagactcaga tctattggga gatttgggtcc tgtattagtc ccttc 175

<210> 279
<211> 28
<212> DNA
<213> Homo sapiens

<400> 279
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<210> 280
<211> 77
<212> DNA
<213> Homo sapiens

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ttccacagaa ctacgtc 77

<210> 281
<211> 91
<212> DNA
<213> Homo sapiens

<400> 281
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gtctgagatg tgggggccct attccgctcc c 91

<210> 282
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 <210> 283
 <211> 87
 <212> DNA
 <213> Homo sapiens

 <400> 283
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 tggggctcgg ctttcacgc ttttgcc 87

 <210> 284
 <211> 30
 <212> DNA
 <213> Homo sapiens

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 <211> 223
 <212> DNA
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 gagctgatgc tcaactccag cctcatgcgg atcacctgc gga 223

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 <211> 418
 <212> DNA
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 cctggctgct ccaaactggg tcatgcacca gcagcgtggt catgcaccag cagtgtcaca 180
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 cccagaaggg acctctaaat gcctttcagc aagcacagac tctgggccag acagcctggc 360
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 <210> 287

<211> 231
 <212> DNA
 <213> Homo sapiens

<400> 287
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 tcattgtccc acagtaattt ctcagggatc tagtcccac tctttattcc tttactcgtt 180
 ccctgggata taattacagc ctgataacca ggctatgact acggacttat c 231

<210> 288
 <211> 103
 <212> DNA
 <213> Homo sapiens

<400> 288
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 ttatgggtag ggctctgaca aagcttcccg attaactgaa ata 103

<210> 289
 <211> 341
 <212> DNA
 <213> Homo sapiens

<400> 289
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 tgctccaacc agcctgagga tgaggcacag ggaggcaggg cccatcactc aggaggccat 240
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 cctaggaccc gcatcgaggc aggggacctc attcctagtg c 341

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 <211> 102
 <212> DNA
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 ttaatgatca ttgttctttc cttctggggc ataacaaagc ag 102

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 <211> 249
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 <213> Homo sapiens

<400> 291
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gtaacttct 249

<210> 292
 <211> 380
 <212> DNA
 <213> Homo sapiens

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 <211> 98
 <212> DNA
 <213> Homo sapiens

<400> 293
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<210> 294
 <211> 30
 <212> DNA
 <213> Homo sapiens

<400> 294
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<210> 295
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<210> 296
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 <212> DNA
 <213> Homo sapiens

<400> 296
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<210> 297
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<213> Homo sapiens

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<210> 299
 <211> 473
 <212> DNA
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<400> 299
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<210> 300
 <211> 70
 <212> DNA
 <213> Homo sapiens

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 ccttgggatt 70

<210> 301
 <211> 190
 <212> DNA
 <213> Homo sapiens

<400> 301
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 ttggagaacc ctaccaagcc cgttccctct tctaccatta ccaattctgc agtacagtct 180
 acctcgaacg 190

<210> 302
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 <212> DNA
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<400> 302
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 aaaatctgat gagaattatg taggccatct gccctaactt cacaaatgag agaaaaggag 180
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<210> 303
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 <212> DNA
 <213> Homo sapiens

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 <212> DNA
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<211> 84
<212> DNA
<213> Homo sapiens

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agaagtgggtg cttcggaagc aaat 84

<210> 308
<211> 125
<212> DNA
<213> Homo sapiens

<400> 308
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ggcgc 125

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<211> 1866
<212> DNA
<213> Homo sapiens

<400> 309
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gaatgacctg gaacaggcct tagaaacaat tgatttattc caatagttaa ccaactggctg	1800
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 <212> DNA
 <213> Homo sapiens

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ctgttgggtgt aattatcatg tcaggagacag aggtgaatc acccagggat ctcagttggc	180
tgccgagagg gaacgatgct ggcccacttc ctggggctcag agagatgaga gtggatggcg	240
gcggcggtgg tgttgcttct cagcctgtct ggaaatctca gagccaatga ccaaagcgct	300
gtgctgcctt g	311

<210> 311
 <211> 90
 <212> DNA
 <213> Homo sapiens

<400> 311	
caaaaagcct tacagcagtg cgaactggtc caaaacatga tagacttgag catctccaac	60
ctggaagggc ttaggaccaa atgtgctacc	90

<210> 312
 <211> 118
 <212> DNA
 <213> Homo sapiens

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<400> 312
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 gaggaattt cctgaagagg gggagcatca tcaacggggc ggactggtac agcttcac 118

<210> 313
 <211> 80
 <212> DNA
 <213> Homo sapiens

<400> 313
 aatggcaaag gaccacggtg ccctgcccag ccgcctgctg caggagagagc agctccctca 60
 gacccggagt gctctgctgt 80

<210> 314
 <211> 443
 <212> DNA
 <213> Homo sapiens

<400> 314
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 gcgggaaaag ccaagttggt ggcaggagga gcccaccacc aaggcgatct cactgcggaa 180
 aaactcgacc ctccgccttc acgtctaggg cggcaggtgg tagagctggg cctctcaggc 240
 ccatgcccga gggcaggcga gacaaggagc gcccccaagt ggccatgcgg tgtcctcacg 300
 gaaggcaggg agggcgctac gggccttggg gaccttgaca caacctggag cacgaggctg 360
 agaaaccac cacgcaggcc agctggaggc tgccgcccag ccgggagtca gaagctggag 420
 ccactgggtg ctcccgaagc cat 443

<210> 315
 <211> 151
 <212> DNA
 <213> Homo sapiens

<400> 315
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 ggggctgtca atgaaaaaac cacctacagt ggagaaaaga gcagagaagc aaaacttcat 120
 gttaatctca ggcaatttgg tgaagccaag a 151

<210> 316
 <211> 134
 <212> DNA
 <213> Homo sapiens

<400> 316
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 ttaagcttag tggt 134

<210> 317

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<211> 152
<212> DNA
<213> Homo sapiens

<400> 317
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tgtgccacta gaacctcctg tctctccaat agctgcttct ctctaattct tcaccatagt      120
tttctttctg tggctttttg aggttctctc ct                                     152

<210> 318
<211> 170
<212> DNA
<213> Homo sapiens

<400> 318
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gcctaaggcc ccataactgg gaggctgtat gtgcttcatg tcagctccat tagtgtctgt      120
tttatttagt gctgttttcc attatctcga acagagtcag tcatatagta                  170

<210> 319
<211> 361
<212> DNA
<213> Homo sapiens

<400> 319
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aggggagggt gttgaattga ggactgaagg tggagcaaga gccaagggtcc ctcagggtct      120
tctgtggaga tttggggctt ttgtcaaaag ctactcaaca tgtttctaatt tctttttccc      180
catttagaat atatgagtag tatttgtccc caccctatct tacaaagcct tcagagtgtt      240
ttgaggaat gcttaciaag tctcccagag aaaagcagag gtcctctaca tccagtatca      300
taatgaaaag caaaaataaa cttacatagt gtggtagggt ggctctactc aaagaactag      360
a                                     361

<210> 320
<211> 108
<212> DNA
<213> Homo sapiens

<400> 320
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agtaaaactt ttaacgtggt ttgcctggca tgaagtaagg taatgaga                  108

<210> 321
<211> 116
<212> DNA
<213> Homo sapiens

<400> 321
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gaacatggga tgagagagcg aaatggtgga aaaaggggag ataggctaatt tccaga      116

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<210> 322
<211> 43
<212> DNA
<213> Homo sapiens

<400> 322
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<210> 323
<211> 62
<212> DNA
<213> Homo sapiens

<400> 323
aggtgattct gacgtgctgc ccgccaggcc tgccctgttc gtcacctggt gcatggagcc 60
gg 62

<210> 324
<211> 168
<212> DNA
<213> Homo sapiens

<400> 324
agcgtggtt tcgacttcag cttcctgccc cagccacctc aagagaaggc tcacgatggt 60
ggccgctact accgggctga tgatgccaat gtggttcgtg accgtgacct cgaggtggac 120
accaccctca agagcctgag ccagcagatc gagaacatcc ggagccca 168

<210> 325
<211> 418
<212> DNA
<213> Homo sapiens

<400> 325
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caaatttgat atcatataat ttaagaagct ctcataatca ggtatggaca ttggcttata 180
caacatacac tgtgaatcag gcacagcaac ctgcaaacca catcatccca acagttttcc 240
attcttccta ttgacaaaca cttaaacaca gcattttcat catatgaaag taaacaaaaa 300
caacaacaga ataagctttc cccacactaa tttctaatac aaagagcttt actgcaatta 360
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<210> 326
<211> 74
<212> DNA
<213> Homo sapiens

<400> 326
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aaaagcgaag gaaa 74

<210> 327
<211> 359
<212> DNA

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<213> Homo sapiens

<400> 327
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 ttcaagagaa ctagactgta agaactaacc tcacattgtg ggaaaataaa aattttaacc 180
 ttttccccct ttatttgaaa tgttctatga ctacttgaaa gaatttaaaa atgaaagtat 240
 ttgtcagttt tgtccttgaa tatctttcat ttgttataga atacatattt tgtccatagt 300
 attttgtttt ataagtgtga gggtagattt ttttattgag agcctactaa tatgcctgg 359

<210> 328
 <211> 85
 <212> DNA
 <213> Homo sapiens

<400> 328
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 agctcgctac ttatactgat gattc 85

<210> 329
 <211> 223
 <212> DNA
 <213> Homo sapiens

<400> 329
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 ttccctcccc tggaccccca agccttccca gatagtcacc ttctctttcc atatgtccat 120
 ggcacctagt ttgaaatggt cttacctcat gcatcatggt ctgccttgtg ttagaccctt 180
 taagcttttg tgtctcatta agatattgaa ctcggtgcg tgc 223

<210> 330
 <211> 494
 <212> DNA
 <213> Homo sapiens

<400> 330
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 ctgtgggaga gcagggaagg ccacaggaaa cctgaccctt aagacctggg tccgggactc 120
 aagagaatgg aaatggagag gaaccaagag gaagcacaga ctggtagtgg gcaccctgtc 180
 attggagcta tgtgaggcga taaggtttgg ctgtgtcccc acccaaattc catcttgaat 240
 tgtagtcccc ataatcccca cgtgtcatgg gagggaccg atgggaggta attgaatcgt 300
 gggagcgggt tccccatgc ttttctgtg atactgagtc agttctcaca agatctgatg 360
 gttttataag gggctttttc ctttttctg ggcacttctt gctgccgcca tggaagaagg 420
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 aaacttggtc aatt 494

<210> 331

<211> 111
 <212> DNA
 <213> Homo sapiens

<400> 331
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 gcagtttaaa aatactttgc ttagcccca ggcagaggct taacctccag g 111

<210> 332
 <211> 123
 <212> DNA
 <213> Homo sapiens

<400> 332
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 aaatgtaaaa tctgaaacca taaaaactct agaagtaa at cggggcaaca ccatttagga 120
 cat 123

<210> 333
 <211> 70
 <212> DNA
 <213> Homo sapiens

<400> 333
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 agagatcaga 70

<210> 334
 <211> 123
 <212> DNA
 <213> Homo sapiens

<400> 334
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 ggacacaagg gtacaaagtt ccatgctgta tctgtagttt ataatttaga acactctgtc 120
 ctc 123

<210> 335
 <211> 128
 <212> DNA
 <213> Homo sapiens

<400> 335
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 gatgctagac tgctggcaga aggagaggag cgacaggcct aaatttgggc agattgtcaa 120
 catgttgg 128

<210> 336
 <211> 143
 <212> DNA
 <213> Homo sapiens

<400> 336
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ggctggcaca cacgtggtct accttgggaa tcctaaagga caaagagtta caacctccac 120
gacaggcctt tgccgtgtat ccc 143

<210> 337
<211> 85
<212> DNA
<213> Homo sapiens

<400> 337
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tatgacctgt gtgccaaaga aaaac 85

<210> 338
<211> 320
<212> DNA
<213> Homo sapiens

<400> 338
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gtgaggcaga gccatgctgt gcaagtgtca taagtcatcc cactttcaac tctcaggaac 120
actcgcagcc agtgccacgc tgtcctcgcc atccaatatt gatagccacc ccagttcctg 180
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tcttaaaactg cgcttctagt gacatggcct taaacgatgg ggtccccaaa tgtacagtgc 300
tcctcgatgg caaggttgta 320

<210> 339
<211> 151
<212> DNA
<213> Homo sapiens

<400> 339
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aggccccgc gtcggcaag tgagcctggc t 151

<210> 340
<211> 164
<212> DNA
<213> Homo sapiens

<400> 340
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ggaagtgggtg gcctgcagcc ccaaattggc ttgggaggat cataccatga tgacagggaa 120
gcctgcagta ctccagcaga catgagagtc acccagagct tata 164

<210> 341
<211> 133
<212> DNA
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gcacactcag tccccctgcc tggcattcct gccgcagctc tgacctggcg ctgtcgcctt 120
ggcatcttaa taa 133

<210> 342
<211> 648
<212> DNA
<213> Homo sapiens

<400> 342
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caggtggaca cccaccatgc taaatagaat tccaagccac tagcctctag ccacacaggt 120
tccatcccaa cactcctgtc tgtgggactt gatctgaaaa gccacacttt ggttgggaac 180
cttgcccagg gctggctgga gaggggcctg ttgtgccact caggggaaggc cttatggttc 240
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cagtcaccag cactgctggc tctgagtcct gatttcttac tttggctttc ctggtggcac 360
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aatgagtcac tccatggctg ctgttttctc ctctgtaaag caggggaagat agcgcccact 540
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gacgtgggag tcactattgt taccaccctc ttgttctagc aggagaca 648

<210> 343
<211> 40
<212> DNA
<213> Homo sapiens

<400> 343
gataaatcat gtgcaagtgt catcgataga ctaacaagag 40

<210> 344
<211> 195
<212> DNA
<213> Homo sapiens

<400> 344
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caaaatttca agaaacaggt gaggttgagc agcttggtgc aaccccatgg ggcctggagt 120
tgagactcaa cagcaatgga tttcagagac caccctgaaa ctcccagtaa aaaagacttg 180
ggagacatgt taata 195

<210> 345
<211> 29
<212> DNA
<213> Homo sapiens

<400> 345
aaaagatggt gaagttggtc cttctggtc 29

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<210> 346
 <211> 212
 <212> DNA
 <213> Homo sapiens

<400> 346
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 ccctgccttg tccctctcac tccccagccc caccctaag tgcccaaagt ggggaggagac 120
 aagggattct gggaagcttg agcctcccc aaagcaatgt gagtcccaga gcccgctttt 180
 gttcttcccc acaattccat tactaagaaa ca 212

<210> 347
 <211> 210
 <212> DNA
 <213> Homo sapiens

<400> 347
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 tgtcagagac agctgcgttt gtaaaagcaa gtctggatga cacagtgatg attacatcat 120
 ctccatcttc atcgccatct catagtaaag ttaaccact gtggcatctg gctgatggtt 180
 ttgtgggaga ggattctatg tcccaccgca 210

<210> 348
 <211> 114
 <212> DNA
 <213> Homo sapiens

<400> 348
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 ctgcagaccc gtcattcaca cctatttcaa caagccgaat aactggagt ttag 114

<210> 349
 <211> 83
 <212> DNA
 <213> Homo sapiens

<400> 349
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 cgtaacacga gaagtgattc cta 83

<210> 350
 <211> 46
 <212> DNA
 <213> Homo sapiens

<400> 350
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<210> 351
 <211> 41
 <212> DNA
 <213> Homo sapiens

<400> 351
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<210> 352
 <211> 387
 <212> DNA
 <213> Homo sapiens

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 ggcggccatc accactgctg cagctgcctg ctttctaagc cagctgagct ctttggggga 180
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 aagccctgat gagtgagttt ccctcca 387

<210> 353
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 <212> DNA
 <213> Homo sapiens

<400> 353
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agtttgatat gtatagaata taattgaagg aggtatacac atattgatgt tgttttgatt	1320
atctatggta ttgaatcttt taaaatctgg tcacaaatTT tgatgctgag ggggattatt	1380
caagggacta ggatgaacta aataagaact cagttgttct ttgtcatact actattcctt	1440
tcgtctccca gaatcctcag ggcactgagg gtaggtctga caaataaggc ctgctgtgcg	1500
aatatagcct ttc	1513

<210> 354
 <211> 98
 <212> DNA
 <213> Homo sapiens

<400> 354	
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tggcgggaga cttttctgga taatcttcgt gcggctgg	98

<210> 355
 <211> 81
 <212> DNA
 <213> Homo sapiens

<400> 355	
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gccaccctaa actgcagtgt g	81

<210> 356
 <211> 96
 <212> DNA
 <213> Homo sapiens

<400> 356	
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agggtcctcg gccgaaaaac tccatggggg atcatc	96

<210> 357
 <211> 123
 <212> DNA
 <213> Homo sapiens

<400> 357	
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ctctagggct caagctctta acactatccc aagtaggggtg ggaaaggaca atttgcctca	120
ctc	123

<210> 358
 <211> 108
 <212> DNA
 <213> Homo sapiens

<400> 358	
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ctctttgcct attgggaaaa actaatttac ctcttgccgc cacccatg 108

<210> 359
 <211> 41
 <212> DNA
 <213> Homo sapiens

<400> 359
 acagttcttg ccacaggaag actcgataaa aacagattat t 41

<210> 360
 <211> 36
 <212> DNA
 <213> Homo sapiens

<400> 360
 aatctgaaag ggcttgaaaa gttaggatgt agactg 36

<210> 361
 <211> 72
 <212> DNA
 <213> Homo sapiens

<400> 361
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 cgcttctgag gc 72

<210> 362
 <211> 380
 <212> DNA
 <213> Homo sapiens

<400> 362
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 gggtaacatg aagataaatg agacgagaga ggacatggat gcacagttgt tagaacaaca 180
 aagcacgaac tcaagtgaat ttgaggctcc atccctcagt gacagtatgc cttctgtagc 240
 agattctcac tctagtcatt tttctgaatt tagttgttct gacctagaaa gcatgaaaac 300
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 tgaggtagaa aatgaccgtc 380

<210> 363
 <211> 123
 <212> DNA
 <213> Homo sapiens

<400> 363
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 acaaattgga gaaatgactc tccttaagat atcttaaatgt cggctgggca ccgtcgttca 120
 tgc 123

<210> 364
 <211> 84

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<212> DNA
 <213> Homo sapiens

<400> 364
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 tgtagctct gctgtgcaa aaca 84

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 <212> DNA
 <213> Homo sapiens

<400> 365
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 aatacacacc tggggagtac atttgacaaa tttcccttag gatttcgtta tctcaccttg 120
 accctcagcc aagattgga aagctgcgtc ctggcgattc caggagaccc agctggaaac 180
 ctggcttctc catgtgaggg gatgggaaag gaaagaagag aatgaagact acttagtaat 240
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 ggacaggatt ttccagatcc taattggaaa tttagcaata aggagaggag tccaagggga 360
 caaataaagg cagagagaag agacagaact aaaaatacga ggaaaggaga gtgaggattt 420
 tcattaaaag tctcagcagt gggtttcttg ggttatttaa aacatcacct aaataggcct 480
 tttcttcta attggccatc aaattaaagc ctatcctttc tcaagcagga gctggtattg 540
 tagggagtgg ccgggtattc tgggctgggc tcttctggag taggggggtca gcaaacattg 600
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 <212> DNA
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 tctttgaacc tctgtttact ctggaaaatg cccaagtctg cagatttttg atagaactaa 180
 atgaactagt agtccagcaa catgata 207

<210> 367
 <211> 228
 <212> DNA
 <213> Homo sapiens

<400> 367
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 gggaaaaaat acagcaagat gaaaaatgag tgttactagg ttctttcaaa gatgactgat 180
 gaatggttga cacaacact gagaaggga accatgagac ctgcctcc 228

<210> 368
 <211> 393
 <212> DNA
 <213> Homo sapiens

<400> 368
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 gatctgtaaa ttagcaataa aaactaatgt gccttccaag gttatggtaa aaatcaaata 180
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 tttttccata tttgctctag ttttaaattt gcaaatttta attcagtatt gtttataata 360
 agacaaaagc tcttctttaa gggtggggca tta 393

<210> 369
 <211> 199
 <212> DNA
 <213> Homo sapiens

<400> 369
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 ctatctagtg tcctattta 199

<210> 370
 <211> 394
 <212> DNA
 <213> Homo sapiens

<400> 370
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 ttcaactaaa taagatactt gggaatttat atctaaagga agaattctcag tcattgtaaa 300
 taaatgacct aaagtcatta ttgtggaaat caatcagaga aatccctttc tggagtttta 360
 catccttttt ggaactcttt tggtatgaca gcta 394

<210> 371
 <211> 35
 <212> DNA
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<400> 371
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<210> 372
 <211> 69
 <212> DNA
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 <400> 372
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 agcaacctc 69

 <210> 373
 <211> 578
 <212> DNA
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 caattttttt cttccttttag ggtgggggat tggtttggtt ttcttttggt gtggtttttt 180
 gttttatttt tgtcaagatt gattttttaga tgcaaggact tgaaaagacc cagaaggatg 240
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 <210> 374
 <211> 108
 <212> DNA
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 <400> 374
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 ctttgtgggt gtcttctaac aggagcagtc cacgcaaagc cttcctga 108

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 <211> 161
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 <213> Homo sapiens

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 <210> 376
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 <400> 376

GBX1170_3WO_ST25.txt
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<210> 377
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 <212> DNA
 <213> Homo sapiens

<400> 377
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<210> 378
 <211> 63
 <212> DNA
 <213> Homo sapiens

<400> 378
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 agc 63

<210> 379
 <211> 181
 <212> DNA
 <213> Homo sapiens

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<210> 380
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 <212> DNA
 <213> Homo sapiens

<400> 380
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 tattttgacg gcatca 76

<210> 381
 <211> 111
 <212> DNA
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<400> 381
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 cagttaagac ttgtggcctt atcaactctg tgaagttcta ccaagcctca a 111

<210> 382
 <211> 73
 <212> DNA
 <213> Homo sapiens

<400> 382

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aacacgagtc cca 73

<210> 383
<211> 117
<212> DNA
<213> Homo sapiens

<400> 383
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<210> 384
<211> 35
<212> DNA
<213> Homo sapiens

<400> 384
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<210> 385
<211> 1906
<212> DNA
<213> Homo sapiens

<400> 385
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ggctagaccc taaatccaat ggctgtgttc ttataagaag caggaaactt ggacaaacac 180
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gaatggatgg tagataaatg gatgggtagg tggatggata gatggatgaa tgggtagacg	1380
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gatgggtaga tggatggata gatggatgaa tgggtagatg gatggacagg tagatggatg	1560
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agccctgtat gacaaattaa aaactgagtg ggtttgaata aagggccacg aagcccccat	1860
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 <212> DNA
 <213> Homo sapiens

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ctcttagcaa gcaaac	136

<210> 387
 <211> 46
 <212> DNA
 <213> Homo sapiens

<400> 387	
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<210> 388
 <211> 119
 <212> DNA
 <213> Homo sapiens

<400> 388	
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ggcagcaggt gtcacagaat ctctgtctga acacaggggtg ggcgcattac aaatcaatc	119

<210> 389
 <211> 55
 <212> DNA
 <213> Homo sapiens

<400> 389	
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<210> 390
 <211> 71
 <212> DNA
 <213> Homo sapiens

<400> 390
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 ggagtcggat g 71

<210> 391
 <211> 442
 <212> DNA
 <213> Homo sapiens

<400> 391
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 cctggcatgg atcttgagaa ta 442

<210> 392
 <211> 70
 <212> DNA
 <213> Homo sapiens

<400> 392
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 agcctaagtt 70

<210> 393
 <211> 279
 <212> DNA
 <213> Homo sapiens

<400> 393
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 cctgccccgc ggcgcccccc caccctgcac agctgtcacc tctgaccacc tcaactccct 240
 gctggggaat atcctgagaa tcatcgtaa caacctggg 279

<210> 394
 <211> 189
 <212> DNA
 <213> Homo sapiens

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<400> 394
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 cattctgcaa ggaaggttgc tctctgggcc tataagcaaa cagtccagaa aagggttagc 180
 catcctctt 189

<210> 395
 <211> 87
 <212> DNA
 <213> Homo sapiens

<400> 395
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 cctgcagctg cgctcgccct agactcc 87

<210> 396
 <211> 200
 <212> DNA
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<210> 397
 <211> 772
 <212> DNA
 <213> Homo sapiens

<400> 397
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 gggtgcttgt ctgtttccgg gttgggggga aagttggttg ggtgggaggg agccaggttg 720
 ggatggaggg agtttacagg aagcagacag ggccaacgtc gaagccgaat tc 772

<210> 398
 <211> 57
 <212> DNA
 <213> Homo sapiens

<400> 398
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<210> 399
 <211> 804
 <212> DNA
 <213> Homo sapiens

<400> 399
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 cagagcattt ttattatagt gctagagggt ttggaaggct atctatthtt ctctgaggaa 180
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<210> 401
 <211> 224
 <212> DNA
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<210> 402
 <211> 37
 <212> DNA
 <213> Homo sapiens

<400> 402
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<210> 403
 <211> 135
 <212> DNA
 <213> Homo sapiens

<400> 403
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 tgcggaaaac tcaca 135

<210> 404
 <211> 56
 <212> DNA
 <213> Homo sapiens

<400> 404
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<210> 405
 <211> 79
 <212> DNA
 <213> Homo sapiens

<400> 405
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 gcacaccacg atcagggtc 79

<210> 406
 <211> 138
 <212> DNA
 <213> Homo sapiens

<400> 406
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 gtctggacgt tgcattga 138

<210> 407
 <211> 166
 <212> DNA

<213> Homo sapiens

<400> 407
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gtgttcctag agcacaggac gctgtctgcg gctccccatc ttccctgcca gctccagcct 120
gaactcaagg attgttaaga ccactccact gatccctaaa gctgtt 166

<210> 408
<211> 48
<212> DNA
<213> Homo sapiens

<400> 408
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<210> 409
<211> 815
<212> DNA
<213> Homo sapiens

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accaccaact gacactttag catgaagaaa aaaacaaacc taacagactg tcagctctaa 180
agacattaca gagcagaaac ttccaaaagc gttatacaag ctgtctttct gggcaaatga 240
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<210> 410
<211> 585
<212> DNA
<213> Homo sapiens

<400> 410
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<210> 417
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<210> 418
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<400> 419
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<210> 422
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<400> 423	
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<212> DNA
<213> Homo sapiens

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<210> 426
<211> 104
<212> DNA
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<212> DNA
<213> Homo sapiens

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<212> DNA
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 <212> DNA
 <213> Homo sapiens

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<210> 432
 <211> 76
 <212> DNA
 <213> Homo sapiens

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<210> 433
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 <213> Homo sapiens

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 gc 242

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 <211> 202
 <212> DNA
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<400> 434
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 <212> DNA
 <213> Homo sapiens

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 attgacgcag agtccgag 138

<210> 436
 <211> 90
 <212> DNA
 <213> Homo sapiens

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<210> 437
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 <212> DNA
 <213> Homo sapiens

<400> 437
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<210> 438
 <211> 193
 <212> DNA
 <213> Homo sapiens

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 <212> DNA
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<210> 440
 <211> 58

<212> DNA
 <213> Homo sapiens

<400> 440
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<210> 441
 <211> 532
 <212> DNA
 <213> Homo sapiens

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<210> 442
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 <212> DNA
 <213> Homo sapiens

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gtgccatggc tgatgag 137

<210> 444
<211> 54
<212> DNA
<213> Homo sapiens

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<210> 445
<211> 328
<212> DNA
<213> Homo sapiens

<400> 445
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gtgaggaatt acctctgctc gggacaga 328

<210> 446
<211> 114
<212> DNA
<213> Homo sapiens

<400> 446
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<210> 447
<211> 402
<212> DNA
<213> Homo sapiens

<400> 447
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<210> 449
 <211> 248
 <212> DNA
 <213> Homo sapiens

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 <211> 61
 <212> DNA
 <213> Homo sapiens

 <400> 450
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<210> 451
 <211> 242
 <212> DNA
 <213> Homo sapiens

 <400> 451
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<210> 452
 <211> 76
 <212> DNA
 <213> Homo sapiens

 <400> 452

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 tttcaggaca aaaatc 76

<210> 453
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 <212> DNA
 <213> Homo sapiens

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<210> 454
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 <212> DNA
 <213> Homo sapiens

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<210> 455
 <211> 258
 <212> DNA
 <213> Homo sapiens

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 gaactgaact caggggtggc tgtggcttca ggcattggtg tatccaggga gaacagtatg 240
 gccaagatcc ttccctca 258

<210> 456
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 <212> DNA
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<400> 456
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<210> 457
 <211> 114
 <212> DNA
 <213> Homo sapiens

<400> 457
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<210> 458
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 <212> DNA
 <213> Homo sapiens

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<400> 458
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agttgtcaga gaggagtttt gaggaggccc tgaaggctcg ccggctgtta aggcctgagc 180
tgtagtgggc aagaagagat ggccagttca ggtagaggaa gcctgctttg agctgaagac 240
cggaggtgaa tctggacagg gcttccc 267

<210> 459
<211> 102
<212> DNA
<213> Homo sapiens

<400> 459
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aaaggatgat ggaaatgctg ctatcacagg ctataccatt ca 102

<210> 460
<211> 88
<212> DNA
<213> Homo sapiens

<400> 460
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atccctgaag gacggagtgg aggcttag 88

<210> 461
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<212> DNA
<213> Homo sapiens

<400> 461
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cctctgtagg ctggagacct cgggttcagc tccatttatc agggcacagg accttcctgt 180
tctgagactt tgttccaggg gactttcaca cttcagagaa tagcacatgt catcctgcac 240
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aactggcctc agccagaaaa gcagggaagg cacccccagt ttgcagctga gagactccag 360
cctgggagag ctgaataaat cttttgccca gaggggttcc tcagtaaattg ctggagatga 420
ggctcagacc tgacctttgg attcccagat g 451

<210> 462
<211> 29
<212> DNA
<213> Homo sapiens

<400> 462
atgacacca caagtgcacg aaaaagcta 29

<210> 463

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<211> 347
<212> DNA
<213> Homo sapiens

<400> 463
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ggcagaagta gatccacatg tgtatagacc gtggatttta gaccaaggca tgggggcaat      120
tcagtggaga aaggattaat ttttcaacaa atagtgtcaa aacaagatat ccataagcaa      180
aaaatgaaca tcaaaccata ttttataata tatacaaaaa tgaacaccac atggacatat      240
atgtaacacc taaaactata aatcttgtgg aagaaaacct aagaaataat ctttgtgaga      300
ttgggttaga caaagatttc ttagatatga cactgaaagt gcaattc      347

<210> 464
<211> 176
<212> DNA
<213> Homo sapiens

<400> 464
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tgctctgggc tgtgaagggg tggagcaggc agtggccagc tttgcccttc ctgctgtctc      120
tgtttctagc tccatggttg gcctgggtggg ggtggagttc cctcccaaacc accaga      176

<210> 465
<211> 53
<212> DNA
<213> Homo sapiens

<400> 465
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<210> 466
<211> 122
<212> DNA
<213> Homo sapiens

<400> 466
tccggttggc taggcctgaa ttcccagcag tttccaagtg ccttggacgt tggctccatt      60
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tc      122

<210> 467
<211> 87
<212> DNA
<213> Homo sapiens

<400> 467
gacacattca gctaacgtat tttagcaggt ggagtgaggt tgaagattcc tgtgacagcg      60
atgccataga gagaatgtac tgtgccc      87

<210> 468
<211> 173
<212> DNA
<213> Homo sapiens

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<400> 468
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 agcatctcaa gggcactgtg gtatggaaaa ggacgccaca tgagtaaatt tta 173

<210> 469
 <211> 37
 <212> DNA
 <213> Homo sapiens

<400> 469
 aaatgagaag taacgtcagc agctccgtag gttctga 37

<210> 470
 <211> 74
 <212> DNA
 <213> Homo sapiens

<400> 470
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 actgagcact ctag 74

<210> 471
 <211> 123
 <212> DNA
 <213> Homo sapiens

<400> 471
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 aaaatgcggg tgaagaccag atttcttgca catggcggtg acgggatgct ccctagagag 120
 ctt 123

<210> 472
 <211> 37
 <212> DNA
 <213> Homo sapiens

<400> 472
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<210> 473
 <211> 548
 <212> DNA
 <213> Homo sapiens

<400> 473
 ccttggcaaa ctgacaagga tgtcatatat gtattgtagt ggtcaaaatt aatgttttgt 60
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 gatctcggct cactgcaacc tccgtctcct aggttgaagc aattctccta cctcagcctc 180
 ctgagtagct gggattacag gcacgtgcca ccacaccgg ctaatttttt ttttttttat 240
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gcatttataa gatgactcac tattagtagt cctatcccca tattatttaa gctctaaatt	480
tcctgtggaa atttagactt ggaatataga cttggaaaac ccctcaagcg ttgcttctca	540
atgtgctc	548

<210> 474
 <211> 282
 <212> DNA
 <213> Homo sapiens

<400> 474 gtacccgggt gatttgctca gattgttatg acaatgccaa catctactcc aggacccgag	60
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tcatgggtcca aatgcctaaa gagacatatt tagtacatcc tccccaggat actactgccc	180
tagagagcct gataccgtca gccaacagag agccatctgc ctttcccacc aaccatgaga	240
ggataagtga gaagaaactt ccctccacac agatgagcgg tg	282

<210> 475
 <211> 107
 <212> DNA
 <213> Homo sapiens

<400> 475 tgtaagtacc cttgttatcc aagcggcaaa tgtgtcagct ttgtacaaat gtgaagcgggt	60
caacaaagtc gggagaggag agagggtgat ctccttcacac gtgacca	107

<210> 476
 <211> 160
 <212> DNA
 <213> Homo sapiens

<400> 476 cccttggtgact gggagttag cactatcacc tgcacactag acctgcagtc tatgaagaga	60
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tccacacac acaggcagca gcctcatctc aaatggactg	160

<210> 477
 <211> 31
 <212> DNA
 <213> Homo sapiens

<400> 477 atggaatatg gagcaaaagg ggtcctgtgc t	31

<210> 478
 <211> 156
 <212> DNA
 <213> Homo sapiens

<400> 478 tttcttagcg caaagcagtg agggcagtac atgttctttt tgcattttta attattgtaa	60

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atcctaacgc tacctctgac tcaacctgac tttgta 156

<210> 479
<211> 31
<212> DNA
<213> Homo sapiens

<400> 479
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<210> 480
<211> 30
<212> DNA
<213> Homo sapiens

<400> 480
gagaaacatc gaaagcgcag cctgcagccg 30

<210> 481
<211> 742
<212> DNA
<213> Homo sapiens

<400> 481
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tatcctttaa ttcctttggc caaaggccat ttcaaataaa atgtttattt cagaatgcat 120
ataaaaagtc agtagtgctg ctgggcgtgc tggctcatgc ctgtagccca agcactttgg 180
caggctgaag caggaggatc acttgagccc aggagtagaa gaccagcctg ggcagcatag 240
tgagaccccc atttctacaa aaaaaaaaaa aaaattagcc aggtgtggtg gcacacatcg 300
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cccaacctct cacatctagt tcattagtgt ttggtgagaa ttgtcttccc gtttcccttt 660
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ttgccttcat gtacacctgt ca 742

<210> 482
<211> 195
<212> DNA
<213> Homo sapiens

<400> 482
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attatgaccg gggcttgctg ctgagctgca ggggttcaga gtactgctac ctgtgcaatg 120
gcagcttccc cagagcgccc aggggctccg aggccacaga cagaaaatat ctttgctacc 180

acgtgctgaa aaata

195

<210> 483
 <211> 387
 <212> DNA
 <213> Homo sapiens

<400> 483
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 ctccccaccc cacctccctc acttcactgc attccagatg ggacatgttc catagccttg 120
 ctggggaagg gcccaactgc aactccctct gcccagccc cacccttggc catctccctt 180
 tgggaactag ggggctgctg gtgggaaatg ggagccaggg cagatgtatg cattcctttg 240
 tgtccctgta aatgtgggac tacaagaaga ggagctgcct gagtgggtact ttctcttcct 300
 ggtaatcctc tggcccagcc tcatggcaga atagaggtat ttttaggcta tttttgtaat 360
 atggccttctg gtcaaaatcc ctgtgta 387

<210> 484
 <211> 63
 <212> DNA
 <213> Homo sapiens

<400> 484
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 tga 63

<210> 485
 <211> 37
 <212> DNA
 <213> Homo sapiens

<400> 485
 ttgccattca cctgtcccgt ctccaacatt aaagctt 37

<210> 486
 <211> 49
 <212> DNA
 <213> Homo sapiens

<400> 486
 ctttccctga tacacctgcc tgtgaaccac cctgatcgct cttcgtgcc 49

<210> 487
 <211> 429
 <212> DNA
 <213> Homo sapiens

<400> 487
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 taaaatcctg atttatctta aactagtgtg tagacatgac tgtggttcaa gtttggcaga 120
 caggtttaaa tgtcaaatcc aacactagag acaataccat ttatttcagt taaggaatat 180
 agactttgcc accaaataat tacatatctt tcattcctgt atgacatgga tgcctctatt 240
 tgcattgacct ctgagtatga agtaataata tattaatttt caacaactga tctgtctgaa 300

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aaatacaaaag aaacagcaaa atggtgatat taaaactgac tcaccactgt cctctgtttg 360
 ttgggcagga agactctaac gataggtttt tgtggtgact tggggttgct ccgtgccaca 420
 tctgtggga 429

<210> 488
 <211> 245
 <212> DNA
 <213> Homo sapiens

<400> 488
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 cacagccatg ctcttgagga gcttacaatc caagctggag gcaggggagg gtatagtctt 120
 taaatatgct taagtgttgt agggaaggac agagttacca ataaacatgt aactagaaag 180
 ccaggctcag ttcttacctc tgggaatcag aactctttat gaaacttgat tgatagaatc 240
 tacta 245

<210> 489
 <211> 74
 <212> DNA
 <213> Homo sapiens

<400> 489
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 ttcaggcagc agct 74

<210> 490
 <211> 67
 <212> DNA
 <213> Homo sapiens

<400> 490
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 tggcatg 67

<210> 491
 <211> 567
 <212> DNA
 <213> Homo sapiens

<400> 491
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 ttttgaagt ctgctattaa aaagccttta aggatttact aacttcgagt ctaagtgcaa 180
 ggggacgaaa gcttaagcct gtcagacatt ctttttcttg gacaaaaaga tcaaagtttc 240
 ctacaaattg ctaagctttg cacaagggag aagcctacat gtactagtgc atggaatcag 300
 tttcatctta tttcatgggg actcttctcc cactggaaag aacagaatg aggaatgaat 360
 cttaattggt ctcttcatca gaagtggtaa acttgggtctc tatattcacg aagtcagaca 420
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gggcaagggt caccactaca aaaagga 567

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<213> Homo sapiens

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gccaagatga atacaatcaa tgcagcagaa cctcatgtgg tgacagtcac catgaatggt 240
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cctttactga gacgagagca acaagctggc catgatgaag gtgttctgga tcgtcttctg 480
gacaggaggg aacggccact agaaggtggc cgaactaatt ccaataacaa caacagcaat 540
ccatgttcag aacaagatgt tcttgcacag ggtgttcca 579

<210> 493
<211> 86
<212> DNA
<213> Homo sapiens

<400> 493
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gaaggggcct catTTTggct gaagat 86

<210> 494
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<212> DNA
<213> Homo sapiens

<400> 494
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<210> 495
<211> 34
<212> DNA
<213> Homo sapiens

<400> 495
ctgagcacct ccaccgactg gaaggaggcg aaat 34

<210> 496
<211> 32
<212> DNA
<213> Homo sapiens

<400> 496

atggcacaaa acgatgcaga tgggcatcac ct 32

<210> 497
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 <212> DNA
 <213> Homo sapiens

<400> 497
 gaatgtaagg gccagaaagc ttgaatgccc agaa 34

<210> 498
 <211> 119
 <212> DNA
 <213> Homo sapiens

<400> 498
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 cccccagacc acattggtgc agcagggttta gatggctatg tgctagagta ttgctttga 119

<210> 499
 <211> 100
 <212> DNA
 <213> Homo sapiens

<400> 499
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 ttaaaggttt tgaatctgcc tgctgttcca gacatgggga 100

<210> 500
 <211> 139
 <212> DNA
 <213> Homo sapiens

<400> 500
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 gggccagact cttgagcca 139

<210> 501
 <211> 210
 <212> DNA
 <213> Homo sapiens

<400> 501
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 aaatctttga aggggtgatag ggtagggcg gtgggatgtt ggggtattggt atttatgaag 120
 gtgctctagg tgattctagt atgtaaccag gggagaacca gtgttttgga gcattcattt 180
 aaaaataaac tgactttggc gggcgacatg 210

<210> 502
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 <212> DNA
 <213> Homo sapiens

<400> 502

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<210> 503
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 <212> DNA
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<400> 503
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<210> 504
 <211> 31
 <212> DNA
 <213> Homo sapiens

<400> 504
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<210> 505
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 <212> DNA
 <213> Homo sapiens

<400> 505
 aggatccaga gagcacccaa tttaccaga cccagcgag 39

<210> 506
 <211> 49
 <212> DNA
 <213> Homo sapiens

<400> 506
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<210> 507
 <211> 29
 <212> DNA
 <213> Homo sapiens

<400> 507
 aacagaacag aagttaggaa tggtgaaat 29

<210> 508
 <211> 386
 <212> DNA
 <213> Homo sapiens

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 ctaccgaatt ggatacgttg agtcaacgg tgctctcaga agcgcggtgg ctcatgcctg 60
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 ctctgggcct ttctccgtat gtttgc 386

GBX1170_3WO_ST25.txt

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 <212> DNA
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 gatccaaagt tggaggtgaa atggtataaa aatggtcaag aaattcgacc cagtaccaa 119

 <210> 510
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 <212> DNA
 <213> Homo sapiens

 <400> 510
 acaagaagat atacgatgga ggtgcccga c 31

 <210> 511
 <211> 189
 <212> DNA
 <213> Homo sapiens

 <400> 511
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 gggctcgggg atactggata caccctgac ctcaaccaag gcccgagcg gggccccagg 120
 tggaaagtga ggccgctgtg ctgtgtgtgg ggacaacgct tcatgccagc attatggtgt 180
 ccgcacatg 189

 <210> 512
 <211> 48
 <212> DNA
 <213> Homo sapiens

 <400> 512
 gaaccaacca cactgtacca aatgagctg ttccctaggt cttgtccc 48

 <210> 513
 <211> 202
 <212> DNA
 <213> Homo sapiens

 <400> 513
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 cagtgagcaa catgatggct tcagagtgag caggcccat gggagagggc ccagctgtgt 180
 cttcctggag cgtaacacc tt 202

 <210> 514
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 <212> DNA
 <213> Homo sapiens

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gggctgtgtc tc 132

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<212> DNA
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actccagacc aaattcccct cccagctcat gtgctgcgat caagacagat gc 172

<210> 516
<211> 80
<212> DNA
<213> Homo sapiens

<400> 516
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ctgccttttg atccctcctc 80

<210> 517
<211> 298
<212> DNA
<213> Homo sapiens

<400> 517
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acatgcacaa atgaattgac aggaagctgc tgtttcagag tccaaatgtc cttattctct 180
tcccattaat atctttaagg tctttctacg gccatctctc ctccctctct tcacatgctc 240
tggccagtca ctcaccgtag gaatcataag tctcctcact gagtccatgt ccgtaatc 298

<210> 518
<211> 119
<212> DNA
<213> Homo sapiens

<400> 518
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aagccagaga ggaattgaga ggcgctctgg cccaatttcc ataattgctc actgccttt 119

<210> 519
<211> 125
<212> DNA
<213> Homo sapiens

<400> 519
cccagaaaat gagaacacgg acacagaatc tccatctcac attgtttcct gctctgccta 60
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 <212> DNA
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<400> 520
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 tctcttcctc ctccttattc taatcaagat attttaagtt ttgaattaaa aatttatctc 180
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 ggagcgttct tccagtagca tgccttcca 390

<210> 521
 <211> 112
 <212> DNA
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<400> 521
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<210> 522
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<400> 522
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<210> 523
 <211> 98
 <212> DNA
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<400> 523
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 caggttaccg ccctgactgc cccgctgagt cggtctggc 98

<210> 524
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 <212> DNA
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<400> 524
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<210> 525
 <211> 228
 <212> DNA
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<400> 525
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 tgaagttag aaataatgaa attgaccaat gcttcctatc tctgtagttg gccattgtgg 180
 ggtcagtgtt tactgatctt tgctcactgt cctgatgaga taaacttg 228

<210> 526
 <211> 42
 <212> DNA
 <213> Homo sapiens

<400> 526
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<210> 527
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 <212> DNA
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 tacggcccca ctagtgggtg aagtctcact tcaagaacat gatggcttga ctacatatgc 180
 aataataaga gaagatgaaa tcacactcca gagagccagt acaccaccgt ggaagaaaga 240
 tatttg 246

<210> 528
 <211> 146
 <212> DNA
 <213> Homo sapiens

<400> 528
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 gtgttggtga ctccaagcaa tctgtc 146

<210> 529
 <211> 74
 <212> DNA
 <213> Homo sapiens

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 agtcctttc ctgc 74

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 <211> 704
 <212> DNA
 <213> Homo sapiens

<400> 530
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tgtggggttaa tgttctgtgc	ctatctcatc ggtgcactta	gcacagtgt	ttataat	240
gtatgttctt tctccctcgc	agcagtcgga gtccttgag	agcaaggacc	atgtacctt	300
tcacttttac atatccattg	cctacatatt tgttgaacga	aagttcctag	cacagcccct	360
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tgatgggaac cttcgtggg	aaaattgagt agagcctga	aggttggtgg	aaaagctt	660
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 <213> Homo sapiens

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cactaa					486

<210> 532
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 <212> DNA
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<400> 532	ggaatgccta ttgggaaggt	gctccagcca aagaattcaa	gggaccagag	gtcaagaaag	60
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<210> 533
 <211> 57
 <212> DNA
 <213> Homo sapiens

<400> 533	cttatcttcg ggagatacat	tccaaggccc ccagtgaact	cctgaaacct	caaacag	57

<210> 534
 <211> 80
 <212> DNA
 <213> Homo sapiens

<400> 534
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 cactcggata cctctaacta 80

<210> 535
 <211> 71
 <212> DNA
 <213> Homo sapiens

<400> 535
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 aatgtgcaga c 71

<210> 536
 <211> 111
 <212> DNA
 <213> Homo sapiens

<400> 536
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<210> 537
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 <212> DNA
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<400> 537
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 cagttcacag acagtcatag ctctctgcag cctcgaaatc ctggggtcaa gcaaccctcc 180
 catctcagtc acatgagtag ctgggactac aggcattgcac ctccatgacc agctcctggc 240
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<210> 538
 <211> 380
 <212> DNA
 <213> Homo sapiens

<400> 538
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 aggatttgta attcaaatca tcacagcatc ctaaagaaat actgtgtgaa tggaatgcac 180
 acaattccta cagaacacac aaactgatgt ccaaaaggca cagagtaatg ctggtggctc 240
 tttctagtca gttaagaaac aataaaaagt ctgcattatt ctttcataat ttaaatactt 300

aagtaatctc cactttatta ttttataaca atgacttcaa atttacatta ttttaagtac 360
cattgtaata gcttagtgta 380

<210> 539
<211> 115
<212> DNA
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<400> 539
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<210> 540
<211> 57
<212> DNA
<213> Homo sapiens

<400> 540
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<210> 541
<211> 223
<212> DNA
<213> Homo sapiens

<400> 541
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accgattggg aaaaaaatat atttatattt gatTTTTTTT ttctttttaa atttatatgg 180
tatccatccc agccaaagtc gtgcccggtc atctggtaga act 223

<210> 542
<211> 30
<212> DNA
<213> Homo sapiens

<400> 542
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<210> 543
<211> 465
<212> DNA
<213> Homo sapiens

<400> 543
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aatggttttt gtaccaaggt ttggcccacg ctgagattca caaagaactg gctttcagtt 420

cttatcttta ttttgattta aactggccca tcatgttgtc ctttg 465

<210> 544
 <211> 75
 <212> DNA
 <213> Homo sapiens

<400> 544
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 ctgaagcctc ttatt 75

<210> 545
 <211> 488
 <212> DNA
 <213> Homo sapiens

<400> 545
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 tatgctacaa ccaacagcga tttattaact acactagaga tgggtgttaa ggaatagctg 180
 agcaattagg ggctactagc cggatggctt gggaaaatag gataggctta gacatgataa 240
 tagcagaaag aggaggagtt tgcctcatga ttaaaactca atgttgtacc ttcatcccaa 300
 acaacactgc ccctgatgga agtataacaa aggcatcgca aggtctgact gccctgtcca 360
 atgagtttagc caacaactca gggttaaatg agccctttac aggatggcta gaaaagtgg 420
 tcagtaaag gaaaagaatt atagcctcaa ttctcacttc cctggcagcc gcaatgggtg 480
 tattttatt 488

<210> 546
 <211> 222
 <212> DNA
 <213> Homo sapiens

<400> 546
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 gggttcatgg acacggaagg gagggttgtt gttacttctg ttttactggg gaagaaaaca 180
 cccgtgttca ctactgtcct attggcagcg aatttgaaca cc 222

<210> 547
 <211> 55
 <212> DNA
 <213> Homo sapiens

<400> 547
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<210> 548
 <211> 32
 <212> DNA
 <213> Homo sapiens

<400> 548
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<210> 549
<211> 59
<212> DNA
<213> Homo sapiens

<400> 549
atggcgctcg gaagagccag ggacccggct gtgcgcttgg atccatcact gctctgggc 59

<210> 550
<211> 135
<212> DNA
<213> Homo sapiens

<400> 550
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tatgcctttg cattcgctc tctccagata ccaaagcact gtgatttccc atggcttcag 120
gaggcgacta gtcta 135

<210> 551
<211> 195
<212> DNA
<213> Homo sapiens

<400> 551
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ccctctattt ttagttatac atatcttgaa gccatttctt ctgttttaga atgtcagcat 180
atgatttgct aggtc 195

<210> 552
<211> 80
<212> DNA
<213> Homo sapiens

<400> 552
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cttcacgat aactctgagg 80

<210> 553
<211> 33
<212> DNA
<213> Homo sapiens

<400> 553
gcttggtaaa ttggcgttcc aactcccaga aca 33

<210> 554
<211> 34
<212> DNA
<213> Homo sapiens

<400> 554

agaagaggag cttggggcaa taacatgaat tctg 34

<210> 555
 <211> 280
 <212> DNA
 <213> Homo sapiens

<400> 555
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 ggcaaaccag gcagtcgcaa gctccagtgc ctactgggac caatgaggtt acgtgagtaa 180
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 tcccgctctaa aacaaaagac tccaggttct cactgcagga 280

<210> 556
 <211> 277
 <212> DNA
 <213> Homo sapiens

<400> 556
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 ttgaagaggg tccagtgaga gcctattaga ggcttcacaa ctcaattgcc agcagcagat 120
 ttctcccatc gcttagagac tgctcactca caccactcct cagaagacct ccagcaacat 180
 acacagccag gaacgacagg aaggaaggga catgacattt actgaacggc agtgctgaac 240
 caggcactga gccagggcct gttactaagg gcaaagc 277

<210> 557
 <211> 66
 <212> DNA
 <213> Homo sapiens

<400> 557
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 agttga 66

<210> 558
 <211> 143
 <212> DNA
 <213> Homo sapiens

<400> 558
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 attgaagaaa acagacaagt ccaaggagga aatgcataca aggcagaggt ggtaggcaaa 120
 gaggagtata agattgacaa gga 143

<210> 559
 <211> 169
 <212> DNA
 <213> Homo sapiens

<400> 559
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gccctgagca tgtacctggc tccccagtg taccgaggg ccttgctgtc actggatgga 120
 ttgaacaact caaccgagtg tgcattgctca tgctaaccac cattcagtc 169

<210> 560
 <211> 107
 <212> DNA
 <213> Homo sapiens

<400> 560
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 agccatgggc acacctgctc ccaagacggc cttctccttc aacactt 107

<210> 561
 <211> 191
 <212> DNA
 <213> Homo sapiens

<400> 561
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 aactgcaggg gagccaacaa acatctaact ctgccactc attttaccac tggggcgaac 120
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 tcaggccatt g 191

<210> 562
 <211> 86
 <212> DNA
 <213> Homo sapiens

<400> 562
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 atggcgatgg tataggggat gcctgt 86

<210> 563
 <211> 82
 <212> DNA
 <213> Homo sapiens

<400> 563
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 ggggatgtta tgacctaga ta 82

<210> 564
 <211> 245
 <212> DNA
 <213> Homo sapiens

<400> 564
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 tgcctgtaat cccagcactt tgggaggctg aggaaggcag atcgcttgag cctaggagtt 120
 caagaccagc ctgggcaaca tagtgagacc cccatctcta caaaaaatac aaaaattaac 180
 cagatgtagt ggtgtgctag tccaagctac tccaaaggct gaagtgggag attgggtaga 240

gcca

245

<210> 565
 <211> 318
 <212> DNA
 <213> Homo sapiens

<400> 565
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 gcatcagttt tgggtctgcct tatgagttct gttttgaaca agtgtaacac actgatgggt 180
 ttaatgtatc ttttccactt attatagtta tttcctaca atacaatttt aaaattgtct 240
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 ccagtagtat tcacatta 318

<210> 566
 <211> 173
 <212> DNA
 <213> Homo sapiens

<400> 566
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 aataaatgtg gccgctttgt ttttttcct aattatttca ttcgtaaaag tcttatcttc 120
 ccaataaaga tggtaactcc tctggactgg gtctgctttt cgcattttcc ttc 173

<210> 567
 <211> 116
 <212> DNA
 <213> Homo sapiens

<400> 567
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 gcagcccata ttaatgagat ctctgtttct ctcaagacag tcagggccgt ctggtc 116

<210> 568
 <211> 266
 <212> DNA
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<400> 568
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 gagtgacagg cgccgtggtg acgatggtgg tttctttcct cgaacactgg aaatccattg 180
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 tctaatacgt gtgcttcgga atgacc 266

<210> 569
 <211> 70
 <212> DNA
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<400> 569
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 ctctcccttc 70

<210> 570
 <211> 47
 <212> DNA
 <213> Homo sapiens

<400> 570
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<210> 571
 <211> 101
 <212> DNA
 <213> Homo sapiens

<400> 571
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 ctctccatgg tttctctcag gttctgagac tctaggcagg c 101

<210> 572
 <211> 792
 <212> DNA
 <213> Homo sapiens

<400> 572
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 tcagtgggtca caagtgagag aaaccagctt cgtggagaat tagatactat gtcaaaaaaa 180
 accacggcac tggatcagtt gtctgaaaaa atgaaggaga aaacacaaga gcttgagtct 240
 catcaaagtg agtgtctcca ttgcattcag gtggcagagg cagaggtgaa ggaaaagacg 300
 gaactccttc agactttgtc ctctgatgtg agtgagctgt taaaagacaa aactcatctc 360
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 ctggaaaacc aaattgcaca actgaataaa gagaaagaat tgcttgtcaa ggaatctgaa 480
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<210> 573
 <211> 70
 <212> DNA
 <213> Homo sapiens

<400> 573
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aggccatgag 70

<210> 574
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 <212> DNA
 <213> Homo sapiens

<400> 574
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 actaggggtca gccctaaatt cacttctaag agacagaagg acaccagga atacatggaa 180
 ggccatgtga aaatggaggc agagcttga gtgatgccg ccacaagtca agggatgctg 240
 ggagccacca aaaactggaa gaggcaagga aagtttctcc ccgagagccg ttagtgggag 300
 tgtggctctg ctggcaactt gatttcagac ttctagcctc cagaactctg aggtaataag 360
 tttctcttgt ttaagacct caggtttgaa gtagtttgtt acagcagccc aagaaacaat 420
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 aacata 486

<210> 575
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 <212> DNA
 <213> Homo sapiens

<400> 575
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<210> 576
 <211> 170
 <212> DNA
 <213> Homo sapiens

<400> 576
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 tcaaattggg aggggtattc ttcattgcagg agaccccagg ccctggaggc tgcaacatac 120
 ctcaatcctg tcccaggccg gatcctcctg aagccctttt cgcagcactg 170

<210> 577
 <211> 188
 <212> DNA
 <213> Homo sapiens

<400> 577
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 ttacctggct ggactttgac tatgagcggg agctgatgtt ctgcctcgag tgccgccagg 120
 ccctggtacg gaacaagcat ggcaaagccg aaaacgcctt cactgtgggc acagacaact 180
 tccagcgc 188

<210> 578
 <211> 221

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<212> DNA
 <213> Homo sapiens

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 gagtggagta gaaaagagtt tagtgtctcc ccaaactact gggttcttca aaaagttgtt 180
 gggcaaatgc tcagaacca agttaaggtc tcaagcaagt c 221

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 <211> 402
 <212> DNA
 <213> Homo sapiens

<400> 579
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 aaccatccac ctcataatgc acagtggaat gaatgccacc acaatacatt ttaatctcac 120
 gtttcaaaat acaaacgatg aagagttcaa aatgcagata acagtggagg tggacacaag 180
 ggagggacca aaactgaatt ctacagccca gaagggttac gaaaatttag ttagtcccat 240
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 <212> DNA
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 atatgaagtg ggtaaattct gcaagctaag agcttggcaa gggctgttgt aagttagttt 180
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<210> 581
 <211> 134
 <212> DNA
 <213> Homo sapiens

<400> 581
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 ggccttctac ccaggacgtc agcatgacta cctagtccca cctgctggca cagctggcat 120
 tcctgttcaa aatc 134

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<400> 582

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cgggagaca 69

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<212> DNA
<213> Homo sapiens

<400> 583
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<210> 584
<211> 65
<212> DNA
<213> Homo sapiens

<400> 584
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ttttc 65

<210> 585
<211> 73
<212> DNA
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ctttacatgg gct 73

<210> 586
<211> 44
<212> DNA
<213> Homo sapiens

<400> 586
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<210> 587
<211> 96
<212> DNA
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<400> 587
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gatctcccaa gagacatcag cagttgtggt cttgcc 96

<210> 588
<211> 76
<212> DNA
<213> Homo sapiens

<400> 588
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tgattataa cagctg 76

<210> 589

<211> 203
 <212> DNA
 <213> Homo sapiens

<400> 589
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 gcagtcttag aggtttctag gta 203

<210> 590
 <211> 210
 <212> DNA
 <213> Homo sapiens

<400> 590
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 ttaaaaaagc tttctttgtg attatctggg atctgggttg gtctccagaa aatacataga 180
 cttggagata ggaaggcctc acaggacttc 210

<210> 591
 <211> 47
 <212> DNA
 <213> Homo sapiens

<400> 591
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<210> 592
 <211> 86
 <212> DNA
 <213> Homo sapiens

<400> 592
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 atgactggat tggtaatgac aaatgg 86

<210> 593
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 cactgaagga ggcaatgatg acgctggtac agatttcact tcagcatggg ctggaatctg 120
 taaatgatgc ccagaaggca aaactggaga cttcacagtc actggaagac tctgggtatt 180
 aactacaata aaagatgagt ctttttgtgt tgagggagga acagcaaagc tttgcatggt 240
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 gtttgaagaa ctggctggct gaaaaatggg caattgaact gatgcacttg tggaagagct 420

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<210> 594
<211> 34
<212> DNA
<213> Homo sapiens

<400> 594
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<210> 595
<211> 391
<212> DNA
<213> Homo sapiens

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acctgacatc tatagcatct tagcctcatc ttcagagatg ccattggtaa aattataggc 300
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atcaccta at gcactcacgt agcccta atg g 391

<210> 596
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<212> DNA
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tgattaaatg gcaaaagtaa atcttgtttt agtaatcaca ttaaatagaa aaggatgaag 540
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aaaacaagac tcatctacat gctgtctata agagacttgc cttagatata aggacacaaa 660
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tatgtactta ataatacagc ctcaaaatat atgaagcaat aattgctata atttaagggg	900
gaaaagaaca gttctatgaa aagttagaga atgaaatatt ccactttcaa catgagatta	960
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tgaaaatttg aagtcataaa aagtatcttt tgcaattaca atggaatgaa gctagaaatc	1200
aataactaga aaaaccagaa aagtcacgca tatgtagaaa tttaaaaacc cgctcttcaa	1260
cagccattgg tcaaagaaga aatcacaagg gacattagaa aataccttga gacaaatgaa	1320
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<210> 597
 <211> 223
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 <213> Homo sapiens

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gcttcagccc cttttaaaaa aaaaaaaga gagagagaga tacttttaac acacagaaaa	180
attcgggtgtg gtatataaca agcaccag tagcatgtgt cta	223

<210> 598
 <211> 260
 <212> DNA
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<400> 598	
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taaatttgag gtcagaccag ttctctgctc tagaaccctg ttttctgttg ttttaagatgt	180
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<210> 599
 <211> 240
 <212> DNA
 <213> Homo sapiens

<400> 599	
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gaacaggaag taaaatgggc cgagatggag cgagcccca gtgtgcttcc aaggccactc	180
ccacctccct gaaacaccct gctacgtact gatccaatgc cctgcgctgt gtatgagagc	240

<210> 600
 <211> 86
 <212> DNA
 <213> Homo sapiens

 <400> 600
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 agatgttaat acctttcctc actaaa 86

 <210> 601
 <211> 34
 <212> DNA
 <213> Homo sapiens

 <400> 601
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 <210> 602
 <211> 29
 <212> DNA
 <213> Homo sapiens

 <400> 602
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 <210> 603
 <211> 123
 <212> DNA
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 <400> 603
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 tggtggttgg ctctcgtat gcatctctac cattcctaatt gcggtttgaa aattgtgctc 120
 agc 123

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 <212> DNA
 <213> Homo sapiens

 <400> 604
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 accaacctga gcaacatggc gaaaccccgct ctgtaataaa aatacaaaaa aattagctgg 180
 gcatgggtggc atgtgcctgt aatcccagtt actggggagg ctgaggcagg agaatcactt 240
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aggcctagcg ttgcgcctcg gacacggtgg ccggcccgtc aaagggacca cgcagaagga	600
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ggtgaggggt ctggctcctt cctggagaga ggagggcagg ggaggcggag ctggtccggg	780
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<210> 606
 <211> 123
 <212> DNA
 <213> Homo sapiens

<400> 606

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ctg 123

<210> 607
<211> 91
<212> DNA
<213> Homo sapiens

<400> 607
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tccatcacca gagcaagttc agccaccagg c 91

<210> 608
<211> 196
<212> DNA
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<400> 608
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gccaggagaa gagaggggccc cctgagcatc caggaccagc tcctgaccct ggaatgtgtt 120
cagcctggag ctctgtgtcc tgatgttcta gaatagggcc aaagccaccc ctcctcttg 180
ggctgactg attagg 196

<210> 609
<211> 36
<212> DNA
<213> Homo sapiens

<400> 609
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<210> 610
<211> 563
<212> DNA
<213> Homo sapiens

<400> 610
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 aagcttcctt ctccccaggc aggcccagca aaatctgtag ga 162

<210> 612
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 <212> DNA
 <213> Homo sapiens

<400> 612
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 cagatgctac attttcaaaa ggcaagggtc ttttagaatg cttgatgtct gtgaggttga 180
 caggagcaat attaaataaa tatacataca ctgtttaagg attctgtg 228

<210> 613
 <211> 74
 <212> DNA
 <213> Homo sapiens

<400> 613
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 ggaggactgt ggca 74

<210> 614
 <211> 86
 <212> DNA
 <213> Homo sapiens

<400> 614
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 ttggcaaaaa gggcaagaca aggtga 86

<210> 615
 <211> 89
 <212> DNA
 <213> Homo sapiens

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 gagaaatttc tgcattgaggc taagcaaag 89

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 <212> DNA
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<400> 616

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 aagctgctgc agctcatcca cagtctttgc gatgttattg ctctgtaaga gaagcacttg 360
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<210> 617
 <211> 110
 <212> DNA
 <213> Homo sapiens

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 agagggccag ggatcctccc tcacccacc ttctgcacgc ttctgtaggg 110

<210> 618
 <211> 68
 <212> DNA
 <213> Homo sapiens

<400> 618
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 atgcaaga 68

<210> 619
 <211> 213
 <212> DNA
 <213> Homo sapiens

<400> 619
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 cagtaggagg agccaggatt ggttactccc tgc 213

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 <212> DNA
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 aaacagtcaa gaatttattt ttgaatttaa ttattcattc atatgtttaa caaaagttta 180
 ttaaagtctt actgagggca agaaaccgtg taggcaaat agataagaaa tgaacagcgg 240

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<400> 621
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<210> 622
 <211> 149
 <212> DNA
 <213> Homo sapiens

<400> 622
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 <212> DNA
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 atcccac 127

<210> 624
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 <212> DNA
 <213> Homo sapiens

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 taacatactg catagatgta attccagcaa aaagcaaaga aacaagacat cttacatagc 360
 ttgtgtggtc ttaccaaggg aaaattcatg gtttgtgttc atcttttgaa atagtaaaaa 420
 taactcgtga gtttcatttc tactttcttg gagccccagt cattgcagaa tctaccacag 480
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GBX1170_3WO_ST25.txt

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<212> DNA
<213> Homo sapiens

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<211> 382
<212> DNA
<213> Homo sapiens

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aagcttgga accaatccaa aatccctcag atccacacct atacactcag tgactcatgt 180
ctatgagcca tggtgaccat gccaggggtt ggggtcagaa gaatcagggg aagtgaata 240
gcaaggggac tcttcacag ctttttttga gggttcttca gtcctggcta actctgcatt 300
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cctggagctc accgaagtca ga 382

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<211> 543
<212> DNA
<213> Homo sapiens

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ccagttaatg tcctcagcag ggaattaata atattattgt atattcatga aattgacacc 360
atgtggccac acaaatgcat tacacaggcc tctatgtaac ataggatatt cattagagaa 420
ttgtttttca agaggacaaa gtactttcat ttttgctag aaaatggggg aagacaaaaa 480

GBX1170_3WO_ST25.txt

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 tga 543

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 <212> DNA
 <213> Homo sapiens

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 gctttgcact aaagtcaacc tcaaaaatta atatcccaca atcacatata gcagaaacgc 120
 agagcaaaga gtt 133

<210> 629
 <211> 95
 <212> DNA
 <213> Homo sapiens

<400> 629
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 tgtgatgatt ctctgagtcc aggatttatc cagcc 95

<210> 630
 <211> 36
 <212> DNA
 <213> Homo sapiens

<400> 630
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<210> 631
 <211> 77
 <212> DNA
 <213> Homo sapiens

<400> 631
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 cactttctga tcctgag 77

<210> 632
 <211> 278
 <212> DNA
 <213> Homo sapiens

<400> 632
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 cttctcccag tgtctaaaat gatcaatatg cctagagtag atgctgctga agaggcaaag 180
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 ctgatgataa gccctaggag gctcctgagt catattcc 278

<210> 633

<211> 29
 <212> DNA
 <213> Homo sapiens

 <400> 633
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 <210> 634
 <211> 273
 <212> DNA
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 ctttagggcc aaaaaataga cctaggtttg tattactatt tcagcttaat cgtgtatacc 180
 ttgtgtttcc tcggccaaca atggctaatt atggtaaata ctatttagaa ttatgtgcta 240
 tgtactaagt gtttgacata tggatatctca ttt 273

 <210> 635
 <211> 223
 <212> DNA
 <213> Homo sapiens

 <400> 635
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 tgaccctcgc tgtctgataa aaaagcactg gccacatggc cgctgggaaa tttgaatgtg 120
 gccagtctga atttagatgt gatgtgtgag ctacaaacta gatcttaaaa aactaatgca 180
 aaaaacgtaa aaatatgagt aacgatttct tatggcccac atg 223

 <210> 636
 <211> 157
 <212> DNA
 <213> Homo sapiens

 <400> 636
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 cggggcgatg cgtgcgacga cgacatcgac ggcgacc 157

 <210> 637
 <211> 39
 <212> DNA
 <213> Homo sapiens

 <400> 637
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 <210> 638
 <211> 978
 <212> DNA
 <213> Homo sapiens

 <400> 638

GBX1170_3WO_ST25.txt

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 caactgcgag tggcctacgg tcattttttc aaatgagaag actggagaga gagaacaaca 660
 gtaatcacia aacctctgtt gcccttagtc catgacaatg ttttaaggaaa ctttaaaaaa 720
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 aatattttaa atgggggtatt tagtggaat gcaatcagta gaaaacattg ctttttagtg 840
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<210> 639
 <211> 165
 <212> DNA
 <213> Homo sapiens

<400> 639
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 aatttattcc ttattccctc ttggcagcta atgggctctt accaagttta aacacaaaat 120
 ttatcataac aaaaatacta ctaatataac tactgtttcc atgtc 165

<210> 640
 <211> 271
 <212> DNA
 <213> Homo sapiens

<400> 640
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 tggggcaaag ctgtgtttca gccacactga acccaattac acacagcggg agaacgcagt 180
 aaacagcttt cccacaagag ccgtctcctg tcctcctgtt ccccagggca gggagcccca 240
 ggacaacacc agacttcagc tgtactgtgg g 271

<210> 641
 <211> 84
 <212> DNA

<213> Homo sapiens

<400> 641
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 ttggttctag cagaaggact tacc 84

<210> 642
 <211> 115
 <212> DNA
 <213> Homo sapiens

<400> 642
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 acggcacaca gactggcatc gcctgggcgt gcgctgctcc atgtttctca gaaaa 115

<210> 643
 <211> 181
 <212> DNA
 <213> Homo sapiens

<400> 643
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<210> 644
 <211> 168
 <212> DNA
 <213> Homo sapiens

<400> 644
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 acaacttaca tcccaggagg cagtacgtgg tccgagctag agtcaaca 168

<210> 645
 <211> 293
 <212> DNA
 <213> Homo sapiens

<400> 645
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 aattttttta gtatagcgta tcgcaagggt ttgacacggc tgccagcgac tctaggcttc 180
 cagtctgtgt ttggttttta ttcttatcat tattatgatt gttattatat tattatttta 240
 ttttagttgt tgtgctaaac tcaataatgc tgttctaact acagtgtca ata 293

<210> 646
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 <212> DNA
 <213> Homo sapiens

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<210> 647
<211> 88
<212> DNA
<213> Homo sapiens

<400> 647
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aactgatttt caagcctgac taacttgt 88

<210> 648
<211> 2245
<212> DNA
<213> Homo sapiens

<400> 648
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ataatactca ggtcaggaag acagattcct gtttataaaa aaagagaacc aaggtgtact 180
gtggcacctt taaaactcaa gccctgggct ggggtgcagtg gcccaggcct gtaatcccag 240
cactttggga tgccgaggca ggcagatcac ttgaggtcag gagttcgaga ccagcctggc 300
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cagagtagct gggattacag gcattcgcca ccatgcctgg ctaattttgt attttttaga	2040
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ccacacattc atagggagg gactg	2245

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 <211> 32
 <212> DNA
 <213> Homo sapiens

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<210> 650
 <211> 42
 <212> DNA
 <213> Homo sapiens

<400> 650	
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<210> 651
 <211> 206
 <212> DNA
 <213> Homo sapiens

<400> 651	
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ggacacgtat ttacaaaatg cattgatgag taagagagaa aacttatcca aggcagtgc	180
aagagactcc tgagacaact ggcaca	206

<210> 652
 <211> 38

<212> DNA
 <213> Homo sapiens
 <400> 652
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<210> 653
 <211> 68
 <212> DNA
 <213> Homo sapiens
 <400> 653
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 gccctga 68

<210> 654
 <211> 579
 <212> DNA
 <213> Homo sapiens
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 cctgatgttg ccaggagtag gatgctgatg ctgccagaga gtaggtgggc tccaaacccc 120
 aggcttctca cttgcttact aagcacagca gtctgaagct tgggacctgg cagtgcgtct 180
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<210> 655
 <211> 437
 <212> DNA
 <213> Homo sapiens
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 cgaggacagc gtggcactgg ctgcgagtgt tcctgagagt tgaaagtggg atgacttatg 180
 aacttgac agcatggctc tgcctcaca tgatgcagtc agccacctgg tgaagaagtg 240
 acctgcgaca caggaaacga tgggacctca gtcttcttca gcagaggact tgatattttg 300
 tatttgga ctgtgggcaa taatatggca ttttaagagg gaaagagttc agacttatca 360
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 aaatcgccca agtgatg 437

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<210> 656
 <211> 96
 <212> DNA
 <213> Homo sapiens

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<210> 657
 <211> 66
 <212> DNA
 <213> Homo sapiens

<400> 657
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 gaagtt 66

<210> 658
 <211> 493
 <212> DNA
 <213> Homo sapiens

<400> 658
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 agagtaagag cagcagctgt accccaatgg cacagcaaag caaatcccc tacaggcacc 180
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 tcagaacttc tgactctgag gaagaggtac aagacctctt ttactgcag aagtatccca 420
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 tgtccaatga agg 493

<210> 659
 <211> 266
 <212> DNA
 <213> Homo sapiens

<400> 659
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 agaaattaat caaaagaaga attaatctct ccaatcagcc ttggcatttt ctttctatct 180
 ttgatatgtt gttttttaca gtgtcttggg tttcagaata agctgtttgt aactacttcc 240
 tccactatat tgtgagcctc tggagg 266

<210> 660
 <211> 242
 <212> DNA
 <213> Homo sapiens

GBX1170_3WO_ST25.txt

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 taggtactcc ataaatgtaa gactatggca gctgtctagt acaagtgctt ctactgatt 180
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 ag 242

<210> 661
 <211> 50
 <212> DNA
 <213> Homo sapiens

<400> 661
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<210> 662
 <211> 105
 <212> DNA
 <213> Homo sapiens

<400> 662
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 agtcgcaagg gcaaccacca ccgcttcac accgagaaaa gggtc 105

<210> 663
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 <212> DNA
 <213> Homo sapiens

<400> 663
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 caggtgggga aactgaggca ctggaagggg aaggaactcc cacagctagg tagtggcagc 240
 ttggcaatgg cgctccccg tgtgcacaca agcctgggaa gggccaggca ccaggaccac 300
 attccttcca attacagtgg ccttccaacg gtcagg 336

<210> 664
 <211> 34
 <212> DNA
 <213> Homo sapiens

<400> 664
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<210> 665
 <211> 91
 <212> DNA
 <213> Homo sapiens

<400> 665
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agcgtgaccg ttgatgatgc agggaaccgt c 91

<210> 666
 <211> 76
 <212> DNA
 <213> Homo sapiens

<400> 666
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 tcagcaggaa gcttcc 76

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 <211> 298
 <212> DNA
 <213> Homo sapiens

<400> 667
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 cattgtttct tatacctaaa attgcctatt aattagctaa ttcctaaaat tcctaattac 180
 aatatgaatt ttttttaaga gacaggttgt cactctgccca cccaggcttg ggtacagctg 240
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<210> 668
 <211> 403
 <212> DNA
 <213> Homo sapiens

<400> 668
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 tgtggaacta tccgggtgat gccaatacac actaaagttt tagaggccct ggtctagaga 180
 gagagagtat ggagtgagaa gaatttttgt ctagagttga accttgagaa ggtttgactt 240
 ttaaagactg ggaagtgaag gatgactttg caaaggaggt tggaagtagt gtttagaggg 300
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<210> 669
 <211> 172
 <212> DNA
 <213> Homo sapiens

<400> 669
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 ttcattaccc actttcacgg ccggtgccca atgggacgtt gagctgctgt tt 172

<210> 670
 <211> 299

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<212> DNA
<213> Homo sapiens

<400> 670
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ggcccaggag cccttctgct gacagtggga actcccagct acgtgtgggg gtccccatac 180
cagacaaagg tccttgacct tagtcttgcc cgagaggccg acacagccca gctttggggg 240
ctggctttac ccacaagagg ccacaccttg ccacagcact gtttatcttg cctgtttca 299

<210> 671
<211> 68
<212> DNA
<213> Homo sapiens

<400> 671
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ggagatta 68

<210> 672
<211> 549
<212> DNA
<213> Homo sapiens

<400> 672
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gcatttaact catatatgac cttccttttag gaaggcttga ctggtaaggg aaaaactcct 180
ccagtgaaca cgtgcacaac ttcagtaaaa aactgcaca tgcgtcccct cccaagtgtc 240
ggcaggccac tgtgcatgca gacagcccgc cccaaagaaa aatcagagga ggagaaatgg 300
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gatttgctg 549

<210> 673
<211> 29
<212> DNA
<213> Homo sapiens

<400> 673
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<210> 674
<211> 89
<212> DNA
<213> Homo sapiens

<400> 674

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acaccctaca ctgcctccat tgaaaaaca 89

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<211> 237
<212> DNA
<213> Homo sapiens

<400> 675
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gcaccctgag agcgcacctg gacatcagcc attacacgtg agggggagga acttttctga 180
gtttccctaa aaggcttaaa gtaaggggtt gttgggtgga ccacacatga catatta 237

<210> 676
<211> 121
<212> DNA
<213> Homo sapiens

<400> 676
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g 121

<210> 677
<211> 93
<212> DNA
<213> Homo sapiens

<400> 677
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gtgtcaagac gtggcacgtg tcagagaatt tga 93

<210> 678
<211> 42
<212> DNA
<213> Homo sapiens

<400> 678
aaggatctga tggaagcacg tcatctgata ctacctcaaa ta 42

<210> 679
<211> 141
<212> DNA
<213> Homo sapiens

<400> 679
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tggtgggtac ccgtgcccag gaggacgccg agctccagcc ccgagccctg gacatctact 120
ctgccgtgga tgatgcctcc c 141

<210> 680
<211> 467

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<212> DNA
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 ggaaagaaca accgattcac caactccact ttttctatatt tacaactttc tacatctcac 180
 tcttgattttt ggccttcctg gctgaaacag cctggcagtc cctagagccc ctgagaagag 240
 ccctggttct ccaaaagaca gaggaggaga agccctgcag gatgcgctga ccacttccca 300
 gagaactgac agtccgtgct cccaaaagtt tgaaccaaca gcctaattgtg aaaagaaact 360
 gcaactgaaag gtaaaggagg aaatggtgat gaactgggct tatgtgagaa tgtctatatt 420
 ttcataacac agccccagaa tctttctctc agttacagcc tcaggca 467

<210> 681
 <211> 65
 <212> DNA
 <213> Homo sapiens

<400> 681
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 atttt 65

<210> 682
 <211> 404
 <212> DNA
 <213> Homo sapiens

<400> 682
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 gcatccattc tctctttctc ttgatgacgc agctgtcatt tggctgtgcg tgctgacagt 120
 ttgcaacag gcagagctgt gtcgcacagc agtgctgtgc gtcagagcca gctgaggaca 180
 ggcttgccctg gacttctgta agataggatt ttctgtgttt cctgaatttt ttatatggtg 240
 atttgtattt aaattttaag actttatttt ctcactattg gtgtacctta taaatgtatt 300
 tgaaagttaa atatatttta aatattgttt gggaggcata gtgctgacat atattcagag 360
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<210> 683
 <211> 131
 <212> DNA
 <213> Homo sapiens

<400> 683
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 ctgctttaga g 131

<210> 684
 <211> 76

<212> DNA
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 cgtctgcttt gggttt 76

<210> 685
 <211> 283
 <212> DNA
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 aaacagagga ttgcctgtca acagatgggc tacaattgct tctctttgga gaaccaagag 180
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 caacaggtgg gttcccagtg ctcttatctg gtcgcaggta ctg 283

<210> 686
 <211> 40
 <212> DNA
 <213> Homo sapiens
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<210> 687
 <211> 307
 <212> DNA
 <213> Homo sapiens
 <400> 687
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 gtgcaaaatg catgtgccct ctagaccag aatcctgtga aatgaagttg ttaatgtaat 180
 aataaaatgt agcatttttg atcagacaaa aaggccatgg gccttctcca cctaattggcc 240
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 aatattg 307

<210> 688
 <211> 185
 <212> DNA
 <213> Homo sapiens
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 gacaagcaag gcagaaggaa agcaccctga gaagacagga aagaaagaat gcagcactgg 120
 ttaccaggat gaaagcccag aggccagagg aatgcttaaa acacatcatt gtagtgctgg 180
 atcca 185

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<210> 689
<211> 58
<212> DNA
<213> Homo sapiens

<400> 689
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<210> 690
<211> 30
<212> DNA
<213> Homo sapiens

<400> 690
ctggcaaggc ataccgcctg acctgcacac      30

<210> 691
<211> 154
<212> DNA
<213> Homo sapiens

<400> 691
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acagacagag cacacaccac ttctaagctc aacactgctc accaactaga agcacctcgg      120
ttaagcacat gtgagacact cttgcatagg aaag      154

<210> 692
<211> 50
<212> DNA
<213> Homo sapiens

<400> 692
agaagctgcc cttggctgct cgtagcgccg ggccttctct cctcgtcatc      50

<210> 693
<211> 248
<212> DNA
<213> Homo sapiens

<400> 693
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gaaaactgtt acaaatcaag ctgtgtatct tcagacttgt caaatctatc ccatgattaa      180
ataattctgc ttgtgagatc tgcttggaact ctgtatgatt ttctgatct tgataccctg      240
tgaggaac      248

<210> 694
<211> 314
<212> DNA
<213> Homo sapiens

<400> 694
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 gggctgactt gactgtatag tgcattggct tttCaacag taaatctgca aaatctaact 300
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 cattcctaca aaagaggcag aaactttgag caatctaggt tttttttttt ttttaagtttt 180
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 cgtgatccaa gcagatgcca catggaagag gaatcgccat ttactcagaa aaaatgtccc 300
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<210> 696
 <211> 87
 <212> DNA
 <213> Homo sapiens

<400> 696
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 acttttgaag catggttttc ttgaaga 87

<210> 697
 <211> 590
 <212> DNA
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<212> DNA
<213> Homo sapiens

<400> 698
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actaagtatc ctgggttttg caaaatatgg aggatctgtt taccttatcg ctaatgggta      180
cagcagagag tggct                                                    195

<210> 699
<211> 32
<212> DNA
<213> Homo sapiens

<400> 699
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<210> 700
<211> 107
<212> DNA
<213> Homo sapiens

<400> 700
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taagtaatgg attctgtgtt cccagaccac tcgacccgga gttaaatt                    107

<210> 701
<211> 791
<212> DNA
<213> Homo sapiens

<400> 701
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ataatatata ttgtatgtga taatatgatc gtattctata aatacatata cacacgatac      180
tcctttccag aagttcctgg ggctccgtgt tgcagttcag gactccttgc ttcttggacc      240
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 <211> 89
 <212> DNA
 <213> Homo sapiens

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 ccttattatt ttgctacggc ctcaaaaga 89

 <210> 703
 <211> 119
 <212> DNA
 <213> Homo sapiens

 <400> 703
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 ggatctgcgt ctgcgacaac ggcaaggtgt tgtgcgatga cgtgatctgt gacgagacc 119

 <210> 704
 <211> 250
 <212> DNA
 <213> Homo sapiens

 <400> 704
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 <211> 32
 <212> DNA
 <213> Homo sapiens

 <400> 705
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 <210> 706
 <211> 100
 <212> DNA
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 cagccctgtg gcagctttgc tgaccgccta tcacctggga 100

 <210> 707
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 <212> DNA
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 <400> 707
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taatcaggtc tcagaggata gacccgtgtg tacagtcact attcagggaag agagtttgaa	300
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cagggatatt ctctctcttg tccattacca tatccttaga gtcagaagg ggtgtctggc	180
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gagaggaaaa tactatttcc cattaaaatg aagaaagagt ttttattaga agggaaggcc	300
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<210> 709
 <211> 81
 <212> DNA
 <213> Homo sapiens

<400> 709 cagaacaagt gcatctgctg gcagccagct taaggagtta gcagccctca attccaataa	60
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<210> 710
 <211> 178
 <212> DNA
 <213> Homo sapiens

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<210> 711
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 <211> 31
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 <210> 713
 <211> 30
 <212> DNA
 <213> Homo sapiens

 <400> 713
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 <210> 714
 <211> 83
 <212> DNA
 <213> Homo sapiens

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 <210> 715
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 <212> DNA
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 <210> 716
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 <212> DNA
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 <400> 716
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 gaagaaggcc tgccagaggt tcctcgactg a 91

 <210> 717
 <211> 147
 <212> DNA
 <213> Homo sapiens

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 ctcccagat cttcacctgt tagtgtc 147

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tgggtggaag gactggagc caccgaagtg gaggaagaat gaagtgagaa aggagagtac 180
cgatggagtc agggtccta gaatccagaa t 211

<210> 719
<211> 274
<212> DNA
<213> Homo sapiens

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tgctgatccg cgtcccgccc ggcgccagg accctcagag ggaggagagc tcaaagacct 180
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actcaggga cagtgagagc gcagggcgcc tccc 274

<210> 720
<211> 281
<212> DNA
<213> Homo sapiens

<400> 720
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aacattaata taagaagcca aattgtaatg atacagcaaa atgaggccac tggattaat 180
acaggtagca aagggtccaca tccaggtggg actgacatca gggaaatttc caaaaccagt 240
tgctgctgcc taagagtggg tgccactgac gaaagcttga a 281

<210> 721
<211> 353
<212> DNA
<213> Homo sapiens

<400> 721
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tagagatggg cttggggctc catgccttgg ctttggtggg cttctgcttc ctcaggaact 120
cacactacct gtacataccc tgggactcac cagaaagctt taggctctgt ttgattgggc 180
cattctatcc ttgactgttt tcatatactc aagtggttga ttttgccaat gggcctaagc 240
catgtcagtc ttaggggaag tttttgtttt ttcctttata gtgggtctaa ttttcctaac 300
tgcathtagc aaatagcaat tcctggggcc actgttgggc tgaccctgat tta 353

<210> 722
<211> 146
<212> DNA
<213> Homo sapiens

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<400> 722
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 gtcagcattg actgggtgac ctgtatacca gggagaatgc ttttacacac gcgcggagcc 120
 cccctaggag actgccgatt ttatgt 146

<210> 723
 <211> 87
 <212> DNA
 <213> Homo sapiens

<400> 723
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 gacataccct tccaccgatg cattata 87

<210> 724
 <211> 144
 <212> DNA
 <213> Homo sapiens

<400> 724
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 ttctgggctt ccgggaccaa ggggactcag gctgggattt ctttgttgaa ttcaatgtag 120
 tcctttccat cataggcatt cttc 144

<210> 725
 <211> 87
 <212> DNA
 <213> Homo sapiens

<400> 725
 aatctcaatg ctaggggaaa taaccacact tcagaccatc tcggaagatc taaaaagcct 60
 gaccatggac cctcaciaac tgcctc 87

<210> 726
 <211> 198
 <212> DNA
 <213> Homo sapiens

<400> 726
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 agactgggca ttggatcttc aggaattatc aatttgaagg gggagttggg aagtgataat 120
 agactgtgtt tatatgagaa aattatccat aatttttaga aatgcaaact gaaataggct 180
 aaaacgacat gtggtctg 198

<210> 727
 <211> 57
 <212> DNA
 <213> Homo sapiens

<400> 727
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<210> 728
 <211> 37
 <212> DNA
 <213> Homo sapiens

 <400> 728
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 <210> 729
 <211> 176
 <212> DNA
 <213> Homo sapiens

 <400> 729
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 ccggctgccc ctctagccc ctcttcaggg ggtcccatg tctcagcccg agggagaagt 120
 tggctctggc cagagccacg ctcacactcc cacaggatgc cgcaagtccc aggcct 176

 <210> 730
 <211> 83
 <212> DNA
 <213> Homo sapiens

 <400> 730
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 gataatgtaa gagttggatg gca 83

 <210> 731
 <211> 372
 <212> DNA
 <213> Homo sapiens

 <400> 731
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 cccggagcag gggctctgagc cacagccgtg ctgcccaca aactgatttc tcacggcgtg 120
 tcacccacc agggcgcaag cctcactatt acttgaactt tccaaaacct aaagaggaaa 180
 agtgcaatgc gtgttgtaga tacagaggta actatcaata ttttaagtttg ttgctgtcaa 240
 gatttttttt gtaacttcaa atatagagat atttttgtac gttatatatt gtattaaggg 300
 cattttaaaa gcaattatat tgtcctcccc tattttaaga cgtgaatgtc tcagcgaggt 360
 gtaaagttgt tc 372

 <210> 732
 <211> 237
 <212> DNA
 <213> Homo sapiens

 <400> 732
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 aggtttttgtg cacagatgcc tttaggaaac actgggctaa acaaaggtaa gtggctttct 120
 tgactgcagg acttctagag cttcatttgc cacagtgggt taagtgcaaa gttaggggca 180
 ttggatgtac tgttgcctag actttgtggc caccggacca tcttgtgaac caaatga 237

GBX1170_3WO_ST25.txt

<210> 733
 <211> 301
 <212> DNA
 <213> Homo sapiens

 <400> 733
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 caacagtgca ctttgggtga tgtggaccat tctgtattga gcagaaattt tctaattggaa 120
 ggaaggttcc tctgcagaac aactacagag gattttcact taacactgca gcagttcttg 180
 atgaatctgg tcatgattct cagtctccca aggggctcag gggcccacaa ggcaggaaca 240
 tcctttgggg gtttgtgctg ctgtcatacg gttcctgtgt tcagtccta gctaccatgt 300
 g 301

 <210> 734
 <211> 79
 <212> DNA
 <213> Homo sapiens

 <400> 734
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 ttcaatagga agtgagagg 79

 <210> 735
 <211> 52
 <212> DNA
 <213> Homo sapiens

 <400> 735
 tgtgcaaagt acgttcccgga gaattcagtg agttcttctg gacaaaataa ac 52

 <210> 736
 <211> 257
 <212> DNA
 <213> Homo sapiens

 <400> 736
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 ttttcttttc tttttctttt ttttttttat cacactccta aaaccaagta gaaggggaat 120
 gctgggcttt gtactggata atgtgagtcc ccatgtaaat tgtgagcgat tgcaaagtac 180
 ggaaagggtt attacctaag gtgagccctc ccagagctcc cggagtataa aagcattaag 240
 cgcatgttct aacaaac 257

 <210> 737
 <211> 69
 <212> DNA
 <213> Homo sapiens

 <400> 737
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 cggcaggca 69

<210> 738
 <211> 65
 <212> DNA
 <213> Homo sapiens

 <400> 738
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 ttctc 65

 <210> 739
 <211> 32
 <212> DNA
 <213> Homo sapiens

 <400> 739
 ttactcgcct tcaggtgtca tgttcttggt cc 32

 <210> 740
 <211> 399
 <212> DNA
 <213> Homo sapiens

 <400> 740
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 gtctcaaaact cctgacctca ggtgatctgc ctgcctcggc ctcccaaagt gctgggatta 120
 caggcgtgag acaccacacc cagccataac taagcattat gttttctaaa acttctaaga 180
 tcctccctaa acccgtctgg agacatgggt tttagcccag actctgcctc aaactcattg 240
 tagtcccag cacattaccc agttgctctg ggccttggtg ttatgctctg ggaagtagat 300
 gttgatgctg tggccttagt gccttctggc cccagcattc catgggcctg tgatcttgac 360
 caacctgaga aaacagtaac agcccatcca ctggaaata 399

 <210> 741
 <211> 88
 <212> DNA
 <213> Homo sapiens

 <400> 741
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 agtgaccaac gcgatcctgg gcattctg 88

 <210> 742
 <211> 248
 <212> DNA
 <213> Homo sapiens

 <400> 742
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 tggaaacttg gctaggtccc atggcccctg gtgtgtgtgt ctttttttct gttaatatatt 120
 tcttattttg ttcaacttgc ggagagattt tctctacttt tatcttctaa ccccttctgt 180
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 cttacatc 248

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<210> 743
<211> 413
<212> DNA
<213> Homo sapiens

<400> 743
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gacaactcca tcacaaacaa taaaagatcg gggagagaaa agccatttag cctgataaag      120
tacatctcaa tttagctagc agatcagtac ccacaggaat aatctggaag gcatgttccc      180
taccctctcc accttctggt atttgcattt ctagcagtga tcaactgaagc atcaggattt      240
gtggggattc acaagtaaca tcatgatggg aggaggcagc cctgcctccg atgatgagct      300
gaaaatagct gaagatggta aaaccaagag caaagcaacc cggctcatag ccgaaatttc      360
atctcctcct cagcctctca cagagaagcc aggaagagtc tgattggctt gca          413

<210> 744
<211> 37
<212> DNA
<213> Homo sapiens

<400> 744
cctcaggaac aggaaccttc tcttgcccaa caaagtc                                37

<210> 745
<211> 95
<212> DNA
<213> Homo sapiens

<400> 745
ctcccgcgga tgttgaaagt acgggacccg cggccctggc tcctcttcct gctgcacaac      60
gtgggcctgc tgggcggctg gaccgtcctg ctgct                                95

<210> 746
<211> 54
<212> DNA
<213> Homo sapiens

<400> 746
tgagacaggc gaacagggcg acagaggcat aaagggtcac cgtggcttct ctgg          54

<210> 747
<211> 37
<212> DNA
<213> Homo sapiens

<400> 747
ggctttgtga caaccaggac gactgtggcg atggctc                                37

<210> 748
<211> 86
<212> DNA
<213> Homo sapiens

<400> 748
gggaagctgc gcctccgcaa acgctcagaa gcagcttcgc cagacagccg caacgtacat      60

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gttgactgcc cgaggcggaa gtcgat 86

<210> 749
 <211> 215
 <212> DNA
 <213> Homo sapiens

<400> 749
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 gcccaaataa atgaattaat ttcattattg gaagaaatag ttttgttata aaaatgaatt 120
 tggcttattt tgcacatgtg catgtgttct cctacccttc caacatgaga tgacacagca 180
 agaaggccct caccagatgt gagcgccttg acttt 215

<210> 750
 <211> 296
 <212> DNA
 <213> Homo sapiens

<400> 750
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 caggagccca gtacagagga tgaagccact gatggggctg gctgcacatc cgtaactggg 120
 agccctggct ccaagcccat tccatcccaa ctgagactct gagtctcacc ctaagaagta 180
 ctctcatagt ttcttccta agtttcttac cgcatgcttt cagactgggc tcttctttgt 240
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<210> 751
 <211> 36
 <212> DNA
 <213> Homo sapiens

<400> 751
 tgaaacatat tgtacgcacc aggaactact tgctgg 36

<210> 752
 <211> 30
 <212> DNA
 <213> Homo sapiens

<400> 752
 gacaagctgt taagattccg gaagcaaaga 30

<210> 753
 <211> 92
 <212> DNA
 <213> Homo sapiens

<400> 753
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 ccaacacttg aaaccgacac gcacacgcgc gg 92

<210> 754
 <211> 108
 <212> DNA
 <213> Homo sapiens

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<400> 754
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gcatcccca aacagtcacc cccaacaacc gagagtcctg gaacgtga 108

<210> 755
<211> 82
<212> DNA
<213> Homo sapiens

<400> 755
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acccgagatt aacagctgga ac 82

<210> 756
<211> 42
<212> DNA
<213> Homo sapiens

<400> 756
gggtggtcct ctaaagaatt gcaacttctg gcccttgaaa aa 42

<210> 757
<211> 219
<212> DNA
<213> Homo sapiens

<400> 757
ccagaggtgt atgtgaccag gccagctag aggaggcagc ttcaggctag caccccaaca 60
ggaaagaaca gtccttaggc ccggtggctt cagcaattaa atcagggttg catctcatca 120
tgagtggatc ccacagccag gcagattgat agctgtgatc gtcctgacgt gttatgtgtc 180
cctctctgga tgcaggggcc atagtactga cctcactga 219

<210> 758
<211> 111
<212> DNA
<213> Homo sapiens

<400> 758
tcaaagaaga cgacattccc agatagaaaa ggaagcaaac gttttttgag aatggagaca 60
aaaactatatt tgcacatcat aattttttcca ttagcaagca caatgccaga a 111

<210> 759
<211> 48
<212> DNA
<213> Homo sapiens

<400> 759
cagtcgggct gggagaaaca tatggtgccca caaatatccc ttttccaa 48

<210> 760
<211> 38
<212> DNA
<213> Homo sapiens

<400> 760

ggaagttagc ttttgggtcca ccagcgagtt tgaatgga 38

<210> 761
 <211> 231
 <212> DNA
 <213> Homo sapiens

<400> 761
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 tgggcatgtt ttatttggtt tcacaggagt taaaaaccta atttaaaaag tcaacatttt 120
 aaaaagagag ttttcacatg aaaattcagt tggaagatca gctgtgttca gttggctttc 180
 ctacaagggtg tctcattagc tggagtggag gaggcacctga ctctatgtat g 231

<210> 762
 <211> 557
 <212> DNA
 <213> Homo sapiens

<400> 762
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 gctgggctgg gctgggctga gccctggtc ttctctacag ttcacagagg tctttcagct 120
 catttaatcc caggaaagag gcatcaaagc tagaatgtga atataacttt tgtggaccaa 180
 tactaagaat aacaagaagc ccagtgggtga ggaaagtgcg ttctcccagc actgcctcct 240
 gttttctccc tctcatgtcc ctccagggaa aatgacttta ttgcttaatt tctgcctttc 300
 cccctcaca catgcacttt tgggcctttt tttatagctg gaaaaaacia aataccaccc 360
 taaaaacctg tatttaaaaa gaaacagaaa tgaccacgtg aaatttgcct ctgtccaaac 420
 atttcatccg tgtgtatgtg tatgtgtgtg agtgtgtgaa gccgccagtt catcttttta 480
 tatgggggtg ttgtctcatt ttggtctgtt ttggtcccct ccctcgtggg cttgtgctcg 540
 ggatcaaacc tttctgg 557

<210> 763
 <211> 207
 <212> DNA
 <213> Homo sapiens

<400> 763
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 tgttgccctc cctgtgaaat ccagaccag acgtcctctg gcgggaggag ctaccattac 120
 ttggtccgtt tgtcagacga ctgcagtctt tacttgtggc ctctgactgt tctacagggt 180
 cagaagctgt agtcctgctg gtacttg 207

<210> 764
 <211> 114
 <212> DNA
 <213> Homo sapiens

<400> 764
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ggggacagtt tcttcgtcca cctttggtct tgggtccatg cttccatgtc cttc 114

<210> 765
 <211> 83
 <212> DNA
 <213> Homo sapiens

<400> 765
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 ccacatctca cccagctttt ttg 83

<210> 766
 <211> 271
 <212> DNA
 <213> Homo sapiens

<400> 766
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 ttctttgaaa tgtccttggtg ccaagtacga gatctattgt tggaagtctt tggatatatgc 120
 aaatgaaagg agaggtgcaa caacttagtt taattataaa agttccaaag tttgtttttt 180
 aaaaacatta ttcgaggttt ctctttaatg cattttgcgt gtttgctgac ttgagcattt 240
 ttgattagtt cgtgcatgga gatttgtttg a 271

<210> 767
 <211> 140
 <212> DNA
 <213> Homo sapiens

<400> 767
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 tgggtgtgag tcctgtacat tccaggatgt ttagcagcat ttccagcttc tactagatgt 120
 cagtagcaaa ccaccttcc 140

<210> 768
 <211> 312
 <212> DNA
 <213> Homo sapiens

<400> 768
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 gtaggagcac ccccttcaga acctaggaac cctcagagct caccatgctc ccatgagcag 120
 gcagtaggag cacccttcc agaacctaca gccatgcccg ggaaccctca gagctcaccg 180
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 cctcagagct caccgtgctc ccagctcctc cagagggga gagtcctctg tctgcatcca 300
 gctgaaccct ga 312

<210> 769
 <211> 78
 <212> DNA
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<400> 769
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 cactccctgc catggcgc 78

<210> 770
 <211> 109
 <212> DNA
 <213> Homo sapiens

<400> 770
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 aacataaaac cccagccat atcaaacacc acttttcatc tgatcagtc 109

<210> 771
 <211> 72
 <212> DNA
 <213> Homo sapiens

<400> 771
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 ccgggtgaat tc 72

<210> 772
 <211> 43
 <212> DNA
 <213> Homo sapiens

<400> 772
 atatgtggac attggagtct tagcgtctga tttacaaaga gtg 43

<210> 773
 <211> 87
 <212> DNA
 <213> Homo sapiens

<400> 773
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 tgggagcacg ctgagaacat ttggcag 87

<210> 774
 <211> 99
 <212> DNA
 <213> Homo sapiens

<400> 774
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 gtggtgccct ggagcactga gatcttgtgc cagctctaa 99

<210> 775
 <211> 102
 <212> DNA
 <213> Homo sapiens

<400> 775
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 ggcaggtaat gagaccagct gaatccgggt cttggtgttt ta 102

<210> 776
 <211> 48
 <212> DNA
 <213> Homo sapiens

 <400> 776
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 <210> 777
 <211> 135
 <212> DNA
 <213> Homo sapiens

 <400> 777
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 tcattcattc attctttaag taatttttaa aaagaagatt attagattgt ctccctcact 120
 cactactaag aatgg 135

 <210> 778
 <211> 31
 <212> DNA
 <213> Homo sapiens

 <400> 778
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 <210> 779
 <211> 96
 <212> DNA
 <213> Homo sapiens

 <400> 779
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 ggtggacaga aacacattct ccacggaaga agtgcc 96

 <210> 780
 <211> 72
 <212> DNA
 <213> Homo sapiens

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 ggtggtggtc ga 72

 <210> 781
 <211> 207
 <212> DNA
 <213> Homo sapiens

 <400> 781
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 tatatgctgg gtccaaaca gagcctgata tatagcaagc attcagtga tcttaaccag 120
 catcattgtg attccacaca ggagcccatc tgcttgagga atttagctgt aaaaataaaa 180
 gtttgaacac tactggatgg gatgatc 207

<210> 782
 <211> 133
 <212> DNA
 <213> Homo sapiens

<400> 782
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 tctgtctctc ctctgttctg aaatttagca tctgggcttg ttgatattcc ttgttagagg 120
 tcaagagcag gtt 133

<210> 783
 <211> 521
 <212> DNA
 <213> Homo sapiens

<400> 783
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 tttttcaatt aagttaggaa aagagtaaatt catgatcaat gaaaactaaa tttgaactat 120
 taagaagcct atggggagca gtttatgttt ctgatatgat ttatgctcta aaatttcact 180
 agtttccttt acactcttaa cttttcatag ttaggcctaa actaaaccaa atattcatgt 240
 gctttattat tcttccttgc ttctcagtat cactttcctt atcacctaaa aggcattatt 300
 aaaaatcaaa aaacaaaaaa tctgcacatc tattatagtc tgaatgtatg tttttagaga 360
 atagaaataa gaaaaaaggg aggtatttaa aatgttgaag taagttgtgg cagacctgga 420
 agacaatgca tggctaaagt acagaattac tttctctgaa aaatctttta aacaaggaaa 480
 ccagttcatg tctgttcagg gaccttgcca atttcttcat c 521

<210> 784
 <211> 264
 <212> DNA
 <213> Homo sapiens

<400> 784
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 gtccctgctc cggtcttacc cctctcccc actctctcca accaaccac ttctgactct 120
 gagtcctctc tgctctctcc cctcaccgc tctcggggcc aatgtgctca gcaaccagct 180
 cccttgcttc ctctccggga agtagcggga gttgagggga tcgtccatgt ccacgtccct 240
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<212> DNA
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<210> 798
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<210> 801
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 <212> DNA
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<400> 801
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<400> 802
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 <211> 81
 <212> DNA
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 aagaagtgtc cggacacgct agcaggattt cagcatacag agctaacaag atgcgggg 118

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 cattcaagaa ataatcacct ctcatctggg atagcttaag agaaacagga gaccacaaca 540

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aggctgaact catt 674

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aaagggcagg tattggcaag gcttcgggac taattta 277

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attttcag 68

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<210> 818
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 <212> DNA
 <213> Homo sapiens

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<210> 819
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 <212> DNA
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 <212> DNA
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<400> 822

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 <213> Homo sapiens

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tcaggagtaa ggagactgca tt	142

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 <212> DNA
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ggagtcacac tactcaatct atacatcagt gttaaataatg atttttacta attttttttt	120

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ttttttacca acactatctt aaaaaatctg acagcataga gcagtgatta aaggcatttg	180
cttcaggggtc aaatatagtt acactgctgt tttttggaca atttgttatt ttgaaccatt	240
gtttcttacc ttataaaat gagcataaga taatgttctt ttaagggtgag tatgagatac	300
aaatgagaaa agcaataata ataaagattc aacaatggaa actgctatctt acattatgat	360
tgttataatt agaaggacaa actgtaattt aacgttccta tagtaataaa atggcatcta	420
cagagcaaat ctaaacagac ttaatcttca tataacaatt catcccagat aatttgaatt	480
gaccataata acatgtttga aaggaggctg aaataaaaca gggtttgctc ttttcaactc	540
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gaaaacattt aggcaactca ctgaatcaaa aataaatata gacaaattta attaatatat	960
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<210> 838
 <211> 60
 <212> DNA
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<210> 839
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 <212> DNA
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<400> 839	
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tagttactgc actgaaatgc agacgagaag acaaaga	97

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 <212> DNA
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<400> 840

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<210> 841
 <211> 85
 <212> DNA
 <213> Homo sapiens

<400> 841
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 gttacaagga atacactaga ggcca 85

<210> 842
 <211> 230
 <212> DNA
 <213> Homo sapiens

<400> 842
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 acaactggct ggggctggct atgtgtttgg tcaactgtaat ctctgatatg gccctgctgg 180
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 <212> DNA
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<400> 843
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<210> 844
 <211> 63
 <212> DNA
 <213> Homo sapiens

<400> 844
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 agt 63

<210> 845
 <211> 29
 <212> DNA
 <213> Homo sapiens

<400> 845
 agagaaaaat aggctagctg gagagttgc 29

<210> 846
 <211> 175
 <212> DNA
 <213> Homo sapiens

GBX1170_3WO_ST25.txt

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 cacagcgccc gccgcctgag ttagcctgaa ttagcagtc cgcagtaaca gcagc 175

<210> 847
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 <212> DNA
 <213> Homo sapiens

<400> 847
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 gggtcagtgg tgtgactgaa gctgggagtt agctcgtgtc tgtgggtgcc tcggtgtgtg 180
 tctctggggc tctgagtcct tgtgcgtgcg tgtgtgtctg tgaacccgac aggaagctcc 240
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 ata 303

<210> 848
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<210> 849
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 <212> DNA
 <213> Homo sapiens

<400> 849
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 aaccctttct ctactaaaaa tacaaaaatt agctgagcgt agtggcaggt gcctgtaatc 180
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 gagccgagat cgcgctactg cactccaggc tgggtgacag agtgagactc tgtctcaaaa 300
 aaaaaaaaaac accaatatct gtcatcatgt aggcacagcc aaggtgaact gaagcaggat 360
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<210> 850
 <211> 28
 <212> DNA
 <213> Homo sapiens

<400> 850
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<210> 851
 <211> 75
 <212> DNA
 <213> Homo sapiens

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 gggtagccac cacc 75

 <210> 852
 <211> 140
 <212> DNA
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 <400> 852
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 gaccctgct aatatatgca 140

 <210> 853
 <211> 118
 <212> DNA
 <213> Homo sapiens

 <400> 853
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 <211> 130
 <212> DNA
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 atttgctctg 130

 <210> 855
 <211> 77
 <212> DNA
 <213> Homo sapiens

 <400> 855
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 gtcaagaagc aaaagga 77

 <210> 856
 <211> 200
 <212> DNA
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<212> DNA	
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<212> DNA	
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<210> 859	
<211> 84	
<212> DNA	
<213> Homo sapiens	
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atcattccgg agagtctaag tggc	84
<210> 860	
<211> 48	
<212> DNA	
<213> Homo sapiens	
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<211> 106	
<212> DNA	
<213> Homo sapiens	
<400> 861	
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tcaagggtc acacctctca ggaatgaaga gttggttcac accacc	106
<210> 862	
<211> 160	
<212> DNA	
<213> Homo sapiens	
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gcgcccggga cccccagggc ggcgacgctg ccgccggtgc cgccgagcct ttgttccgcc	120
gccggggccg gtttcacgcc tgtcgccctc gcaagcagcc	160

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<210> 863
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<212> DNA
<213> Homo sapiens

<400> 863
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<210> 864
<211> 1103
<212> DNA
<213> Homo sapiens

<400> 864
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gcatcttctc agtgctacta gta 1103

<210> 865
<211> 44
<212> DNA
<213> Homo sapiens

<400> 865
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<210> 866
<211> 57
<212> DNA
<213> Homo sapiens

<400> 866
ccagaaactt cttacccgta ttgagctgcc agaagctgca agtgctgttg caagatg 57

<210> 867
<211> 181
<212> DNA
<213> Homo sapiens

<400> 867
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tttcattaat ctttttctgc atctcactca tctcttcttg tacattaaga agttgttgct 180
g 181

<210> 868
<211> 121
<212> DNA
<213> Homo sapiens

<400> 868
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aatccccca aaccaaaggg aaagcctcct gtcccaaac cagccagtcc caagaagaac 120
a 121

<210> 869
<211> 69
<212> DNA
<213> Homo sapiens

<400> 869
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gacccatgg 69

<210> 870
<211> 108
<212> DNA
<213> Homo sapiens

<400> 870
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ccaggatgac caggccaagc aggtgctgaa gggcatgtca gatgttgc 108

<210> 871
<211> 32
<212> DNA
<213> Homo sapiens

<400> 871
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<210> 872
<211> 176
<212> DNA
<213> Homo sapiens

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<400> 872
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atccaaggta agaaccacct ttttagttag gtctgatggg tagaaagctt gagttgaagc 120
gtgcccttct ggaattgcca ctttggggccc aattttgtct acacgggaac tgctta 176

<210> 873
<211> 337
<212> DNA
<213> Homo sapiens

<400> 873
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tggaaagctg tctgtttctt agaaagttaa gcatacacta ctctatgggc tagcaaggcc 180
agtctcaat atttaacaa aaaattaaaa caaaaacat gaatacgga ggactggaag 240
gcatgattat gtgttattta tcatcgcccc aaactgcaa caattcaa atctatgaac 300
aggagaatgg aggaacgccg tggagagtat ttttaca 337

<210> 874
<211> 42
<212> DNA
<213> Homo sapiens

<400> 874
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<210> 875
<211> 65
<212> DNA
<213> Homo sapiens

<400> 875
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ctaca 65

<210> 876
<211> 54
<212> DNA
<213> Homo sapiens

<400> 876
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<210> 877
<211> 47
<212> DNA
<213> Homo sapiens

<400> 877
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<210> 878
<211> 397

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<212> DNA
 <213> Homo sapiens

<400> 878
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 gaggctcgag agcaggccat ttccaagaa gatgaagaat ggtgactgtg tttttattga 180
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 cgcggaagca tggagggaaa ggaggttgta aaatagactc catggagact cttaggaagc 300
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 aatggaaagc agtcacagct gagttttcgg agaccaa 397

<210> 879
 <211> 94
 <212> DNA
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<400> 879
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 gcgatcctga gggaccctg atgcttctag ccca 94

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 <211> 309
 <212> DNA
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 tatcataaca gaactagggc tgggcacagt ggctcacacc tgcaatctca gcactttggg 240
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<210> 881
 <211> 191
 <212> DNA
 <213> Homo sapiens

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 ggtagtactt g 191

<210> 882
 <211> 41
 <212> DNA
 <213> Homo sapiens

<400> 882
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<210> 883
<211> 112
<212> DNA
<213> Homo sapiens

<400> 883
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<210> 884
<211> 178
<212> DNA
<213> Homo sapiens

<400> 884
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aaagatgtca ataagtctgc ttcagatgac caatctgac agaaaactac accaaagaaa 120
aaaggggttg ctgtggatta cctgccagag agacagaagt acgaaatgct gtgccgtg 178

<210> 885
<211> 40
<212> DNA
<213> Homo sapiens

<400> 885
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<210> 886
<211> 208
<212> DNA
<213> Homo sapiens

<400> 886
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cagaagttgc ccagcaacta ttttcattcc ccagaggcag agagtataat ggaaaggagg 120
aatttggggt gagatgtctt tcttgtgttt aaattttcta ctctgaactt ggacaagtca 180
cttatcttcc taaatcccaa ttcctcat 208

<210> 887
<211> 33
<212> DNA
<213> Homo sapiens

<400> 887
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<210> 888
<211> 124
<212> DNA
<213> Homo sapiens

<400> 888

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tgta	124
<210> 889	
<211> 49	
<212> DNA	
<213> Homo sapiens	
<400> 889	
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<210> 890	
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<212> DNA	
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<210> 891	
<211> 42	
<212> DNA	
<213> Homo sapiens	
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<212> DNA	
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<211> 33	
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GBX1170_3WO_ST25.txt

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 <210> 896
 <211> 32
 <212> DNA
 <213> Homo sapiens

 <400> 896
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 <210> 897
 <211> 101
 <212> DNA
 <213> Homo sapiens

 <400> 897
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 gggccctcct cgaggagcag gagcaagcta gtgggctgcc a 101

 <210> 898
 <211> 186
 <212> DNA
 <213> Homo sapiens

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 agctta 186

 <210> 899
 <211> 80
 <212> DNA
 <213> Homo sapiens

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 <210> 900
 <211> 401
 <212> DNA
 <213> Homo sapiens

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 aatttcctaa attactaaat acacataact cttattgttc atgctttaat ccatgggtctt 180

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tgccatatta ttggcctgtt aaatgctaataaacctttgt ttctcagcat gtagtttaca	240
tgatggggac ttgattaaga aagtactttc aagcatctta ttcatagga aactttatta	300
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<210> 901
 <211> 640
 <212> DNA
 <213> Homo sapiens

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 <212> DNA
 <213> Homo sapiens

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ggcttgatta cccactcagt gccagctgg tcatcatcat gttggccaac caccagaggg	180
ga	182

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 tctaccaag 129

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 <211> 76
 <212> DNA
 <213> Homo sapiens

<400> 905
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 tttggctttc ccgtgt 76

<210> 906
 <211> 53
 <212> DNA
 <213> Homo sapiens

<400> 906
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<210> 907
 <211> 36
 <212> DNA
 <213> Homo sapiens

<400> 907
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<210> 908
 <211> 28
 <212> DNA
 <213> Homo sapiens

<400> 908
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<210> 909
 <211> 95
 <212> DNA
 <213> Homo sapiens

<400> 909
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 cggttcccca aggtcgctgc cgacctaga ccgcg 95

<210> 910
 <211> 407
 <212> DNA
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<400> 910
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cagccaggag ctatttccta agttgtcttt ctggtggaaa gctcagctcc tactaagcag	300
tccttgcttc aaaatggctt tgatgaatga cccaaaggag ccaggccagt ccctgagtca	360
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<210> 911
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<210> 912
 <211> 137
 <212> DNA
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<400> 912	
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tccgtggaca ttgatgg	137

<210> 913
 <211> 75
 <212> DNA
 <213> Homo sapiens

<400> 913	
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cgctttccgg agacg	75

<210> 914
 <211> 270
 <212> DNA
 <213> Homo sapiens

<400> 914	
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GBX1170_3WO_ST25.txt

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 tcgtgtgtct ggatgaaggg gccacggcaa gatcctcctg gctcaggggt tcacacctgg 180
 gcacacatgc aggattctgc aggccagtgt gcaccgagcc tccaacttgt 230

<210> 916
 <211> 134
 <212> DNA
 <213> Homo sapiens

<400> 916
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 aggccaagc acgggctatt gcggaaaatg agcgggtcat gagccaggct ggagtacagg 120
 acctcgagag cctt 134

<210> 917
 <211> 269
 <212> DNA
 <213> Homo sapiens

<400> 917
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 gccctgcagc ctgccctgcc atcctagagg tgggagctgc agtgcacctg gcagccaggc 180
 cctggccagt cgaggggtggg gctgtgaggc agcagggaga ccttcgtgct cccagtgagc 240
 ggagccgact ccactgctag cggactaga 269

<210> 918
 <211> 375
 <212> DNA
 <213> Homo sapiens

<400> 918
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 catagaactg gcagagggca tggcatggag gcagcgccat cagaggaaga tctgaggaac 180
 cagcagagga agataaggag ggatggtggt ttgaaagacc acagctaaag gcaaagtaaa 240
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<210> 919
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 <212> DNA
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gattctcc 68

<210> 920
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 <212> DNA
 <213> Homo sapiens

<400> 920
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 ttgggatggg gactttttca agtcattaag agtgtttggt taaggatgac tcattgatgg 180
 tagttctcag ccgtctcaaa aactgcaagc taatcagtca gacattc 227

<210> 921
 <211> 42
 <212> DNA
 <213> Homo sapiens

<400> 921
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<210> 922
 <211> 94
 <212> DNA
 <213> Homo sapiens

<400> 922
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 cgcgggcaga gaggatgttg tagggccggc atgc 94

<210> 923
 <211> 119
 <212> DNA
 <213> Homo sapiens

<400> 923
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 gcactcccaa ggagtttggg tttgtttggg tttgttctag gtatggtccc agggatccc 119

<210> 924
 <211> 79
 <212> DNA
 <213> Homo sapiens

<400> 924
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 ctttcacaaa ggccttcac 79

<210> 925
 <211> 362
 <212> DNA
 <213> Homo sapiens

<400> 925
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ttttatatgt aaacgtcatt ctttttaaac aaacaagaaa aagcaatgta atggcatgcc	120
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atgttcatct ctgagttcca ttgatattta tcctctgaag gcacttgggt ttggggttgc	240
tggcaggagg tgaagaacca tcagagttaa ggtcaaggga caggaggtgc tgctagagag	300
agaagccaca aggaccacaa tgaactgagg tgtctaggga ccatggcatg cacagggcat	360
tg	362

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 <212> DNA
 <213> Homo sapiens

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 <211> 380
 <212> DNA
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ttcccaactc ctgccaacca gaacttaact actcctttgg attctgcttt tcacttgttc	240
ttcatcagac tatggaagct tagacttcat aatttggtctg agacttcaaa aatagtttta	300
aagaaagcta ttccaccct gctaaagtaa ttacatgatt ctgccccctt aaacacccaa	360
agccctaatac tgtgtttctca	380

<210> 928
 <211> 77
 <212> DNA
 <213> Homo sapiens

<400> 928	
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gcgtcatcgc cagcacg	77

<210> 929
 <211> 102
 <212> DNA
 <213> Homo sapiens

<400> 929	
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gtgacctcca cctaccatgg ctctgtagac gccagctcct ca	102

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<210> 930
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 <213> Homo sapiens

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 aaaatgttca ggaagagagg gaagggcacg cacagggcaa gataaagttg ggaagtaggc 180
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 atgttgagg gtaaaggag ctaggtcttc tactctgggc tctgcatgca ggtaactgtg 780
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 <213> Homo sapiens

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<210> 932
 <211> 408
 <212> DNA
 <213> Homo sapiens

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 agtgatatta ggttaaaaaa atattttacag ttttcattct ggtccacctt ccttccttat 180
 ccttatactg aatccatttc tctacttttc aggtaagtga aaggggtcac aaaattttta 240
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 ccttctctga aaaaagagaa ggaattactt attaaaacta agcacactta gcaacttctt 360
 tcccaatcct atctttattc gtttgcctgg tgccaaattt ttctggcc 408

<210> 933
 <211> 81
 <212> DNA
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 ggggtatgct ggatttccaa a 81

<210> 934
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 <212> DNA
 <213> Homo sapiens

<400> 934
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 ggtctgcgcc ctaggatgca ctgag 85

<210> 935
 <211> 36
 <212> DNA
 <213> Homo sapiens

<400> 935
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<210> 936
 <211> 234
 <212> DNA
 <213> Homo sapiens

<400> 936
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 actttgatgg tgatgagatt ttccatgtgg atatggcaaa gaaggagacg gtctggcggc 120
 ttgaagaatt tggacgattt gccagctttg aggctcaagg tgcattggcc aacatagctg 180
 tggacaaagc caacctggaa atcatgacaa agcgtccaa ctatactccg atca 234

<210> 937
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GBX1170_3WO_ST25.txt

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<210> 938
<211> 181
<212> DNA
<213> Homo sapiens

<400> 938
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accagttgac agggcccccc agtccccacc gccaccacc tggccggcta cttgtcagac 180
a 181

<210> 939
<211> 35
<212> DNA
<213> Homo sapiens

<400> 939
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<210> 940
<211> 44
<212> DNA
<213> Homo sapiens

<400> 940
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<210> 941
<211> 96
<212> DNA
<213> Homo sapiens

<400> 941
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acccagtcgt gtgccctttt ccacaaattc tcccag 96

<210> 942
<211> 78
<212> DNA
<213> Homo sapiens

<400> 942
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ctcggtttta catcacat 78

<210> 943
<211> 131
<212> DNA
<213> Homo sapiens

<400> 943
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GBX1170_3WO_ST25.txt

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ccagcgggtc a 131

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<211> 238
<212> DNA
<213> Homo sapiens

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atcaacttca acagcaagcc catctctgga agctcccaga ccattgtgcc aatcaagtgg 120
aggaggcact ttcatttaga gaggcttatg tgaaccttat atgagaaact tgccaacctg 180
cctctttgat ttttagcct tactatttct aatacttagg tgctatcttt tagagacc 238

<210> 945
<211> 96
<212> DNA
<213> Homo sapiens

<400> 945
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gttgtggggg gcattctgca gccagtcttc aggcaa 96

<210> 946
<211> 43
<212> DNA
<213> Homo sapiens

<400> 946
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<210> 947
<211> 79
<212> DNA
<213> Homo sapiens

<400> 947
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gtaactcttt aagaacagc 79

<210> 948
<211> 37
<212> DNA
<213> Homo sapiens

<400> 948
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<210> 949
<211> 155
<212> DNA
<213> Homo sapiens

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GBX1170_3WO_ST25.txt

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ctggtgttta tgcccttact gtgccctatt tatag 155

<210> 950
<211> 99
<212> DNA
<213> Homo sapiens

<400> 950
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gttcacagga cggtgccagg caggttctca tggactcac 99

<210> 951
<211> 279
<212> DNA
<213> Homo sapiens

<400> 951
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tttgggttgc cgtgctccca aaacatttta aatgaaagta ttggcattca aaaagacagc 120
agacaaaatg aaagaaaatg agagcagaaa gtaagcattt ccagcctatc taatttcttt 180
agttttctat ttgcctccag tgcagtccat ttcctaattg ataccagcct actgtactat 240
ttaaaatgct caatttcagc accgatggcc atgtaaata 279

<210> 952
<211> 130
<212> DNA
<213> Homo sapiens

<400> 952
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ccctcatatc tcgaggagat ttgtcagtca ctgcctcaac tcggccgcgg tcaccagtag 120
gggaaaatgc 130

<210> 953
<211> 1545
<212> DNA
<213> Homo sapiens

<400> 953
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aaaacgtcta cctattccat ttaatttcct gctgataaat gtattttatc tacaagcaag 180
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gactatttct ctttacttcc tgcagaattt catttcaagg gaccacagca cacccttgaa 360
aattaccatt tatttaatgc cagttgaacc aatgggtagc aaaagaggag ggaggggaaca 420
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ctcactaaca ggtcctttcc tggaagaaat aacctcatct cctgccatat tagttttacaa	660
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 ctttccctct ctgtgcttca gttccctcat ctgtagagtg ggaatgataa caggatctaa 180
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 tgtgcagcag cagtctctaa ccatta 266

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 <212> DNA
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 tccctggatg aactgagcac ttata 86

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 <212> DNA
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<210> 961
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 <212> DNA
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 <212> DNA
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 aaaatcaaat tcaacattcc acctaggagg cttccatctc tgcttaggag ctgagtaatg 180
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 tgtaaaaacc cagcttcagg aggtgatgaa ataggtgcag tggctctggc gtaagctctg 240
 aagccccagg ctgaggctct attgaaaaat tacttttgct gaaatattcc tgtttttagg 300
 aacttccatg gaacttgagc cttcacgcag catattttgg catctgattc aaagctaata 360
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<210> 965
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 <212> DNA
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 gcc 183

<210> 967
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<210> 968
 <211> 130
 <212> DNA
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 cgtggccacc tctgataagc tagccacagc tgagctcacc attgccaaag accag 115

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 gatggttaca ccatga 76

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 aaaatttcta cataactgca tggggtcagt tacagatata tccaga 226

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<210> 974
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<400> 974
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 gaaaacaaac acatggagcc ttgccagctg gatcaggcac cactgtttac agcaggagca 180
 aagtgtgggg aattggagag gcatgaagaa gggaaggagc agaggggggtg gggataattc 240
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<210> 976
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 <213> Homo sapiens

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<210> 977

<211> 33
 <212> DNA
 <213> Homo sapiens

 <400> 977
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 <210> 978
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 <212> DNA
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 gcggcagtga cccgccctgg gagctgccc 89

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 <210> 982
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 <212> DNA
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<210> 983
 <211> 33
 <212> DNA
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<400> 983
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<210> 984
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 <212> DNA
 <213> Homo sapiens

<400> 984
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 cccaggatat gtatggg 137

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<400> 985
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<210> 986
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 <212> DNA
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<210> 987
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 <212> DNA
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agaaaaaagt gtgttggcct tttttttttt tagaaagtta gaattgtttt taccaagagt 240
ctatgtgggg cttgattcac ccttcatcca tt 272

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<212> DNA
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<212> DNA
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<210> 993
<211> 296
<212> DNA
<213> Homo sapiens

<400> 993
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ctccaacctc ctcataatcc ttctcaaggg cagccatgtc ctcacgggcc tctgaaaact 180
cgccttcctc catcccctca cccacgtacc agtgaacaaa ggcacgcttg gcatacatca 240

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gggtcaaactt gtggtccagg cgagcccagg cctcggcaac agctgtggta ttgctc 296

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 <213> Homo sapiens

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 tctgtagaga tttgtttta 79

<210> 995
 <211> 232
 <212> DNA
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<210> 996
 <211> 103
 <212> DNA
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 ccggctgcag caacatcaac atgagctctg caacctcaa gca 103

<210> 997
 <211> 73
 <212> DNA
 <213> Homo sapiens

<400> 997
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 gccatccctc ggc 73

<210> 998
 <211> 257
 <212> DNA
 <213> Homo sapiens

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 tcattacgat tcagcagaag cgatgtgcca ggctcagcaa tacaactgca aaaccggggc 180
 ctg 183

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 <211> 119
 <212> DNA
 <213> Homo sapiens

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<210> 1003
 <211> 400
 <212> DNA
 <213> Homo sapiens

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 tggtgtcccc tgtcctctgt aagaacgcaa ggctgcaga tgttcccaa atggaggtcc 180

GBX1170_3WO_ST25.txt

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<210> 1004
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 <212> DNA
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ctcccctggg cctggtgacc aagccagcct tgtccac	97

<210> 1005
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 <212> DNA
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gctgttagac taaatgtcgt aggttgtaa ccacatagaa acacactagt atgaagaaaa	120
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<210> 1007
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 <212> DNA
 <213> Homo sapiens

<400> 1007	
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<210> 1008
 <211> 463
 <212> DNA
 <213> Homo sapiens

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agaactctta gtttgaaaag atcgagtact agcatataga atccccaaa ccactttaaa	300
ttaatgagtc atacaatata tctgacatgt taccaaattc tcccagacc caaggctcaa	360
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gccacgtgc tcgtggccat ctggtgggcg tcatgtgcct tgtgtcccag cacctgcagg	240
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<210> 1010
 <211> 83
 <212> DNA
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catttgcccg cggtcttcat tca	83

<210> 1011
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 <212> DNA
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<210> 1029
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 <212> DNA
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<211> 190
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 <212> DNA
 <213> Homo sapiens

<400> 1036
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 <211> 70
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<211> 161

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<213> Homo sapiens

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<213> Homo sapiens

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<211> 63

<212> DNA

<213> Homo sapiens

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 <212> DNA
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 <213> Homo sapiens

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<213> Homo sapiens

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<211> 133

<212> DNA

<213> Homo sapiens

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120

agttccagag cca

133

<210> 1057

<211> 157

<212> DNA

<213> Homo sapiens

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120

gcgctgcact cctgaccgct tccctgaagg ctgcacg

157

<210> 1058

<211> 280

<212> DNA

<213> Homo sapiens

<400> 1058

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atctcgggga gggaaagcct atgtagttac aaatggaaac ttctctttct tccattcatt

120

ttggtgggtg ggacaaagga aaagaaggtg aatatatatg tgattgcaa gcaggaagtc

180

tgcattttgtg tgtgaactcc ccaagtgatt cccacgtgca cctcactgtc ctttccttac

240

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280

<210> 1059

<211> 748

<212> DNA

<213> Homo sapiens

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120

tctctgacct tgagggtccc tggctctggg gagggagctc gcagggtccc tctctgacac

180

tgagggtccc tggctctggg gagggagcac tgtgttttca gtgccacat gttgccaac

240

cgcgctccag aaagctgccc agtttctgtc cctgccgaac gcaggagaat gcagggaagg

300

atgttgact ttttctccag agctgcttcc cttgaggggg gccctgcct acaggtcaga

360

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420

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 cgccaggaga gctgcctccc tgagcctcat ttccccctgt gctgagggct gggcatgctg 660
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 <212> DNA
 <213> Homo sapiens

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 aggaagtgtt gagtgggtggc ctgccctagg accgactcca tgggtgtgta acgagtgtag 180
 ttgcacaggg ccccatatgc agaagggggc tctgcacttg gaatttaatg ctatgtggct 240
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<210> 1062
 <211> 380
 <212> DNA
 <213> Homo sapiens

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 ctgctacttt ttgcatctat aaaatggtaa cactgctact tatacctcag gatgttgtga 180
 ggattaaaaa ttgagtaagc taagtgcctg gtgcagtcct ggcacagtca ctaagcattt 240
 actatcttta tgcagtttct ttttgaatg ctaactgccc tccaaattcc tccaaagtaa 300
 acacatggat tagtaaatga gaaagaaaca atgcttaaaa caactatggg taacatacct 360
 gtttcaagtc gcgtagaata 380

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 <212> DNA

<213> Homo sapiens

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<210> 1064

<211> 467

<212> DNA

<213> Homo sapiens

<400> 1064

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gaatgactag ttacacagtt caggtgctag gaggcagtat aaaagtcaga gagcaaatgc	180
tttaagaaac tgtagtatac accaggaaat gcaattcttt agttagatac cttctccttt	240
cagtaaaatt atgttcagt ctgtaaatag gcaactttca gtgatttggt tttcaaacia	300
gtggcttttt atcttttct cttgacagt agtgtctctc catgtgtgaa gtattttctc	360
ctctcatatc tgtgaagtcc tgcttgtaag tgtttcggtt atgcaacatt tcatggggaa	420
tttgagcact ggaattcttg gtcgctagtt aggtgggtct taccgca	467

<210> 1065

<211> 48

<212> DNA

<213> Homo sapiens

<400> 1065

ctatggcagg tataccaggc ccagagcaat gagcgagaga ggtgggtca	48

<210> 1066

<211> 183

<212> DNA

<213> Homo sapiens

<400> 1066

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tgcactagcc aagagacttt acttttaaga agtattaaaa ttctaaaatt ctattaatct	120
ctcattaata gtatttaata taaagattct taaaattact gacgttatga attggtttga	180
tgc	183

<210> 1067

<211> 207

<212> DNA

<213> Homo sapiens

<400> 1067

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ttttctcccc accaagcccc cacccttgct gtgtcaccat cactactcaa gaccggaggc	120

GBX1170_3WO_ST25.txt

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<212> DNA
<213> Homo sapiens

<400> 1068
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ctcaggc 127

<210> 1069
<211> 64
<212> DNA
<213> Homo sapiens

<400> 1069
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cctg 64

<210> 1070
<211> 238
<212> DNA
<213> Homo sapiens

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ggatttcaac ccctggagaa aacgatgtca ttgttcagca gctgagagcc caggcgctcg 120
cggcgacttg ccgtctctcc attccactgc ctgttgacaga gtttttctgt aactaagggg 180
gttgaggta ttgtagacgt tagattgcgg gcaccgccag ggattttgca gcgcttca 238

<210> 1071
<211> 251
<212> DNA
<213> Homo sapiens

<400> 1071
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gtgaaaaagc actttgaaaa ttgtaaaact ccctacaaat gtaagatatt gttaatgacc 180
ttacaaaaac caccttttta aaatgatttg gaatcataga ctctaaaagt tgattctagt 240
ggctagtcc a 251

<210> 1072
<211> 102
<212> DNA
<213> Homo sapiens

<400> 1072

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 tcaccctctg gctttgatgg tccttggtc cgtgatgctc ag 102

<210> 1073
 <211> 99
 <212> DNA
 <213> Homo sapiens

<400> 1073
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 ccatggagga gctaaaagca gagcgagaaa aacgaaaga 99

<210> 1074
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 <212> DNA
 <213> Homo sapiens

<400> 1074
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<210> 1075
 <211> 129
 <212> DNA
 <213> Homo sapiens

<400> 1075
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 gaacaagagc cctctgagac agtgatggga accatctgca tcacagaagc acaagctctg 120
 gtgatgatg 129

<210> 1076
 <211> 160
 <212> DNA
 <213> Homo sapiens

<400> 1076
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 aagggtcttt ctttcttgtc tgctctgtgt actacagggc 160

<210> 1077
 <211> 40
 <212> DNA
 <213> Homo sapiens

<400> 1077
 ttcttgatg atgtgacagt ggcggataat gcagaaaagg 40

<210> 1078
 <211> 98
 <212> DNA
 <213> Homo sapiens

<400> 1078
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 taaatagagt tgctaggcct gtctagtgtgta agcattca 98

<210> 1079
 <211> 101
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 aattgctcaa ggaaggggca gtcaagaact tggatgagt a 101

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 <212> DNA
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<400> 1080
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 tgggccaagg gtggaggcca agttacgggg acagagaggc gaagacaagg gcagcagtgc 120
 ccacaacagg aattcctacc cttcaacttt gttcatagtgtgtccctactt tta 173

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 <211> 33
 <212> DNA
 <213> Homo sapiens

<400> 1081
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<210> 1082
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 <212> DNA
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 gaaataattt gggcttaaaa gtgaacataa attatagagt ggaaggtaag ggacaaaagc 180
 cttttacctt taattttcct ggagaattat ataaaggttt tcttagaaca attttgccct 240
 gattactgaa gcgtcaaata aagctgg 267

<210> 1083
 <211> 325
 <212> DNA
 <213> Homo sapiens

<400> 1083
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 ttcacttcct ggagagacag attttgtaaa ctttacagag cagcttttaa tcattcggtg 120
 gttcccagat tcctaggcca gagtctctat actgaataat ttataataga ggtcatatcc 180

GBX1170_3WO_ST25.txt

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 cctgtgaatg ggaccttatt tggaaatgga gtctttgcag gtgtaattca gttaagatga 300
 ggtaggccccg aaaagcaatg actga 325

<210> 1084
 <211> 118
 <212> DNA
 <213> Homo sapiens

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 agactataac actaattatt tttctagagg atgcatttga catgccaaact ctcattca 118

<210> 1085
 <211> 36
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<210> 1086
 <211> 39
 <212> DNA
 <213> Homo sapiens

<400> 1086
 aacctgtgca ctacctgact caggaatcgg ctctggaag 39

<210> 1087
 <211> 43
 <212> DNA
 <213> Homo sapiens

<400> 1087
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<210> 1088
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 <212> DNA
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<210> 1089
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 <212> DNA
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<210> 1090
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<212> DNA
 <213> Homo sapiens

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 tctgttagaa tgaaatgggt cccataaata aggggcatga gccc 104

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 <212> DNA
 <213> Homo sapiens

 <400> 1091
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 <210> 1092
 <211> 138
 <212> DNA
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 ccgctttgga gcatggat 138

 <210> 1093
 <211> 199
 <212> DNA
 <213> Homo sapiens

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 cccgcttgct tggcgagaa 199

 <210> 1094
 <211> 35
 <212> DNA
 <213> Homo sapiens

 <400> 1094
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 <210> 1095
 <211> 35
 <212> DNA
 <213> Homo sapiens

 <400> 1095
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 <210> 1096
 <211> 120
 <212> DNA
 <213> Homo sapiens

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<210> 1097
 <211> 68
 <212> DNA
 <213> Homo sapiens

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 agtcattt 68

<210> 1098
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 <212> DNA
 <213> Homo sapiens

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 aagagcctcc gagaggttct gtgctagtct ggctgtgccg agtgcacggg gggaaccagg 180
 ctttcaggac tctctggcct cttttccct ctctgggagg agttgagaca agtcttgctt 240
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<210> 1099
 <211> 274
 <212> DNA
 <213> Homo sapiens

<400> 1099
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 atattgtgtg tgctgagcat cccaccgtgc aaggcagtgt ttaaagctgt gaacacacag 180
 atgcagggac tgtggtctcc cttttcatgg tgttctcacc cttcatggca tccttggtca 240
 aggtagggag gccagagaga gctataaaga tata 274

<210> 1100
 <211> 85
 <212> DNA
 <213> Homo sapiens

<400> 1100
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 gcaaacacgg ctaagctctt tccct 85

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 <211> 262
 <212> DNA
 <213> Homo sapiens

GBX1170_3WO_ST25.txt

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tttcaaattc aaatgggtata attggggcctt ggtagttgat gtttatctta attgaaacag 180
attctcttca tccttttgcct ctgagactcc cactttgagg ctgaaagggtc attttaaadc 240
tgcagagcac tcgagaagcc ac 262

<210> 1102
<211> 230
<212> DNA
<213> Homo sapiens

<400> 1102
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taggggatgg ggcagttagt ggggacagag ggcagatggg taagattcag agcacaggct 120
agtgtgacgg aagtttaaac ttgtgagtta aatagggttt ggcaatctag ctggatagca 180
tccctgcccc ttgaagagat gtttttgtgg cgccacacta ctgacttagg 230

<210> 1103
<211> 95
<212> DNA
<213> Homo sapiens

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tgcttcaaaa tgtgcctaca agtgcagtct ggggt 95

<210> 1104
<211> 41
<212> DNA
<213> Homo sapiens

<400> 1104
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<210> 1105
<211> 36
<212> DNA
<213> Homo sapiens

<400> 1105
ctggattctg cagtatgaac agggcaacct caccaa 36

<210> 1106
<211> 58
<212> DNA
<213> Homo sapiens

<400> 1106
aagccaatgc tgaggtgatg cgagagatga ccaagaagct gtacagccag tatgagga 58

<210> 1107
<211> 314
<212> DNA

<213> Homo sapiens

<400> 1107

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atgcaaaaaa tctacttctt tattttccca cattctgtat tatatatatg aaccaaaaat	180
gcacagagag gcctaagttc cccagcctgt ggcacattgt cagggggcca agcatggtcg	240
ggactgcagg gcctttcttg ggctaggatt gccacgtgg ttatgactga ggattcttat	300
gctctcacc acga	314

<210> 1108

<211> 105

<212> DNA

<213> Homo sapiens

<400> 1108

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<211> 161

<212> DNA

<213> Homo sapiens

<400> 1109

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tcacaatgac agttgtatca atggtgtttt tttccactaa gcttatgtgg ccatgacatg	120
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<211> 60

<212> DNA

<213> Homo sapiens

<400> 1110

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<211> 47

<212> DNA

<213> Homo sapiens

<400> 1111

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<210> 1112

<211> 174

<212> DNA

<213> Homo sapiens

<400> 1112

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gtcactgact catcagaagg ctactttggt ctcactccat caggtggccc aagg 174

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 ggagttcccc gaaacatctt ttaggctggg gggagggtgc tgaccaagag gccagaggag 240
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 gtctctctga 70

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 <212> DNA
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tgagagggag cgcgcgggca gccgagcgcc ggtgtgagcc agcgctgctg ccagtgtgag 180
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gcaaaccg agcgtctacg ctg 263

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<400> 1118
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<210> 1119
<211> 86
<212> DNA
<213> Homo sapiens

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gcagacagcg ggtcggaagt ttggtt 86

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agggcaaagg aagcagtact ggatcctttt cc 212

<210> 1121
<211> 409
<212> DNA
<213> Homo sapiens

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<210> 1122
<211> 198
<212> DNA
<213> Homo sapiens

<400> 1122
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 ggactcaaca tgttaagtga ctccagcatg ggcctgctgg acccctctgt tgaagagacg 180
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<210> 1123
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 <212> DNA
 <213> Homo sapiens

<400> 1123
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<210> 1124
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 <212> DNA
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<400> 1124
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 gtagcctgca 130

<210> 1125
 <211> 117
 <212> DNA
 <213> Homo sapiens

<400> 1125
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 aacccccctgg cgaacatctc atgcaataaa atggaggata aacccttcag cataatc 117

<210> 1126
 <211> 1492
 <212> DNA
 <213> Homo sapiens

<400> 1126
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 gtttgaattt ctgctttcag aaaggaaatc gatggggcgt gttgtcagaa gttaggggcc 180
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 cctaagtgca aaagttaaaa ataattttgt gtgtctaatt acattgcttt gtacgagtca 420
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<211> 41
<212> DNA
<213> Homo sapiens

<400> 1127
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<210> 1128
<211> 240
<212> DNA
<213> Homo sapiens

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ctcctgagcc catttccac tcaccttttc cttcatgggt ccctggtgat ggcaaccccg 180
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<210> 1129
<211> 71
<212> DNA
<213> Homo sapiens

<400> 1129
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gcgccccac t 71

<210> 1130
 <211> 259
 <212> DNA
 <213> Homo sapiens

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 aaccagctca tctaagcacc agacacaaga ttttactgct tttgtcaggt ggagtgggaa 120
 gtcgcaccca cgtctggcca gttgggtcgg ctgtaactca gactttggac tgacttgtca 180
 cccagctcat atagcaagga gttcctgatg gcagctgggg gagctgacat cagtgtcagc 240
 tcagactctt aggcagtta 259

<210> 1131
 <211> 640
 <212> DNA
 <213> Homo sapiens

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 cctctgcctg tcctctccca actcaagggt ctagtgggaa ggggtgcccc caggctctca 180
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 cccatgaaaa aatacagggt tctagactgc caggagagacc ctggcccca gtagtgtgtc 420
 ctggggactt cctcagagcg agaaacctcc cccaatgtct tcaagacttt tctctcccc 480
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<210> 1132
 <211> 225
 <212> DNA
 <213> Homo sapiens

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 ggacaggggc atgagctcac tttctacaag gaccagttag ctgtcctcgg ttcagggaca 180
 gcaccctgtg ccgtcattgc acttgacgc tgttcaatgt gcata 225

<210> 1133
 <211> 39
 <212> DNA
 <213> Homo sapiens

<400> 1133
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<210> 1134
<211> 84
<212> DNA
<213> Homo sapiens

<400> 1134
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aaacacggag gatgacgaca ccct 84

<210> 1135
<211> 159
<212> DNA
<213> Homo sapiens

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ttttagttc tgtacttttc gagagaaggg aatagggaag acagcaaaga aagattcaga 120
tttctaacc tgcaactttt gccaagcttt attgccctg 159

<210> 1136
<211> 95
<212> DNA
<213> Homo sapiens

<400> 1136
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accaatgaa acatcaccta gcttctcaaa agctg 95

<210> 1137
<211> 171
<212> DNA
<213> Homo sapiens

<400> 1137
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aattagtcca gttatttttg aaagcagtct ggagatttct caaagaactt aaaacagaat 120
taccatttga cccagcaatc ccattaccag gtatatactt ccacaaaaat a 171

<210> 1138
<211> 125
<212> DNA
<213> Homo sapiens

<400> 1138
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cacccattgg accaacta tagaaaccta cattgtgcct tgcgccccct tgaccatgaa 120
agtta 125

<210> 1139
<211> 31
<212> DNA

<213> Homo sapiens
 <400> 1139
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<210> 1140
 <211> 87
 <212> DNA
 <213> Homo sapiens
 <400> 1140
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 tttgcaccca ctgaagtcaa tgacata 87

<210> 1141
 <211> 61
 <212> DNA
 <213> Homo sapiens
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 g 61

<210> 1142
 <211> 103
 <212> DNA
 <213> Homo sapiens
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 cgtccagatg caggagctgt ccctgggcat gaaagccctg gcc 103

<210> 1143
 <211> 44
 <212> DNA
 <213> Homo sapiens
 <400> 1143
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<210> 1144
 <211> 550
 <212> DNA
 <213> Homo sapiens
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 aagagatgca agattttctc agatgatttg tgtgtcagtc agagttccgc cagagaaaca 120
 caaccagtag gatataattct atcttgtctg tttcatatc catgtatctg tcatctacct 180
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 ccacagggca ggccgtgtgg aaggagggtc tggaaactct cagacaagac ctgacattgc 300
 agtccactgg tggaatttct ctttcttcag ggaaacctca gctttcaacg gagtggatca 360
 gaccaacca tattatccag gataatctcc ttacataaa gttaactgat tgtagatgta 420

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 ttatagcata gccagggtcaa cacgtaaaat tgatcaccac agtccatgtc ttgttaactt 540
 ggcacctgta 550

<210> 1145
 <211> 412
 <212> DNA
 <213> Homo sapiens

<400> 1145
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 gtggggaatc tgtaggcaca gaaatgagac tcagcagcag aggacagaca gcacctgcct 360
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<210> 1146
 <211> 68
 <212> DNA
 <213> Homo sapiens

<400> 1146
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 ccacaggc 68

<210> 1147
 <211> 98
 <212> DNA
 <213> Homo sapiens

<400> 1147
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 gggaagagtg cagattggag cagctatcca aaaatata 98

<210> 1148
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 <212> DNA
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 caagcaggca agatcagatt caca 84

<210> 1149
 <211> 59
 <212> DNA
 <213> Homo sapiens

<400> 1149
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<210> 1150
 <211> 86
 <212> DNA
 <213> Homo sapiens

 <400> 1150
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 gaagcccta agtgggacag cagtgc 86

 <210> 1151
 <211> 66
 <212> DNA
 <213> Homo sapiens

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 ggtcca 66

 <210> 1152
 <211> 107
 <212> DNA
 <213> Homo sapiens

 <400> 1152
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 gctaatacagc acttgatcgg aagtccaggt tagtatgtga agccagg 107

 <210> 1153
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 <212> DNA
 <213> Homo sapiens

 <400> 1153
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 ctgagactcc cctgccgctc caagcccga agaactggag cctggagggg ggtgagggga 120
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 <210> 1154
 <211> 154
 <212> DNA
 <213> Homo sapiens

 <400> 1154
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 ttctggcata tttcaaaatt gttccttttc ccctctggct gccagagcat gagggatttt 120
 ccttaatat cacttttgga acctttaga gctt 154

 <210> 1155
 <211> 320
 <212> DNA
 <213> Homo sapiens

 <400> 1155
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<210> 1156
 <211> 136
 <212> DNA
 <213> Homo sapiens

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 ggcaaagggc ttcctg 136

<210> 1157
 <211> 117
 <212> DNA
 <213> Homo sapiens

<400> 1157
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 ttaagatgaa gtttcgcttc ttaggaaaat taatggccaa ggctatcatg gatttca 117

<210> 1158
 <211> 149
 <212> DNA
 <213> Homo sapiens

<400> 1158
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 acaaacatat tcctttgccg atgctgacc 149

<210> 1159
 <211> 48
 <212> DNA
 <213> Homo sapiens

<400> 1159
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<210> 1160
 <211> 90
 <212> DNA
 <213> Homo sapiens

<400> 1160
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 ctctctcaaa ccttgttcag atgctgcaga 90

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 <212> DNA
 <213> Homo sapiens

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<210> 1162
 <211> 507
 <212> DNA
 <213> Homo sapiens

<400> 1162
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 gcaagtcccc gaaatgcact tccaaagaca ggaaagattg cagtgggaca gaaccagaa 180
 aatctctcac attctcgaaa acccgaaaga gaacctcaa gaaagacgtt tgcctctcct 240
 ccacctcttt atctcggcgg gagaggaagc ctgcgccccca ttcaccccg cctttctccc 300
 caccgcgccc cagggagaag ttaccatgg ctgcctgcgg ccccttact tccggtgccg 360
 gtgccgctag ggctgcgcca tccccccagt caatcggaca accatagcct ccaactgacc 420
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 gaggacggcc gcacaaaaac caatcta 507

<210> 1163
 <211> 52
 <212> DNA
 <213> Homo sapiens

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<400> 1163
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<210> 1164
 <211> 28
 <212> DNA
 <213> Homo sapiens

<400> 1164
 ctgcagtgtg gtgaactcca acttttag 28

<210> 1165
 <211> 81
 <212> DNA
 <213> Homo sapiens

<400> 1165
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 atgacgacta tgcgggcttc a 81

<210> 1166
 <211> 373
 <212> DNA
 <213> Homo sapiens

<400> 1166
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 gcttttagata tttcagaact tcattcccca aatgaaagct aatctggaca aactatatat 120
 tgcatagatt tctctacaga ttctttgctt taaaacctaa atgcaactaa catagtgtaa 180
 ttttaacctt tttgccccac agtaaaaact atctgtcctg aaaaatatga tggatatatc 240
 ctgtgatttt ccagttaaca gaattgttct acttcaaaga taattattat catatatcaa 300
 aataaccagc tcaacatagg acattacttc agtctttact gactcatagg catatgaact 360
 tgtgcccagc ttt 373

<210> 1167
 <211> 218
 <212> DNA
 <213> Homo sapiens

<400> 1167
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 ggggggagga aggaatgcat gggctctgcc cttagagcaa gtctgaaacc agaatcaaga 120
 gtcctcctcc ccagtgggcc tgtgtggggg aagaggggca gcctgccccca ggggtgcaag 180
 aggacagcaa ttcagcttcc aggccaaagc agtttaga 218

<210> 1168
 <211> 37
 <212> DNA
 <213> Homo sapiens

<400> 1168
 cccggggccc atagcccaca ccgtgccctg cgtttca 37

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<210> 1169
 <211> 186
 <212> DNA
 <213> Homo sapiens

<400> 1169
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 ccttctcacc cttccatggc cctcaacacc cgctttgctg aggtggagtg tttggcggaa 120
 agtcatcagc acctgtccaa ggagtcaatg gcaggaaaca agccagccaa tgcagtcctg 180
 caaaaa 186

<210> 1170
 <211> 162
 <212> DNA
 <213> Homo sapiens

<400> 1170
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 ccagagttct aacttctgca gctaaaacac aggaccctag ctgccttctc accccagcta 120
 gtggcaggcc tcagtaaag acagaacagt ggaatgctcc tc 162

<210> 1171
 <211> 145
 <212> DNA
 <213> Homo sapiens

<400> 1171
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 agaagagctg gccccaggaa tctaacttga atcggaagaa aaagaaagaa cagcctaaga 120
 gctctcaggc taacccccgg aggca 145

<210> 1172
 <211> 115
 <212> DNA
 <213> Homo sapiens

<400> 1172
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 tctaggtttg gtcagagtct acatgaaaac agaccacaag gacagccaac atata 115

<210> 1173
 <211> 467
 <212> DNA
 <213> Homo sapiens

<400> 1173
 ccatttcacc agagcgtcct taggggctgg ggggtgggttt gttaatgggg tggaggcaat 60
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 ccctcttctc tccctaactt tggttctcta ccctccttct cactcctcac ctgattctct 180
 ctcttcctcc tccttatatc tgtgaggcag aaggcatctg aagctcatat tagcccccac 240
 tgggtgggaa ttaggagtgg gtagttaaact caggagagact tgagataccc tggaaaaaat 300

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gctattgaga tgtcctgaca ttaggcaggg tggatggaac aagaaggagc aagaaaggaa	360
cctcaggcag atgttaggac atggacttga tcatgtggcc tgggagttta gaaatgggga	420
gagacatcct cctagatcag atcgtgggct cagtaggcat gttgatt	467

<210> 1174
 <211> 1183
 <212> DNA
 <213> Homo sapiens

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ataaccatat ctccaaacta aattaacgtt actaaagtgg ggaattttccc cttcctatat	180
tctcataagt gattgagcat ctgtcctcat ataggacttg ctgccttgga ggggaggggc	240
cagacctggg aaaaagagga gccatgaata actctgcttc ctacatttggt cttcttctct	300
tcctccatat ccatgattta tatatgtgaa ggaagaacaa gaaataactt aataggccat	360
ttgtcaatga gactacagt taggaagggt ggaaagtga tataaaatct agattggggc	420
ttctgggttc ctgttcagcc tataaggagc ttagaatttg ccactcagtc ttgacaacaa	480
gtaaaatgct gaacaaactg aaaaatcaat aattcttctc agatccataa gagaagtga	540
attacagggc aaactactac cttcagcatc accccgcacc cccaaccca ctaaatagaa	600
agacaggaga atacagagaa tcataacaca ggcgcagaaa cctccttgag agagccaggg	660
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tcgttcttaa caatgtctgc cctcaggaga agatgtttta ccagagccta atcttctggg	960
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<210> 1175
 <211> 224
 <212> DNA
 <213> Homo sapiens

<400> 1175 atgggccata gtgacgatgg tggttttgtc aaaaagaaaa ggggggggata tgtaaggaaa	60
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gatctgtact aagaaaaatt gttttgcctt gagatgctgt taatctgtaa ctttagcccc	180
aaccctgtgc tcacggaaac atgtgctgta aggtttaagg gatc	224

<210> 1176
 <211> 130
 <212> DNA
 <213> Homo sapiens

<400> 1176
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 ttttatttgt ttgtttgttt ctgatggaga ttatagtttt gtgacagcta ggcccttgtc 120
 tgttgtttca 130

<210> 1177
 <211> 43
 <212> DNA
 <213> Homo sapiens

<400> 1177
 caagggagg ctccgaaaag gacatggcga agtggcaaaa aga 43

<210> 1178
 <211> 353
 <212> DNA
 <213> Homo sapiens

<400> 1178
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 gatgtataca aggtaattgc agttgacaaa gagtaggtgt ggctaattgg agcagattat 120
 gtccatggtg tagtggattt tatgctgttt ttaacagaag aaaccacctc aatttttttt 180
 ttttgaggtt aaacttcagt atatgaaaga gggggcaacc cagcagttgt ttgattgaa 240
 gcagagttct aggtctccag gaatagttta aaaactgtaa ctaggctggg cagcatggct 300
 catgcctgta atccccaaca ctttgggagg ctgaggtcga aacatctctt gaa 353

<210> 1179
 <211> 630
 <212> DNA
 <213> Homo sapiens

<400> 1179
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 ttggaacttt tctcctgcat gtgtatatat gtcaaattgt cagcatgaca aaagtgacag 120
 atgttatttt tgtattttta aaaaacaatt ggttgatatat aaagtttttt tatttctttt 180
 gtgcagatca ctttttaaac tcacataggt aggtatcttt atagttgtag actatggaat 240
 gtcagtgttc agccaaacag tatgatggaa cagtgaaggt caattcagtg atggcaacac 300
 tgaaggaaca gttaccctgc tttgcctcga aagtgtcatc aatttgtaat tttagtatta 360
 actctgtaaa agtgtctgta ggtacgtttt atattatata aggacagacc aaaaatcaac 420
 ctatcaaagc ttcaaaaact ttgggaaagg gtgggattaa gtacaagcac atttggctta 480
 cagtaaata ga actgattttt attaactgct tttgccata taaaatgctg atatttactg 540
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gtgcaggcaa tcgtggatgt ctctgacaaa 630

<210> 1180
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 <212> DNA
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<400> 1180
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 tcctggctcc ctacctgaag aaagcgctc gccagcaagg tgcattgatcg tccaccaggg 120
 cacca 125

<210> 1181
 <211> 35
 <212> DNA
 <213> Homo sapiens

<400> 1181
 cagagagggg ccgtggcatg tccaagggtta ctctg 35

<210> 1182
 <211> 51
 <212> DNA
 <213> Homo sapiens

<400> 1182
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<210> 1183
 <211> 107
 <212> DNA
 <213> Homo sapiens

<400> 1183
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 ttaatgagta ttgactgct ctctgggtctg tgggactggg cattcaa 107

<210> 1184
 <211> 32
 <212> DNA
 <213> Homo sapiens

<400> 1184
 gggcgagcag ccctacgagc acctgaccgc ag 32

<210> 1185
 <211> 30
 <212> DNA
 <213> Homo sapiens

<400> 1185
 ccatgccagt ctgagcactc catttaatta 30

<210> 1186
 <211> 314
 <212> DNA
 <213> Homo sapiens

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<400> 1186
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cgatgcccag ccatccctcc atctccctga cccgggcact cttgcctcag gcagcctcac 180
caggaaaggc ggaggcacat tgatgagggc cccccgggag tccatgatgc tgatggcctc 240
cagcccgtgc cgctgccc aa cttcatagtc attttgggtca tgtgcggggg tgatcttcac 300
agcacctggg tgta 314

<210> 1187
<211> 142
<212> DNA
<213> Homo sapiens

<400> 1187
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acaaacgctc tacttatctt gccggggcct cagccagaag tctcctataa ctctgcggat 120
gtttatacat gccctctgct tc 142

<210> 1188
<211> 253
<212> DNA
<213> Homo sapiens

<400> 1188
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gcaaagcaga gccaggcgtg cagggcacgg ggctggccct tttcccagct cggaaagaga 120
aagaaaatct gcctacagct ccttcgctcc acgaccctc ccccgacttt gggggggcgt 180
gtgaacgcgg cagcggcggc gtgctgctgc tcaccgcacg agctggaatg cagagtgcc 240
cattagggac gcc 253

<210> 1189
<211> 28
<212> DNA
<213> Homo sapiens

<400> 1189
tttagacatg aagtatgagg ccggcatc 28

<210> 1190
<211> 157
<212> DNA
<213> Homo sapiens

<400> 1190
acctgaaaga accaagtcgc cagactccc aagtgccacc tcagtaaggg acctcaacgg 60
gacgaccaag gcccagtga agcctcgacg gcccttgacc atggaagctg cccagagcat 120
ctcaaataag tcagcagcct ttccactggg cctattc 157

<210> 1191

<211> 106
 <212> DNA
 <213> Homo sapiens

<400> 1191
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 tgtctgagcc tgagcagtgg gccagatgga ctatcggtct gcctca 106

<210> 1192
 <211> 818
 <212> DNA
 <213> Homo sapiens

<400> 1192
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 cttatctggg ccggagaggg gcgttggcag cgggggtctt gccgccttcc ggtcctctgc 120
 atgccaggca ccacctgggg ccggggccagg gcaggctgcc tggacaccat ggacctgccc 180
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 gactgaggac ggctgacccc cttggtgact gcctgggccc agaggggagt tgggggagtg 300
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 tgccccgttt gatggctgac aaagtgccct tgaatgcgtc agaccagcg tgggtcccagg 540
 gtcctgacct taacatacca ccccaaatta ccctacccc agcctacccc tgccctaaat 600
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 acacccaag ccctaattcc taaccgtag cctcaccta accttctac cggatgccac 720
 ctggcaaaca tcctcctggc ccctatctgc ccctccccg gggatccggg aggcagtggg 780
 gtccctggga ggctgctccc tgcagaacgc gatggaca 818

<210> 1193
 <211> 121
 <212> DNA
 <213> Homo sapiens

<400> 1193
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 cagtcaagta gcagtgggaa tgaattatct aaaagctctc tgctagcata cacgtgaaat 120
 a 121

<210> 1194
 <211> 297
 <212> DNA
 <213> Homo sapiens

<400> 1194
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 ggctgtgtga taggaaacaa atgccttaca gatgtgccta ggtgttctgt ttacctagt 120

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tcttactctg ttttctggat ctgaagacta gtaataaact aggacactaa ctgggttcca 180
 tgtgattgcc ctttcatatg atcttctaag ttgatttttt tcctcccaag tcttttttaa 240
 agaaagtata ctgtatttta ccaaccccct ctcttttctt ttagctcctc tgtggtg 297

<210> 1195
 <211> 82
 <212> DNA
 <213> Homo sapiens

<400> 1195
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 gcgaatgtat gcaggacttc aa 82

<210> 1196
 <211> 305
 <212> DNA
 <213> Homo sapiens

<400> 1196
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 actagggtaa taacagtatg gtgattccaa attatttggg tcctgagttt gaattcagct 180
 tgtcaggtga gttttagctt taatttccta acttgcaaaa tgggattaat aatatcttag 240
 agggttcaat ataaagtatc acgcagtaga aggtcaacaa atggggctta tgacgatgac 300
 agtta 305

<210> 1197
 <211> 66
 <212> DNA
 <213> Homo sapiens

<400> 1197
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 gctcga 66

<210> 1198
 <211> 156
 <212> DNA
 <213> Homo sapiens

<400> 1198
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 gagtgagctg ggcattccga tctctggggt ttgtgtgcgt ggggttaaca ctccatctga 120
 gtgagctggg tgactgcctc catgagtcct gttgtg 156

<210> 1199
 <211> 28
 <212> DNA
 <213> Homo sapiens

<400> 1199
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<210> 1200
<211> 293
<212> DNA
<213> Homo sapiens

<400> 1200
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tccctatcac aaggtcattt gaaaacggac tcaggacaaa cccatatacg tgtagctcta 180
ggccaataac ataaaaataa cagtataatc tatagaaatt tataaaaagg aataaatggc 240
aataaattct aaccgaaagt aactctgacc tggtttgtgc tgtaagttt tga 293

<210> 1201
<211> 100
<212> DNA
<213> Homo sapiens

<400> 1201
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taatctcggg gggtaggaaa ggacacgtct gcatttttga 100

<210> 1202
<211> 50
<212> DNA
<213> Homo sapiens

<400> 1202
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<210> 1203
<211> 32
<212> DNA
<213> Homo sapiens

<400> 1203
ggtggaagcc gaagtatctc agcttcttct gc 32

<210> 1204
<211> 140
<212> DNA
<213> Homo sapiens

<400> 1204
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tggggctgga gaaacctaac ctggctcatg aactgtccaa acgatgagac aagttgccct 120
gacagggcag ttgtttggaa 140

<210> 1205
<211> 129
<212> DNA
<213> Homo sapiens

<400> 1205
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cttcgctcaa ggacacttgg gggaagggcc cctgattccc tattcttcac ctcgtgaagg 120
gcgggcatg 129

<210> 1206
<211> 28
<212> DNA
<213> Homo sapiens

<400> 1206
gttcttgagc cccttcacga ccgtcacc 28

<210> 1207
<211> 224
<212> DNA
<213> Homo sapiens

<400> 1207
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gaactgtagg gaatagtggg tgatggcgac agtggtgaaa tatagctcgg gctttaggat 120
ttgtcatatg tctaattgagg cttgacatgc aagtactatt aaaatctcct tagcatacat 180
tgttttcctg attactgggg gggaccttaa gttgtctcat gtaa 224

<210> 1208
<211> 92
<212> DNA
<213> Homo sapiens

<400> 1208
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agccaacaca acaaattattc tgctcccttt tc 92

<210> 1209
<211> 374
<212> DNA
<213> Homo sapiens

<400> 1209
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cagcattggc agcctccgcc tccccatgtc ccaaaagagg aaactgggct ggagaaagtt 120
tcgcagccca aggacgcgtg gctggaagtg gcagaacccg ggcttccgag gttgggagag 180
tggggtcctc caaggccctc agcacgggtc ggagggattg ggactgaacc cgccatcccc 240
ctggaccttg gtgccctcca agccccgcgc tcgcgccctg tccgtcgcct cccccagaga 300
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gaacgattga catc 374

<210> 1210
<211> 2423
<212> DNA
<213> Homo sapiens

<400> 1210

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ggcctggtgt	gagggcacga	gactcaccga	catccctgat	gacaagcctg	taggtccctc	180
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ccctgaggaa	agaacacagc	agaaacaggt	ggaaggcgtg	ggccagagag	ctgaccttcc	300
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ttttggagac	agggctctac	tctgttatcc	aagctggagt	gcagtggcat	gatcacagct	600
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<212> DNA
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<213> Homo sapiens

<400> 1263

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<210> 1264

<211> 30

<212> DNA

<213> Homo sapiens

<400> 1264

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<210> 1265

<211> 64

<212> DNA

<213> Homo sapiens

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<210> 1266

<211> 140

<212> DNA

<213> Homo sapiens

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<210> 1267

<211> 31

<212> DNA

<213> Homo sapiens

<400> 1267

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<211> 45

<212> DNA

<213> Homo sapiens

<400> 1268

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<210> 1269
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 <212> DNA
 <213> Homo sapiens

<400> 1269
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<210> 1270
 <211> 53
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<210> 1271
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agactatggg aaaagtaacg gcaaagttaa cttactaggg tctggggggc atacatggaa	180
aaagcactta attcaagctc aggggaagtga gcatggggag ctggaaggat tcctgaaaga	240
caatacaaca aaactgagaa cctaagaaaa agtggcaatt agctaggcta catggaccct	300
ta	302

<210> 1274
 <211> 28
 <212> DNA
 <213> Homo sapiens

<400> 1274	
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<210> 1275
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 <212> DNA
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<400> 1275	
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acgcatttct gctgtttgtt ctgtgaatgg aaacactgtg ccaagcccca agaggattac	180
gcttccaggt gtgtaacgtg ttttctgtgt ctgccgttc cagcagctga tatctttgga	240
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gttaagcaca cacacactca cacaacaggc ttacgaggct caggcctggc gggtcagaaa	420
gccactccc tctccaagg ccactggatc ccaggagaag ccagactgg cgatactaca	480

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cacaatccca acaaacatct cctgtgacat taagttgtca tcagcttgcg tgatccccag	180
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 <212> DNA
 <213> Homo sapiens

<400> 1278	
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<210> 1279
 <211> 50
 <212> DNA
 <213> Homo sapiens

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 <210> 1281
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 <212> DNA
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 <211> 28
 <212> DNA
 <213> Homo sapiens

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 <210> 1283
 <211> 65
 <212> DNA
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 ctgct 65

 <210> 1284
 <211> 45
 <212> DNA
 <213> Homo sapiens

 <400> 1284
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 <210> 1285
 <211> 114
 <212> DNA
 <213> Homo sapiens

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<210> 1287
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 <212> DNA
 <213> Homo sapiens

<400> 1287
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<210> 1288
 <211> 89
 <212> DNA
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<210> 1289
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<210> 1290
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<211> 141
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 tccagtttagc catcacgctg c 141

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<210> 1294
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 <212> DNA
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<210> 1295
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 <212> DNA
 <213> Homo sapiens

<400> 1295
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<212> DNA
<213> Homo sapiens

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<210> 1297
<211> 522
<212> DNA
<213> Homo sapiens

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<211> 283
<212> DNA
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<212> DNA
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<210> 1300
 <211> 53
 <212> DNA
 <213> Homo sapiens

 <400> 1300
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 <210> 1301
 <211> 151
 <212> DNA
 <213> Homo sapiens

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 <210> 1302
 <211> 408
 <212> DNA
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 <213> Homo sapiens

 <400> 1303
 accaaacaga tgaacgaacg gagcacagca gtgctatgaa ag 42

 <210> 1304
 <211> 72
 <212> DNA
 <213> Homo sapiens

 <400> 1304
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 caaagaacca gt 72

 <210> 1305
 <211> 102
 <212> DNA
 <213> Homo sapiens

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<400> 1305
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 aaaaagaagc ctctcacttt cagtccaagc taattacacc tc 102

<210> 1306
 <211> 137
 <212> DNA
 <213> Homo sapiens

<400> 1306
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 aaatgcatcc aacagcc 137

<210> 1307
 <211> 72
 <212> DNA
 <213> Homo sapiens

<400> 1307
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 actacctaata ca 72

<210> 1308
 <211> 69
 <212> DNA
 <213> Homo sapiens

<400> 1308
 ggaggtacaa gaaagatcca caaaccagag aaagctttcc agcagtcagt tgaacaagac 60
 aacttatttt 69

<210> 1309
 <211> 36
 <212> DNA
 <213> Homo sapiens

<400> 1309
 tgaagtttagc tgttcctca gtagctcttt gttccc 36

<210> 1310
 <211> 144
 <212> DNA
 <213> Homo sapiens

<400> 1310
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 gtgcctgcac tcacagccca gtcccaggac agcgggcttt gctgccccat tgcccattac 120
 ttagccaagt cgatctccat gaaa 144

<210> 1311
 <211> 210
 <212> DNA
 <213> Homo sapiens

GBX1170_3WO_ST25.txt

<400> 1311
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 cagccatcct ggtactgtag tttagggggt gatgggtggt gaaattgatt tctggctggt 180
 tactaagggtg cctgctagcc attgtataaa 210

<210> 1312
 <211> 86
 <212> DNA
 <213> Homo sapiens

<400> 1312
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 gttggagaac gcgtgtggaa attgac 86

<210> 1313
 <211> 60
 <212> DNA
 <213> Homo sapiens

<400> 1313
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<210> 1314
 <211> 28
 <212> DNA
 <213> Homo sapiens

<400> 1314
 aaactacaaa aagctctggt gaccacca 28

<210> 1315
 <211> 46
 <212> DNA
 <213> Homo sapiens

<400> 1315
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<210> 1316
 <211> 408
 <212> DNA
 <213> Homo sapiens

<400> 1316
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 tacaagcaaa atgaaatatg tttagcctca taaaaaatca tctacaatat tgagacttga 120
 gagtatggca aactctggta aagttaataa attaatgtgc tgcctaggggt ttgtttatat 180
 ctggaaaaca ggaaacggta ggtaggtagg taggtaggta cataggtaga tagatataga 240
 tagatagata gatagataga tagatagata gatagataga tataatacaa tacttttctt 300
 agagtcagag cctggacatg acaacactaa caatagggat attctgaact gctccaagga 360
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<210> 1317
<211> 746
<212> DNA
<213> Homo sapiens

<400> 1317
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cgctgggttag gagcttgagc tgtctgaggc ctgtgggagc ctcaagttgg ttttcttctg 120
tgagttggat tctccccctc ttgaaaaaaa atcgattttt caggatttaa ttaatacaaa 180
ccttatttta ggttggtgct taactggagg tgatgcataa gtctgatttt tttttccaag 240
atagaaaaag catttatcct aacaaattgg tattttttat taagcctcca tgtggctctg 300
aatgcaagct atatatagtg agtttttcta aattaaggga actctgcttt tttttttttt 360
ttttaagtaa ctggctctga agtgcataat tctagaacgt ccccgagat gaatgagggc 420
cagtgccctt ggcagaggca ggtgtggcct cgtagaggca gtgctggccg cgccagggca 480
tcagtgtgta tgtgggagct gtgcttccac ctaagccgtt ggtaggggac tgtggcattt 540
aagaatgtag agagcgcac ctttttgatc tcctgggcgg agtgaacctg caggggccac 600
cccagaaacc ttggttctga tgcactgcaa gcaagtaacc agcttctcac tccagtttca 660
agtggctatt atgtaatata aattcaaagc acattgtgaa tagaacctac atgaaaacat 720
acactttgtt gccactgac atgtta 746

<210> 1318
<211> 70
<212> DNA
<213> Homo sapiens

<400> 1318
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gtggaagagt 70

<210> 1319
<211> 109
<212> DNA
<213> Homo sapiens

<400> 1319
aggatgaagga agacagtgcg tacgggagcc agtcagtgga gcaggaggca gagaagctgg 60
gcccaccccc tgagccacca ggagggtctt gccacgggca cccccagcc 109

<210> 1320
<211> 89
<212> DNA
<213> Homo sapiens

<400> 1320
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aaaggcagtg gaagcagaga ctcgtggca 89

<210> 1321

<211> 71
 <212> DNA
 <213> Homo sapiens

 <400> 1321
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 acacttatgg a 71

 <210> 1322
 <211> 79
 <212> DNA
 <213> Homo sapiens

 <400> 1322
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 attgtcacac ctttgaaac 79

 <210> 1323
 <211> 45
 <212> DNA
 <213> Homo sapiens

 <400> 1323
 tttaggaaaa ggctgctata ctgtggacga agtctcagat cagaa 45

 <210> 1324
 <211> 104
 <212> DNA
 <213> Homo sapiens

 <400> 1324
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 tgaggtctgg atgagaagtg tgaccaggcg tgtttgactc atgc 104

 <210> 1325
 <211> 79
 <212> DNA
 <213> Homo sapiens

 <400> 1325
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 cctcgttagga aggcagtgt 79

 <210> 1326
 <211> 28
 <212> DNA
 <213> Homo sapiens

 <400> 1326
 gtaagggatg tctctgcgcc atcctcag 28

 <210> 1327
 <211> 60
 <212> DNA
 <213> Homo sapiens

 <400> 1327
 tgctggccca aagccagtcc agcactgcct cctctgactc taaaatcaga agagtcttga 60

<210> 1328
 <211> 120
 <212> DNA
 <213> Homo sapiens

<400> 1328
 atgacctccg gcttcctgcg gggctccatg tggctcggac agacacggaa gcacagcagc 60
 gtgagcgcca ggaccacett catctcagcc attgcaaacg cctgcccaat gcagttcctg 120

<210> 1329
 <211> 677
 <212> DNA
 <213> Homo sapiens

<400> 1329
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 cttgaactcc tgggctcaag caatcctctt acctcagcaa ctaggactac aggcacatgc 120
 caccacgctt ggccttctaa tttattttctg tgtcaacaaa ataaaactca ggcctaggaa 180
 tagcttgggt cagaaatcac agagggactt agtattccat taatacaaat ggaaacatta 240
 agttcatcat cagatgataa aaggaaaaaa aaaaacctga tactcatctc aaaagacgca 300
 gaaaagacat ttgcataaat ccagtaccta ttattatttc aaatttaaaa actttcttctt 360
 ttttaagaga tagggatatca ctatgttgcc caggctgatc ttgaactctt ggcctcagat 420
 gatcctcctg cctcagcctc ccacagtgtc gggactacag gcatgagcca ccacacccat 480
 cataaattaa aacttctgaa caatctagta acaaattggaa atgctttccc atgatccagc 540
 acatctagca gggggtgtct gctgacattc tacacaaaga gacacactgg agttgtgctt 600
 ctcatcattt cacattaaga acccaactgc acctttttct gtgcctctaa acacctgtag 660
 tctgataggg gacaccc 677

<210> 1330
 <211> 115
 <212> DNA
 <213> Homo sapiens

<400> 1330
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 aacacaatgg gtggaagtgt ggttcagtgt ctaagaaagt ctccagcaca gtgtg 115

<210> 1331
 <211> 179
 <212> DNA
 <213> Homo sapiens

<400> 1331
 gttactcagt tttcgcttac acatgccaga aaggcatttc cttgttttga tgagccaatc 60
 tacaaggcta ctttcaaaat cagcatcaag catcaagcaa cctatttatc tttatctaata 120
 atgccagtgg aaacttccgt gtttgaggaa gatggatggg ttacggatca cttttcaca 179

<210> 1332
 <211> 161
 <212> DNA
 <213> Homo sapiens

<400> 1332
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 gtggacccgc ttacaaaatc agcttaagaa acgtaacctt aaattttaga attacagatt 120
 ttaatgactt catattccac gactgaccct ctgagttttt t 161

<210> 1333
 <211> 160
 <212> DNA
 <213> Homo sapiens

<400> 1333
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 cttccaggat ggggtggctg agaagtgtgt tgattatattt cagagattcc gacgttctac 120
 ccacgtgacg cccaaatcat acctctcctt tattcagggc 160

<210> 1334
 <211> 1546
 <212> DNA
 <213> Homo sapiens

<400> 1334
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 ctaacagaaa aaaaccact gaaaatatta tcatagacct ggacaaagag gacaaggatt 120
 taatattgac aattacagag agtaccatcc ttgaaattct acctgagctg acatcggata 180
 aaaatactat catagatatt gatcatacta aacctgtgta tgaagacatt cttggaatgc 240
 aaacagatat agatacagag gtaccatcag aaccacatga cagtaatgat gaaagtaatg 300
 atgacagcac tcaagttcaa gagatctatg aggagctgt caacctttct ttaactgagg 360
 aaacatttga gggctctgct gatgttctgg ctagctacac tcaggcaaca catgatgaat 420
 caatgactta tgaagataga agccaactag atcacatggg ctttcacttc acaactggga 480
 tccctgctcc tagcacagaa acagaattag acgttttact tcccacggca acatccctgc 540
 caattcctcg taagtctgcc acagttattc cagagattga aggaataaaa gctgaagcaa 600
 aagccctgga tgacatgttt gaatcaagca ctttgtctga tgggtcaagct attgcagacc 660
 aaagtgaat aataccaaca ttgggccaat ttgaaaggac tcaggaggag tatgaagaca 720
 aaaaacatgc tggtccttct tttcagccag aattctcttc aggagctgag gaggcattag 780
 tagaccatac tccctatcta agtattgcta ctaccacct tatggatcag agtghtaacag 840
 aggtgcctga tgtgatggaa ggatccaatc ccccatatta cactgataca acattagcag 900
 tttcaacatt tgcgaagttg tcttctcaga caccatcatc tcccctcact atctactcag 960
 gcagtgaagc ctctggacac acagagatcc cccagcccag tgctctgcca ggaatagacg 1020
 tcggctcatc tgtaatgtcc ccacaggatt cttttaagga aattcatgta aatattgaag 1080

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cgactttcaa accatcaagt gaggaatacc ttcacataac tgagcctccc tctttatctc	1140
ctgacacaaa attagaacct tcagaagatg atggtaaacc tgagttatta gaagaaatgg	1200
aagcttctcc cacagaactt attgctgtgg aaggaactga gattctccaa gatttccaaa	1260
acaaaaccga tgggtcaagtt tctggagaag caatcaagat gtttcccacc attaaaacac	1320
ctgaggctgg aactgttatt acaactgccg atgaaattga attagaaggt gctacacagt	1380
ggccacactc tacttctgct tctgccacct atggggtcga ggcaggtgtg gtgccttggc	1440
taagtccaca gacttctgag aggcccacgc tttcttcttc tccagaaata aaccctgaaa	1500
ctcaagcagc tttaatcaga gggcaggatt ccacgatagc agcatc	1546

<210> 1335
 <211> 238
 <212> DNA
 <213> Homo sapiens

<400> 1335	
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ctgtggctct tccctgctcc cttaccctc tcaggaccag tcacaggatg ggggccagcc	120
tcccgtccc tatatgccca tcagtccccg aggtgcgggg tgggaacttg gagagcacgc	180
tgctgcatgg aacgctcttg tcaccagcaa atgcctcagt ggctatgtgg gaacacaa	238

<210> 1336
 <211> 31
 <212> DNA
 <213> Homo sapiens

<400> 1336	
aggccaagag cggatgttct tcatttcact t	31

<210> 1337
 <211> 89
 <212> DNA
 <213> Homo sapiens

<400> 1337	
ctgagatgc cattgtaact gctttcatta ctttcattcc caagttcatc gagtcacagt	60
ttggtatccc agcctccaat gccagcatc	89

<210> 1338
 <211> 31
 <212> DNA
 <213> Homo sapiens

<400> 1338	
agaagaataa tggaaccact ttggaaatag g	31

<210> 1339
 <211> 537
 <212> DNA
 <213> Homo sapiens

<400> 1339	
cacacatggc gctgtcagga tacacaagga caatagccaa agagttacaa aaaataaatc	60

GBX1170_3WO_ST25.txt

catgattctt aaacaattgc aaccaaaaaa aaaaaaaagt tacaagtatc aaaactttca 120
gatgcattgc attgaaaaga aggtttgtgc acgtcataat ttaaagaggc aaaaccaagg 180
agctactgaa acctcacgtt aaacagttta ttataaagct gatggaaagg agcaagttgt 240
ctctctgtat cagcttcctt taacagtttt ccattaattg aagaaagagg tgggaggggt 300
gaattcattt ttgcatgcac aagatgtact gcttaacgaa acactatcag cttgttttaa 360
atggatcttt taaatatcaa ctgtagcctg gttggctaata tctttctaata cttccccatt 420
actttcgctt agatttccca tagatcaaca ggcataagtaa aatgcctcat cagaacacac 480
ttctccacac aattcaaaaa gggagctcct gtggggtcaa agcaaccatc agtccag 537

<210> 1340
<211> 104
<212> DNA
<213> Homo sapiens

<400> 1340
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ggctcagagc ttcttcacc tgcccgttaa cattcgaaaa tgtc 104

<210> 1341
<211> 124
<212> DNA
<213> Homo sapiens

<400> 1341
acccttgggt ggctctccgg cattccagct gcagctgctg gggctggctg caggcacgtc 60
tgactgttct cccctttgga gtagacaggg ttgttctggc tgtcccatgc attgcctttc 120
aata 124

<210> 1342
<211> 331
<212> DNA
<213> Homo sapiens

<400> 1342
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cagcaccggg gcctcaaccg tgcaggggtg ggataaaccc atcgtaagtt gaaaataacct 120
gaagtggaaa gtgcgctttc agcttagacg accgttttat ctggacgcag ccccatcgga 180
cgtcgaggag cctatgaatg cgtatcagcg ttatcagaaa gccgaaaaaa acttaagttg 240
aaccatccta agtcggggac tgtctgtcca cccttgccga cttgacctct ttttcccgg 300
tctctagagt cagtatacca ccagcccgtt c 331

<210> 1343
<211> 91
<212> DNA
<213> Homo sapiens

<400> 1343
gtccacaga tcgttctcaa cattgacttg gccccacga tcttgatat tgctgggctc 60

gacacacctc ctgatgtgga cggcaagtct g 91

<210> 1344
 <211> 894
 <212> DNA
 <213> Homo sapiens

<400> 1344
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 ccccgaggag tccccagagt ccctctagtg gggccgaggc tgcagatgag gacagcaatg 120
 actcccctgc ctccagctcc tctaggcctc ttaaggtgcg gatcaagacc attaaaacat 180
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 ccttggtgta gggggccttc ttggctgagg ctagcctctt gaagctgtcc cctgcaacac 300
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 gtgtggctcg caaggctgtg gtgctgcctg gggggactgc caccagccct aagatgattg 480
 ctaagaacgt gctaggcctg gtgccccaaag ccctgcctaa ggctgacggg cgggcagggc 540
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 tggaggcctt caacaagatc ctcaacagca agaactgct ccctgcctat aggccaaacc 720
 tgagcccacc agctgaggct gggctggccc tgcctccac cggtaccgc tgcctggagt 780
 gtggggatgc cttctcattg gagaagagcc tggcacggca ctatgaccgt cggagcatgc 840
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<210> 1345
 <211> 63
 <212> DNA
 <213> Homo sapiens

<400> 1345
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 cag 63

<210> 1346
 <211> 80
 <212> DNA
 <213> Homo sapiens

<400> 1346
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 gtgtgtgacg tttcgggttt 80

<210> 1347
 <211> 28
 <212> DNA
 <213> Homo sapiens

<400> 1347
 acccccagtc ggcctactgt gcctcagc 28

<210> 1348
 <211> 64
 <212> DNA
 <213> Homo sapiens

<400> 1348
 ggccagaggtt ctatgcctct gtccttgaga acttctccag gatcttgga attcctggcc 60
 ttca 64

<210> 1349
 <211> 78
 <212> DNA
 <213> Homo sapiens

<400> 1349
 aacggcgtgc tgacctacca tccaaattta catgattaca tgaagaatat tcatggtaaa 60
 gagattgacc ttgggaga 78

<210> 1350
 <211> 102
 <212> DNA
 <213> Homo sapiens

<400> 1350
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 atcaagggga aagtgccttt gtactcaatg gcgcaattgg ta 102

<210> 1351
 <211> 54
 <212> DNA
 <213> Homo sapiens

<400> 1351
 tgccgaccg taccatcaca ccacggggc cgcggcgacc tacagcattg gaac 54

<210> 1352
 <211> 347
 <212> DNA
 <213> Homo sapiens

<400> 1352
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 aaaatgccag acaagatata cagtggaggg atgcacatac aaagagttgg gaaaaaggaa 120
 aaataattac atggggaaga ggatttgctt ctgtctctcc aagtgacaat caggtgcctc 180
 tgtgggtgcc caccaaact ctgaaggtct atcatgagcc acaccaggaa gagaggactc 240
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 gaaaagacca agaatactca ccaggcagac cctccaacat ggggaca 347

<210> 1353
 <211> 129
 <212> DNA

<213> Homo sapiens

<400> 1353

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ctggaccca acgaggtgtg ggagatcgtg ggcgagctgg gcgacggcgc cttcggcaag 120

gtttacaag 129

<210> 1354

<211> 33

<212> DNA

<213> Homo sapiens

<400> 1354

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<210> 1355

<211> 33

<212> DNA

<213> Homo sapiens

<400> 1355

gagaatttgg cttgcgggag tactcagaag tta 33

<210> 1356

<211> 326

<212> DNA

<213> Homo sapiens

<400> 1356

aggtttcatt ggacatatac ttccatgtgg ctggggagat ctcagaatca tgacagggag 60

gtgaaaggca cttcttacat ggtggtggca agagaaaatg aagaagatgc aaaagcggaa 120

acccctgata aaaccatcag atcttgtgag acttattcac tatcacaaga acagtatcat 180

ggggaaaccg accccatgat tcaaattatt tcccacctgg tccctccac aacacgtagg 240

aattatggga gctacaattc aagatgagat ttgggtgggg acacagagct aaaccagggg 300

aaaagcacat tctggggcct atcaga 326

<210> 1357

<211> 149

<212> DNA

<213> Homo sapiens

<400> 1357

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gccctgaaag gaggcctgcc agcagcccgc ttctcgccgg ctgtgcccag tgtggacagt 120

gctgtggagt cttgggacag ctcggccac 149

<210> 1358

<211> 33

<212> DNA

<213> Homo sapiens

<400> 1358

ggctgatgcc agcccgggcg tgcccctcaa cac 33

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<210> 1359
 <211> 120
 <212> DNA
 <213> Homo sapiens

 <400> 1359
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 tcaacagaat acagtgccca ataagaaaag caaaaccagg atatcttcta ccttaatatata 120

 <210> 1360
 <211> 64
 <212> DNA
 <213> Homo sapiens

 <400> 1360
 agctacacag gaaataacac caccaaaaat aacacattca aactcagagg gcaatcttcc 60
 ctaa 64

 <210> 1361
 <211> 112
 <212> DNA
 <213> Homo sapiens

 <400> 1361
 ggcttcgcg cccaatttct aacagcctgc ctgtccccc ggaacgttct aacatccttg 60
 gggagcgccc cagctacaag acactgtcct gagaacgctg tcatcacccg ta 112

 <210> 1362
 <211> 50
 <212> DNA
 <213> Homo sapiens

 <400> 1362
 gaacagaatt tacactcagc cctggtaacc agtctatccg tcagtaccag 50

 <210> 1363
 <211> 343
 <212> DNA
 <213> Homo sapiens

 <400> 1363
 tagggtcttg gggatatcaat gtctcccact ccatttcctg ctcatcttcc aggactgggt 60
 ctagtcttccc attcacacac ctctgtggct cctccctgggt tacctaattc ttgactctgt 120
 caatttaagg agcagcagat aaggcttagt aacttactat tgatgttttg gatccatgag 180
 catcagctaa ggcctgctgg aaagcttcag gcaacgcaca gagcacagca gtcaccagg 240
 actgaccctc aactggggcc cggtggtgtg cactccacca gactaactc gtcatgtctc 300
 tcatcaaaaa atttggcatg tccactgtgc caacaaagtc ctg 343

 <210> 1364
 <211> 252
 <212> DNA
 <213> Homo sapiens

 <400> 1364

GBX1170_3WO_ST25.txt

tggctccctg ttgttcttag cacaatgacc caaatcctca gcatggcctc taaggccctg	60
tactggtgcc agctgccttg ccagcccacg cctggtaact ccgacccttg ctgtgcactc	120
atcccccagc atctccagtt cccagcactc agactcctgc cagctctagg cctctgcaca	180
cagtgcactt cagctcagag cacaccccct ctcccagttc actcctgtgt gtcctcagg	240
tcggtgtcta ct	252
<210> 1365	
<211> 35	
<212> DNA	
<213> Homo sapiens	
<400> 1365	
atgccatggg ccctagacac ctcagttcat tgtgg	35
<210> 1366	
<211> 285	
<212> DNA	
<213> Homo sapiens	
<400> 1366	
acgcttcgtt ggtctcggga atacagctcc acacgcaaaa aagtaaaaag tgcagcaaaa	60
caacaacaca acgatcaacc tcaaaggaaa caacaaaatt aattttatca aaatgcaatg	120
tgtacattaa gactaaagtt atggattgtt cctgtttggc atagaaatgt gatgactatt	180
aacagaaagg ggaaaaagat ttgcccccta tccatcatca gacagacaga cttctcttac	240
taaacccctt atgtggagtg ggatgagtga ctatttcctg cagaa	285
<210> 1367	
<211> 57	
<212> DNA	
<213> Homo sapiens	
<400> 1367	
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<210> 1368	
<211> 111	
<212> DNA	
<213> Homo sapiens	
<400> 1368	
tttactgaaa taagccattc aatcaatggg caataatcct tggatataaa tgcccaggct	60
ttgccacca ctagggtgac tctaagccaa gtcacttcat ctatgaatgc c	111
<210> 1369	
<211> 77	
<212> DNA	
<213> Homo sapiens	
<400> 1369	
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gaagtcaggc acggtgg	77

GBX1170_3WO_ST25.txt

<210> 1370
 <211> 54
 <212> DNA
 <213> Homo sapiens

 <400> 1370
 gagcagaggc ttgaggggta tggttgggta gccatggatg cagcgggtac gtac 54

 <210> 1371
 <211> 81
 <212> DNA
 <213> Homo sapiens

 <400> 1371
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 gcagccttat gattaaactt c 81

 <210> 1372
 <211> 109
 <212> DNA
 <213> Homo sapiens

 <400> 1372
 acgtgtgaat gcagcgctgt gtctttaagg ggcacgcgcg gaggttttcc gtccgggaca 60
 aaatgtcagc gaggcgcctg gagggggatc taccatctcg gactcccga 109

 <210> 1373
 <211> 121
 <212> DNA
 <213> Homo sapiens

 <400> 1373
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 gaaaggggtg cccggcagtt gggcctggca ctggggccag cgctgggtct cctaggtgac 120
 c 121

 <210> 1374
 <211> 375
 <212> DNA
 <213> Homo sapiens

 <400> 1374
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 aattttaaat gtctgtaaaa atttgtgagg gaacaaagtt attttctatt atgaatttac 120
 taaacactag atgacatttt aagccatcat atgttatcaa taaaaattag cacaagagaa 180
 attccagcac agggcacagg atatagtagg caataatata ccttagagag agagaagaag 240
 gaaaatgaga gacagaggaa ggctctatth taaaatgaca taaatcattt tcctgatctt 300
 gaagactaat ggagataggg agaaaggata aaataagccc atgtaaaatt gcctagactc 360
 tgaacaagca acaag 375

 <210> 1375
 <211> 602
 <212> DNA

<213> Homo sapiens

<400> 1375

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acgactccta gcatcttcgg gaggtcctg aaggactgaa gcaaaggaaa tctctgaagg      60
gatttagtcc ttgaaagggg gtagggatac ttaggggtgtt ctgtgttgag cgcttcttcc    120
tatctctcca gttcatgta tgtgtgtctt tatgtccaag caattgagcc aacaagtcct      180
cagaattcct tgtgaaaaaa acgttttttt tttttgagac ggattctcac tctgtcgccc    240
aggctggagt gcaatggtga aattcagctc actgcaacct ccgcctccgg ggttcaagcg     300
attctcctgc ctacgcctcc cgagtagctg ggattacagt cacgcgccac cagccccagc     360
taattttgta tttttagtag agacaggatt tctccttggt caggctgggtc tggaactccc    420
gacttcaggt gatccgcccc cctcggcctc ccaaagtggg gggattacag gtgtgagcca     480
ccgtgcccag ccctgaaata gtcttaattg cttgtttttc tttttgtct gaggtgtgct     540
ttttaaaatc tctatggaga tggagaagac tgacattctc tggcctgatg tgaaaacctc    600
tc                                                                           602

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<210> 1376

<211> 87

<212> DNA

<213> Homo sapiens

<400> 1376

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aggctttgtc tttcacctgg agagaaaata ggcagcttag ctctctctcg actttgggga      60
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```

<210> 1377

<211> 65

<212> DNA

<213> Homo sapiens

<400> 1377

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cagatacaca aaattccacc ccatgatcaa gaatcctgct ccactaagaa tggtgctaaa      60
gtaaa                                                                      65

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<210> 1378

<211> 86

<212> DNA

<213> Homo sapiens

<400> 1378

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ccacactttg attagcaagg atttagagcc aaggggcttc catagcacag acaatattgg      60
atccaccacc aaaagggttac aatca                                           86

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<210> 1379

<211> 39

<212> DNA

<213> Homo sapiens

<400> 1379

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agtttctgtc agcagtagtt tcaccattt gcatggaaa                               39

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<210> 1380
 <211> 553
 <212> DNA
 <213> Homo sapiens

<400> 1380
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 ataaagcctt gattaaacca ttcataccct atattactca tacctttact tcagagattg 120
 aggaactata tacaacaaat taattttattt tcaccatagg gataacatac tgtacctctc 180
 tgccaatgtt acttgaaaat cttccatgtc aaaacaactt gacagtagat ataaacaatt 240
 caataaatat gcaatgatct ttcattacag tccttttaaag acgcatgtta attcatgctg 300
 ttaaccttag gatcacagtg catagaatcc aaatataaac agttgggggtg actttttaaag 360
 taatgttgga tccctcactt tatttatatt cccactataa ccagtaagtt catttcatag 420
 gccctatcat gcattaatca ttgaatggca ggagttaatg aaaacttttc ctgttacaac 480
 gccattgcc ggcaatgaac gtacaaaac cgccaaggaa gtcattgtta ttgcacaata 540
 catgaggacc tgg 553

<210> 1381
 <211> 30
 <212> DNA
 <213> Homo sapiens

<400> 1381
 gaggtgatac cagagccttc gcaacaccag 30

<210> 1382
 <211> 68
 <212> DNA
 <213> Homo sapiens

<400> 1382
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 tgaatccc 68

<210> 1383
 <211> 71
 <212> DNA
 <213> Homo sapiens

<400> 1383
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 cacttgcaaa c 71

<210> 1384
 <211> 50
 <212> DNA
 <213> Homo sapiens

<400> 1384
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<210> 1385

<211> 765
 <212> DNA
 <213> Homo sapiens

<400> 1385
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 tcttcgtttg tcagtgtttc tgaacaagca gagattgatg tctttttata accttaaagg 120
 ctgaaattcc acaagccata agcaggtcca gtccggtttc ctggaggccc ggggaggcct 180
 cattcccact tttgaagtgc agtccttggt tcttactctc aggcttgtca tgcctaatta 240
 aatgaaattt gtctttaact gtgacatttc tggcacagcc atggttacaa atttgattta 300
 cccaattata tcctgttagg aaggaggaca gattcttaca gatcctgttt acagaactaa 360
 tgatcgtaaa agaaaagggc ctcagcaaag gtactttgaa gagtttttag ctattattcc 420
 tagtagtttt gtagataagg ccaattacat ttgttgtttt caatagaatg attatttgaa 480
 catttccttg atgatttatt atttcatatc tatgttaggt ttttatagtc cccctccac 540
 cctcaccccc agaattctga agagttagtt ggaagaagga agaaggcacc attttaggaa 600
 tattttattc cagtttattg aatacagcct cctaaattga ggattagcga cagtaataaa 660
 gaaaaaaaaa gacctttaga aaattagaac attaagggtg aaatcagttt catccagtcc 720
 tggggaaaaa ttcctgttcc tctgatcctg ggtagtttag cctgc 765

<210> 1386
 <211> 94
 <212> DNA
 <213> Homo sapiens

<400> 1386
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 gctgcagtca gccagcagct tgctccccgt gagg 94

<210> 1387
 <211> 500
 <212> DNA
 <213> Homo sapiens

<400> 1387
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 gctcaaaaca aaactttgtg ttcagtctga gttatcttgt attatgtttt aatgggttag 120
 ttttattttt cagtgttttt catataaact gcctccaatc ttttctctaa aggagtagag 180
 gtataaacat acacatagag gactgagtga tggtaggacc ttgggtgagg agaggaggga 240
 ttagaagaaa acaattctga aagaaagaag gagcacaaga gggtcagagg tgagaaggat 300
 agaaaggtaa gtgttgaaga aaagaaagtg gaaaagtctt agaatatctc tagctggcag 360
 gagaagggag agggagctgg cctcagggaa aggtgatctt cctaaacagg tcctccattt 420
 ccctttgggt ctgggtctag gccggggcct tgtctgaata ggcttaaca tgaaagcgag 480
 cgttcttgag ttctggtttc 500

<210> 1388
 <211> 31
 <212> DNA
 <213> Homo sapiens

 <400> 1388
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 <210> 1389
 <211> 65
 <212> DNA
 <213> Homo sapiens

 <400> 1389
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 ctacag 65

 <210> 1390
 <211> 145
 <212> DNA
 <213> Homo sapiens

 <400> 1390
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 gtcagccttt tccatattta ggacatttct ctccccctg gagaaagtcga accgctggat 120
 ctacatagcg ctttatctgg gatcg 145

 <210> 1391
 <211> 82
 <212> DNA
 <213> Homo sapiens

 <400> 1391
 ggtctcggga aaatgctgcc cgcgacaacc cactgcggga ccctaaatgt ctcgacaata 60
 aggcctcctc ggcacgtctc tg 82

 <210> 1392
 <211> 96
 <212> DNA
 <213> Homo sapiens

 <400> 1392
 ggcccagctt catggatata caaactatac attcacatgg gttccacacc tagatgggct 60
 cttacatcat gtagctgggc ctacctggga gagagc 96

 <210> 1393
 <211> 198
 <212> DNA
 <213> Homo sapiens

 <400> 1393
 agtacaatgc atactcctta ggttcttaaa ctctaccagt ctaacagaaa gcaccaagat 60
 acagatgcc aagtcagaaa aaatacaaag cagctcagaa tcaatatcat atatcttatt 120
 caaggtaa at tttatgtag attctttgtc tggcatttgg gaggctaaat taacttagga 180
 ggctagagat cccatctc 198

<210> 1394
 <211> 109
 <212> DNA
 <213> Homo sapiens

<400> 1394
 catcaagtag tggtagcaga cttcatagag gttatgtaga agaagccaca ttagaagaca 60
 agccatcaca gactacccat attgtatttg ttgtgcatgg cattgggca 109

<210> 1395
 <211> 567
 <212> DNA
 <213> Homo sapiens

<400> 1395
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 aaactgatct ttctaaacac aggtcagctc atgtcactca cctcctcaga aatcttcagt 120
 agctcttcat taaccaacag ggggttccta actccccgtc ttggcattgg aggacctttc 180
 cctgcctgat ccccgcatc atcttttcct gcaatattta ctcaggccag tgctcacccc 240
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 ttccctgtca agacttcaca taggtggact gatgctagac tatgatgatg agtctccagt 360
 gaaagtttct aagtagaact ctctcagggt ttctagaagc atttttgttt aagaaaatat 420
 tgtgggggga gcgggatttt taaatgggtg agctcatggt aaacaaaatt atgtgtgcaa 480
 aatgttaata gagcctttct aatattcttg tgattaactc tgggtgacagt tggctgagtg 540
 ttcttgtttc tgcaacgcct gtctttg 567

<210> 1396
 <211> 152
 <212> DNA
 <213> Homo sapiens

<400> 1396
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 agagtagctg tctggctttt gtgtagacaa aatactttct caactccacc gcttgggcaa 120
 aggcaaggct gtgctgacct aatttcatt cc 152

<210> 1397
 <211> 88
 <212> DNA
 <213> Homo sapiens

<400> 1397
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 acttgcggcg atgtcacccc tgccctgc 88

<210> 1398
 <211> 237
 <212> DNA
 <213> Homo sapiens

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<400> 1398
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aactacactg cctgggttgat cttctctctg aatatttcgg tgctatctct ttccttcagt 120
ttgcatcttc ccctctcaga aatgtatgtc aatctaaaag tccaatccca tccactttct 180
gtattgggtca tttcatcatc ttccagggct tcatccatga cttgcacctg tgtgacc 237

<210> 1399
<211> 115
<212> DNA
<213> Homo sapiens

<400> 1399
atgctgcgta aggcctcaat cccactgaaa gctggaagca gtgggacaga agggttccag 60
agagagggtta aagaagaaag tgaaggggga gaatatggaa atcataggga gatca 115

<210> 1400
<211> 192
<212> DNA
<213> Homo sapiens

<400> 1400
agtcactctg gcatcgctg caacagcaaa taaatgagtg gcaaacaagc tctcgcgag 60
ggattttaaa tattttatgt gactaagaag aatgagatac gtccatttgc tgtgataaga 120
aaagatattc cacagtttcg tatttggttaa gtattttcag caaatcatgg aacacgatgc 180
aacacccgat tc 192

<210> 1401
<211> 63
<212> DNA
<213> Homo sapiens

<400> 1401
gagggctctg gacgtcctca gggcagcgga gtgacagaaa tgcaagggtg accccaaccg 60
cag 63

<210> 1402
<211> 113
<212> DNA
<213> Homo sapiens

<400> 1402
cgagactccc ctcgactgtt gttgggatgg tggtagcgt ggtagagccg tctgctttga 60
gtcaccgggc tggctagaa tatagaactg acagtccaaa tgctatcct ttc 113

<210> 1403
<211> 81
<212> DNA
<213> Homo sapiens

<400> 1403
gatgcgcgcc gtacatccgg cactgggtct ctgcctcctc ccagctcctt cgtgtggaaa 60
agtgttgta gcaggcgccc t 81

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<210> 1404
<211> 66
<212> DNA
<213> Homo sapiens

<400> 1404
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cagctt                                                                    66

<210> 1405
<211> 43
<212> DNA
<213> Homo sapiens

<400> 1405
caaggagatt ccagcggtg cccatactgt ttgtgccagg cag                          43

<210> 1406
<211> 95
<212> DNA
<213> Homo sapiens

<400> 1406
atgtgcaaat atcaccacta attccagaat atttaatcac ctcaaaaaga acccccctga      60
cacacacacc cagtagcagt ccatgccccca cttcc                                95

<210> 1407
<211> 96
<212> DNA
<213> Homo sapiens

<400> 1407
gtggaggatg gtcataaca cttctcggaa tcctccatca aatgtgcact ccactctcct      60
ctccttctct cccctaaatc cacatcacca gcttgg                                96

<210> 1408
<211> 89
<212> DNA
<213> Homo sapiens

<400> 1408
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ctacgttgtc ttttcgcttc tctggggag                                       89

<210> 1409
<211> 135
<212> DNA
<213> Homo sapiens

<400> 1409
agaagtccac ttggctctat cctgggtcct gaaggagaag caagaagaag gtcttcgcag      60
ggaagtctct gctcaaagca aaatctcttt atggaatggc atgagctatc tcattattaa    120
attcaccagc agcca                                                         135

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GBX1170_3WO_ST25.txt

<210> 1410
 <211> 284
 <212> DNA
 <213> Homo sapiens

 <400> 1410
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 tttagaattc aaaaactttt tatatgtttt tcctgataaa tagtgcttaa attacttgtc 120
 aatattctgt tccaaagaat gcatacaaat tggattttgt ttttcatttg atgtgtgtta 180
 agagtggaaa agatgcataa ctgacgtgca tctggcatat ctgatgtgcc gcaactgcca 240
 acagttcaga taactttatg gtggtcacag gtcagtcata atga 284

 <210> 1411
 <211> 60
 <212> DNA
 <213> Homo sapiens

 <400> 1411
 tggaagcgcc actaccagcc cacgaaactc tttgaggcca gaaatagcgt cttgaccccc 60

 <210> 1412
 <211> 51
 <212> DNA
 <213> Homo sapiens

 <400> 1412
 ggacctcttc gaagggctgg gagtagagag agaataccac cccgaagagc t 51

 <210> 1413
 <211> 178
 <212> DNA
 <213> Homo sapiens

 <400> 1413
 gaatttagac cttttccctg caccactctc ttcattctgg gggctctgtt acactaattt 60
 gaataaactc tcccctttct ttgcaacttc ccagcaacaa taatgatttt cttgccaggc 120
 cgtctcttgc tccctaattc atttcccagg aagctgtgat acagggtgaa ataaagtc 178

 <210> 1414
 <211> 81
 <212> DNA
 <213> Homo sapiens

 <400> 1414
 tgccttcgt gcagagatca cagatgctga aggctgggt ttgaagctcg aagatcgaga 60
 gacagttatt aaggagttga a 81

 <210> 1415
 <211> 357
 <212> DNA
 <213> Homo sapiens

 <400> 1415
 atcagtggat tctcgggggtt tggacttaat gttgagctaa gaagcattaa gtctttgaac 60
 tgaatgtatt ttgcatccct ggttttggac gacagtaaac gtaggagcac tgttgaagtc 120

GBX1170_3WO_ST25.txt

ctggaaggga gatcgaagga ggaagattga cttggttctt tcttagtcct atatctgtag	180
catagatgac ttggaataaa agctgtatgc atgggcatta cccctcaggt cctaagaaat	240
aagtcctgaa tgcattgctg tccaaactaa cactctgtaa tttttctttt atgtcttatt	300
ttccaagagt cctccatttt ttgcaccccc tcaccgcaa ctctgttatt cagtaga	357

<210> 1416
 <211> 61
 <212> DNA
 <213> Homo sapiens

<400> 1416	
tggactttga gaaaagccga agtcagcggg agcaggaaga aaagctgctc atcagtcct	60
g	61

<210> 1417
 <211> 70
 <212> DNA
 <213> Homo sapiens

<400> 1417	
tgctcctttc ctttatgtca actctccac aggtcttagg gaatcccttc tcctctctta	60
atggcaagca	70

<210> 1418
 <211> 47
 <212> DNA
 <213> Homo sapiens

<400> 1418	
caatcctaaa catatttggg agctgcacac ctaaaagagg agctccc	47

<210> 1419
 <211> 33
 <212> DNA
 <213> Homo sapiens

<400> 1419	
aggaggtggc aaaactaggc gactttccaa atc	33

<210> 1420
 <211> 284
 <212> DNA
 <213> Homo sapiens

<400> 1420	
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cccgcgcggc tcccgctcgg cgcccgctag cactggggcg cgaccaactg tttaccgaga	120
gaggggggat gttgcagcac ccggcgaagc tgtgtggctc cgaagcggat tttctggaaa	180
ccctacgtcc ccaagttcgc tttcatgtaa caggtgcatg cagatggaga ggaagacgca	240
agcgaagaag aaaggactgg gcgaaaatag ctcggcctgc cgca	284

<210> 1421

<211> 58
 <212> DNA
 <213> Homo sapiens

<400> 1421
 agatataatt ggttgtggac ggctaaatga acctattaaa gtcttgtgtc ggagagtt 58

<210> 1422
 <211> 130
 <212> DNA
 <213> Homo sapiens

<400> 1422
 gattctacct ctgctctttc cgcaatccac caagccccgt aaacttgcca gaagttacat 60
 tgtgtctgca gttataatgt ttaaaacatg ctctcacttg accccaggat tctcattagc 120
 tgggttaccc 130

<210> 1423
 <211> 405
 <212> DNA
 <213> Homo sapiens

<400> 1423
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 ccaaactacc aaaagtttgc tccatgtcac aacctgccct aggcctccag gccaatgtga 120
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 <212> DNA
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 gataaaacca atgatgggca cacatttacc tgtgtaacaa acctgcacgt cctgcacatc 240
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tg 302

<210> 1426
 <211> 201
 <212> DNA
 <213> Homo sapiens

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 gacagtacac ctcgaggagag a 201

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 <212> DNA
 <213> Homo sapiens

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<210> 1428
 <211> 195
 <212> DNA
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 tcctgcgccc gagaa 195

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 <212> DNA
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<400> 1430
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<210> 1431
 <211> 84
 <212> DNA
 <213> Homo sapiens

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 atggatgccc agtccaacaa tcct 84

<210> 1432
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 <212> DNA
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 <210> 1438
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 tatggagcag gtatta 196

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 cagaagg 127

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 catgcaagca tcaaggta 139

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<211> 37
 <212> DNA
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<210> 1442
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 <212> DNA
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<210> 1444
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 <212> DNA
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<210> 1446
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<212> DNA
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 tgcattgacat atatacc 317

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<210> 1449
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 <212> DNA
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 gtacctgtgc ctga 74

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 ggttgtaaat ctccagaagt ggtggaatta aacacaagca cacacacaca tacacacaaa 180
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<210> 1451

<211> 203
 <212> DNA
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 gtatcctgac agcgccatgt gtg 203

<210> 1452
 <211> 1050
 <212> DNA
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 cctcctgggc atcgaggccc atctccacag cagagtatgc cctcctctac cacaccctgc 180
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 <212> DNA
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<210> 1454
 <211> 90
 <212> DNA
 <213> Homo sapiens

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 ctaaccaaat tacagccact tcttaataag 90

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 <212> DNA
 <213> Homo sapiens

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 <210> 1456
 <211> 187
 <212> DNA
 <213> Homo sapiens

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 <212> DNA
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 <210> 1458
 <211> 104
 <212> DNA
 <213> Homo sapiens

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gtggtgttaa gccttgggcc ttc	83

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tcttgata	189

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actc	124

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<211> 176
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<210> 1466
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<212> DNA
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<210> 1467
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<212> DNA
<213> Homo sapiens

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tccatgtaca agta 134

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<210> 1469
<211> 253
<212> DNA
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GBX1170_3WO_ST25.txt

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<210> 1474
 <211> 41
 <212> DNA
 <213> Homo sapiens

<400> 1474
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<210> 1475

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<211> 74
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<212> DNA
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<212> DNA
<213> Homo sapiens

<400> 1477
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<210> 1478
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<213> Homo sapiens

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<211> 266

<212> DNA

<213> Homo sapiens

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tggagtaggc caagttcaaa gcctggaaaa cagggcacag agctctcagc atgggtccccg 180

cacacatgtg cagatgaaga actgtgtgag aagatcactc aacacacaca ggctcaggtg 240

agcgggtctg agtctactga cttgta 266

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<211> 86

<212> DNA

<213> Homo sapiens

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gcgacaccgc acagagcttc ttcccg 86

<210> 1482

<211> 28

<212> DNA

<213> Homo sapiens

<400> 1482

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<210> 1483

<211> 69

<212> DNA

<213> Homo sapiens

<400> 1483

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tgcccttg 69

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<211> 51

<212> DNA

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<400> 1484

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 <213> Homo sapiens

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 <210> 1486
 <211> 57
 <212> DNA
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 <210> 1487
 <211> 119
 <212> DNA
 <213> Homo sapiens

 <400> 1487
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 <212> DNA
 <213> Homo sapiens

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 <212> DNA
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 atggtgtcca acacgcctct ctgtt 325

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 <211> 168
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 <213> Homo sapiens

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 gcctgccatc accaccacaa gcaccagtag gaaatctctc cttggtgc 168

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<210> 1491
 <211> 68
 <212> DNA
 <213> Homo sapiens

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<210> 1492
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 <212> DNA
 <213> Homo sapiens

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 cccacagtgc taggcttggc ccgcctaagg cactgggtgt acctg 165

<210> 1494
 <211> 107
 <212> DNA
 <213> Homo sapiens

<400> 1494
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 ggcgaggttg ctcacgggga acaccattgc ctttgtgcta ggcgggg 107

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 ttctcgtgaa ggaaatcata g 81

<210> 1496
 <211> 78
 <212> DNA
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 actcagctac aaatagaa 78

<210> 1497
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 <212> DNA
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<210> 1498
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 <212> DNA
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<400> 1498
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<210> 1499
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 <212> DNA
 <213> Homo sapiens

<400> 1499
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<210> 1500
 <211> 145
 <212> DNA
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<400> 1500
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<210> 1501
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 <212> DNA
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<400> 1501
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<210> 1502
 <211> 142
 <212> DNA
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 tcttgggtct ttcacagtcc tc 142

<210> 1503
 <211> 35
 <212> DNA
 <213> Homo sapiens

<400> 1503
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<210> 1504
 <211> 456
 <212> DNA
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<400> 1504
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 taaatccagc aacatataaa aaagatcata tgctgtaacc agtaaaattt atctcagaaa 180
 tgcaagggtg gttcaacata caaatcaat caatgtaata aagcatacta aaggacaaaa 240
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<210> 1505
 <211> 91
 <212> DNA
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<400> 1505
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 tggggacagt tgaagcacia cctccacaaa g 91

<210> 1506
 <211> 115
 <212> DNA
 <213> Homo sapiens

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<210> 1507
 <211> 53
 <212> DNA
 <213> Homo sapiens

 <400> 1507
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<210> 1508
 <211> 214
 <212> DNA
 <213> Homo sapiens

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 aataataaaa cacaggaaac aacttacatg tacataggctc ttgaagtgag tgaagcggct 120
 gtattttttt ggggggggca ttgcttttgt tttttagata gagattgaga tgatactcta 180
 ttctaataca aattagagat ttgtagtggg acca 214

<210> 1509
 <211> 146
 <212> DNA
 <213> Homo sapiens

 <400> 1509
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 agaacagggc ttcagagacc gcagaaactc cacaccacga gaacagggct tcagagacca 120
 gagtaactcc acaccgtgag aacagg 146

<210> 1510
 <211> 1112
 <212> DNA
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 gttggcactg acagtcttgc atggtcatat gccagtgttt ttgcttttagc ttttctttga 300
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<210> 1511
<211> 123
<212> DNA
<213> Homo sapiens

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ttt 123

<210> 1512
<211> 123
<212> DNA
<213> Homo sapiens

<400> 1512
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cctggcatct ggcccacagg agtggcaccc ctccccaaga cttccacac agtttctata 120
tta 123

<210> 1513
<211> 253
<212> DNA
<213> Homo sapiens

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tcccatcctg tta 253

<210> 1514
<211> 225
<212> DNA
<213> Homo sapiens

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 <212> DNA
 <213> Homo sapiens

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 ttcatgaaga agggcc 136

<210> 1516
 <211> 370
 <212> DNA
 <213> Homo sapiens

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 ataatatattc 370

<210> 1517
 <211> 101
 <212> DNA
 <213> Homo sapiens

<400> 1517
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 ggctaccccg atgtatccag tgggtacacc ttggcccaca g 101

<210> 1518
 <211> 69
 <212> DNA
 <213> Homo sapiens

<400> 1518
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 ctaccattc 69

<210> 1519
 <211> 194
 <212> DNA
 <213> Homo sapiens

<400> 1519
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 ctgccagata ccta 194

<210> 1520
 <211> 113
 <212> DNA
 <213> Homo sapiens

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 <213> Homo sapiens

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 <212> DNA
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<210> 1524
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 <212> DNA
 <213> Homo sapiens

<400> 1524	
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gtgtgtttcg aatgagaaaa aacaaattgc ttattcggac ctctagcaac tgccaata	118

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acgatgtgtc ctgtcgctgc tcttg	145

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 <212> DNA
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<210> 1527
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 <212> DNA
 <213> Homo sapiens

<400> 1527
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 accacggtga ccgagtgtct gcaca 85

<210> 1528
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 <212> DNA
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 tgttggaggt cagtagcaca gtttggtgta gatgcatggt a 221

<210> 1529
 <211> 312
 <212> DNA
 <213> Homo sapiens

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<210> 1530
 <211> 100
 <212> DNA
 <213> Homo sapiens

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<210> 1531

<211> 1046
 <212> DNA
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 <210> 1537
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 <212> DNA
 <213> Homo sapiens

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 gtgcttacac tttaccgcta g 81

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 tgcttttacc tg 252

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<212> DNA
<213> Homo sapiens

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<210> 1547
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 gggcattgct cattttcatg tactatt 147

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 <212> DNA
 <213> Homo sapiens

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 <212> DNA
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<210> 1559
 <211> 99
 <212> DNA

<213> Homo sapiens

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<211> 32

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<210> 1561

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<212> DNA

<213> Homo sapiens

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tga 63

<210> 1562

<211> 218

<212> DNA

<213> Homo sapiens

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aaacattcca ggtcgttagg gaatagcata gattatttaa tccctgtgga ttaaagcccc 180

actgaaatca aagcctgagc ttttccactg tgaagggtg 218

<210> 1563

<211> 326

<212> DNA

<213> Homo sapiens

<400> 1563

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cattgattca ctggaaagca aagtacagct tccaccataa aaccctgcag ctgaaaaagg 180

acaaactgag cagctctcaa ataaagacag cctcagccgt cttgcacagc acggccccctc 240

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<211> 195

<212> DNA

<213> Homo sapiens

<400> 1564

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cacaagacgt ggga                                              74

<210> 1575
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<400> 1575
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<210> 1576
 <211> 273
 <212> DNA
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<400> 1576
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 aggacacaaa attgctttat tctacaactg ccagctccag gcagaaatag gaaggcaaag 180
 agataagaga aggaaaaatg agagaatgaa gtctgtatag ggtagagcaa tagaaagtaa 240
 gcttcgggtg cctccaacgt tcatggctgc ctg 273

<210> 1577
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 <212> DNA
 <213> Homo sapiens

<400> 1577
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<210> 1578
 <211> 33
 <212> DNA
 <213> Homo sapiens

<400> 1578
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<210> 1579
 <211> 68
 <212> DNA
 <213> Homo sapiens

<400> 1579
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 ggaagggg 68

<210> 1580
 <211> 231
 <212> DNA
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<400> 1580
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 accttgaggg cagtcagaag cacagaaggg ctggataact atgggaaatg actggtcgct 180
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<210> 1581
 <211> 81
 <212> DNA
 <213> Homo sapiens

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 gaagcgatct gagaagttga a 81

<210> 1582
 <211> 165
 <212> DNA
 <213> Homo sapiens

<400> 1582
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 gatagccaca taaagaattc ttgcagcaca gccacgaaag gtttc 165

<210> 1583
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 <212> DNA
 <213> Homo sapiens

<400> 1583
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<210> 1584
 <211> 78
 <212> DNA
 <213> Homo sapiens

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 ctgcaatagg tcatttga 78

<210> 1585
 <211> 34
 <212> DNA
 <213> Homo sapiens

<400> 1585
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<210> 1586
 <211> 67
 <212> DNA
 <213> Homo sapiens

<400> 1586
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 agatgcg 67

<210> 1587
 <211> 106
 <212> DNA
 <213> Homo sapiens

<400> 1587
 ctgcgagtc cagcctttct cctgttgggt gatgctgcta agcatgctcc caggatagag 60
 gaagcatctg ccatgcttgt gggtagacat gggttactaa gtaaca 106

<210> 1588
 <211> 213
 <212> DNA
 <213> Homo sapiens

<400> 1588
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 gagaaggctg caggagtcct ttgttgctca gcagggcgct ctgccctccc tccttccttc 180
 ttgcttctaa tagccctggt acatggtaca cac 213

<210> 1589
 <211> 305
 <212> DNA
 <213> Homo sapiens

<400> 1589
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 cagccgcgag aaggcgggga ggcgcggaca gccgcaaact tccccttctt cgcgcaagct 180
 tcgcagacgt gtccgggtcg tttgctctta aaggggcccgg cgctctacct ggcgaagcca 240
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<210> 1590
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 <212> DNA
 <213> Homo sapiens

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 agtaaatagg ctatTTTTTc ttactgggtc tggcttctct ggcccttcgc atacgtgtgt 180
 ctgctgagtg ttctgcatg taagaattaa gaccaaggga ggggagagag aaaccacac 240
 ataaacaatg cactaaagat cactgaactg tttaaacatt tccacttgcc agtttaattt 300
 cttgaagact gttgcttggt tggaatgttt cttgtcactg attttaaggt tgcattctgga 360
 aaagactaaa ggcttcagtc ccctcccacc accagaaatg aacaaaaagc attttaccta 420
 aaaatacacc agcaaaatgt actcagcttc aatcacaaat acgactgctt aaaactgcag 480
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<210> 1591
 <211> 35
 <212> DNA

<213> Homo sapiens

<400> 1591

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35

<210> 1592

<211> 293

<212> DNA

<213> Homo sapiens

<400> 1592

agtcccgctg ggccctagac caagacacgg gagaacctgt gaccacccgc cccctggtta 60

gggcacagag gatccacacc ttgccgtgcc ctggactaca gcacggaggg accccgatct 120

gccgggcaact gggctcctgc acagaggagc ccctgccatg gaggtctgga ctgtccttgc 180

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gcatgggaga accctgcccc gcagagccct ggactccgcc actggaggac tcg 293

<210> 1593

<211> 1053

<212> DNA

<213> Homo sapiens

<400> 1593

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cagggtaaac acacaaccta cggaatggga gaaaatatat gcaaactatg catacagcaa 180

agatctaata ttcagaatcc attaggaact taaacagatt aacaagcaaa aaaaacaagc 240

aaccaccatta aaaagtgggc aaaggacatg aacaaacact tttcaaaaga agatatacac 300

atggccaaca aggatatgaa aaaatacctg atatcactaa tcattagaga aatgcaaadc 360

aaaaaaatgc catcacacta atcagaatgg ctgttattaa aatgccaaaa aattacagat 420

gctggcgagg ttgcagagaa aggggaatgc ttatacactg ctagtgggaa aataaattag 480

ttcagccatt gtggaaagca gttgggtgat ttctaaaaga acttaaaaca gctaccattc 540

aagccagcaa tctcatgact gggatatatg ccaaaggaat ataaattggt ctaccataaa 600

gacatgcaca tatatgttca ctgcagcact attcacaata gcaaaacatg aaatcaacct 660

aaatgcccat caatggtaga ctggataaag aaaatgtgac acatatacac catagcatac 720

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ctacttgagg gtggaggggt ggaggagggt gaagactgaa aaactgccta tgggggtacta 960

tgcttattac ctgggtgatg aaataatctg aacacaaaac cctggtgaca tgcagtttac 1020

ctatataaca aaactgcaca tggactctta aac 1053

<210> 1594

<211> 2099

<212> DNA
 <213> Homo sapiens

<400> 1594

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gaggcaacta cagtcagatt tatagccagc catctatcac ctctagaagg ttccagagac	240
agtgaaactg caagatgctc tcaacaggat tatgtctcat ggagaccagt aagaaaatca	300
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aatgctgggg tccctgggtg ggtaagaaac tcaacatcag acgggtatgc agaaggatgt	540
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ataaaaggta cagtcagggg aaaatagatc taggcagagt gccttagtca gggaccacgg	1860
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gcctttctccc acagctgcct acaacagagt ctcccagcct tctcagagag ctaaaaccag 1980
aaatttccag actcatgaaa gcaaccccc agcctctccc caaccctgcc gcattgtcta 2040
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<211> 111
<212> DNA
<213> Homo sapiens

<400> 1595
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<210> 1596
<211> 629
<212> DNA
<213> Homo sapiens

<400> 1596
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ggtctcctcc tcccgaactc taaacctgcg tgtgtggctg tgcaccgctc gttttagcgc 540
tcacctcagg tctggggaag tctgtgctgg catctcctca ttgtgccttc atcagagctg 600
gtgccttcgg gccagaaaga ctctcgttc 629

<210> 1597
<211> 78
<212> DNA
<213> Homo sapiens

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tacaagcatg tagttaac 78

<210> 1598
<211> 422
<212> DNA
<213> Homo sapiens

<400> 1598
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ttttttcaaa ttcacacatg tgaatttgaa ttccaggctc atcacatcca ggtgtgttcc 120

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 ctgtcagcag gtcccaaata tctagaattt gattgcttca catccctata gcaactctcc 360
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 tc 422

<210> 1599
 <211> 129
 <212> DNA
 <213> Homo sapiens

<400> 1599
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 cagggatcag gagccagggt catagcttga aaccaggcac tatagtgaga ttcccgtgtt 120
 catgaagga 129

<210> 1600
 <211> 271
 <212> DNA
 <213> Homo sapiens

<400> 1600
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 gaaagtttta gtgttgctg aaatgcaaga gggaagggtga ttggtagtga gttaaaagaa 120
 aaagagagga aaagagagta gttttgtctt caagtaaaat gtctggttgt gccagacatt 180
 tcacaagtgt gaaaggagat aggagaagct caacttgagg gcgtgtagta agttgtagaa 240
 ggctcgaggg gacgtggact tatttgcctt g 271

<210> 1601
 <211> 333
 <212> DNA
 <213> Homo sapiens

<400> 1601
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 ggtgattcca cctcgggtga atcccagcca acttgggagg ctgaggctga aggatcactt 180
 gaacccagga gtttgagtcc agcctgagca acataacgag acttctgtct ctaaaagaaa 240
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 cacacaatcc gtttttggga gatgtattca gcc 333

<210> 1602
 <211> 221
 <212> DNA
 <213> Homo sapiens

<400> 1602

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cctcacagat gaatgaggtc atgctgggaa ttccctctgc agggaaactgg cctgactgac 180
atgcagttcc ataaatgcag atgtttgtct cattaccttt t 221

<210> 1603
<211> 57
<212> DNA
<213> Homo sapiens

<400> 1603
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<210> 1604
<211> 329
<212> DNA
<213> Homo sapiens

<400> 1604
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ggttcacaca tttttcatca taatccattt atataagata acttggaataa gaatctgtaa 240
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accagtactg tgcattgacc cttggcata 329

<210> 1605
<211> 30
<212> DNA
<213> Homo sapiens

<400> 1605
atattaggct caattagaga aacaataaag 30

<210> 1606
<211> 88
<212> DNA
<213> Homo sapiens

<400> 1606
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cacgcccact gttgtggttg tgctggct 88

<210> 1607
<211> 128
<212> DNA
<213> Homo sapiens

<400> 1607
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agcccaga 128

<210> 1608
 <211> 77
 <212> DNA
 <213> Homo sapiens

<400> 1608
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 ctacagccaa gcacact 77

<210> 1609
 <211> 688
 <212> DNA
 <213> Homo sapiens

<400> 1609
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 tcacgcctcc tgcaggatct gggagtggagg gtggagagtc tttcctcacg ctccagcaca 120
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 aagaaaagca gctcagctca ggatgagtct tctgcctga aactgagaga gtgaagaacc 240
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 agctgataag gttcacagtt tctctcacc aggtgtaact ggattttttc tggggcctca 600
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 ctattttccc aggggtggctt caatctcc 688

<210> 1610
 <211> 81
 <212> DNA
 <213> Homo sapiens

<400> 1610
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 acccagact gccactcaca a 81

<210> 1611
 <211> 87
 <212> DNA
 <213> Homo sapiens

<400> 1611
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 catgagagat gaacacgaac aagtgtg 87

<210> 1612
 <211> 180

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<212> DNA
 <213> Homo sapiens

<400> 1612
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 aaggggggtcg gaggaggcgc gggagagaaa agcccagggc tgtacactcg catccctctg 180

<210> 1613
 <211> 34
 <212> DNA
 <213> Homo sapiens

<400> 1613
 gcccacacca gggacatgt ttcacacctcc taaa 34

<210> 1614
 <211> 385
 <212> DNA
 <213> Homo sapiens

<400> 1614
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 taaatgagca ttctaggcag aggccagtat ttgtaaaggc taggatgtgt gaaacgatat 120
 ggtctggtgg gagcagagta tcagtcagta aactggtggg cattgaagct gggcacatca 180
 gcagaggcaa ggcttgagat tgtgagaagc cattgtctct gtggtttctcc ctcatccct 240
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 aggggaaaac atggagctgg gggctctggat gcctgggcct tcctaggaca cctagtcccc 360
 ttccatctgc accttgggggt ctgtc 385

<210> 1615
 <211> 233
 <212> DNA
 <213> Homo sapiens

<400> 1615
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 aagtaagcct aggtgttgtc agcaggcagg ctggggaggc cagtgtttgt ggcttcctgc 180
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<210> 1616
 <211> 34
 <212> DNA
 <213> Homo sapiens

<400> 1616
 cttgagaagg ttactgagtg agttattggg agtc 34

<210> 1617
 <211> 107
 <212> DNA

<213> Homo sapiens

<400> 1617

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ggatccctga atgacactgt ggggcaaagc taccgaccct ccatgga 107

<210> 1618

<211> 543

<212> DNA

<213> Homo sapiens

<400> 1618

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gtccccccat taggattcta ttacatatgc aattgtaggt tcaacctgtc cttttccctg 120

ccagcaaacc ccaccacct aagagaaatt ttagcttata tatgacggta tatttacaaa 180

aagagaaaga gaaaatctgg tatttgcaat gatctgtgcc ttctttttac caccctcttg 240

attggagctt ttgtgatgca gctaccatga ttcaaaaaaa ttaaaaatta aaaaaaaaaa 300

atctgccact tatccaagtc cactagaggc cactgtcttc aaagcttctc tcaccctagc 360

caaaggctcct aagaggagac agctgtgaag ttgggcgtgc tctgtggtac cagctgtgac 420

ttttctatct ctcctagttt taggttggtc atgaaactag aaatgtcatc ctgcttgatt 480

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atg 543

<210> 1619

<211> 157

<212> DNA

<213> Homo sapiens

<400> 1619

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acaagttgga ttggccacaa gaagtcattg ggattccatc catgaacgtg aactttttat 120

tgtggtttgt ccgttccgag cgctccgag aacagtc 157

<210> 1620

<211> 59

<212> DNA

<213> Homo sapiens

<400> 1620

tctgcctcag agactccctg attggcccct tttctgagag gatgtgctat ctctgcagt 59

<210> 1621

<211> 31

<212> DNA

<213> Homo sapiens

<400> 1621

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<210> 1622

<211> 52

<212> DNA
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<210> 1623
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 <212> DNA
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 tcgtcttcag catcacggca ga 142

<210> 1624
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 <212> DNA
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<210> 1625
 <211> 318
 <212> DNA
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 ccctatagca actgggtg 318

<210> 1626
 <211> 375
 <212> DNA
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<210> 1627
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 <212> DNA
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 catgcgatta tctaccacg tccacgcggc cacctcacc tctccgcaca cctctggctg 180
 tctttttgta ctttttggtc cagagctgct tctgtctggt ttatttaggt tttatccttc 240
 cttttctttg agagttcgtg aagaggggaag ccaggattgg ggacctgatg gagagtgaga 300
 gcatgtgagg ggtagtggga tgggtgggta ccagccactg gaggggtcat ccttgcccat 360
 cgggaccaga aacctgggag agacttgat gaggagtggg tgggctgtgc ctgggcctag 420
 cacggacatg gtctgtcctg acagcactcc tcggcaggca tg 462

<210> 1628
 <211> 42
 <212> DNA
 <213> Homo sapiens

<400> 1628
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<210> 1629
 <211> 136
 <212> DNA
 <213> Homo sapiens

<400> 1629
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 agctgcattg agccat 136

<210> 1630
 <211> 543
 <212> DNA
 <213> Homo sapiens

<400> 1630
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 aagttaatct taattgcaat ttgactccgt ttccttggtg gggatagact ttcttcagat 120
 tccaagtgct ctcttaaag gcaaattaag ttaaagaata ctactgtcc attccccca 180
 cttattctcc agttaattgc ttgtcagttc catttcaaga aagcagtgat gttccagggt 240
 tgattcagtt ttcctgtgca cactattgcc aaatTTTTTT ttagcaaaga ttctgactg 300
 gaacgtagac agttggaaac agtactacct acctagaggt tatgtgtttt ctctttctcc 360
 ccgctttcac ctctttcttt cccaattcaa aacagccaag tgagccctgt tctgggtattt 420
 tgaatcatta gagaaaagaa agggagtggc tgTTTTgagt tgcctttct ttgcagaaag 480

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<400> 1632	
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<212> DNA	
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agtagacccc ttcta	75
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<210> 1636	
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ggtttctaac tggaagtga attttttcta tttttaaac tttttttta tttcatagtt	120
actttttaag cttttttgt taaaaattaa gacacaaaca cacaccttat cctaggccta	180

tacaggggtca ggatcatcag tatccgtctt ctgc 214

<210> 1637
 <211> 125
 <212> DNA
 <213> Homo sapiens

<400> 1637
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 cattcctctc tgcgccaggc tctgcccgt cccacctgcc cccgtggaaa tcgcagggtg 120
 acctg 125

<210> 1638
 <211> 269
 <212> DNA
 <213> Homo sapiens

<400> 1638
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 gaaattacat aatgctttcc aaaggcacct acaacttagt tttaaattac ttgctactgg 180
 ggattacca tggatattcct taataggcag gaagtctggg aattctggtg gcctctaggg 240
 cagtgttctc acagcaccgt tccgacagg 269

<210> 1639
 <211> 156
 <212> DNA
 <213> Homo sapiens

<400> 1639
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 tgtgatgagg gctgtaatgg aaggggcaga gagttccatg gaaaactgga gagaggaggc 120
 agaaactgct gcaatatctg ggcttgagct tcacag 156

<210> 1640
 <211> 98
 <212> DNA
 <213> Homo sapiens

<400> 1640
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 gtgaggggtca tgactaaagt tgcatagctt gcaggtgg 98

<210> 1641
 <211> 32
 <212> DNA
 <213> Homo sapiens

<400> 1641
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<210> 1642
 <211> 123

<212> DNA
 <213> Homo sapiens

<400> 1642
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 ttttaagcaa ggacatttca atgatgtgag gaaaaaaaaa agtgccacaa agctttgaga 120
 atc 123

<210> 1643
 <211> 57
 <212> DNA
 <213> Homo sapiens

<400> 1643
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<210> 1644
 <211> 65
 <212> DNA
 <213> Homo sapiens

<400> 1644
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 cagct 65

<210> 1645
 <211> 500
 <212> DNA
 <213> Homo sapiens

<400> 1645
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 tagaaccagt aatggaattg ctgggccaaa cgggtagttc tggtttttta tttatttatt 180
 tttatctgtc tgtctatgta tctatctgtc tattgagaca gagtttctact cttatcacccg 240
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 gatcctccca agtagctggg accacaggta catgccacca tgctggctaa tttttgtatt 360
 ttttttttgt agagatgggg ttttgccttg ttgccaggc tggctttgaa ttcttggtc 420
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 ctggcttagt tctattttta 500

<210> 1646
 <211> 176
 <212> DNA
 <213> Homo sapiens

<400> 1646
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 cttggtaact gtcacaactg cccttaacta atgatttgtg cattgccacc tgaggc 176

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<210> 1647
 <211> 738
 <212> DNA
 <213> Homo sapiens

<400> 1647
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 gctgtgagtg aaccatccac actcttaggg agaccaagcc ttccatttgt gcgctgcatt 180
 ccattttctt tggcctactg aaggacatcc atctctgcta gatgtttcgt atcagcatat 240
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 ccgggttcaa gtgattctcc cacctcaacc tctcaagtag ctgggattac aggtgcatgc 480
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 cagctgttga ctcctttc 738

<210> 1648
 <211> 186
 <212> DNA
 <213> Homo sapiens

<400> 1648
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 ggtcctcctg ggggctgtct gtgggggtcgt gctgtactgt gcctgttggc ataatgggat 180
 gtcaga 186

<210> 1649
 <211> 118
 <212> DNA
 <213> Homo sapiens

<400> 1649
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<210> 1650
 <211> 1348
 <212> DNA
 <213> Homo sapiens

<400> 1650
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gcaaagcaag caaggaacat ttggggtaag aaaacaaaca tgaggcaaaa gaaaaaatac	240
atgtttttaa gaaaacattg agcagagaac tgcagccagg atgcgctcag cagacattca	300
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<210> 1651
 <211> 60
 <212> DNA
 <213> Homo sapiens

<400> 1651	
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<210> 1652
 <211> 61
 <212> DNA
 <213> Homo sapiens

<400> 1652	
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<210> 1653
 <211> 125
 <212> DNA

<213> Homo sapiens

<400> 1653

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 tgta 125

<210> 1654

<211> 100

<212> DNA

<213> Homo sapiens

<400> 1654

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 tacggcatcc tggaccaac caccgagac tggacagatg 100

<210> 1655

<211> 900

<212> DNA

<213> Homo sapiens

<400> 1655

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<210> 1656

<211> 43

<212> DNA

<213> Homo sapiens

<400> 1656

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<210> 1657

<211> 75
 <212> DNA
 <213> Homo sapiens

 <400> 1657
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 cggctctcggc caccg 75

 <210> 1658
 <211> 83
 <212> DNA
 <213> Homo sapiens

 <400> 1658
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 ggggaggcag aatatattga aaa 83

 <210> 1659
 <211> 201
 <212> DNA
 <213> Homo sapiens

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 <210> 1660
 <211> 36
 <212> DNA
 <213> Homo sapiens

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 <210> 1661
 <211> 584
 <212> DNA
 <213> Homo sapiens

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 gtttgtgttg ggtaccattt gtacaacaca gttaatttaa acattttcat tttggttgca 180
 catgaaaaag gcggcagtag aaaataaagt cattgagggt ttttaaatac cagaataggc 240
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 aaatatttag ttcaagtcac agaatttttc tcagtagaga cccaatgca atgcataatt 360
 agctgcctta gatggcccggt ttgaaaggat gatatccctt cagagtgtaa ctttactgat 420
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agtcattgca gaatactgtc ttctgtctac agcagggtgct tatt 584

<210> 1662
 <211> 48
 <212> DNA
 <213> Homo sapiens

<400> 1662
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<210> 1663
 <211> 171
 <212> DNA
 <213> Homo sapiens

<400> 1663
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 cactaccacc ttttccttat actgtatatg attatggcct acaatgttgt a 171

<210> 1664
 <211> 275
 <212> DNA
 <213> Homo sapiens

<400> 1664
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 ttacagagc catctaggag attctgatgt atgttagagt ttgagaaccc tctgacccaa 180
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 ttttcatatt gccagcttcc taggcaatct gattt 275

<210> 1665
 <211> 34
 <212> DNA
 <213> Homo sapiens

<400> 1665
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<210> 1666
 <211> 66
 <212> DNA
 <213> Homo sapiens

<400> 1666
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<210> 1667
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 <212> DNA
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<400> 1667
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<210> 1668
 <211> 93
 <212> DNA
 <213> Homo sapiens

<400> 1668
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 cgtccatggc cttgaaagca cttactacaa ttg 93

<210> 1669
 <211> 247
 <212> DNA
 <213> Homo sapiens

<400> 1669
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 tccatgcctc ctaagccagt gcgtcccagg cactggggcca ggctctgccc accttatcac 180
 cagtcctcct gacagcactg caagccagct acctttatca acacaccggg ttgatagatg 240
 gctcatg 247

<210> 1670
 <211> 169
 <212> DNA
 <213> Homo sapiens

<400> 1670
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 <212> DNA
 <213> Homo sapiens

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<212> DNA
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<212> DNA
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<210> 1687
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 <212> DNA
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<210> 1688
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 ggatagggta ggtcagtgag tagcgtagtt gatggaca 218

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 aattatttta gtagtgtttc agtaatgttg actgtatttt ccaacttggt caaattatta 120
 ccagtgaatc tttgtcagca gtgc 144

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 <211> 31
 <212> DNA
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 <210> 1693
 <211> 130
 <212> DNA
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<210> 1696
 <211> 238
 <212> DNA
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<210> 1697
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<210> 1698
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 <212> DNA
 <213> Homo sapiens

<400> 1698
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<210> 1699
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<210> 1700
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<400> 1700
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acatttt 367

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<212> DNA
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<400> 1701
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<210> 1702
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<212> DNA
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<212> DNA
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<210> 1704
<211> 338
<212> DNA
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<211> 170
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 <212> DNA
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<400> 1707
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<210> 1708
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 <212> DNA
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<210> 1709
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 <212> DNA
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<211> 212
<212> DNA
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<212> DNA
<213> Homo sapiens

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 <212> DNA
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<400> 1738

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ggattgggaa ccactagttc tttcagatgg tattcttcag actatagaag gagcttccag 180
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<212> DNA
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 <213> Homo sapiens

<400> 1752	
gattatgggtg caaggtagaa ggtgagaaag aatgcagaac caagctagac cc	52

<210> 1753
 <211> 70
 <212> DNA

<213> Homo sapiens

<400> 1753

gtgggaagggt ggcattgggat gaagttgtca ttactgagca tcttctctgt gtaaataaag 60

ggcagtagca 70

<210> 1754

<211> 123

<212> DNA

<213> Homo sapiens

<400> 1754

ggaccgcgct aataaaaact gccgaatcct gcagtaccgt cttcggaaag ccgagcagaa 60

aagcctgaaa gtggctgaga cgggtcaggt ggatggtag cttattcgaa gcctggagca 120

gga 123

<210> 1755

<211> 341

<212> DNA

<213> Homo sapiens

<400> 1755

gtaggctccc tatcattata tatagagttt cttttccac ggtagtcagt gacttaacct 60

gaattgtaaa tgtttgtaaa ggggttaattg tcctacatca aacttagtta aataattcca 120

tccacttatg gaggaggagg agaattgtga agaggtaaaa agctgggcac aagttcatat 180

gcctatgagt cagtaaagac tgaagtaatg tcctatgttg agctgggttat tttgatatat 240

gataataatt atctttgaag tagaacaatt ctgttaactg gaaaatcaca ggatatatcc 300

atcatatattt tcaggacaga tagtttttac tgtggggcaa a 341

<210> 1756

<211> 261

<212> DNA

<213> Homo sapiens

<400> 1756

gccatgaat ctatcaggct ttatcatgaa agtttattgt ttttaatcct agtacaatca 60

gctaccagtt acatacagta aaaaacagaa acagccacaa agcaatgatg atagagatag 120

tctgtgacat tgtacagtgg aggaaatact ctctgttgga atcctccagc agacccccgc 180

ctggcttcag cagttaagct atcactccct ccctcccaa aacagttaaa agaaaaatta 240

acgtcttgct tgggtacagc a 261

<210> 1757

<211> 87

<212> DNA

<213> Homo sapiens

<400> 1757

tgtctgcaca aggattaaga cctcgactg tgtccagccc gatcccttac acaccttctc 60

cgagttcaag caggcctata tcacctg 87

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<210> 1758
 <211> 372
 <212> DNA
 <213> Homo sapiens

<400> 1758
 cgtttttttaa ccagggatga tgccatcccc ctccccgaag ggacagatat ctagagacag 60
 ttatggttgt cacaactggg gggggcagct acttagcatt tggtagatga aggctgttaa 120
 acatcttaca cgtacaggac agctctccac aacaaataat tatctggccc aaaatgtcag 180
 tagtgctaatt ttgggaaacc tttatctaaa caataattat caatggccac tcaagcagta 240
 agataaaaaa gaagtttgat ggggatattt atgatgggtg gaacaagctg ttaacacctg 300
 accgaaactc aaccactga ttgaccttaa atgggaaact gatattaggt gcctcctgtg 360
 gggatataat ag 372

<210> 1759
 <211> 537
 <212> DNA
 <213> Homo sapiens

<400> 1759
 ttgactgtct gaagagtcac tatgagcaaa ataaaacaaa taagactcaa actgctcaaa 60
 gtgacgggtt cttggttgct tctgctgagc acgctgtgtc aatggagatg gcctctgctg 120
 actcagatga agaccaagg cataagggtg ggaaaacacc tcatttgacc ttgccagctg 180
 accttcaaac cctgcatttg aaccgaccaa cattaagtcc agagagtaaa cttgaatgga 240
 ataacgacat tccagaagtt aatcatttga attctgaaca ctggagaaaa accgaaaaat 300
 ggacggggca tgaagagact aatcatctgg aaaccgattt cagtggcgat ggcattgacag 360
 agctagagct cgggcccagc cccaggctgc agcccattcg caggcaccgc aaagaacttc 420
 cccagtatgg tggctctgga aaggacattt ttgaagatca actatatctt cctgtgcatt 480
 ccgatggaat ttcagttcat cagatgttca ccatggccac cgcagaacac cgaagta 537

<210> 1760
 <211> 49
 <212> DNA
 <213> Homo sapiens

<400> 1760
 tggcttgctt ggcacccagg gacagtagct gtttggctct ccaccaat 49

<210> 1761
 <211> 82
 <212> DNA
 <213> Homo sapiens

<400> 1761
 aggccagtat ggggtgcaagg ggcccgcgtt ggtagtcatt tctttgtggg ctgatggctg 60
 cgtgtgtata ggcaggaagt ta 82

<210> 1762
 <211> 35

<212> DNA
<213> Homo sapiens

<400> 1762
aaagcccacg gtcatagaca gcaccataca atcag 35

<210> 1763
<211> 229
<212> DNA
<213> Homo sapiens

<400> 1763
cacctataat gagctggaca ctctatgggc cttgcaattt agacatgaat agagttctca 60
ggtaccttac attctaatta gaaggagaac tttgacctct aaccaagacc tgtttaattc 120
ataggagggt ttcttttctt ttttttaaac tgcactcacg gtcacccccc caaaggatga 180
gggtttctta agttatgttg aaaattcaaa ccttgagtcc gggcatggt 229

<210> 1764
<211> 867
<212> DNA
<213> Homo sapiens

<400> 1764
agctgcatgg tggctcgaag agatctcaag tcttgctgac atgcatatag ggtacaactt 60
attacagggt cataacattt gcttctcaat tcacataaaa gagcaaattg ctgtggcttt 120
gctttttaat tttttttttt ttttttaaga gagagaggag ccactcttgc ccaggctgga 180
gtgcagtggc taactgcagt ctctcactcc tgggctcaag ggatcctcca gcctcagctt 240
cctgaatagt tgggactaca ggcacaagcc actgtacaca gctgctttgt tatcttctac 300
atatatacca aagggaagag ttaggaacac cagaaactca gtagtaactc actttaacct 360
tgcttctggg gctccaattc aagtgatgct caatttcaag gtacaaggaa aaccatgaga 420
atataaagtc ataatgcat ttccactcag atgaaaagat ttatctatct ttagatactc 480
aaaattattc ttggcatttt agcacttttg gtacacattt cctgatgtag gaaatagtaa 540
aatttcagag cctatggcat tggctttcac cacctatgca attttctaca catctgaaaa 600
ttaccagttt atctaactcc ttaaagtgtc ctctcttcaa caacaaaaaa cacaacaaaa 660
aattgctgga agaaacagga agcatccagg tccaaatgac agcataacag actatgaaga 720
aacagggtt aagtgcccat ctagaacaag atgggtctaga ttacaataag gaccccatgg 780
gacagaacat caaaacattc aactttcaag taaatgtctt ggaagtaaac attttaaatt 840
tataggactt cctctggcat gtaggta 867

<210> 1765
<211> 78
<212> DNA
<213> Homo sapiens

<400> 1765
accacccttc ccaacaatcc actagcaatc cagaggccac cacccttcc caacaatctg 60
gcaacgaccc agaggcca 78

<210> 1766
 <211> 137
 <212> DNA
 <213> Homo sapiens

<400> 1766
 aataatgtac aaattggtga ataaacacaa cagagccaac aaacatccca cccgagccca 60
 tacagcaaac aggaaatgag aacatttcag caagatttca agcaagcaag agatgatggg 120
 tcattgttca ggtgact 137

<210> 1767
 <211> 61
 <212> DNA
 <213> Homo sapiens

<400> 1767
 aagcatgttt ggtgagctgc tgcagaatgc cagcaccatg ggggatctgc ggaactgtcc 60
 a 61

<210> 1768
 <211> 354
 <212> DNA
 <213> Homo sapiens

<400> 1768
 gccaatcatg aaggaccgcg tgctgtatga ctctgtttat aggaaatggt ctggaatagg 60
 caaatctgta gagaccgaaa gtaaattatg gtttcctagg cctaggaacc agtgaggggt 120
 gaggaggata gctaaggggt agaaggtttc tttggggata atgaaaatac tctaaaattg 180
 attgtggtga aggttgcaca attctgtgga tatactaagc acaattctgt ggatatacta 240
 aaagcaattg aattgtacac tttatgtggg tgaattgtat gccgtatgaa ttatatctca 300
 acattgtatt agaaaataaa attaatgaag catagaagtt acggagaact actg 354

<210> 1769
 <211> 47
 <212> DNA
 <213> Homo sapiens

<400> 1769
 acagttgcag gcacgcagcg gtctcccagc gtcagggcgc accgcga 47

<210> 1770
 <211> 273
 <212> DNA
 <213> Homo sapiens

<400> 1770
 gtggtttaat gtcttcaaga acttcctgta gttaaattta tttcagtgag atacttttgg 60
 aattaatgtc cttttactga gacctgatgg cttttatgta ttttagggta aatttctgaa 120
 gttttatatt cttgttttaa aattgtttaa atgtgtttgg taactattgg aaaattttct 180
 cttcttaatt atgttctgtg tattgtattg atcctgaatt gtatagttaa tagtgacttt 240

tcaagatggg gcatgctcaa gatcgaacag ata 273

<210> 1771
 <211> 358
 <212> DNA
 <213> Homo sapiens

<400> 1771
 cctcagtgtg taagatgtgc aagacaaata tgcttatttc cttttctaga atataagtga 60
 tattatttgc ttatgacact aacactatta atgacaggag tcaatcagcc ttacagcta 120
 tcaaaatata atgagatccc aatgatgatt cttttttact ttgaatgtta attagtttgg 180
 gactttgatt ggctggcaaa cattttatca ttgtcagaat ttaatttaga tttcaaaaat 240
 agcttacagg attttaaaca tgggtgtggtt ttctaaagcc ttttttttaa aaaaagagat 300
 ctttttgaga gaaacaaatg aggattgtaa agtttgggga cttacctctg tagcattg 358

<210> 1772
 <211> 38
 <212> DNA
 <213> Homo sapiens

<400> 1772
 tgatcagaaa cattggggac ttggcactta tcatgaaa 38

<210> 1773
 <211> 104
 <212> DNA
 <213> Homo sapiens

<400> 1773
 acttcgggct gtcggagttt attgaatcca ccctttcagg acacagcctc cccttgctca 60
 gatacgatag ctcccttgag gccatggtca ctgcattagg aaaa 104

<210> 1774
 <211> 421
 <212> DNA
 <213> Homo sapiens

<400> 1774
 tgctaaggcc atccattgtc ttttgttagg agtcaaaca aatttttagta accaaaacat 60
 attttcaata aaattttata tgtatataag taaataacaa aacaacaaaa aacaaaaaaa 120
 gaacaaaaca gcaccaagaa cctatgtaaa atttcatcat acaatttcta tgcaagctgc 180
 ttgattacag aaaactgttc aaactgttca tcaaaaactg agtgggattt tccattgata 240
 tttcagatat tcaaatcaac ccatattctg agtatcaatc tgaattgcac aggttaagat 300
 gtgaaccctt cacatagtgt tgaagatgtg ttgaaatctg tacttgaatt ggcattgttt 360
 tcctcagagt taggctgcct tcatgagaaa tatcttctat ccctgagaga tcagctacat 420
 c 421

<210> 1775
 <211> 83
 <212> DNA

<213> Homo sapiens

<400> 1775

gtgtttacaa tccacttttc tccaaatgtg ccatcacgct gtctgttgct tgaactcctg 60

gatgtcagtg tttcgggaatt gct 83

<210> 1776

<211> 60

<212> DNA

<213> Homo sapiens

<400> 1776

ccagaaactc atctcgaatg aagtacttgg cccgggtcac gcgtgggtcc tctccgggct 60

<210> 1777

<211> 157

<212> DNA

<213> Homo sapiens

<400> 1777

gtctattatg ggaggagcag tctttgagac gctggaagga aatacaattg agataggatg 60

tgacggtgac agtataacag taaatggaat caaaatggtg aacaaaaagg atattgtgac 120

aaataatggt gtgatccatt tgattgatca ggtccta 157

<210> 1778

<211> 33

<212> DNA

<213> Homo sapiens

<400> 1778

ttttttggct tagtatgttg aaataaacta tgg 33

<210> 1779

<211> 43

<212> DNA

<213> Homo sapiens

<400> 1779

aatactatgg gagttggcag ctagaaacac aagttaggaa agg 43

<210> 1780

<211> 207

<212> DNA

<213> Homo sapiens

<400> 1780

ctggtggctc ccaacatgat aggacacaga aactcatgct caatggtacc cgtacttcga 60

taaggagcaa cagcaaagtc agatggtgga agatctgtca ggtgtttact tatgtttag 120

atatggttac aaagctcagg gagcccctgt ctaatgggaa atatggctac caaactgatg 180

atggcctccc aggaatcca attctgc 207

<210> 1781

<211> 137

<212> DNA

<213> Homo sapiens

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<400> 1781
 tgcttctacc catgcccga ggtgaactcc aacaagtgtg ggcccgagtg ccgctgcaac 60
 cgacggtggg tttacgatgc catcgtcact gagtcaggag aggtcatcag cacgctgccg 120
 tttaatgttc ctgacta 137

<210> 1782
 <211> 40
 <212> DNA
 <213> Homo sapiens

<400> 1782
 atcttgccat ttgtgatgag tgctacatta cagaaatgga 40

<210> 1783
 <211> 153
 <212> DNA
 <213> Homo sapiens

<400> 1783
 tgtagaaagc atggggctaa aagtattttg acataattta tccaaattta gcctggctat 60
 aatttctgta agccttgagt tagtcagagg atgagtaaca atagagaaca tttttaaaaa 120
 actaattacg gttgaatatt aagtctgacc caa 153

<210> 1784
 <211> 29
 <212> DNA
 <213> Homo sapiens

<400> 1784
 agaacaagcc ttcagacatt tgctatatt 29

<210> 1785
 <211> 103
 <212> DNA
 <213> Homo sapiens

<400> 1785
 ggcaagagt gtccctcggt ctctcttcc caggagcac tcggggcttc ggactctgca 60
 gtggtttgca aggccagggc caagtgggtca cttcactcac tga 103

<210> 1786
 <211> 29
 <212> DNA
 <213> Homo sapiens

<400> 1786
 ccatgcgccg aggcacttcc aggcttcac 29

<210> 1787
 <211> 68
 <212> DNA
 <213> Homo sapiens

<400> 1787
 catttattta tgatcaacca gagagactaa acagtggact catggggttg gactctattg 60
 caattcaa 68

<210> 1788
 <211> 48
 <212> DNA
 <213> Homo sapiens

<400> 1788
 tgagtgaacac cgtgggattg cagaaccaca cgctaaccat gaagaatt 48

<210> 1789
 <211> 705
 <212> DNA
 <213> Homo sapiens

<400> 1789
 cccggactct tggaactgag tttcttcct ctcacccatc ctgaccctaa gaagctgaga 60
 gaatctgtgc cctcttggg agactgggaa ggcgggggag aagccccctc gccctcgtca 120
 cccagcaagg gctagtgcag cctcacgttc atgtggattc acagccagac cctgtttcaa 180
 ggcagaggca gtctgggtcag gacctggcag aatacacatg ggggtccaggc agtccccgag 240
 ggagatgccc caagggtacc tgcgatgctg ttccgggttg aacctgtgtg atagtttttt 300
 tttttttttt ttggagactg agtctcattc tgttgcccag gctggactgc aatggcacia 360
 tctcagctca ctgcaatctg tgcgtcctga attcaagtga ttctcatgcc tcagcctccc 420
 aaatagctgg gattgcaggc gccaccacc acgcctagct aatttttgca tttttagtag 480
 agacgggggt tcaccatgtt ggccaggctg gtctcgaact cctgacctca aatgattcac 540
 ccacctcggc ctcccaaagt gctgggatta caggcgtgag ccaccacgcc cggccccatg 600
 taaacacttt acacgttcaa aatacaatta aaaaaagaaa ggaaggaaaa tcctgaaata 660
 gaactgagtc agaataagt accctccgtg cgctcatgtt atagc 705

<210> 1790
 <211> 191
 <212> DNA
 <213> Homo sapiens

<400> 1790
 tccaggggaa atacacatat ggccaacagc accagcaaag gtgcttgata gcactactca 60
 tcagagaaat gcaaatccaa atgacaccag aggctacttc acactcatta gaatgattat 120
 aaccagaaag tcagataata actagtgttg gcaagaatgc gcagaaattg gaaccctctt 180
 acttactggt g 191

<210> 1791
 <211> 119
 <212> DNA
 <213> Homo sapiens

<400> 1791
 tgtccaatct gtcactaggt ccatgtgtca ttgtttttcc tccaaaatat tccttcatcc 60
 tgagctcttt gtcacctagg acctggacta ctacagtaac cttgctcctt gacttcaga 119

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<210> 1792
 <211> 426
 <212> DNA
 <213> Homo sapiens

<400> 1792
 atggttctac catgaagaca cacgcactca aatgcccact gcagcaccac tcacaacagc 60
 accgacatgg aatcaagctg gggcctgtca gcggcagacg gataaagagg atgtggtcca 120
 tatacaccgc ggaatactat gcagccataa aaaggaacaa gatcatgccc tttgcaggaa 180
 cttggatgga gctggaggcc attatccttc gcaaactaat gcggggacag aatccccggc 240
 actacacttc ccacttaca agtggaagct gaatgatgag aacacaggga cagaaagggg 300
 ccaacaacac aactgggggc cggcctgagg gaagagggag aggctcagaa aaccatttta 360
 acaaaactgt caggtacca tgcttggtac ccggtgctga aatgatctgt aggacaaacc 420
 ctagtc 426

<210> 1793
 <211> 30
 <212> DNA
 <213> Homo sapiens

<400> 1793
 gggccagctt tgataatgga gcgagatgcc 30

<210> 1794
 <211> 269
 <212> DNA
 <213> Homo sapiens

<400> 1794
 cctctatcat ggcagggact tcccaataaa ttctatactc attgtggcca gctgaacgcc 60
 tgacatttag tagactcctc aaaaatgatt tttgaatgaa tgatgactga ccaactgaat 120
 gaatgaccaa tcttaaagca ccagtgaatg tttttactgt cttcacagag ctcagaatag 180
 atccttggaa gccattctgg aaaagggcaa ctttccaagg atgttttcaa aaagaccaac 240
 atataagcac gtgtatttgg ttgaccctc 269

<210> 1795
 <211> 96
 <212> DNA
 <213> Homo sapiens

<400> 1795
 tcttgcagtc ccaagtagag ggatgcgtga gcaccatgct gagcttgggg ccacctcctg 60
 acagcagccc tgagacgccc atccaaaacc ctgttg 96

<210> 1796
 <211> 98
 <212> DNA
 <213> Homo sapiens

<400> 1796
 tggactctgg acttcgcagg ttctgcctg tcacgccacc cccttcctgg gagcagcgag 60

cagtgccccca ggcccagatt ggagcacggt ctctatgg 98

<210> 1797
 <211> 776
 <212> DNA
 <213> Homo sapiens

<400> 1797
 ccatcacgta tgtcgcagca gcatttcacc cctgaagtct ctaaactctg agcctgaaaa 60
 gatttgtatt taatacacat aacatttttt agttcattct gcctttccta tttgttccag 120
 tttttgcttg gttttagttt ggaggggaac ttaagtacac agatccttat ctctcccat 180
 cccctagcct cacaaaacac agttgagagt cttttaagta cctgagctct cgaagctacc 240
 cagaactgaa ctagactccc ctaccttaga ctggtaccct caaacacagg actgaagctt 300
 aattgggaat ttggctttat ggagaaaaga atctttttca aagtttgtgt cggaagggga 360
 gggtgagggt tgcccactgt ctctgcagga aggtccggc ttaatctagg aagtagattc 420
 cagctgcacg atgaggaaca cattagcttt tgggatcaaa ccaggaatat gaatctgtaa 480
 ttattaagct cattgccaac ccacaagata tgtttctgaa aacctgtagt ttcttaattt 540
 aagtccatcc ctttcattaa cgctacagtt gtgactcaca ctgatcccaa acttttaagt 600
 gctaaatatt aacatttagc attaactgtc ttgtcaagcg aaaggccttc tctacaacct 660
 agtccatctc acttctggtg ctacctgagt tggacagaat tctagctcat ggttgctagg 720
 aaagctaggc ctctgatcat agaagcagat agcttcagtc ccagtctagg cctaga 776

<210> 1798
 <211> 103
 <212> DNA
 <213> Homo sapiens

<400> 1798
 atgtctgcag gtttctcctt gaagcaaagtg tgtgggatca ttgcatttcc agaaatctgc 60
 ctccctcacc ctccgttgac agtatatgtc atgcctcact ttc 103

<210> 1799
 <211> 32
 <212> DNA
 <213> Homo sapiens

<400> 1799
 atttgagac tttcggcttg tttcaaatga ta 32

<210> 1800
 <211> 48
 <212> DNA
 <213> Homo sapiens

<400> 1800
 atggctcgga gtctcggggt cctggtggca ctgccattcc cgctcccg 48

<210> 1801
 <211> 114
 <212> DNA

<213> Homo sapiens

<400> 1801

gctctgtgag gctgagtaaa cactattctc taacataggg acgacatggg caactgaaag 60

gattcaatgt aagtaatctc tgtgaagctc ctagcagagg gttagatgca caac 114

<210> 1802

<211> 449

<212> DNA

<213> Homo sapiens

<400> 1802

gagcactgac ctttgacgtc ctttgttgtg aggaaagtcc atctatgtgt tagttatgga 60

attaaacact aatacaaaaca aattatcata aaaatgaaac aaaaacaaaa ccccagctgt 120

ttatagactc cccttcccag atgtatagct gggagaggctc cgtctcacac tggcttcccc 180

ctctctctgg ccacactcc tgtcaccatc tccattgcac ccatagtgga aatagctagg 240

aagtgaaaac agctaggaag aagaaagaga aacaaaaaca aaaagaagca ataatatcca 300

agacaagccc tccccacatc taaattacaa aattgttata agtaactaa aaagcacatt 360

ttcttttagcc aggtagaaaa attaatatgt caactgtgaa aaaacttctt ttgatttgat 420

agaatagaca gccatggtgt tgtttttca 449

<210> 1803

<211> 217

<212> DNA

<213> Homo sapiens

<400> 1803

atagcgctct ctcgacgtca ctgtgtcccg gcttacaact agagggtgtcg cacacacca 60

cttgggtgcc tccccctcca aaaccaagca gaaaggcgtc tagaaaatta gaagggtttg 120

ccagttggtg ctggcgtaga ggacgtttcg aaggcgcttg gagcacccca ccgttgcaact 180

ggatgtagct accccggctt gtggtcaata gagctcc 217

<210> 1804

<211> 227

<212> DNA

<213> Homo sapiens

<400> 1804

ggaccgttga gtcactacc acctggagtt tgagttgaag catgaaaatg gtgcccattgc 60

ctgacgtcc agcgcttga tctgcacgtg cccttgtaga ggatccttac cgtcctagag 120

agcagacgtt ttctgaaaac tacttgctcc aaaagaccct ctgagttaac gtttcagctg 180

tatcattaga cttgtattta gagcgtgtca cttcctctga actgtta 227

<210> 1805

<211> 199

<212> DNA

<213> Homo sapiens

<400> 1805

tgccttcaag tgttcgtaag ctagcttctt ctgcgcagc catcctctct cttctcgctg 60

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aattctgaga agcgtgaaga ggatgatttg gatgtccagg atcaccagca gatgctaattg 120
 cagaaccata acgtaattga gcttcagtag aatccataat actgaccatc cagttccaag 180
 tggaataag cttttcttc 199

<210> 1806
 <211> 100
 <212> DNA
 <213> Homo sapiens

<400> 1806
 atcttcagct cctgctaggc gccggggaaa gtaccaggcg ctggcctgta acctccttcc 60
 ggctctgtcc ccatcagcgg ctccccaga agtcatggcc 100

<210> 1807
 <211> 130
 <212> DNA
 <213> Homo sapiens

<400> 1807
 gtgctgcctt tgcttcttat cattcatggc agattgtttg tgctttcaac atttcatttg 60
 aaatgggaga agataaaatc acttgatgta acctggaaac tatgctttac atggcaatca 120
 aagccttttg 130

<210> 1808
 <211> 277
 <212> DNA
 <213> Homo sapiens

<400> 1808
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 ttttgccctca tgtttgtttt cttaccccaa atgttccttg cttgctttgc acatgcccga 120
 cctcccaccc accaagaccc attggaatcc caccactgcc tctactaggc tgcttgagtt 180
 cagataatga tctcaaaaac agcactcgct cccctcacc actaaccccc tggctctaag 240
 cagcttcctt tctcagaggg ccttgcaaat tgtcaga 277

<210> 1809
 <211> 99
 <212> DNA
 <213> Homo sapiens

<400> 1809
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 ggggagcaga aggcagaatt gccatgccca agcccagac 99

<210> 1810
 <211> 64
 <212> DNA
 <213> Homo sapiens

<400> 1810
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ggaa

64

<210> 1811
 <211> 377
 <212> DNA
 <213> Homo sapiens

<400> 1811
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 aaccttttaa ttttcacaat tgatgacagt gtgagtttga tgaaaatata tgaagctatt 120
 atggaaatac catgtaatag ggagagttga acatgaatat tagagaagga atccagttac 180
 ttttttaaatac tacacctgtg tgcacctgta ttactgaata taggaaagag ataccatta 240
 catagttact cagtaaacia aagagaaata ccaggttaga aagaagagtt actattcctg 300
 agaaataatc aagaacatat ttaattttaa ctaatgatgt gaactattta gttttgatgt 360
 ccggttatgtg attctgc 377

<210> 1812
 <211> 186
 <212> DNA
 <213> Homo sapiens

<400> 1812
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 gtcaggaagt agagggcttt tcctgggtgtt agggacaata taaatgaaga catggagaca 120
 ggagtgggct tggcgaacac aggatgatgg gcatcagcct gagtgaccag gtgttcgtag 180
 ctgaga 186

<210> 1813
 <211> 75
 <212> DNA
 <213> Homo sapiens

<400> 1813
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 gattaatggg aacc 75

<210> 1814
 <211> 301
 <212> DNA
 <213> Homo sapiens

<400> 1814
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 aggaataaga tttatgttaa gactatcaaa cacagtgttg cctacaatag caaaaatgtg 120
 aaaataacia caacaacaaa acagcagagg aattgttatg tttttgtag tctatctata 180
 tgatgcctat ttttaggctt taaaaagtct tcaaaatctt taatgactga tttatctagt 240
 taaatgctta atccttagca ggctcttatt ctttaattaa acgtgccttt gagtagatgt 300
 g 301

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<210> 1815
<211> 495
<212> DNA
<213> Homo sapiens

<400> 1815
gcagacttct tggagtggta gttcatggtc ttcttctaag aaggctgtgg atgccttaaa 60
agcattatntt gacgctggct cccatatctc actgccctct ccaaaaaatg tgttacccta 120
acatagaagt atcttttctc agaattcttc agtatattat gaatcagtga ctaccttttc 180
tctcccttga aatttttctg taacttaatg ttcatttctt tttgtttcag taaaccagtc 240
tcaactcttt tccttttctc tttctgttgt acctctcatt tccccgacct ttctgtctct 300
gtagatggca tttcataatt cacattgata ataattgcta gaatttatag gcattttattg 360
tagattaagt agagcattta ttatagatta agcctatacg taacttgttg aattctcata 420
acaaccttag gaagtacatg ttgttacttc cacattttat agataaggta gccagtctgc 480
tctagagaaa tttta 495

<210> 1816
<211> 107
<212> DNA
<213> Homo sapiens

<400> 1816
gactcttcca ggcaatttcc atagatctgc agtcctgcct ctgccacagt ctctctgttg 60
tccccacatc tacccaactt cctgtactgt tgcccttctg atgttaa 107

<210> 1817
<211> 192
<212> DNA
<213> Homo sapiens

<400> 1817
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cctccccctgc cctgcctac accccctccc ctgccccctgc ctacaccccc tcacctgtcc 120
ccacctacac tccatcccca gcaccagcct atacccccctc acctgcccc aactataacc 180
ctgcaccctc gg 192

<210> 1818
<211> 115
<212> DNA
<213> Homo sapiens

<400> 1818
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ccagaccaa atgagtgcc gcgaccccaa ctctccatc ttcttcaccg acacg 115

<210> 1819
<211> 200
<212> DNA
<213> Homo sapiens

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<400> 1819
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ctctgcttac accacgtggg ggtaggtcca gaactcaggc cttgggaaca tatgctgtgc 180
tctcttctac aggcgctgtg 200

<210> 1820
<211> 670
<212> DNA
<213> Homo sapiens

<400> 1820
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attataactt ttaaaaaaaaa tgtataaatt atacctggcc tgtacagctg tttcctacct 120
actcttcttg taaactctgc tgcttcccaa cacaactaga gtgcaatttt ggcattcttag 180
gagggaaaaa ggacagttaa caactgtggc cctatttatt acacagtttg tctatcgtgt 240
cttaaattta gtctttactg tgccaagcta actgtacctt ataggactgt actttttgta 300
ttttttgtgt atgtttattt tttaatctca gtttaaatta cctagctgct actgcttctt 360
gtttttcttt tcctattaaa acgtcttcct ttttttttct taagagaaaa tggaacattt 420
agggtaaatg tcttttaaatt ttaccactta acaacactac atgcccataa aatatatcca 480
gtcagtactg tattttaaaa tcccttgaaa tgatgatatc aggggttaaaa ttacttgtat 540
tgtttctgaa gtttgctcct gaaaactact gtttgagcac tgaaacgtta caaatgccta 600
ataggcattt gagactgagc aaggctactt gttatctcat gaaatgcctg ttgccgagtt 660
attttgaata 670

<210> 1821
<211> 91
<212> DNA
<213> Homo sapiens

<400> 1821
agacagatta tggttgattg agaaatgggt gacagtttaa gatgtcgggc aggaagtgta 60
ggctcctctt ttaagaaaca tgaggtgcct g 91

<210> 1822
<211> 33
<212> DNA
<213> Homo sapiens

<400> 1822
aagaaagcgc aaggaatgtc ctgaccaact tgg 33

<210> 1823
<211> 55
<212> DNA
<213> Homo sapiens

<400> 1823
tcttggcatc gccacacca ggacttgctc gtgccgcaat tccccacgga aacaa 55

<210> 1824
 <211> 73
 <212> DNA
 <213> Homo sapiens

<400> 1824
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 caaacgagca gaa 73

<210> 1825
 <211> 101
 <212> DNA
 <213> Homo sapiens

<400> 1825
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 tgactctcgc taccagggcc cggtgggtcac tatgccacaa a 101

<210> 1826
 <211> 494
 <212> DNA
 <213> Homo sapiens

<400> 1826
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 atagtcacat atatacaatg aaggcagttt cttcagaggc aaccaggggt tatagtgcta 180
 ggtaaatgtc atctcttttg tgctactgac tcattgtcaa acgtctctgc actgttttca 240
 gcctctccac gttgcctctg tcctgcttct tagttccttc tttgtgacaa accaaaagaa 300
 taagaggatt tagaacagga ctgcttttcc cctatgattt aaaaattcca atgactttcg 360
 cccttgggag aaatttccaa ggaaatctct ctcgctcgct ctctccgttt tcctttgtga 420
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 gtgaggtata atcc 494

<210> 1827
 <211> 103
 <212> DNA
 <213> Homo sapiens

<400> 1827
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 cactggcctc accttccct ggatggagag taaccgcaga tac 103

<210> 1828
 <211> 409
 <212> DNA
 <213> Homo sapiens

<400> 1828
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cttcttcaca agatgacttg ctcgctgtta cctgcttccc cagtcttttc tgaaaaacta 120
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 gttgttttgc ctgttagttt tgaggagcag gaagctcatg ggggcttctg tagccccctc 240
 caaaaggagt ctttattctg agaatttgaa gctgaaacct ctttaaactc tcagaatgat 300
 ttattgaag agggccgcaa gcccctaatg gaaaactgtt tttagaaaat atgatgattt 360
 ttgattgctt ttgtatttaa ttctgcaggt gttcaagtct taaaaaata 409

<210> 1829
 <211> 115
 <212> DNA
 <213> Homo sapiens

<400> 1829
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 acctatctag cccattaaga actgctttaa agggacacat ctggcaacag taaaa 115

<210> 1830
 <211> 318
 <212> DNA
 <213> Homo sapiens

<400> 1830
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 gtgttacagt ttaaaatctt actgtattac ctacatcatt gaaagaatca tcatgcagcc 120
 tttctcaaca aaggcttatt tagagaatta taccctaata tcctaaagta tatttaata 180
 attaataaat atttaataaa ttaacttact cattcctggg agaattgaga atagagtcac 240
 tcaaatcatt ttctatgggg ttaaattctt tggctgaacc cgagttgaga aaggctgcta 300
 gagaatgcat tgaagacc 318

<210> 1831
 <211> 67
 <212> DNA
 <213> Homo sapiens

<400> 1831
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 cacacca 67

<210> 1832
 <211> 250
 <212> DNA
 <213> Homo sapiens

<400> 1832
 ccggaacatc gtctagctgg tgttaggaat gtttgcttaa tttccagact tttttttaa 60
 aacacatcgt ggggtttttt aggtccaac ctgattagt catggtcagc cctcaatgaa 120
 ggctgaggca tctctgactg aggtgttttt gtttggtttt gtttttttaa atcatgtatt 180
 tgctacaaag tattgtactt gtctcaatgg gaatggtgta aaaaacaaaa ggccttatgt 240

gatctgtatc 250

<210> 1833
 <211> 70
 <212> DNA
 <213> Homo sapiens

<400> 1833
 caaaggcgag tgcagcttta gctgccttgg agaaactggt ttctggaccc aatgcggcaa 60
 ataataagaa 70

<210> 1834
 <211> 102
 <212> DNA
 <213> Homo sapiens

<400> 1834
 ggcagcttat tcacgtggcc tttcctccgc tgctgtgatt ttatctttga atgtggcctt 60
 tggagtgggt aaagtaggac ttagacgctc agtgaagtgg ct 102

<210> 1835
 <211> 251
 <212> DNA
 <213> Homo sapiens

<400> 1835
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 cattttcacc cattctgtgg ttcattgtag ttttaaggaaa ccaagcatat agatgcatta 120
 gtgattttgt ttatattatg taaaatataa cgatctctta aaaataccac agtttgtatt 180
 ttttctttaa ggagtaaaga tttgccttta aataacttgg tattttcctg gctttcgttt 240
 aatacaatag a 251

<210> 1836
 <211> 45
 <212> DNA
 <213> Homo sapiens

<400> 1836
 ggagatgcac atatttacct gaatcacatc gagccactga aaatt 45

<210> 1837
 <211> 189
 <212> DNA
 <213> Homo sapiens

<400> 1837
 gacttcgcag gtgagcagta acggaaatca gccccgttta ttctctccag cacctgcctt 60
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 attgaactct gtgcagattc gctgttcgta gacatggtac ctgatggaca ccaagctacg 180
 tacagcttc 189

<210> 1838
 <211> 59

<212> DNA
 <213> Homo sapiens
 <400> 1838
 aacaggatgt agaaagaccc atgaagaaag aaagaagaaa gctatggttc cgaaagcag 59

<210> 1839
 <211> 66
 <212> DNA
 <213> Homo sapiens
 <400> 1839
 gacgtgcggg atcaagttgc tattcatgaa gctatggaac agcagaccat atccatcact 60
 aaagca 66

<210> 1840
 <211> 324
 <212> DNA
 <213> Homo sapiens
 <400> 1840
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 taagctgtaa aaaccgtttg aaaatataaa ctcgtttttg gaatacatgt gtcaaaggct 180
 gcccatgtta atacctttgg tataaaacgg taacgattcc cttgacaaac ccatccatca 240
 cctgacgcac attcacatct cctggtaact actctaccta gtctagtctc aaccaccct 300
 gtcagtcacg actcactcct gtcc 324

<210> 1841
 <211> 182
 <212> DNA
 <213> Homo sapiens
 <400> 1841
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 ggggaatcac aaatatattg ctttagtact gcatgttctg ttgtggtgag ggaaagaaac 120
 atgctttgaa ggttttccct tgtcaacaga atgtgtgtct gtagctgtgt attgcgcatg 180
 ta 182

<210> 1842
 <211> 28
 <212> DNA
 <213> Homo sapiens
 <400> 1842
 taaggtccct ccagtgtaca acaatttg 28

<210> 1843
 <211> 175
 <212> DNA
 <213> Homo sapiens
 <400> 1843
 caciaagtgc gccattctga ggatatgcag ttgctttct cttattttta ttatctcatg 60

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agtgcagtgc agccactgaa tatatctcaa gtctttgatg aagttgatac agatcaatct 120
gggtgtcttgt ctgacagaga aatccgaaca ctggctacca gaattcacga actgc 175

<210> 1844
<211> 261
<212> DNA
<213> Homo sapiens

<400> 1844
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gctggaagag accctaaagg ttatataaac caattccctt attttagagc tgagaaatct 120
caggtgcaaa gaaggagag gctataacat ggtggcacta gaataagact gccggggttg 180
aatcctggtg caactactta ttacctgtgt gatcttggga aagtgactta acctttctgg 240
gtcacagttt ggatacctat a 261

<210> 1845
<211> 30
<212> DNA
<213> Homo sapiens

<400> 1845
tctgaatgct gaagtgacag ttggagatgg 30

<210> 1846
<211> 446
<212> DNA
<213> Homo sapiens

<400> 1846
gatccaggca gttagcgata tgttgatga attgagaaaa atgagttttt ctttctctac 60
taactgaatt agattagaaa taagcagtta agtgagaaaa ataggaatt agtgccagat 120
atgttgaggt gtagtggtga cagggggtct tttaccttca gatgtttggt gcaacttaga 180
gaatgcagtg gtagttgctg gccagccca tccaaacaac ctcatcttggt ggggtgatact 240
tcacagatga cttaaaataa atcccctgaa aataagaatc tctggaagag atgacacgtg 300
tatgtgcgtg tgtgcacgtg tgtgcgtgtg tgcacgtgtg tgtgtgtgtg tgttttggtg 360
gagtggtagg aggaggggtg gcttaatgat gagaatcatt atttcttgaa ttggatgaca 420
ctttccattc ctgcaaaggg agcgtg 446

<210> 1847
<211> 40
<212> DNA
<213> Homo sapiens

<400> 1847
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<210> 1848
<211> 268
<212> DNA
<213> Homo sapiens

<400> 1848
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 gaaatctgaa tactcaaaca ccccttctgt attttctactc aaccatcatt gtattagatg 120
 atacataagg aaagtgactt agggaagtaa gttcagaagg aaatgtgttc ctttctccct 180
 catattatct tttcaacaga ggcctggatt gctaaatgga ttatgaaagc aaattgctac 240
 tgggaggtga tgggtcaaaag caaactta 268

<210> 1849
 <211> 140
 <212> DNA
 <213> Homo sapiens

<400> 1849
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 accatgactt aatattttga gccctagaag aaaggggtgt gctgaggaca agagtgggga 120
 aataggaaca ctgaccagta 140

<210> 1850
 <211> 233
 <212> DNA
 <213> Homo sapiens

<400> 1850
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 gagggctgca gtcctagctg gccaaagttc aaagaacat gctgggctgg ggctaaaaga 120
 aaaaccaatg gaattattat gcccccaaac ttagctatctt ggaagaaaaa acacaagatt 180
 taaggtaatc tgttggttaa tgttatttgg atacactaac atcgtgcatg aaa 233

<210> 1851
 <211> 68
 <212> DNA
 <213> Homo sapiens

<400> 1851
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 tgtaataa 68

<210> 1852
 <211> 223
 <212> DNA
 <213> Homo sapiens

<400> 1852
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 catgaacact tctcccaggg tctaaggaca ggctgacata acatgctaata accaccagag 120
 ctggcactca cccagatgta ccacatcagg ccaggaagca gaaactacca acatcccagc 180
 aaaccatgtg gaggccccca aatcagactg cttgggccta aca 223

<210> 1853

<211> 199
 <212> DNA
 <213> Homo sapiens

 <400> 1853
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 agagcaaaac aacaacaaaa aaacataact atgtaaacaa gagaataact gctgctaaat 180
 caagaactgt tgcagcatc 199

 <210> 1854
 <211> 169
 <212> DNA
 <213> Homo sapiens

 <400> 1854
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 ttttgttctc agcatggaga aggcagaaac cagcagtagg gatccacaga gagggcatag 120
 gaaagaagat gttaaagagg ctggacattg gggctgatgc tggatcatcc 169

 <210> 1855
 <211> 186
 <212> DNA
 <213> Homo sapiens

 <400> 1855
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 agaaaacaga agagagaaat caggaacat ttaggaaata ggatcagctg ggcttggtga 120
 tgaaattcag gagatgatgt catgggtgac tcctagtTgg ttcttgaggt tgtgataatg 180
 cccttc 186

 <210> 1856
 <211> 61
 <212> DNA
 <213> Homo sapiens

 <400> 1856
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 a 61

 <210> 1857
 <211> 31
 <212> DNA
 <213> Homo sapiens

 <400> 1857
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 <210> 1858
 <211> 405
 <212> DNA
 <213> Homo sapiens

 <400> 1858

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ttcaagtgga tatgtgcagt tgacagtttg agagatgcat ctagggttca gtaaagacaa	120
cacaagcctg tctttagggc ctacctgtga actgtgaaca cagcaatgag aatgatggac	180
atcaccttta agtatttttc tagactttat tactcatgtg tttgtcatga ggtgtaactt	240
agtagttcat agtcctataa tgtatgttat tgactaggta gcattttatt ttctaattgt	300
ttctgttata gtgctgccac atgtgtttcc cagaaacgca ttttaccac agttcttagg	360
gttggcctga ttagtttaat tgctgtctga acctgcttct tactg	405

<210> 1859
 <211> 72
 <212> DNA
 <213> Homo sapiens

<400> 1859	
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tccgaagccg ga	72

<210> 1860
 <211> 577
 <212> DNA
 <213> Homo sapiens

<400> 1860	
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taatttgaat aacaaatttt agattctaag taggccataa cttctttgca aaacaattga	180
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ttagtagact gctcttctca tccctgggtca aggagcttct ctaactgatg gttgatattt	300
cgcagatggc tttcggtccc cagaagtgtt cttgctttta ataacagagc tggaaggctg	360
gatgaatcat actgttgaaa gaaaattata taattagcaa tatcaaaaac tcataacctt	420
gtccttagat agcccaatct tatgactaat gcaaattttg attgagcttt ccattaacta	480
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gaatataatt gatcaciaag ttgctaggga gctgctc	577

<210> 1861
 <211> 81
 <212> DNA
 <213> Homo sapiens

<400> 1861	
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tcctgtcctg acaccatcct g	81

<210> 1862
 <211> 140
 <212> DNA
 <213> Homo sapiens

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<400> 1862
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gacatgggcc tcggtgtgcc tttcaacatc gccagctacg ccctgctcac gtacatgatt 120
gcgcacatca cgggcctgaa 140

<210> 1863
<211> 99
<212> DNA
<213> Homo sapiens

<400> 1863
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<210> 1864
<211> 272
<212> DNA
<213> Homo sapiens

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agaattgta gtgtccaggc tcttccaagc aaggtcttcc aaagggatat ctcaaaaata 180
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<210> 1865
<211> 52
<212> DNA
<213> Homo sapiens

<400> 1865
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<210> 1866
<211> 231
<212> DNA
<213> Homo sapiens

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gttcctcatg ctgcctcttc ctgctggctt tattctgtgt ttgacttgaa cgtttcgtca 180
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<210> 1867
<211> 78
<212> DNA
<213> Homo sapiens

<400> 1867
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acatacacaa tcagccct 78

<210> 1868
 <211> 42
 <212> DNA
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<400> 1868
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<210> 1869
 <211> 286
 <212> DNA
 <213> Homo sapiens

<400> 1869
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 actaaacccc actgtttcat ttttaatacac ttaatagtcc ttggtttatg aagacattta 180
 tgtgatgatg aaagttattt agcatcttta tggaaggact tagctgagct gtattaggca 240
 aaagaaggaa agaaagtggg tacagggcaa cgggtcagtg agatct 286

<210> 1870
 <211> 630
 <212> DNA
 <213> Homo sapiens

<400> 1870
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 tggcctgaag ccaacaataa ttacaatcag gtcttctgat ctttctccct gcccccaac 180
 cccaccacc ttcttaaaca gctgtgaagg gaagtgtta atggtatcca aaacaaagag 240
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<210> 1871
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 <212> DNA
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<400> 1871
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gcacagtggc agttaggatg gctggagagt aggatagttc tatggggttgc ccaaaaaatg	180
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gttctgtttt gaaggaaacc atgtgcttca tgaaacctac agttgacaag agaatgtaca	360
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catacttaac actactgaat gtatacttaa aaatgattca gatagtcaac ttctattata	300
tgtatttcac cacaaaaatt tcttaaagta gcaagaaata aataaaattg taaaaacctg	360
atgttagtgg ctatgtaggg aaatggatat catatactca caacaggaag tgtagctttc	420
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tgccactcca ggggatacat gtgtacacta aatttacaga gatgctcaca gctgcacgat	540
ttaaagtagt caaaacagtt taacagctca agagatgggc tacatatcct ttagtataag	600
cacaatggca taaaatcatg caatcattca ttcagatctt tttttgagca cgaacaagca	660
gatgaaagtt atgctttcca cagaaaaata caatttcaga gcatttatag acttctagaa	720
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<210> 1873
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<210> 1874
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 <212> DNA
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 agggctggag ctggacagaa gccagtgcct ttaagtcatt tgtgtcaaaa ccctctgggg 180
 t 181

<210> 1875
 <211> 77
 <212> DNA
 <213> Homo sapiens

<400> 1875
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 gcatccgtcc tctccac 77

<210> 1876
 <211> 30
 <212> DNA
 <213> Homo sapiens

<400> 1876
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<210> 1877
 <211> 82
 <212> DNA
 <213> Homo sapiens

<400> 1877
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 atccgatggc tgatgcttca ta 82

<210> 1878
 <211> 201
 <212> DNA
 <213> Homo sapiens

<400> 1878
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 agtccgttgc ctgaggaaag a 201

<210> 1879
 <211> 33
 <212> DNA
 <213> Homo sapiens

<400> 1879
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<210> 1880
 <211> 98
 <212> DNA
 <213> Homo sapiens

<400> 1880
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 aagtgtctag gtaaatagat ggttactgag tgtctccc 98

<210> 1881
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 <212> DNA
 <213> Homo sapiens

<400> 1881
 caagattatc agcaaaatcg agaatcatga 30

<210> 1882
 <211> 98
 <212> DNA
 <213> Homo sapiens

<400> 1882
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<210> 1883
 <211> 91
 <212> DNA
 <213> Homo sapiens

<400> 1883
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 acaacttcga atctgggtca cttaaacaag c 91

<210> 1884
 <211> 96
 <212> DNA
 <213> Homo sapiens

<400> 1884
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 cccatcccag ttgagtcttt agatgatccc ttctg 96

<210> 1885
 <211> 124
 <212> DNA
 <213> Homo sapiens

<400> 1885
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 tttt 124

<210> 1886
 <211> 86
 <212> DNA
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 <400> 1886
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 gtagtgtctg atctcccgtc cggcag 86

 <210> 1887
 <211> 47
 <212> DNA
 <213> Homo sapiens

 <400> 1887
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 <210> 1888
 <211> 178
 <212> DNA
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 <400> 1888
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 cagggccgcg tggtcgggcc ctgcagggcg ggaggcgcg cgcggggcgg ggccggtgac 120
 gggacgcgga gaccccgcg gcggcgggag gggcacgagg cgcgcgtttg cacccgag 178

 <210> 1889
 <211> 54
 <212> DNA
 <213> Homo sapiens

 <400> 1889
 ggggtcaggc cttgcttgca taaaggagaa aacaactcta tgtacatgct gggg 54

 <210> 1890
 <211> 80
 <212> DNA
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 <400> 1890
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 atgtgaacgt tgtcagccta 80

 <210> 1891
 <211> 29
 <212> DNA
 <213> Homo sapiens

 <400> 1891
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 <210> 1892
 <211> 155
 <212> DNA
 <213> Homo sapiens

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<400> 1892
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 atcaggtgga tgtagagatc aaacggagac agaga 155

<210> 1893
 <211> 478
 <212> DNA
 <213> Homo sapiens

<400> 1893
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 aatggcagct ccctgggagg tacttaggga tggtgaccac cagctgatca gcaccaagaa 120
 gatgagcaag agccaggtgt ccacagccct cttgtacctc cccctgact cccttgctac 180
 ctgtgtgttt tctccaggct gtcacactgc ctcccacca ccaatgcagc acacatctgc 240
 tgggaaggcc caaggcttaa caccactgcc tgctggccac tctgctttgt cgctctctgg 300
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 gaaggctggg gtgtcaaagg ataaaaaaaa aatcaaaagg ctacatcatg ctttacttag 420
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<210> 1894
 <211> 203
 <212> DNA
 <213> Homo sapiens

<400> 1894
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 aagaccattt ccatggagct catgtttttc ttttctgtag gaactttttt ttaaccagca 120
 cccaccataa ttccgaaggc cacgtttcat ctttctgga tcactacagt gaagtattac 180
 agttgtacag ttcccagtct ggc 203

<210> 1895
 <211> 57
 <212> DNA
 <213> Homo sapiens

<400> 1895
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<210> 1896
 <211> 61
 <212> DNA
 <213> Homo sapiens

<400> 1896
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 g 61

<210> 1897

<211> 415
 <212> DNA
 <213> Homo sapiens

<400> 1897
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 tatagaaaga atctataaat tcttggggaa gtgtgttata agctttaata attacattga 360
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<210> 1898
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 <212> DNA
 <213> Homo sapiens

<400> 1898
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 aacaagtaga attataaaga agaattagct gaccacggga atgttgacac tgctgccatt 180
 tgagttactg taaatctgca gccagaggaa cttaacgaag gcaacttata agcataaatg 240
 aggaaagtgg ttgtgacaaa aaggatgaag atgtcccaga agaagtaacg ccagcaca 298

<210> 1899
 <211> 122
 <212> DNA
 <213> Homo sapiens

<400> 1899
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 gtccttctgc tccttttagaa aacagaacca gcacagcgtc cacaccgaca gcagttacta 120
 gg 122

<210> 1900
 <211> 528
 <212> DNA
 <213> Homo sapiens

<400> 1900
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 tccagcactc tgcgtgccag ggcctcagct tcatgaggca gtgctcttct gggggttcct 120
 ggggtgcagt tggctgtggg gcttttgggt actttttgtt gcaataatgt tttttcagtc 180
 tgatatattt atatgtatac gtgtgtgtgt gtgtgtgtgc gtgcgtgtgt attttacta 240
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 aaaatatacc cttcgcggtg ttcctaataca catgtttgta ctataatttc acgtgggttc 360

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agttaaacta gagctaaggt tgtccatggc atgttgagtc agttgtcata atggtcagtg 420
 agtaaaacta acctactatg acaaactga cttacacctc tatgtgagca aacaccttgt 480
 gtgtgtgtgt gtgtgtgtgt gtgtgttacc agcatacacc ctagtagg 528

<210> 1901
 <211> 70
 <212> DNA
 <213> Homo sapiens

<400> 1901
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 gagccgggga 70

<210> 1902
 <211> 234
 <212> DNA
 <213> Homo sapiens

<400> 1902
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 tacatttcac ttatataaga tgttcaaat agacaaatct ttagagacag aaagtaagag 180
 actgaggcaa tgaaaatgtt ctaaaattag acagtgatcg tgagggtgc acaa 234

<210> 1903
 <211> 135
 <212> DNA
 <213> Homo sapiens

<400> 1903
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 ccatttcagg caatgccaa tttggagaaa agaagaagtg caaaaaaga tgtttctttg 120
 acctcaccgc aaata 135

<210> 1904
 <211> 32
 <212> DNA
 <213> Homo sapiens

<400> 1904
 tgcttcgatt gctttcgagt catgagttgg tg 32

<210> 1905
 <211> 312
 <212> DNA
 <213> Homo sapiens

<400> 1905
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 acttttaatg tcaagatgaa aaagggtgta aggtgttata ttttcttcaa ttcctttacc 180
 acaggaggct aactccacaa tttccctcat gtttctcatt cagaaaaaaa aatattaaat 240

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acttggctct ca 312

<210> 1906
<211> 436
<212> DNA
<213> Homo sapiens

<400> 1906
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gatccacca tctcgggctc ccatagtgtt gggattacag gcgtgagcca ccatgccctg 420
ccagtaaagt cttttt 436

<210> 1907
<211> 151
<212> DNA
<213> Homo sapiens

<400> 1907
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ctgaagtctg ggggggggtg ggcgccgagc gcgcgggggtg ggggggggtcc tggctcttgg 120
cttctcgact cggctctgtt tcgacagcga a 151

<210> 1908
<211> 33
<212> DNA
<213> Homo sapiens

<400> 1908
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<210> 1909
<211> 81
<212> DNA
<213> Homo sapiens

<400> 1909
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aactcgaatc acaaaagaga c 81

<210> 1910
<211> 45
<212> DNA
<213> Homo sapiens

<400> 1910

gtgagaccct cccgacagga caaaccactc tgccgttata tgtga 45

<210> 1911
 <211> 260
 <212> DNA
 <213> Homo sapiens

<400> 1911
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 atcatctccc aaggaacgag gggaacttct atattaaaca tgcaaaaaca acaaaaaatc 180
 cattcattca ttcagaattg cctcctcccc tgccccctcc cttccccctg ggcttttcta 240
 accagtttga tattgaagct 260

<210> 1912
 <211> 79
 <212> DNA
 <213> Homo sapiens

<400> 1912
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 tagacatctc agaccaaaa 79

<210> 1913
 <211> 38
 <212> DNA
 <213> Homo sapiens

<400> 1913
 tgattctgcc cggagtaaga cattgacggg agctgggg 38

<210> 1914
 <211> 52
 <212> DNA
 <213> Homo sapiens

<400> 1914
 ttggccaaca gcgaaaagca aggcattgagg acacacgccg tctctgtgtc ag 52

<210> 1915
 <211> 163
 <212> DNA
 <213> Homo sapiens

<400> 1915
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 atgacatacc cctgggtcat ttctgggttt ctcctaggc caattcaaaa cttccaaaat 120
 aaggccaagt aacacaatag gctcacactt gcatcacaag ctg 163

<210> 1916
 <211> 253
 <212> DNA
 <213> Homo sapiens

<400> 1916

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 ttctgcagct gtagtcaaag gtgtacacat tgagtattcc acagatatac atggtttaat 120
 atgtggtatc catgggggtat gattctacca cagccttgta agtgctccaa accttaaagt 180
 acccacaatt actacacctg tgactggaac caatgatccc ttttattccc cgccaggaca 240
 aaccagtatg tag 253

<210> 1917
 <211> 145
 <212> DNA
 <213> Homo sapiens

<400> 1917
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 aaagctcgcg gaagacgagg ttctgcggag agagaggctc caagcagtct gggaagtgtg 120
 gtccagttgg cttagcagta gtttc 145

<210> 1918
 <211> 124
 <212> DNA
 <213> Homo sapiens

<400> 1918
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 tcctaccaca gaaacactga gagttacaga atggcaaata tctgtaactg gttccaagca 120
 agag 124

<210> 1919
 <211> 45
 <212> DNA
 <213> Homo sapiens

<400> 1919
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<210> 1920
 <211> 246
 <212> DNA
 <213> Homo sapiens

<400> 1920
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 accttctaata gcctttggct ctaggtggtg gaacaagtaa agtaatggac aaatactttt 180
 tctaccaata tttagtgacc aaatgcagag ttatggagag ggccaggagac ctcatgaacc 240
 atactc 246

<210> 1921
 <211> 348
 <212> DNA
 <213> Homo sapiens

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<400> 1921
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 gcttaggagt gtctgaaaga ttgcagaggt tgacttttcc tgcagtgagt gtaaaagtga 120
 atggatcatga ccagggtcag aatccacccc tggacttgga gaccacagca agatttagag 180
 tggaaactca cacccaaaaa accataggcg gaaatgtgac aaaagaaaag ccccatctc 240
 tgattgttcc actggaaagc cagatgacaa aagaaaagaa aatcacaggg aaagaaaaag 300
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<210> 1922
 <211> 100
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 <213> Homo sapiens

<400> 1922
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 aggatacatt attcgtgttt gcaacggtct ttgaagagct 100

<210> 1923
 <211> 44
 <212> DNA
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<400> 1923
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<210> 1924
 <211> 249
 <212> DNA
 <213> Homo sapiens

<400> 1924
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 tctcaccttt ctttaaaaac aaaacaaaac gatccttttg aatgtgtggt gcagacgcag 180
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 gcgcggcgg 249

<210> 1925
 <211> 51
 <212> DNA
 <213> Homo sapiens

<400> 1925
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<210> 1926
 <211> 174
 <212> DNA
 <213> Homo sapiens

<400> 1926
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tgggcagaag gcgatggctg gttggagaga agccaggccg tctagtgggg gaggatgggt 120
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<210> 1927
 <211> 436
 <212> DNA
 <213> Homo sapiens

<400> 1927
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 catgttattt ggttgcatga agttgccctt aaccactaag gattatcaag atttttgcgc 180
 agacttatac atgtctagga tccttttatc aaggcagtta tgatcatcgt tttcctgcct 240
 tgacccacc atcatcaaac actcagttaa atataaatta acatttttta gatgaccact 300
 caacataatg cttagaatg gaatttcctc tctgtgacag aaccaggaa ttaattccta 360
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 gtgtaaagtt taacca 436

<210> 1928
 <211> 97
 <212> DNA
 <213> Homo sapiens

<400> 1928
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 aaattctcag taagatccca gatgagatca atgacag 97

<210> 1929
 <211> 36
 <212> DNA
 <213> Homo sapiens

<400> 1929
 acacaccgt gaggaagttg caagccaaca aaaaag 36

<210> 1930
 <211> 110
 <212> DNA
 <213> Homo sapiens

<400> 1930
 aagaggaact tccgccctgt ccctggacct cacattttcc tggaaaagaa agcttctggc 60
 actggtgcac acattaggcc aagaggagcc tgctttcctt gacttttctg 110

<210> 1931
 <211> 331
 <212> DNA
 <213> Homo sapiens

<400> 1931
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 attatggata agataatagg caaagacttt gatcagaaaa gtaatctata aaaatcaaat 120

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ggatattcta gaactgaata cagtgtcttg agttgagaac acagtaggtg gatgtaatag 180
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 tggagtcttg gaatagaatg gggccaaagt a 331

<210> 1932
 <211> 256
 <212> DNA
 <213> Homo sapiens

<400> 1932
 ctggcatcct ctgggcgtcc catgatccct tctgtgtctg cgtgtccgaa tccccgtgtg 60
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 tctcctgctg cccaccacc tgccagtgtt atttatgctc ccttcgtggg tgatggccac 180
 gccctacca tgtccctggc agagggcttc cctccgggat cccctgcctg gtgcccacac 240
 tgcctcgcaa gcgctc 256

<210> 1933
 <211> 32
 <212> DNA
 <213> Homo sapiens

<400> 1933
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<210> 1934
 <211> 270
 <212> DNA
 <213> Homo sapiens

<400> 1934
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 atcatgtaga tagagtcaat tattgtttgt ggagtttttc agctataggg gaggggaact 180
 attaaaatcc atttgtttct attcaatagg taataaaaat tagttgtccc tgggtttggg 240
 aaacttaa at gccattaca gccctgggga 270

<210> 1935
 <211> 72
 <212> DNA
 <213> Homo sapiens

<400> 1935
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 tgtttagaga tg 72

<210> 1936
 <211> 73
 <212> DNA
 <213> Homo sapiens

<400> 1936
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 aatcagagta tag 73

<210> 1937
 <211> 578
 <212> DNA
 <213> Homo sapiens

<400> 1937
 ctacacagta gcacaggagg cattgggaaa tcacaggagg ctgcacagaa tgattacaaa 60
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 tatagtaata ctttttacat tatgggtttg ttatgagaat taaataagtt agtttatgta 240
 aagtgcaaag agcaaggaga agcatgggcc tgtcccagga agggagaacg ggcagttcct 300
 gcaggatcatg ggagggtgag agagcccagt tgggtatttc gaagtacgtt tatgtggcac 360
 ttgtgtgtta tgtgccaggt tctctgttag tagtgaattg gacacagacc aaaaagatac 420
 agatcatgca tgcccccttt atctgactgg actagaatga attcaagtta tgaaaacatt 480
 ttattatagt aataatttag tgtaatagga aattaagggc agcctatatg taccaaagtg 540
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<210> 1938
 <211> 60
 <212> DNA
 <213> Homo sapiens

<400> 1938
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<210> 1939
 <211> 33
 <212> DNA
 <213> Homo sapiens

<400> 1939
 ttccactgga ctcaacatcc ttttgcccgt atc 33

<210> 1940
 <211> 171
 <212> DNA
 <213> Homo sapiens

<400> 1940
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 tgTTTTtgtt ttttccaga cttctatact attgtctgcc ctaggctgta gggaatgctg 120
 gttagtttgc tgaacagaca ctgtgttcag cagggtttgt ggtatctcaa a 171

<210> 1941
 <211> 273
 <212> DNA

<213> Homo sapiens

<400> 1941

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 gggaagtgtg ctctgaaacc cggggacaga ggacgcagga cagactagga gggagccggg 120
 aggatgggct gcagctgtgg aggagggttt cagaggagag aggtcggaga gcagaggcct 180
 gagaagccag aggcaggtgg agagagggtg gaaagtgagc agcgggctgg gctggagccg 240
 cacacgctct cctcccatgt taaatagcac ctt 273

<210> 1942

<211> 235

<212> DNA

<213> Homo sapiens

<400> 1942

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 acattttggg ttgccttttg gaattcatgc actctccagc cttctacatg actactgctt 180
 cttactgtgt tagaatcaac tcctacacc tacctggccc tagaaagcat taagt 235

<210> 1943

<211> 83

<212> DNA

<213> Homo sapiens

<400> 1943

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 agtttaataa agattcacca agt 83

<210> 1944

<211> 58

<212> DNA

<213> Homo sapiens

<400> 1944

gaaaactaca ttcagaccc aactatctta tggagggctt atccccataa cctgatga 58

<210> 1945

<211> 252

<212> DNA

<213> Homo sapiens

<400> 1945

agtatggagt actgaaggcc aagtaaagag tttttcaggg agaaagtgac caactgtgtc 60
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 taataggaag gtccttggtg accttgcaag agcactttca ggagaatagt gaggaagaaa 180
 acctgattgg tgtggtttca agagacaaca ggaggaagag cattggagac tgcagtatgg 240
 acagctcttt gg 252

<210> 1946

<211> 977

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<212> DNA
 <213> Homo sapiens

<400> 1946
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 gttcttccag atcatattct ggctattggc atggctggcc tttctgaagg taccctgctt 180
 gtctattttc ctgactcagc tcttgccctgc ctttttcaca tgttgctgca attagactca 240
 ccgtgaggac tacagtcaat ttcagtctat cttgtgcccc atacaacaag gatttttaat 300
 agtaacaacc cacacctcac ccactaggac tcaatgttca caacaggaag gaccattgct 360
 gcatactcct tgaccagcaa cttttttgaa gatattttta agtgcagagt aggcctctat 420
 tcctgtatgt aattgttcat tttcagcacc tggaacctca tctatcgggt ctggaaggaa 480
 tacagcagtt cgaaagccgc gtccatttct ctccttcagt agtgcagaaa tgagtccgat 540
 tcaccagtac acacagaact gtaccagttc aacctagcaa aagaagaaaa gtttccactg 600
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 ttgtcttact tcagatcagc aggacagttg ggctctcaga ctcatgacca ctgagtttgc 720
 ttgtgttgaa actgtggttt catccaacat atgctattgg acatgattat tattccattc 780
 aaatggatta cagacttctt gaggacagga caaacttatc tctcatggtg tttttttaga 840
 atacttttat aaccaaggaa gaaaccatgc cagctgttac cattcaactt ctttaagcaga 900
 gattaagctt tttcatatct gttcttatcc tggacatcag tagtttttaa ttgccagca 960
 tccgttccat cttgtaa 977

<210> 1947
 <211> 449
 <212> DNA
 <213> Homo sapiens

<400> 1947
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 atatgcacct aaaaattcag tgtaaatcaa gtttactaaa ccctgaaatt ctatagccaa 120
 atgcttctgt gatagaaata atcagccctc agtatctgct aagcgtaaatt tttttcccta 180
 gtttgagag agaaactggt tgggtgcagt ggctcacacc tgtaatccca gcactttgaa 240
 ggctgaggtg ggaaaatcgc ttgagctcag gagttcaaga ccagcctggg caatgcagcg 300
 agacattgtg tctacaaaaa aatttaaaaa ttagccatgc attggtgaca cgtgcctgga 360
 gtcccagcta ctcgggatca ggaagccgag gtgggaggat ggcttcagcc aaggaagtca 420
 aaactggagt gagtcatgtt caggccaca 449

<210> 1948
 <211> 901
 <212> DNA
 <213> Homo sapiens

<400> 1948

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ccgtggttga agtcagccta cactacagtg cacagttgag gagccagaga cttctttaat 60
 catccttaga accgtgacca tagcagtata tattttcctc ttggaacaaa aaactatttt 120
 tgctgtattt ttaccatata aagtatttaa aaaacatgaa ttgagtttct gtagatttct 180
 agttctcaac tttagcctga acgccaacac ttgaaggtgt ttttcacct ctgtatgttg 240
 aaggtggtta tttgtatgta ggaacaggac tgccatccca gctttgcatg ccaaagaaat 300
 aaagaacaca ctttaaaggg caaactgaag agatgagcga gcaaaggtgc ccttcaggtc 360
 tactgaaaag ttagagtaca aaacaacact gttgatctgg acaaaagaag aaaaattacc 420
 ctttttgctt gtgttgtagac aacttcattt aatatggttt aaagatttat gagactgtca 480
 gctaaaagtc ttttcacaag aatgtcaaca gagaatggca tctcaaata tatatatattc 540
 tttgcacaat ttgtgaaacc ttataagcca ttttccccag gtacaatgta gttcctgctg 600
 atagaaagga aatattttgt caagagcttt catttaaaag ctactacctc cacaatcacc 660
 cccaaacca gaaaatcccc actggctctt gccagtctgg ttttcgtatt gcagttattc 720
 caattgtatt tgatctccct gataacgtat tttcatgggt ttgggtagaa gatgctaadc 780
 agattagaag caggaatagt ttttgctgt ctgtgaaatt gagccttttg gtgcgccacg 840
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 a 901

<210> 1949
 <211> 144
 <212> DNA
 <213> Homo sapiens

<400> 1949
 ctctcgggta ttgaggcaga agaaaacttt gaagaagact cacacaggcc attaattaat 60
 ggtggtgaaa atgaagacga atatgagccg aattattcaa tccaagatga tagttctggt 120
 gcccaagtca aggcgataag cttc 144

<210> 1950
 <211> 229
 <212> DNA
 <213> Homo sapiens

<400> 1950
 aaggttttcc ttgagctggt ctctctctac tttgagagtc tcctccacac tcctaaggtc 60
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 ccttatattc tccgtttcta tgttttccag gtttaacttc tgggtctcaa attgctcctt 180
 caagtgttct atttcacaca ttttctcctg agtctcattg acagctgtc 229

<210> 1951
 <211> 152
 <212> DNA
 <213> Homo sapiens

<400> 1951
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GBX1170_3WO_ST25.txt

agatgtgcta ctacaccaat ggctgtacac agagtaaaag tcacatttaa ggatgagcca 120
ggagaggggca gtggtgtagc acgaagtttt ta 152

<210> 1952
<211> 110
<212> DNA
<213> Homo sapiens

<400> 1952
gggaagcctc tggtcgactg tcagatcccc gaggttcaga ggacggatac agcaggaacg 60
aaaaaacatc cgaccaaca ttattcttgt gcttaccgat gatcaagatg 110

<210> 1953
<211> 331
<212> DNA
<213> Homo sapiens

<400> 1953
agcagtctgg caggccttct caagtaaata ccaaccctgt ttctgcagca gcctcagcag 60
cagctcagtc tagacagggt ttccttcttt ctgtttatct ttcttgctat cagagccctg 120
atgtgtacat tttggaatgc tggagtagct gcttcatttc tattcctcca tctcccctcc 180
ctcattgaag gggctggtgg aactagacca gatgtctaac aaaccccgat tgctagagtg 240
tctggctctg tacgtgactg accaatcata atacggtgtg ccaagttttt ttatacctc 300
tgacaacagc gtacaaaacc tggactgttt c 331

<210> 1954
<211> 49
<212> DNA
<213> Homo sapiens

<400> 1954
tgcgcgcgcg ccagtgaag accgagattg agggaaagca tgtctgctg 49

<210> 1955
<211> 31
<212> DNA
<213> Homo sapiens

<400> 1955
tgagatgcg ggcaacgaca caagaaacac a 31

<210> 1956
<211> 80
<212> DNA
<213> Homo sapiens

<400> 1956
accttgag atgagtatgc atccagcggc aagcgtcca ctctcagtct ttactaagga 60
atctacagcc tccaaacaca 80

<210> 1957
<211> 81
<212> DNA

<213> Homo sapiens

<400> 1957

gagattgcag atgtcagcgt ccagatgtgc agccccagca gagcaggaat gtatcagggg 60

cagtggcgga tgtgcactgc t 81

<210> 1958

<211> 451

<212> DNA

<213> Homo sapiens

<400> 1958

caaagttcag tgctcgggtgt tctcggcaca acaatgcagt gtagttcaga aggtatTTTTg 60

gcaactctta atctgaacaa gaatgggggg ggcgctTTTTg aaaaataagg ctttaagaag 120

gcttgtcatt ttagggctaa atTTtaatag aatgtgagtc tgaactctta catttagaac 180

aaacaaaacc ttaaaattac tgattgggtc aaaaaatggT tttatggaaa aattaatctg 240

taacaaaaag ttggcattga gtgcgaaggc tccaccgttg tttttttttt ttgttttttt 300

tttttgtttt tttttgagca aagcgtacaa aggttccaag ggacaggacc aagaacgagg 360

ggctgagaca ttacaacag caggcatttt ctcttcctct tcttcacggg aggcgggcag 420

aggactgctc ggatcgcttc gtcaaact g 451

<210> 1959

<211> 29

<212> DNA

<213> Homo sapiens

<400> 1959

atgttgctgc cacgatcagt gccacagag 29

<210> 1960

<211> 81

<212> DNA

<213> Homo sapiens

<400> 1960

gtggTccagt gccagagac atttatcaga gaattaaaaa acttgaggat aaaatccttg 60

aattggaagg catctctcct g 81

<210> 1961

<211> 73

<212> DNA

<213> Homo sapiens

<400> 1961

tgTgtacag ggcagcatgt cctgaaaggg gctgcaagaa atgctgattc caagggatgt 60

gtgccagttc tct 73

<210> 1962

<211> 396

<212> DNA

<213> Homo sapiens

<400> 1962

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ttttaaaact ccaccacag ctaacactaa gattacttcc ttcctgaata catatcacca 180
gacgctctcc tttgtcccat tgtcgtata ttgccaaatg ctttctctcg atttttggtc 240
aaagtcctaa tcatttcagg tccaattaaa aactcagtat ctcttgagcc ttccccacac 300
catatgttgc aaaattatct ggtctttcca cattcacagc gttcacaggc cactgttgca 360
ttacctatta gtctgtgagt gtacacgttc ggaccc 396

<210> 1963
<211> 185
<212> DNA
<213> Homo sapiens

<400> 1963
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gggagatgtt tggagtgggc cagatggaga agaaagagtc aagtcacctc caccctagt 120
ggcctgaatg ctgtcatgcg gaattgcctg gtccagttaa caaacctcg cttcattgtt 180
ttatt 185

<210> 1964
<211> 268
<212> DNA
<213> Homo sapiens

<400> 1964
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gagcactgat tatttaaggt gactgaggat tactgtcagt gataggattg tgttataatt 120
ccacttatat acatctgata tggaaaactg aaacttccat tttagaagag aaagaaaata 180
gctgaatttg gcatttcagt agcatgctat agaattcatc atgattaatt tcacattaaa 240
ttatgggcaa tagctgtatc acatttca 268

<210> 1965
<211> 640
<212> DNA
<213> Homo sapiens

<400> 1965
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aagtggagga attagtcaag cagctatctg aggaaagaac attccaagta aagaatatac 120
agcccatata ttgttgatg tgtgtacatt gaaatttttg tgcagtaaaa tgaatatttc 180
atttacctat ataattttac ataaaataaa atatattttg aatgtgagtt tgttccaaac 240
aatcattttt cttgccttca aaaccactga gcttaaagaa ctctttcaag tgtcattaga 300
gatagattcc aactacaatc aacattgtgg aatccagagg aggcaaatg aaggaagcag 360
cactcattac aaaatgctgc tttgtaaaga attaattctg tcctggtatg tttcacatta 420
ggtaatatga aggaaatgaa tatgtcatga accctccttg aggatgtggg ggaattaaaa 480

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gtaatttcgc ttaatatcca actctcactt ttggctttgt agtcagaggg aaacaatgct 540
 ttcccagggt ctaaggtaaa cgttaaaagg ttacaaggag acttggaaga gtcaaggaac 600
 gcttccacca actattcctg ccattccagt tgggaggggt 640

<210> 1966
 <211> 131
 <212> DNA
 <213> Homo sapiens

<400> 1966
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 aggttaacct ctggggaaac aggaagacct gctgatttaa cccctacttc ctttcctata 120
 atccacagta a 131

<210> 1967
 <211> 60
 <212> DNA
 <213> Homo sapiens

<400> 1967
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<210> 1968
 <211> 99
 <212> DNA
 <213> Homo sapiens

<400> 1968
 tgtgtcgtgg tatagcagaa gtgcttgaag atttgtttct ctgccttacc tttagtaatt 60
 gtgtttatgt tggctatctg gctattgccc ttgcgtgac 99

<210> 1969
 <211> 551
 <212> DNA
 <213> Homo sapiens

<400> 1969
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 ctaagctacc tgccttcaaa atagtttagg gaccaccacc atattttatt ttgtttttat 180
 ttttgaacat ttttctaag atttggagag aaaactattt aaaaaattc cacatatcag 240
 tgatacaatt tcttgctgtc accaattttt tataatagca gagtggcctg ttctaagaag 300
 gccatatttt ttaagttatc tttcagggtg acatggaaat actataaagt tggatgtcaa 360
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 aaaaaaagat ttgtaaaatc accggaacaa ttgtgtgctt ttttttatag gtagtgggta 480
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 ttactaacat a 551

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<210> 1970
 <211> 178
 <212> DNA
 <213> Homo sapiens

<400> 1970
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 aaggctgttt aagaatagaa ctcatccccg gtttccacca aattatttcc ctaattctta 180
 aatcctcaaa taagttctta atctccaaag tctcggttgt gggaaaaaca ttaatttgtg 240
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 gggcgctgtg cagtgtggtc agcatggtga agaaagtcatt ttctcgggtg ggcagtattc 360
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<400> 1973
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<210> 1974
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 aaccataagg gtaaccagat tttcatctac agacaagtgg tagtcatttg tgtttatcat 180
 gcaacttact taaaacacc aagatattaa ttgctgcaac ttgatgtcaa atcacattac 240
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 ttgccttagt aatatattag aatatacaaa tatgtgtgta taaaataaac atacacacac 420
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 tgtatgaact accctatgaa atgtaagctg cagaatagat aaaacacagg tttccactaa 540
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 ttttaacatg tttaaccaac agaagttatt tacagaaatt catatatcca ggcaacacaa 660
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 atggagttca 130

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 tgcacatca tgctgcccac atttgcacca acag 94

<210> 1977
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<210> 1978
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<400> 1978

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<210> 1979
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<210> 1980
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 <213> Homo sapiens

<400> 1980
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<210> 1981
 <211> 35
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<400> 1981
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<210> 1982
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 <212> DNA
 <213> Homo sapiens

<400> 1982
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 aacttctcaa taaaagaaaa tcatgaatgc tccacaattt caacatacca caagagaagt 240
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 ctttcagggga aaagggcatt ctttaggaac tgcattctggt aaccacacc ttgatccaag 180
 agctagggaa acttcagttg taagaaagca taatacaggg acagacttta gtaatagttc 240
 cactaaaaca gagccttctg tattcacagc ttcttctagt aatagtgagc ttattcgaat 300
 agtccttgga gtagtaacaa tgagagacgg caggcagctt gatcctgatt tgggtgaggc 360
 ccagcgaaaa aaattgcagg aaatggtttc ttctattcag gcttcaatgg acaggcacct 420
 tcgggatcaa agta 434

<210> 1984
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 <212> DNA
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<400> 1985
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<210> 1986
 <211> 181
 <212> DNA
 <213> Homo sapiens

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 a 181

<210> 1987
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 <212> DNA
 <213> Homo sapiens

<400> 1987
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 g 121

<210> 1988
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 <212> DNA
 <213> Homo sapiens

<400> 1988
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 atagcaagct gcaactgctc aaag 84

<210> 1989
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 <212> DNA
 <213> Homo sapiens

<400> 1989
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 tgtaatttcg ccttaaacctc tggacactct atatgtagtg cttttttaaa cttgaaatat 180
 ataatatcca gccagcttaa acccatacaa tgtatgtaca atacaatgta caattatgtc 240
 tcttgagcat caatcttggt actgctgatt cttgtaaatc tttttgcttc tactttcatc 300
 ttaaactaat acgtgccaga tataactgtc ttgtttcagt gagagacgcc ctatttctat 360
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 tctgagcagg aagggtaaaa gacaggaacc tgcttcactg tattaactag tccatgggct 180
 gagaccgggg catctctttt ctt 203

<210> 1991
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 <212> DNA
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<210> 1993
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 <212> DNA
 <213> Homo sapiens

<400> 1993
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 <212> DNA
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<400> 1994
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 gacttgaatt gcaaaaagat gttagaaaag cagaagaaga actaggtgaa cttgaagcaa 120
 agctcaatga aaacctgcgc agaaat 146

<210> 1995
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 <212> DNA
 <213> Homo sapiens

<400> 1995
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 tgctgaatgt gggcattaat tttttgactg cagctctgct tctccagccc cgccgtgggt 180
 ggcaagctgt gttcacact aaattttctg gaaggggaca gtgaaaagag gagtgacagg 240
 agggaaaggg ggagacaaaa ctctactct caacctcaca ccaacacctc ccattatcac 300
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 <212> DNA
 <213> Homo sapiens

<400> 1996
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<210> 1997
 <211> 219
 <212> DNA
 <213> Homo sapiens

<400> 1997
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 tgggatgggc ggatctcaca ggctgagaac tcgttcacct ccaagcattt catgaaaaag 180

ctgcttctta ttaatcatatc aaactctcac catgatgtg 219

<210> 1998
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 <212> DNA
 <213> Homo sapiens

<400> 1998
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 gtgggtcttga gattttttatt tttgcatatg taatccattc tgtacag 107

<210> 1999
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 <212> DNA
 <213> Homo sapiens

<400> 1999
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<210> 2000
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 <212> DNA
 <213> Homo sapiens

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 ctctctccag aagggtgaaa tgtagtgaa ctcaagactc tcaactgatga tgggtatttta 180
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 aaaatagcag ctctacatgt tgatgaaaag aaatttcaat ttcttcctat ttgtttttac 300
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 aaaacatatg tgtatgtatt tatttatctt accttcaactg aagttctttt ttctggctgg 480
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 ccaaactggc attatggtat tataggcatt tgatttttgt tttcttattt tcagtttgtc 720
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 gcttagtgcg ttctaccttt ttgcc 85

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 <212> DNA
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<210> 2003
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 <211> 173
 <212> DNA
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<400> 2004
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 tagccacctt ctcttctgaa aacaagatgg gaatgacgga actgtattaa aagattaagt 120
 tatccactag ggagcatact agcacacttc cagatcagcc ttgagatgct aga 173

<210> 2005
 <211> 90
 <212> DNA
 <213> Homo sapiens

<400> 2005
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 gctgccctca atctagaacg ctacacaaga 90

<210> 2006
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 caatacagca acaaaaaaaaa aaaaaaacct caactctgaa aagccatgga aagctggaaa 240
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<210> 2007

<211> 163
 <212> DNA
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<210> 2008
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 <212> DNA
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<400> 2008
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 cagtatttag aacatgcatc taag 84

<210> 2009
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 <212> DNA
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<210> 2010
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 <212> DNA
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 <212> DNA
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<210> 2012
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 <212> DNA
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<400> 2012
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 <212> DNA
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 ggtctaccag tcagcacgcc aag 143

<210> 2014
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 <212> DNA
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 <212> DNA
 <213> Homo sapiens

<400> 2015
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<210> 2016
 <211> 204
 <212> DNA
 <213> Homo sapiens

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<210> 2017
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 <212> DNA
 <213> Homo sapiens

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<400> 2017
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<210> 2018
<211> 82
<212> DNA
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gtgactattg tgtgcacata tt 82

<210> 2019
<211> 158
<212> DNA
<213> Homo sapiens

<400> 2019
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aaaatgatat aaatgttggt ggaactaaca cagctgta 158

<210> 2020
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<212> DNA
<213> Homo sapiens

<400> 2020
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<212> DNA
<213> Homo sapiens

<400> 2021
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agtggttggg gatggttttc tgaccctacg gtaactagat c 101

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<212> DNA
<213> Homo sapiens

<400> 2022
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aggggaaagg aaaccatgca acagtcaacc ttctgagct 99

<210> 2023
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<212> DNA
<213> Homo sapiens

<400> 2023
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 <212> DNA
 <213> Homo sapiens

<400> 2024	
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aaactgggggt tctgtcaatg acaacaagga ctatgtgttg gttcatatca aatccaagaa	180
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<210> 2025
 <211> 58
 <212> DNA
 <213> Homo sapiens

<400> 2025	
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<210> 2026
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 <212> DNA
 <213> Homo sapiens

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 <213> Homo sapiens

<400> 2027
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<212> DNA
<213> Homo sapiens

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<212> DNA
<213> Homo sapiens

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<212> DNA
<213> Homo sapiens

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<212> DNA
<213> Homo sapiens

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<212> DNA
<213> Homo sapiens

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cccattggta ttcccgacac ta 142

<210> 2033
<211> 94
<212> DNA
<213> Homo sapiens

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agggcggcag agttgttatt tttcagcgtg aaca 94

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<212> DNA
<213> Homo sapiens

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gtatttttta aaaggctcaa ctgtaagcct cttagccagt tggataaata tttgggggtca 480
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caacgcatag ataaatttag gggaattgga tgtattattc aactttgatt tgggttgtaa	960
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ctccaccaag aggaattaat gatagacatt ttcgaaaacg gtctcattca aaatctccca	780
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gatcaggggtc actagagaga gataggcccg gacatgtttc acaaaaata	1129

<210> 2037
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 <213> Homo sapiens

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ttgaatatcg tagggacata agtatataca tgttatccaa tcaagatggc tagaatgggtg	240
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<210> 2038
 <211> 74
 <212> DNA
 <213> Homo sapiens

<400> 2038	
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 <212> DNA
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tatattgatt taaatgatgt gtgagatgtt tcaccatttt caggcactgt gtaattctat	180
tgtaataaac tggcaggtat ctttgtaact ataaatagtg catgctcagc catgtacact	240
gtaaatagcc ttaccaaac gtgtttgaca aggaccataa ttaacatcac ttagtgaatt	300
gtgataaaga aaaaaagcc atgatttatt cgatgtgatt ggcttgtttt tatgtggcgc	360
caagaacgaa cctgtttaac agctgtaacc aatggtactg atctatccat ccaatgttgt	420
cattatattt gactgtgggt caacagtatt gcgttgctcag actaggaaag ctaaacgaac	480
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<212> DNA
<213> Homo sapiens

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ct 62

<210> 2041
<211> 436
<212> DNA
<213> Homo sapiens

<400> 2041
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ataatgatca agcaaccctg gaaattaaat cccaaagcag tgcaccttta gtttgttcag 180
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ttgcactgag ttgca 436

<210> 2042
<211> 73
<212> DNA
<213> Homo sapiens

<400> 2042
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ggccttagca cat 73

<210> 2043
<211> 544
<212> DNA
<213> Homo sapiens

<400> 2043
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GBX1170_3WO_ST25.txt

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gagt 544

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<211> 97
<212> DNA
<213> Homo sapiens

<400> 2044
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cttacctgtg atgtgtttta cccagcacct ccggaca 97

<210> 2045
<211> 123
<212> DNA
<213> Homo sapiens

<400> 2045
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gta 123

<210> 2046
<211> 282
<212> DNA
<213> Homo sapiens

<400> 2046
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<210> 2047
<211> 320
<212> DNA
<213> Homo sapiens

<400> 2047
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<210> 2048
<211> 389

<212> DNA
 <213> Homo sapiens

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 aatacgtatg gactggataa ctctgagaa 389

<210> 2049
 <211> 933
 <212> DNA
 <213> Homo sapiens

<400> 2049
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<210> 2050
 <211> 1030
 <212> DNA
 <213> Homo sapiens

<400> 2050
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GBX1170_3WO_ST25.txt

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<211> 129
<212> DNA
<213> Homo sapiens

<400> 2051
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tctgtgttc 129

<210> 2052
<211> 473
<212> DNA
<213> Homo sapiens

<400> 2052
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caaactttac tgttctaaca aatttgtatt ttattttgca ttgccacaca tctgcttatt 420
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 <211> 262
 <212> DNA
 <213> Homo sapiens

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 gaaaggtttc cacttgatat ac 262

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 <211> 265
 <212> DNA
 <213> Homo sapiens

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<210> 2055
 <211> 110
 <212> DNA
 <213> Homo sapiens

<400> 2055
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<210> 2056
 <211> 250
 <212> DNA
 <213> Homo sapiens

<400> 2056
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 ttcaatatat tgaaaaatgc ttttcccctc cctcacagca cgtttttata tatagcagag 180
 aataatgaag agattgctag tctagatggg gcaatcttca aattacacca agacgcacag 240
 tggtttattt 250

<210> 2057
 <211> 2168
 <212> DNA
 <213> Homo sapiens

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GBX1170_3WO_ST25.txt

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acaatgaaat tatatttgct gtgtgactat gattcctaag atttccaggg ctttaagggt 2160
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<212> DNA
<213> Homo sapiens

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agacatcttc acaaggaaaa ccaagtacta aaaaaagtat cctcccaact ctgaagagat 120
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<210> 2060
<211> 302
<212> DNA
<213> Homo sapiens

<400> 2060
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gtttctggct cccaagcctg ggtcactgct acatggattg cgccaaaaaa ttcccagctt 180

GBX1170_3WO_ST25.txt

caacactgct agattaaaat tgctggcatt tttaaatac agcaaagctt ttcacaatgc 240
cctcaagtcc aagaggacaa aggagaaagc aacatgaacg gcagatcctc atgtgaaagg 300
ga 302

<210> 2061
<211> 180
<212> DNA
<213> Homo sapiens

<400> 2061
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gacattatgt ggtgttcttt atgaagtgt tagttcctca gcaggacctg cggtcagaca 120
taagtgcctt agagcaattc ttaggataat ttattttgcg gatgctgaac ttctgaagga 180

<210> 2062
<211> 86
<212> DNA
<213> Homo sapiens

<400> 2062
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gcatccttgg ttaggggtcaa cccagt 86

<210> 2063
<211> 397
<212> DNA
<213> Homo sapiens

<400> 2063
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agaatgatcc tttatggacc aaaacttgaa tcactgc 397

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<211> 131
<212> DNA
<213> Homo sapiens

<400> 2064
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ttccacaat gtcatacttt tgacgcagtt gggtttctca taagtatcct agttcatgta 120
catccgaatg c 131

<210> 2065
<211> 72
<212> DNA

<213> Homo sapiens

<400> 2065

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tgcttgaggc ta 72

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<211> 162

<212> DNA

<213> Homo sapiens

<400> 2066

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gaagagtgtg tgaagaaaat tcgagaactt ggatcacttc cc 162

<210> 2067

<211> 176

<212> DNA

<213> Homo sapiens

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taaaagtttc aaatacagtt tcacttagaa actgcaaccc tccaagtaat gttatg 176

<210> 2068

<211> 393

<212> DNA

<213> Homo sapiens

<400> 2068

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tagggacaga tataccacaa ggtacaacat cagtgaata aattcacaaa actatattac 120

agctagttaa tcagtttaag aattgttccc gtcagtcaca ttttttggcc ctcagaagtt 180

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aagtctgctc tcaccaacag cccttgattt tttcagggag aaatctctag gaaaaaagtc 360

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<210> 2069

<211> 31

<212> DNA

<213> Homo sapiens

<400> 2069

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<210> 2070

<211> 116

<212> DNA

<213> Homo sapiens

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<210> 2071
<211> 237
<212> DNA
<213> Homo sapiens

<400> 2071
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taacaaaatt ctcattaata ctgtgtttga tggcctctgc tgtgttttaa catcgtgctt 180
cttatatgga aagtttttgt gagctgtgta atccctctgg tcagtattat gaaatca 237

<210> 2072
<211> 210
<212> DNA
<213> Homo sapiens

<400> 2072
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actttgttta ggatgaggag tctttgtgtc cctgtacagt agtctgacgt atttcccctt 180
ctgtccccta gtaagcccag ttgctgtatc 210

<210> 2073
<211> 221
<212> DNA
<213> Homo sapiens

<400> 2073
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gtggaggcta aaaagaggac acgaaagtga acagaatgat cttcctacgc acaacacaaa 120
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agtccctcta cccccaccc tcacctggta tgcttacatt a 221

<210> 2074
<211> 113
<212> DNA
<213> Homo sapiens

<400> 2074
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<210> 2075
<211> 59
<212> DNA
<213> Homo sapiens

GBX1170_3WO_ST25.txt

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<210> 2076
<211> 69
<212> DNA
<213> Homo sapiens

<400> 2076
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<210> 2077
<211> 110
<212> DNA
<213> Homo sapiens

<400> 2077
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ccccttgccc aaccaatgca cacagtaggg cttggtgaat gctgctgagt 110

<210> 2078
<211> 507
<212> DNA
<213> Homo sapiens

<400> 2078
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gaacttggtc tgcttcagcc caagaggaat caaaagatca aaagcagttt gggaaggcca 300
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ggccagaagg ggctcacaaa ggcttgc 507

<210> 2079
<211> 99
<212> DNA
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<400> 2079
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gccctggatg agtgggccgg ctgcttcggc atcaagcag 99

<210> 2080
<211> 83
<212> DNA
<213> Homo sapiens

<400> 2080

GBX1170_3WO_ST25.txt

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gctctgaata cagtctctgc agc 83

<210> 2081
<211> 65
<212> DNA
<213> Homo sapiens

<400> 2081
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tgcga 65

<210> 2082
<211> 393
<212> DNA
<213> Homo sapiens

<400> 2082
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aaaataatgc ttttgaaaaa aagaaaaaaa aaacggatat attgagaatc aaagtagaag 180
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cccctttagc actgcttttc tgaagacttc agttttgtta aggagattta gttttactgc 300
tttgactggg ggggtctctag aagcaaaact gaggatgata tcattgagaag tactgatagg 360
acctttatct ggatatgggc ctatagggtta ttc 393

<210> 2083
<211> 115
<212> DNA
<213> Homo sapiens

<400> 2083
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