



- (51) **International Patent Classification:**
C12Q 1/68 (2006.01)
- (21) **International Application Number:**
PCT/GB2013/053202
- (22) **International Filing Date:**
3 December 2013 (03.12.2013)
- (25) **Filing Language:** English
- (26) **Publication Language:** English
- (30) **Priority Data:**
61/732,761 3 December 2012 (03.12.2012) US
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(81) **Designated States** (*unless otherwise indicated, for every kind of national protection available*): AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, JP, KE, KG, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LT, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

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

Published:

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

(54) **Title:** MOLECULAR DIAGNOSTIC TEST FOR CANCER

(57) **Abstract:** Methods and compositions are provided for the identification of a molecular diagnostic test for cancer. The test identifies cancer subtypes that have an up-regulation or a down-regulation in biomarker expression related to angiogenesis and vascular development. The present invention can be used to determine whether patients with cancer are clinically responsive or non-responsive to a therapeutic regimen prior to administration of any anti-angiogenic agent. This test may be used in different cancer types and with different drugs that directly or indirectly affect angiogenesis or angiogenesis signalling. In addition, the present invention may be used as a prognostic indicator for certain cancer types. In particular, the present invention is directed to the use of certain combinations of predictive markers, wherein the expression of the predictive markers correlates with responsiveness or non-responsiveness to a therapeutic regimen.



MOLECULAR DIAGNOSTIC TEST FOR CANCER

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of U.S. Provisional Patent Application No. 61/732,761 entitled “Molecular Diagnostic Test for Cancer” and filed on December 3, 2012.

FIELD OF THE INVENTION

[0002] The present invention relates to a molecular diagnostic test useful for diagnosing cancers from different anatomical sites that includes the use of a common subtype related to angiogenesis. The invention includes the derivation of a gene classification model from gene expression levels. One application is the stratification of response to and selection of patients for cancer therapeutic drug classes and thus guide patient treatment selection. Another application is the stratification of cancer patients into those that respond and those that do not respond to anti-angiogenic therapeutics. The present invention provides a test that can guide therapy selection as well as selecting patient groups for enrichment strategies during clinical trial evaluation of novel therapeutics. The invention can be used as a prognostic indicator for certain cancers including ovarian cancer, breast cancer, colon, prostate, lung and glioblastoma. The angiogenesis subtype can be identified from fresh/frozen (FF) or formalin fixed paraffin embedded FFPE patient samples.

BACKGROUND

[0003] The pharmaceutical industry continuously pursues new drug treatment options that are more effective, more specific or have fewer adverse side effects than currently administered drugs. Drug therapy alternatives are constantly being developed because genetic variability within the human population results in substantial differences in the effectiveness of many established drugs. Therefore, although a wide variety of drug therapy options are currently available, more therapies are always needed in the event that a patient fails to respond.

[0004] Traditionally, the treatment paradigm used by physicians has been to prescribe a first-line drug therapy that results in the highest success rate possible for treating a disease. Alternative drug therapies are then prescribed if the first is ineffective. This paradigm is clearly not the best treatment method for certain diseases. For example, in diseases such as cancer, the first treatment is often the most important and offers the best opportunity for successful therapy, so there exists a heightened need to choose an initial drug that will be the most effective against that particular patient's disease.

[0005] Ovarian cancer is the leading cause of death among all gynecological cancers in western countries. This high death rate is due to the diagnosis at an advanced stage in most patients. Epithelial ovarian cancer (EOC) constitutes 90% of ovarian malignancies and is classified into distinct histologic categories including serous, mucinous, endometrioid, clear cell, transitional, mixed, and undifferentiated subtypes. There is increasing evidence that these differed histologies arise from different aetiologies. There have been recent advances in the methodology used to classify epithelial ovarian cancer (McCluggage, W.G. "Morphological subtypes of ovarian carcinoma: a review with emphasis on new developments and pathogenesis," PATHOLOGY 2011 Aug;43(5):420-32). One of the consequences of this is that many tumors that would previously been classified as endometrioid are now being classified as serous.

[0006] The current standard treatment for ovarian cancer is debulking surgery and standard platinum taxane based cytotoxic chemotherapy. However, not all patients respond to this, and of those that do, approximately 70% will experience a recurrence. Specific targeted therapies for ovarian cancer based on histological or molecular classification have not yet reached the marketplace. Similarly for other types of cancer, there is still no accurate way of selecting appropriate cytotoxic chemotherapeutic agents.

[0007] The advent of microarrays and molecular genomics has the potential for a significant impact on the diagnostic capability and prognostic classification of disease, which may aid in the prediction of the response of an individual patient to a defined therapeutic regimen. Microarrays provide for the analysis of large amounts of genetic information, thereby providing a genetic fingerprint of an individual. There is much enthusiasm that this technology will ultimately provide the necessary tools for custom-made drug treatment regimens.

[0008] Currently, healthcare professionals have few mechanisms to help them identify cancer patients who will benefit from chemotherapeutic agents. Identification of the optimal first-line drug has been difficult because methods are not available for accurately predicting which drug treatment would be the most effective for a particular cancer's physiology. This deficiency results in relatively poor single agent response rates and increased cancer morbidity and death. Furthermore, patients often needlessly undergo ineffective, toxic drug therapy.

[0009] Angiogenesis is a key component of neo-vascularisation of tumors and essential to tumorigenesis and metastasis. As such, it is a key area for therapeutic intervention and has been correlated to poor prognosis and reduced survival. This has promoted the development of a number of agents that target angiogenesis related processes and pathways, including the market leader and first FDA-approved anti-angiogenic, bevacizumab (Avastin), produced by Genentech/Roche.

[0010] Treatment regimens that include bevacizumab have demonstrated broad clinical activity¹⁻¹⁰. However, no overall survival (OS) benefit has been shown after the addition of bevacizumab to cytotoxic chemotherapy in most cancers^{8, 12-13}. This suggests that a substantial proportion of tumours are either initially resistant or quickly develop resistance to VEGF blockade (the mechanism of action of bevacizumab). In fact, 21% of ovarian, 10% of renal and 33% of rectal cancer patients show partial regression when receiving bevacizumab monotherapy, suggesting that bevacizumab may be active in small subgroups of patients, but that such incremental benefits do not reach significance in unselected patients. As such, the use of a biomarker of response to bevacizumab would improve assessment of treatment outcomes and thus enable the identification of patient subgroups that would receive the most clinical benefit from bevacizumab treatment. This would be particularly relevant in the case of metastatic breast cancer, where the absence of a clinically beneficial biomarker has undermined the use of bevacizumab. Thus far, no such biomarker has been clinically validated to predict bevacizumab efficacy. Hypertension and VEGF polymorphisms are so far the only biomarkers to show potential, but important questions remain about their use in a clinical setting.

[0011] Another approach to anti-angiogenic therapy is simultaneous targeting of multiple angiogenic pathways rather than selective targeting of the VEGF pathway. Theoretically, multitargeted anti-angiogenic agents should more completely inhibit angiogenesis than agents such as bevacizumab and thus may produce greater therapeutic benefit. It has been postulated that in some tumors, angiogenesis may require VEGF only in the early stages of disease but is driven by additional angiogenic pathways as the disease progresses. Therefore, by targeting multiple pathways, it may be possible to counteract compensatory escape mechanisms that could lead to resistance to VEGF inhibition.

[0012] As for other types of cancer there is still no accurate way of selecting which patients will or will not respond to standard of care with an anti-angiogenic therapeutic or single agent anti-angiogenic therapy.

[0013] What is therefore needed is a molecular diagnostic test that would facilitate the stratification of patients based upon their predicted response to anti-angiogenic therapeutics, either in combination with standard of care or as a single-agent therapeutic. This would allow for the rapid identification of those patients who should receive alternative therapies. Such a molecular diagnostic test should be predictive of therapeutic responsiveness across different cancer types with sufficient accuracy.

SUMMARY OF THE INVENTION

[0014] Disclosed are methods of using a collection of biomarkers expressed in cancer such that when some or all of the transcripts are under-expressed, they identify a subtype of cancer that has an up-regulation or down-regulation in molecular signaling relating to angiogenesis. The collection of biomarkers may be defined by an expression signature, and the expression signature is used to assign a cumulative score to the measured expression values of the collection of biomarkers. The invention also provides methods for indicating responsiveness or non-responsiveness to anti-angiogenic agents as well as identifying patients with a good or poor prognosis, using the collection of biomarkers and expression signatures disclosed herein. In different aspects, the biomarkers and expression signatures may form the basis of a single parameter or multiparametric predictive test that could be delivered using methods known in the art such as microarray, Q-PCR, immunohistochemistry, ELISA or other technologies that can quantify mRNA or protein expression.

[0015] In one example embodiments, the present invention provides an expression signature defining a cancer subtype associated with up-regulation of angiogenesis related biomarkers (“angiogenesis”). In another example embodiment, the present invention provides an expression signature defining a cancer subtype association with down-regulation of angiogenesis related biomarkers (“non-angiogenesis”). In addition, the cancer subtypes described herein are common to many types of cancer and are not limited to a single cancer disease type. Accordingly, the expression signatures of the present invention are not limited to a single cancer type. In certain exemplary embodiments, the expression signature comprises two or more biomarkers selected from the biomarkers listed in Tables 1A-1C. In another exemplary embodiment, the angiogenesis expression signature comprises two or more biomarkers selected from the biomarkers listed in Tables 2A or 2B. In another exemplary embodiment, the non-angiogenesis expression signature comprises two or more biomarkers listed in Table 2C. In another exemplary embodiment, the angiogenesis expression signature comprises the biomarkers listed in Table 2A or 2B and their corresponding weights as determined using a PLS classifier. In another exemplary embodiment, the non-angiogenesis signature comprises the biomarkers listed in Table 2C and their corresponding weights as determined using a PLS classifier.

[0016] In one embodiment of the invention, the expression signatures are useful for evaluating a cancer tumor’s responsiveness to anti-angiogenic therapeutics. The use of the invention to determine a tumor’s responsiveness to anti-angiogenic therapeutics is not limited to a single cancer type. In one example embodiment, the cancer may be ovarian cancer, breast cancer, colon cancer, colorectal cancer, lung cancer, prostate cancer, or glioblastoma. The

present invention relates to prediction of response to drugs using at least or up to different 10 classifications of response, such as overall survival, progression free survival, radiological response, as defined by RECIST, complete response, partial response, stable disease and serological markers such as, but not limited to, PSA, CEA, CA125, CA15-3 and CA19-9. The invention described herein is not limited to any one drug; it can be used to identify responders and non responders to any of a range of drugs currently in use, under development and novel, that directly or indirectly affect or target angiogenic processes. In one embodiment, the present invention may be used to evaluate adjuvant or neoadjuvant bevacizumab or dasatanib, either as single agents, or in combination with standard of care therapy. In another embodiment, the present invention may be used to evaluate Avastin, VEGF-TRAP, treatment in ovarian cancer.

[0017] In another embodiment of the invention, the expression signatures disclosed herein may be used to determine a patient's clinical prognosis. For example, patients identified as having a cancer subtype associated with down-regulation of angiogenesis related biomarkers may exhibit a longer survival rate than a cancer subtype related to up-regulation of angiogenesis related biomarkers. The use of the invention to determine an individual's clinical prognosis is not limited to a single cancer type. In one example embodiment, the cancer may be ovarian cancer, colon cancer, colorectal cancer, breast cancer, lung cancer, prostate cancer, or glioblastoma. The present invention relates to prediction of clinical prognosis using at least progression free survival. Additional prognostic factors that may be considered are ethnicity and race, age, stage of disease, histology, tumor grade, tumor makers (for example, CA125), site-specific surgical treatment, size of residual disease, and tumor response

[0018] The predictive and prognostic uses of the expression signatures disclosed herein may be achieved using a single expression signature or multiple expression signatures. For example, one expression signature may be a non-angiogenesis signature and a second expression signature may be an angiogenesis signature. In one example embodiment, a non-angiogenesis expression signature is used to determine a patient's clinical prognosis and an angiogenesis signature is used to determine a patient's predicted responsiveness to a given class of therapeutic agent or treatment regimen. In one example embodiment, the angiogenesis signature comprises one or more biomarkers from Table 2A or Table 2B, and the non-angiogenesis signature comprises one or more biomarkers from Table 2C. In another example embodiment, the angiogenesis signature comprises the biomarkers in Table 2A or Table 2B, and the non-angiogenesis signature comprises the biomarkers in Table 2A.

[0019] In another aspect, the present invention relates to kits for conventional diagnostic uses listed above such as qPCR, microarray, and immunoassays such as immunohistochemistry,

ELISA, Western blot and the like. Such kits include appropriate reagents and directions to assay the expression of the genes or gene products and quantify mRNA or protein expression.

[0020] Also disclosed are methods for identifying human tumors with or without the non-angiogenesis phenotype. In certain exemplary embodiments, such methods may be used to identify patients that are sensitive to and respond to drugs that inhibit, either directly or indirectly, processes relating to angiogenesis. In certain other exemplary embodiments, such methods may be used to identify patients that are resistant to or do not respond to drugs that inhibit, either directly or indirectly, processes relating to angiogenesis.

[0021] This invention also relates to guiding effective treatment of patients. Further, methods relating to selection of patient treatment regimens and selecting patients for clinical trials of current, or developmental stage drugs that directly or indirectly affect angiogenesis are provided.

[0022] In addition, methods that accommodate the use of archived formalin fixed paraffin-embedded (FFPE) biopsy material, as well as fresh/frozen (FF) tissue, for assay of all transcripts, and are therefore compatible with the most widely available type of biopsy material, are described herein. A biomarker expression level may be determined using RNA obtained from FFPE tissue, fresh frozen tissue or fresh tissue that has been stored in solutions such as RNeasy®.

BRIEF DESCRIPTION OF DRAWINGS

[0023] Figure 1 provides a heatmap representing the hierarchical agglomerative clustering analysis of the most variable probe sets across 199 serous samples of the Almac Diagnostics' epithelial ovarian cancer sample set. The functional analysis of the probe set clusters is summarized on the right hand side of the image. The legend across the top of the image indicates the classifier group each sample was assigned to for classifier generation (i.e. Class labels).

[0024] Figures 2A and 2B represents the functional analysis results of the angiogenesis probe set cluster in the 199 serous only samples in an epithelial ovarian cancer training set using a functional enrichment analysis. Figure 2A shows a histogram representing the significance of the top 10 enriched Gene Ontology Biological processes. Red bars indicate significance of a process at a p-value of 0.05 after false discovery rate correction. Figure 2B represents the subset of the Gene Ontology Biological processes tree where processes include one or more genes encoded by the probe sets in cluster 3. Red coloured processes indicate significance of that process at a p-value of 0.05 after false discovery rate correction. Black coloured processes

include one or more genes encoded by the probe sets in angiogenesis probe set cluster, but are not significant.

[0025] Figure 3 represents the functional enrichment results of the genes within an exemplary 25-gene expression signature that identifies the molecular subtype related to angiogenesis. Red bars indicate significance of a process at a p-value of 0.05 after False Discovery Rate correction.

[0026] Figure 4 provides Kaplan-Meier curves for recurrence-free survival (time-to-event in weeks) following initial surgical resection from patients with high-grade glioblastoma without prior treatment (Phillips HS, Kharbanda S, Chen R, Forrest WF *et al.* "Molecular subclasses of high-grade glioma predict prognosis, delineate a pattern of disease progression, and resemble stages in neurogenesis," *CANCER CELL* 2006 Mar;9(3):157-73. PMID: 16530701; Costa BM, Smith JS, Chen Y, Chen J *et al.* "Reversing HOXA9 oncogene activation by PI3K inhibition: epigenetic mechanism and prognostic significance in human glioblastoma," *CANCER RES* 2010 Jan 15;70(2):453-62. PMID: 20068170).

[0027] Figure 5 provides a diagram of a ROC curve of the classification performance of an exemplary 25-gene classifier model within 16 prostate cell-lines following treatment with Dasatinib. The AUC is approximately 0.84 following application of the classifier model. The 95% confidence limits were determined using 1000 bootstrap iterations (Wang XD, Reeves K, Luo FR, Xu LA *et al.* "Identification of candidate predictive and surrogate molecular markers for dasatinib in prostate cancer: rationale for patient selection and efficacy monitoring," *GENOME BIOL* 2007;8(11):R255. PMID: 18047674).

[0028] Figure 6 provides a heatmap representing the hierarchical agglomerative clustering analysis of the most variable genes across 265 serous samples of an epithelial ovarian cancer sample set reclassified according to updated pathological classification criteria. The functional analysis of the probe set clusters is summarized on the right hand side of the image. The legend across the top of the image indicates the classifier group each sample was assigned to for classifier generation (i.e. Class labels) of both "angiogenesis" and "non-angiogenesis" subtypes.

[0029] Figures 7A and 7B represents the functional analysis results of the angiogenesis probe set cluster of the 265 serous only samples in an epithelial ovarian cancer training set using a functional enrichment tool (FET) algorithm. Figure 7A shows a histogram representing the significance of the top 10 enriched Gene Ontology biological processes. Red bars indicate significance of a process at a p-value of 0.05 after False Discovery Rate correction. Figure 7B represents the subset of the Gene Ontology Biological processes tree where processes include one or more genes encoded by the probe sets in cluster 2 (angiogenesis probe set cluster). Red

coloured processes indicate significance of that process at a p-value of 0.05 after false discovery rate correction. Black coloured processes include one or more genes encoded by the probe sets in the angiogenesis cluster, but are not significant.

[0030] Figure. 8 represents the functional enrichment results of the genes within an exemplary 45-gene classifier model that identifies the molecular sub-type related to angiogenesis. Red bars indicate significance of a process at a p-value of 0.05 after False Discovery Rate correction.

[0031] Figure 9 provides a diagram of a ROC curve of the classification performance of the 45-gene classifier model within 16 prostate cell-lines following treatment with Dasatinib. The AUC is ~0.95 following application of the classifier model. The 95% confidence limits were determined using 1000 bootstrap iterations.

[0032] Figure 10 provides Kaplan-Meier curves for progression-free survival (in weeks) for the non-angiogenesis sample group versus the “other” samples not labelled as “non-angiogenesis” sample group in the reclassified ovarian sample set.

[0033] Figures 11A and 11B provide heatmaps representing the hierarchical agglomerative clustering analysis of the most variable genes across 51 ER negative samples (Figure 11A) of a breast cancer sample set and the most variable genes across 56 ER positive samples of a breast cancer sample set (Figure 11B). The functional analysis of the probe set clusters is summarized on the right hand side of the image for those clusters showing vasculature development/angiogenesis or immune response/IFN signalling.

[0034] Figure 12 provides Kaplan-Meier curves for progression-free survival (in weeks) for the samples identified as “non-angiogenesis” using the example 63 gene “non-angiogenesis” signature, versus the “other” samples not classified as “non-angiogenesis” using the example 63 gene signature, in the 265 reclassified ovarian sample set.

[0035] Figure 13 provides Kaplan-Meier curves for progression-free survival (in weeks) for the samples identified as “non-angiogenesis” using the example 63 gene “non-angiogenesis” signature, versus the “other” samples not classified as “non-angiogenesis” using the example 63 gene signature, in the independent 265 epithelial and serous ovarian sample set.

[0036] Figure 14A and 14B are graphs demonstrating certain classification performance benchmarks of an example non-angiogenesis signature as applied to colorectal cancer samples.

[0037] Figure 15 provides a diagram of a ROC curve of the classification performance of the 45-gene classifier model within 16 prostate cell-lines following treatment with Dasatinib. The AUC is ~0.95 following application of the classifier model. The 95% confidence limits were determined using 1000 bootstrap iterations (Wang XD, Reeves K, Luo FR, Xu LA *et al.* “Identification of candidate predictive and surrogate molecular markers for dasatinib in prostate

cancer: rationale for patient selection and efficacy monitoring,” GENOME BIOL 2007;8(11):R255. PMID: 18047674).

[0038] Figure 16 provides a heatmap representing the hierarchical agglomerative clustering analysis of the most variable probe sets across 199 serous samples of the Almac Diagnostics’ epithelial ovarian cancer sample set. The functional analysis of the probe set clusters is summarized on the right hand side of the image. The legend across the top of the image indicates the classifier group each sample was assigned to for classifier generation (i.e. Class labels).

[0039] Figure 17 provides a process flow diagram example Kaplan Meier curves for the use of a non-angiogenesis signature to classify a patient based on prognosis and then an angiogenesis signature to determine responsiveness to a given therapeutic regimen in accordance with example embodiments.

[0040] Figure 18A and B are graphs demonstrating certain classification performance benchmarks of an example 25 angiogenesis signature as applied to colorectal cancer samples.

[0041] Figure 19A and B are graphs demonstrating certain classification performance benchmarks of a 45 gene angiogenesis signature as applied to colorectal cancer samples.

DETAILED DESCRIPTION OF THE INVENTION

[0042] Unless defined otherwise, technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this disclosure belongs. Definitions of common terms in molecular biology may be found in Benjamin Lewin, *Genes IX*, published by Jones and Bartlet, 2008 (ISBN 0763752223); Kendrew *et al.* (eds.), *The Encyclopedia of Molecular Biology*, published by Blackwell Science Ltd., 1994 (ISBN 0632021829); Robert A. Meyers (ed.), *Molecular Biology and Biotechnology: a Comprehensive Desk Reference*, published by VCH Publishers, Inc., 1995 (ISBN 9780471185710); Singleton *et al.*, *Dictionary of Microbiology and Molecular Biology* 2nd ed., J. Wiley & Sons (New York, N.Y. 1994), and March, *Advanced Organic Chemistry Reactions, Mechanisms and Structure* 4th ed., John Wiley & Sons (New York, N.Y. 1992).

[0043] The singular terms “a,” “an,” and “the” include plural referents unless context clearly indicates otherwise. Similarly, the word “or” is intended to include “and” unless the context clearly indicates otherwise. The term “comprises” means “includes.” In case of conflict, the present specification, including explanations of terms, will control.

[0044] As used herein terms “marker panel,” “expression classifier,” “classifier,” “expression signature,” or “signature” may be used interchangeably.

[0045] All publications, published patent documents, and patent applications cited in this application are indicative of the level of skill in the art(s) to which the application pertains. All publications, published patent documents, and patent applications cited herein are hereby incorporated by reference to the same extent as though each individual publication, published patent document, or patent application was specifically and individually indicated as being incorporated by reference.

Overview

[0046] A major goal of current research efforts in cancer is to increase the efficacy of perioperative systemic therapy in patients by incorporating molecular parameters into clinical therapeutic decisions. Pharmacogenetics/genomics is the study of genetic/genomic factors involved in an individuals' response to a foreign compound or drug. Agents or modulators which have a stimulatory or inhibitory effect on expression of a biomarker of the invention can be administered to individuals to treat (prophylactically or therapeutically) cancer in the patient. It is ideal to also consider the pharmacogenomics of the individual in conjunction with such treatment. Differences in metabolism of therapeutics may possibly lead to severe toxicity or therapeutic failure by altering the relationship between dose and blood concentration of the pharmacologically active drug. Thus, understanding the pharmacogenomics of an individual permits the selection of effective agents (e.g., drugs) for prophylactic or therapeutic treatments. Such pharmacogenomics can further be used to determine appropriate dosages and therapeutic regimens. Accordingly, the level of expression of a biomarker of the invention in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual.

[0047] The present invention relates to a molecular diagnostic tests useful for diagnosing cancers from different anatomical sites that includes the use of one or more common subtypes related to angiogenesis. The invention includes expression signatures that identify a subject as responsive or non-responsive to anti-angiogenic therapeutics and/or having a good or poor clinical prognosis. The expression signature is derived by obtaining the expression profiles of samples from a sample set of known pathology and/or clinical outcome. The samples may originate from the same sample tissue type or different tissue types. As used herein an "expression profile" comprises a set of values representing the expression level for each biomarker analyzed from a given sample.

[0048] The expression profiles from the sample set are then analyzed using a mathematical model. Different mathematical models may be applied and include, but are not limited to, models from the fields of pattern recognition (Duda *et al.* Pattern Classification, 2nd ed., John Wiley, New York 2001), machine learning (Schölkopf *et al.* Learning with Kernels,

MIT Press, Cambridge 2002, Bishop, Neural Networks for Pattern Recognition, Clarendon Press, Oxford 1995), statistics (Hastie *et al.* The Elements of Statistical Learning, Springer, New York 2001), bioinformatics (Dudoit *et al.*, 2002, J. Am. Statist. Assoc. 97:77-87, Tibshirani *et al.*, 2002, Proc. Natl. Acad. Sci. USA 99:6567-6572) or chemometrics (Vandeginste, *et al.*, Handbook of Chemometrics and Qualimetrics, Part B, Elsevier, Amsterdam 1998). The mathematical model identifies one or more biomarkers expressed in the sample set that are most predictive of a given disease phenotype. These one or more biomarkers define an expression signature. Accordingly, an expression signature includes the biomarkers identified as most predictive of a given disease phenotype. In certain exemplary embodiments, the mathematical model defines a variable, such as a weight, for each identified biomarker. In certain exemplary embodiments, the mathematical model defines a decision function. The decision function may further define a threshold score which separates the sample set into two disease phenotypes such as, but not limited to, samples that are responsive and non-responsive to anti-angiogenic therapeutics. In one exemplary embodiment, the decision function and expression signature are defined using a linear classifier.

[0049] To classify new samples using a defined expression signature, the biomarkers defined by the expression signature are isolated and an expression profile of the biomarker(s) determined. The new sample biomarker expression profile is analyzed with the same mathematical model used to define the expression signature. In certain exemplary embodiments, the mathematical model defines an expression score for the new sample. The expression score may be determined by combining the expression values of the biomarkers with corresponding scalar weights using non-linear, algebraic, trigonometric or correlative means to derive a single scalar value. The expression score is compared to the threshold score and the sample classified based on whether the expression score is greater than, or equal to, or less than the threshold score. In one exemplary embodiment, a sample expression value greater than the reference expression value indicates a patient will be responsive to an anti-angiogenic therapeutic. In another exemplary embodiment, a sample expression score below the threshold score indicates the patient will not be responsive to an anti-angiogenic therapeutic. In another exemplary embodiment, a sample expression score below the threshold expression score indicates the patient has a cancer type, or is at risk of developing a cancer type, that is not responsive to an anti-angiogenic therapeutic. In another exemplary embodiment, a sample expression score above the reference expression score indicates the patient has a cancer type, or is at risk of developing a cancer type, that is responsive to an anti-angiogenic therapeutic. In another example embodiment, a sample expression score above the threshold score indicates the patient has a cancer sub-type with a good clinical prognosis. In another example embodiment, a

sample expression score below the threshold score indicates a patient with a cancer subtype with a poor clinical prognosis. Where an expression signature is derived from a tissue sample set comprising one type of cancer tissue, the expression signature is not limited to identifying the same cancer sub-type only in tissues of the same cancer type, but may be used with other cancer types that share the same cancer sub-type. For example, where an expression signature is derived from ovarian cancer samples, the expression signature may be used to identify a similar angiogenesis sub-type in different cancers such as glioblastoma, breast cancer, lung cancer, colon cancer, or prostate cancer.

[0050] One application of the expression signatures disclosed herein is the identification of patients with good and poor prognosis. By examining the expression of a collection of the identified biomarkers in a tumor, it is possible to determine the likely clinical outcomes of a patient. By examining the expression of a collection of biomarkers, it is therefore possible to identify those patients in most need of more aggressive therapeutic regimens and likewise eliminate unnecessary therapeutic treatments or those unlikely to significantly improve a patient's clinical outcome.

[0051] A patient may be considered to have a "good prognosis" where, for example, the survival rate associated with the cancer subtype is greater than a survival rate associated with other related cancer subtypes. In certain embodiments, a "good prognosis" indicates at least an increased expected survival time. This may be based upon a classification as responsive to an anti-angiogenic therapeutic agent as described herein. The increased expected survival time may be as compared to classification as non-responsive to the anti-angiogenic therapeutic agent.

[0052] A patient may be considered to have a "poor prognosis" or "bad prognosis" where, for example, the survival rate associated with the cancer subtype is less than the survival rate associated with other related cancer subtypes.

[0053] Another application of the expression signatures disclosed herein is the stratification of response to, and selection of patients for therapeutic drug classes that encompass anti-angiogenic therapies. By examining the expression of a collection of the identified biomarkers in a tumor, it is possible to determine which therapeutic agent or combination of agents will be most likely to reduce the growth rate of a cancer. It is also possible to determine which therapeutic agent or combination of agents will be the least likely to reduce the growth rate of a cancer. By examining the expression of a collection of biomarkers, it is therefore possible to eliminate ineffective or inappropriate therapeutic agents. Importantly, in certain embodiments, these determinations can be made on a patient-by-patient basis or on an agent-by-agent basis. Thus, one can determine whether or not a particular therapeutic regimen is likely to benefit a particular patient or type of patient, and/or whether a particular regimen should be

continued. The present invention provides a test that can guide therapy selection as well as selecting patient groups for enrichment strategies during clinical trial evaluation of novel therapeutics. For example, when evaluating a putative anti-angiogenic agent or treatment regime, the expression signatures and methods disclosed herein may be used to select individuals for clinical trials that have cancer subtypes that are responsive to anti-angiogenic agents.

[0054] A cancer is "responsive" to a therapeutic agent if its rate of growth is inhibited as a result of contact with the therapeutic agent, compared to its growth in the absence of contact with the therapeutic agent. Growth of a cancer can be measured in a variety of ways. For instance, the size of a tumor or measuring the expression of tumor markers appropriate for that tumor type.

[0055] A cancer is "non-responsive" to a therapeutic agent if its rate of growth is not inhibited, or inhibited to a very low degree, as a result of contact with the therapeutic agent when compared to its growth in the absence of contact with the therapeutic agent. As stated above, growth of a cancer can be measured in a variety of ways, for instance, the size of a tumor or measuring the expression of tumor markers appropriate for that tumor type. The quality of being non-responsive to a therapeutic agent is a highly variable one, with different cancers exhibiting different levels of "non-responsiveness" to a given therapeutic agent, under different conditions. Still further, measures of non-responsiveness can be assessed using additional criteria beyond growth size of a tumor such as, but not limited to, patient quality of life, and degree of metastases.

[0056] Another application of the expression signatures disclosed herein is the combined identification of prognosis of a patient along with identification of a predicted responsiveness of the patient to a given therapeutic. In certain example embodiments, a non-angiogenesis expression signature defined below is used to identify patients with a good prognosis from those with a poor prognosis, and an angiogenesis expression signature is used to predict the patient's response to a given therapeutic class of drugs.

[0057] The angiogenesis subtype can be identified from a fresh/frozen (FF) or formalin fixed paraffin embedded (FFPE) patient sample. In one exemplary embodiment, the cancer type is ovarian cancer, breast cancer, colon cancer, colorectal cancer, lung cancer, prostate cancer, or glioblastoma. In another exemplary embodiment, the cancer type is a ovarian cancer. In a further exemplary embodiment, the cancer type is breast cancer. In another exemplary embodiment, the cancer type is lung cancer. In another exemplary embodiment, the cancer type is colon cancer. In another exemplary embodiment, the cancer type is prostate cancer. In another exemplary embodiment, the cancer type is glioblastoma

Identifying Expression Signatures

[0058] The expression signatures of the present invention are identified by analyzing the expression profiles of certain biomarkers in a patient sample set. Biomarkers suitable for use in the present invention include DNA, RNA, and proteins. The biomarkers are isolated from a patient sample and their expression levels determined to derive a set of expression profiles for each sample analyzed in the patient sample set. In certain example embodiments the expression signature is an angiogenesis expression signature. An angiogenesis expression signature relates to an angiogenesis phenotype observed in cancer tissues, the phenotype characterized by an up-regulation of biomarkers associated with angiogenesis and vascular development. In certain other example embodiments, the expression signature is a non-angiogenesis expression signature. A non-angiogenesis expression signature relates to a phenotype observed in cancer tissues, the phenotype characterized by a down-regulation of biomarkers associated with angiogenesis and vascular development.

a. Expression Profiles

[0059] In certain embodiments, the expression profile obtained is a genomic or nucleic acid expression profile, where the amount or level of one or more nucleic acids in the sample is determined. In these embodiments, the sample that is assayed to generate the expression profile employed in the diagnostic or prognostic methods is one that is a nucleic acid sample. The nucleic acid sample includes a population of nucleic acids that includes the expression information of the phenotype determinative biomarkers of the cell or tissue being analyzed. In some embodiments, the nucleic acid may include RNA or DNA nucleic acids, e.g., mRNA, cRNA, cDNA etc., so long as the sample retains the expression information of the host cell or tissue from which it is obtained. The sample may be prepared in a number of different ways, as is known in the art, e.g., by mRNA isolation from a cell, where the isolated mRNA is used as isolated, amplified, or employed to prepare cDNA, cRNA, etc., as is known in the field of differential gene expression. Accordingly, determining the level of mRNA in a sample includes preparing cDNA or cRNA from the mRNA and subsequently measuring the cDNA or cRNA. The sample is typically prepared from a cell or tissue harvested from a subject in need of treatment, e.g., via biopsy of tissue, using standard protocols, where cell types or tissues from which such nucleic acids may be generated include any tissue in which the expression pattern of the to be determined phenotype exists, including, but not limited to, disease cells or tissue, body fluids, etc.

[0060] The expression profile may be generated from the initial nucleic acid sample using any convenient protocol. While a variety of different manners of generating expression profiles are known, such as those employed in the field of differential gene expression/biomarker

analysis, one representative and convenient type of protocol for generating expression profiles is array-based gene expression profile generation protocols. Such applications are hybridization assays in which a nucleic acid that displays "probe" nucleic acids for each of the genes to be assayed/profiled in the profile to be generated is employed. In these assays, a sample of target nucleic acids is first prepared from the initial nucleic acid sample being assayed, where preparation may include labeling of the target nucleic acids with a label, e.g., a member of a signal producing system. Following target nucleic acid sample preparation, the sample is contacted with the array under hybridization conditions, whereby complexes are formed between target nucleic acids that are complementary to probe sequences attached to the array surface. The presence of hybridized complexes is then detected, either qualitatively or quantitatively. Specific hybridization technology which may be practiced to generate the expression profiles employed in the subject methods includes the technology described in U.S. Pat. Nos. 5,143,854; 5,288,644; 5,324,633; 5,432,049; 5,470,710; 5,492,806; 5,503,980; 5,510,270; 5,525,464; 5,547,839; 5,580,732; 5,661,028; 5,800,992; the disclosures of which are herein incorporated by reference; as well as WO 95/21265; WO 96/31622; WO 97/10365; WO 97/27317; EP 373 203; and EP 785 280. In these methods, an array of "probe" nucleic acids that includes a probe for each of the biomarkers whose expression is being assayed is contacted with target nucleic acids as described above. Contact is carried out under hybridization conditions, e.g., stringent hybridization conditions as described above, and unbound nucleic acid is then removed. The resultant pattern of hybridized nucleic acids provides information regarding expression for each of the biomarkers that have been probed, where the expression information is in terms of whether or not the gene is expressed and, typically, at what level, where the expression data, i.e., expression profile, may be both qualitative and quantitative.

b. Diseases and Sample Tissue Sources

[0061] In certain exemplary embodiments, the patient sample set comprises cancer tissue samples, such as archived samples. The patient sample set is preferably derived from cancer tissue samples having been characterized by prognosis, likelihood of recurrence, long term survival, clinical outcome, treatment response, diagnosis, cancer classification, or personalized genomics profile. As used herein cancer includes, but is not limited to, leukemia, brain cancer, prostate cancer, liver cancer, ovarian cancer, stomach cancer, colorectal cancer, throat cancer, breast cancer, skin cancer, melanoma, lung cancer, sarcoma, cervical cancer, testicular cancer, bladder cancer, endocrine cancer, endometrial cancer, esophageal cancer, glioma, lymphoma, neuroblastoma, osteosarcoma, pancreatic cancer, pituitary cancer, renal cancer, and the like. As used herein, colorectal cancer encompasses cancers that may involve cancer in tissues of both the rectum and other portions of the colon as well as cancers that may be individually classified

as either colon cancer or rectal cancer. In one embodiment, the methods described herein refer to cancers that are treated with anti-angiogenic agents, anti-angiogenic targeted therapies, inhibitors of angiogenesis signaling, but not limited to these classes. These cancers also include subclasses and subtypes of these cancers at various stages of pathogenesis. In certain exemplary embodiments, the patient sample set comprises ovarian cancer samples. In another exemplary embodiment, the patient sample set comprises breast cancer samples. In yet another exemplary embodiment, the patient sample set comprises glioblastoma samples.

[0062] "Biological sample", "sample", and "test sample" are used interchangeably herein to refer to any material, biological fluid, tissue, or cell obtained or otherwise derived from an individual. This includes blood (including whole blood, leukocytes, peripheral blood mononuclear cells, buffy coat, plasma, and serum), sputum, tears, mucus, nasal washes, nasal aspirate, breath, urine, semen, saliva, meningeal fluid, amniotic fluid, glandular fluid, lymph fluid, nipple aspirate, bronchial aspirate, synovial fluid, joint aspirate, ascites, cells, a cellular extract, and cerebrospinal fluid. This also includes experimentally separated fractions of all of the preceding. For example, a blood sample can be fractionated into serum or into fractions containing particular types of blood cells, such as red blood cells or white blood cells (leukocytes). If desired, a sample can be a combination of samples from an individual, such as a combination of a tissue and fluid sample. The term "biological sample" also includes materials containing homogenized solid material, such as from a stool sample, a tissue sample, or a tissue biopsy, for example. The term "biological sample" also includes materials derived from a tissue culture or a cell culture. Any suitable methods for obtaining a biological sample can be employed; exemplary methods include, e.g., phlebotomy, swab (e.g., buccal swab), and a fine needle aspirate biopsy procedure. Samples can also be collected, e.g., by micro dissection (e.g., laser capture micro dissection (LCM) or laser micro dissection (LMD)), bladder wash, smear (e.g., a PAP smear), or ductal lavage. A "biological sample" obtained or derived from an individual includes any such sample that has been processed in any suitable manner after being obtained from the individual, for example, fresh frozen or formalin fixed and/or paraffin embedded. The methods of the invention as defined herein may begin with an obtained sample and thus do not necessarily incorporate the step of obtaining the sample from the patient. The methods may be in vitro methods performed on an isolated sample.

[0063] As used herein, the term "patient" includes human and non-human animals. The preferred patient for treatment is a human. "Patient," "individual" and "subject" are used interchangeably herein.

c. Biomarkers

[0064] As used herein, the term “biomarker” can refer to a gene, an mRNA, cDNA, an antisense transcript, a miRNA, a polypeptide, a protein, a protein fragment, or any other nucleic acid sequence or polypeptide sequence that indicates either gene expression levels or protein production levels. When a biomarker indicates or is a sign of an abnormal process, disease or other condition in an individual, that biomarker is generally described as being either over-expressed or under-expressed as compared to an expression level or value of the biomarker that indicates or is a sign of a normal process, an absence of a disease or other condition in an individual. “Up-regulation”, “up-regulated”, “over-expression”, “over-expressed”, and any variations thereof are used interchangeably to refer to a value or level of a biomarker in a biological sample that is greater than a value or level (or range of values or levels) of the biomarker that is typically detected in similar biological samples from healthy or normal individuals. The terms may also refer to a value or level of a biomarker in a biological sample that is greater than a value or level (or range of values or levels) of the biomarker that may be detected at a different stage of a particular disease.

[0065] “Down-regulation”, “down-regulated”, “under-expression”, “under-expressed”, and any variations thereof are used interchangeably to refer to a value or level of a biomarker in a biological sample that is less than a value or level (or range of values or levels) of the biomarker that is typically detected in similar biological samples from healthy or normal individuals. The terms may also refer to a value or level of a biomarker in a biological sample that is less than a value or level (or range of values or levels) of the biomarker that may be detected at a different stage of a particular disease.

[0066] Further, a biomarker that is either over-expressed or under-expressed can also be referred to as being “differentially expressed” or as having a “differential level” or “differential value” as compared to a “normal” expression level or value of the biomarker that indicates or is a sign of a normal process or an absence of a disease or other condition in an individual. Thus, “differential expression” of a biomarker can also be referred to as a variation from a “normal” expression level of the biomarker.

[0067] The terms “differential biomarker expression” and “differential expression” are used interchangeably to refer to a biomarker whose expression is activated to a higher or lower level in a subject suffering from a specific disease, relative to its expression in a normal subject, or relative to its expression in a patient that responds differently to a particular therapy or has a different prognosis. The terms also include biomarkers whose expression is activated to a higher or lower level at different stages of the same disease. It is also understood that a differentially expressed biomarker may be either activated or inhibited at the nucleic acid level or protein level, or may be subject to alternative splicing to result in a different polypeptide

product. Such differences may be evidenced by a variety of changes including mRNA levels, miRNA levels, antisense transcript levels, or protein surface expression, secretion or other partitioning of a polypeptide. Differential biomarker expression may include a comparison of expression between two or more genes or their gene products; or a comparison of the ratios of the expression between two or more genes or their gene products; or even a comparison of two differently processed products of the same gene, which differ between normal subjects and subjects suffering from a disease; or between various stages of the same disease. Differential expression includes both quantitative, as well as qualitative, differences in the temporal or cellular expression pattern in a biomarker among, for example, normal and diseased cells, or among cells which have undergone different disease events or disease stages.

[0068] In certain exemplary embodiments, the biomarker is an RNA transcript. As used herein “RNA transcript” refers to both coding and non-coding RNA, including messenger RNAs (mRNA), alternatively spliced mRNAs, ribosomal RNA (rRNA), transfer RNA (tRNA), small nuclear RNAs (snRNA), and antisense RNA. Measuring mRNA in a biological sample may be used as a surrogate for detection of the level of the corresponding protein and gene in the biological sample. Thus, any of the biomarkers or biomarker panels described herein can also be detected by detecting the appropriate RNA. Methods of biomarker expression profiling include, but are not limited to quantitative PCR, NGS, northern blots, southern blots, microarrays, SAGE, immunoassays (ELISA, EIA, agglutination, nephelometry, turbidimetry, Western blot, immunoprecipitation, immunocytochemistry, flow cytometry, Luminex assay), and mass spectrometry. The overall expression data for a given sample may be normalized using methods known to those skilled in the art in order to correct for differing amounts of starting material, varying efficiencies of the extraction and amplification reactions.

[0069] In certain exemplary embodiments, biomarkers useful for distinguishing between cancer types that are responsive and non-responsive to anti-angiogenic therapeutics can be determined by identifying biomarkers exhibiting the highest degree of variability between samples in the patient data set as determined using the expression detection methods and patient sample sets discussed above. Standard statistical methods known in the art for identifying highly variable data points in expression data may be used to identify the highly variable biomarkers. For example, a combined background and variance filter to the patient data set. The background filter is based on the selection of probe sets with expression E and expression variance var_E above the thresholds defined by background standard deviation σ_{Bg} (from the Expression Console software) and quantile of the standard normal distribution z_α at a specified significance α probe sets were kept if:

$$E > \log_2((z_\alpha \sigma_{Bg})); \log_2((\text{var}_E) > 2 [\log_2(\sigma_{Bg}) - E - \log_2(\log(2))])$$

[0070] where a defines a significance threshold. In certain exemplary embodiment, the significance threshold is $6.3 \cdot 10^{-5}$. In another exemplary embodiment, the significance threshold may be between $1.0 \cdot 10^{-7}$ to $1.0 \cdot 10^{-3}$.

[0071] In certain exemplary embodiments, the highly variable biomarkers may be further analyzed to group samples in the patient data set into subtypes or clusters based on similar gene expression profiles. For examples, biomarkers may be clustered based on how highly correlated the up-regulation or down-regulation of their expression is to one another. Various clustering analysis techniques known in the art may be used. In one exemplary embodiment, hierarchical agglomerative clustering is used to identify the cancer subtypes. To determine the biological relevance of each subtype, the biomarkers within each cluster may be further mapped to their corresponding genes and annotated by cross-reference to one or more gene ontology databases containing information on biological activity and biological pathways associated with the gene. In one exemplary embodiment, biomarker in clusters enriched for angiogenesis, vasculature development and immune response general functional terms are grouped into a putative angiogenesis sample group and used for expression signature generation. In another exemplary embodiment, biomarkers in clusters that are up regulated and enriched for angiogenesis, vasculature development and immune response general functional terms are grouped into a putative angiogenesis sample group and used for expression signature generation. In another exemplary embodiment, biomarkers in clusters that are down regulated and enriched for angiogenesis, vasculature development and immune response general functional terms are grouped into a putative angiogenesis sample group and used for expression signature generation. Further details for conducting functional analysis of biomarker clusters is provided in the Examples section below.

[0072] In one exemplary embodiment, the biomarkers useful in deriving an expression signature for use in the present invention are those biomarkers listed in Table 1A, Table 1B, Table 1C, or a combination thereof. These biomarkers are identified as having predictive value to determine a patient response to a therapeutic agent and/or a prognostic value in identifying individuals with a good or poor clinical prognosis.

[0073] In certain example embodiments, their expression correlates with the response, or lack thereof, to an agent, and more specifically, an anti-angiogenic therapeutic agent. By examining the expression of a collection of the identified biomarkers in a tumor, it is possible to determine which therapeutic agent or combination of agents will be most likely to reduce the growth rate of a cancer. By examining a collection of identified biomarkers in a tumor, it is also possible to determine which therapeutic agent or combination of agents will be the least likely to reduce the growth rate of a cancer. By examining the expression of a collection of biomarkers,

it is therefore possible to eliminate ineffective or inappropriate therapeutic agents. Importantly, in certain embodiments, these determinations can be made on a patient-by-patient basis or on an agent-by-agent basis. Thus, one can determine whether or not a particular therapeutic regimen is likely to benefit a particular patient or type of patient, and/or whether a particular regimen should be continued.

[0074] In certain other example embodiments, the expression of the biomarkers disclosed herein correlated with a patient's overall clinical prognosis. By examining the expression of a collection of biomarkers identified in a tumor, it is possible to determine whether the individual has a cancer subtype associated with good clinical prognosis or poor clinical prognosis. Importantly, in certain embodiments, these determinations can be made on a patient-by-patient basis. Thus, one of ordinary skill in the art can use predicted prognosis to help select appropriate treatment regimens to treat the underlying disease while eliminating those treatment regimens most likely to produce undesired or medically unwarranted adverse side effects.

[0075] The SEQ ID NOs listed in Table 1A, Table 1B, and Table 1C refer to probe set identifiers used to measure the expression levels of the genes on an exemplary transcriptome array. Expression signatures of the present invention have been cross-validated using expression data from different arrays with different probe sets as detailed further in the Examples section below. Accordingly, the expression signatures and methods disclosed herein are not limited to expression values measured using the probe sets disclosed herein.

Table 1A: Genes in Clusters of Figure 1

SEQ NO:	Orientation	Gene Symbol
1	Sense	STAT1
2	Sense	PDGFC
3	Sense	TGFB3
4	Sense	RAC2
5	Sense	MARCKS
6	Sense	ALOX5
7	Sense	COL8A1
8	Sense	CTSS
9	Sense	HAVCR2
10	Sense	RAB31
11	Sense	KCNAB2
12	Sense	THBS1
13	Sense	SH3BP4

14	Sense	CTGF
15	Sense	CTGF
16	Sense	VCAN
17	Sense	IGKC
18	Sense	IGKC
19	Sense	IGKC
20	Sense	SGK1
21	Sense	NFATC1
22	Sense	HMHA1
23	Sense	FCGR1C /// FCGR1A /// FCGR1B
24	Sense	EDA2R
25	Sense	COL8A1
26	Sense	COL12A1
27	Sense	HLA-B
28	Sense	HLA-F
29	Sense	HLA-C
30	Sense	SPP1
31	Sense	MYO1F
32	Sense	SPARC
33	Sense	SPARC
34	Sense	UBD /// GABBR1
35	Sense	CCND1
36	Sense	COL1A1
37	Sense	EGR1
38	Sense	EGR1
39	Sense	TNFSF10
40	Sense	SULF2
41	Sense	CERCAM
42	Sense	ATF3
43	Sense	MIR21
44	Sense	BASP1
45	Sense	IFIT2
46	Sense	SULF1

47	Sense	IGLC2 /// IGLC3
48	Sense	IGLC2 /// IGLC3
49	Sense (Fully0Exonic)	IGLC2 /// IGLC3
50	Sense	IGLC2 /// IGLC3
51	Sense	IGLC2 /// IGLC3
52	Sense	IGLC1
53	Sense	IGLC1
54	Sense	IGLC2 /// IGLC3
55	Sense	ANGPTL2
56	Sense	COL5A2
57	Sense	IGJ
58	Sense	THY1
59	Sense	NDN
60	Sense	RGS2
61	Sense	MEIS3P1 /// MEIS3P2
62	Sense	GBP2
63	Sense	CSF1R
64	Sense	C1R
65	Sense	FAT1
66	Sense	COL1A1
67	Sense	RHOB
68	Sense	MMP11
69	Sense	GADD45B
70	Sense	MMP14
71	Sense	MMP14
72	Sense	IGHG4
73	Sense	DDX60L
74	Sense	SPP1
75	Sense	ROR2
76	Sense	CTSK
77	Sense	FCGR2B
78	Sense	PTAFR
79	Sense	ICAM1
80	Sense	HCLS1

81	No Transcript Match	---
82	Sense	SLFN11
83	No Transcript Match	---
84	Sense	JAM3
85	Sense	TMEM49
86	Sense	TMEM49
87	Sense	LTBP2
88	Sense	IRS1
89	Sense	COL5A2
90	Sense	C17orf91
91	Sense	GPNMB
92	Sense	FAM198B
93	Sense	MICAL2
94	Sense	TMEM2
95	Sense	CHST15
96	Sense	SECTM1
97	Sense	DCN
98	Sense	VCAM1
99	Sense	TNFAIP3
100	Sense	C1QA
101	Sense	C1QA
102	Sense	FBXO32
103	Sense	COL12A1
104	Sense	CPE
105	Sense	CIITA
106	Sense	GAS7
107	Sense	COL3A1
108	Sense	FN1
109	Sense	IFI30
110	Sense	ITGB2
111	Sense	ELN
112	Sense	CMTM3
113	Sense	ANTXR1
114	Sense	ARHGDIB

115	Sense	LAPTM5
116	Sense	SOX4
117	Sense	IFI44L
118	Sense	IL4I1
119	Sense	ANTXR2
120	Sense	IGLC2 /// IGLC3
121	Sense	EPSTI1
122	Sense	BIRC3
123	Sense	IGLC2 /// IGLC3
124	Sense	BST2
125	Sense	TNFSF10
126	Sense	COL10A1
127	Sense	IGLC2 /// IGLC3
128	Sense	FBP1
129	Sense	RHOBTB3
130	Sense	CDK6
131	Sense	CD74
132	Sense	ISM1
133	Sense	C1QC
134	Sense	BIN2
135	Sense	CSRNP1
136	Sense	TYROBP
137	Sense	C1QTNF3
138	Sense	DCN
139	Sense	IGFBP4
140	Sense	AOAH
141	Sense	SIRPA
142	Sense	FOSB
143	Sense	CCDC80
144	Sense	IGLC1
145	Sense	HCST
146	Sense	IFI35
147	Sense	BIRC3
148	Sense	COL3A1

149	Sense	IFITM2
150	Sense	ZFP36
151	Sense	MMP11
152	Sense	COL1A2
153	Sense	HLA-DPA1
154	Sense	TWIST1
155	Sense	ZNF154
156	Sense	EGR1
157	Sense	IGLC2 /// IGLC3
158	Sense	TNFSF10
159	Sense	IGKC
160	Sense	IGHG1 /// IGHG4
161	Sense	GBP5
162	Sense	COL1A2
163	Sense	APOC1
164	No Transcript Match	---
165	Sense	COL3A1
166	AntiSense	PXDN
167	AntiSense	EGR1
168	Sense	GBP3
169	Sense	ISG15
170	Sense	---
171	Sense	KIAA0146
172	Sense	CMAH
173	Sense	APBB2
174	Sense	TPM1
175	No Transcript Match	---
176	Sense	DMD
177	No Genome Match	---
178	Sense	IL10RA
179	Sense	---
180	No Transcript Match	---
181	Sense	DUSP1
182	Sense	GBP1

183	Sense	PARVG
184	Sense	MAFF
185	Sense	PDGFC
186	Sense	MSN
187	Sense	RSAD2
188	Sense	TPM1
189	Sense	EMB
190	Sense	C6orf155
191	Sense	FOS
192	Sense	DEXI
193	Sense	RNF19A
194	Sense	FBXO32
195	Sense	DPYSL3
196	Sense	PRICKLE1
197	AntiSense	EGR1
198	AntiSense	NRP2
199	Sense	B2M
200	AntiSense	MIR21
201	Sense	MMP2
202	Sense	CDR1
203	Sense	HLA-B
204	Sense	CTGF
205	Sense	DCN
206	Sense	SOD2
207	Sense	FN1
208	Sense	COL8A2
209	Sense	SGK1
210	Sense	TIMP3
211	Sense	ACTA2
212	Sense	SRGN
213	Sense	LOXL1
214	Sense	CCR1
215	Sense	GBP1
216	Sense	CDH11

217	Sense	FCGR3A
218	Sense	LUM
219	Sense	NNMT
220	Sense	COL1A2
221	Sense	RGS1
222	Sense	GJA1
223	Sense	SPARCL1
224	Sense	DAB2
225	AntiSense	CTHRC1
226	Sense	RGS16
227	Sense	FBLN1
228	Sense	SPP1
229	Sense	CTSB
230	Sense	SPP1
231	Sense	SDC1
232	Sense	PLAU
233	Sense	PDGFRA
234	Sense	SERPINF1
235	Sense	BGN
236	Sense	COL6A3
237	AntiSense	C3
238	AntiSense	C3
239	AntiSense	SPP1
240	AntiSense	HLA-DQA1
241	AntiSense	GAS1
242	Sense	VCAN
243	AntiSense	---
244	Sense	IGHG4 /// IGHG2 /// IGHG1 /// IGHGP
245	Sense	IGHG2
246	Sense	C3orf26
247	AntiSense	ATF3
248	AntiSense	ATF3
249	AntiSense	SULF1

250	Sense	FN1
251	AntiSense	CALD1
252	AntiSense	CALD1
253	Sense	TMEM49
254	Sense	TMEM49
255	Sense	CHD5
256	AntiSense	EGR1
257	AntiSense	SNAI2
258	AntiSense	ITPRIPL2
259	AntiSense	GABBR1 /// UBD
260	AntiSense	GABBR1 /// UBD
261	AntiSense	TWIST1
262	AntiSense	TWIST1
263	AntiSense	BATF2
264	AntiSense	NFKBIZ
265	Sense	C3orf26
266	AntiSense	LOXL1
267	Sense	---
268	AntiSense	TIMP2
269	AntiSense	FN1
270	AntiSense	COL1A1
271	AntiSense	DCN
272	Sense	TREH
273	AntiSense	UBE2L6
274	AntiSense	APOL1
275	AntiSense	BIRC3
276	AntiSense	BIRC3
277	Sense	LILRB4
278	Sense	FGD2
279	Sense	TMEM49
280	Sense	NCF4
281	Sense	COL10A1
282	Sense	GAL3ST4
283	Sense	HCK

284	Sense	TAGLN
285	Sense	TWIST1
286	Sense	HCLS1
287	Sense	LPAR6
288	Sense	ITGB2
289	Sense	LST1
290	Sense	HLA-B
291	Sense	C17orf91
292	Sense	ZC3H12A
293	Sense	KLF10
294	Sense	BASP1
295	Sense	BASP1

Table 1B: Genes in Clusters of Figure 6

SEQ NO:	Orientation	Gene Symbol
2	Sense (Fully Exonic)	PDGFC
3	Sense (Fully Exonic)	TGFB3
4	Sense (Fully Exonic)	RAC2
5	Sense (Fully Exonic)	MARCKS
6	Sense (Fully Exonic)	ALOX5
7	Sense (Fully Exonic)	COL8A1
11	Sense (Fully Exonic)	KCNAB2
12	Sense (Fully Exonic)	THBS1
14	Sense (Fully Exonic)	CTGF
15	Sense (Fully Exonic)	CTGF
16	Sense (Fully Exonic)	VCAN
18	Sense (Fully Exonic)	IGKC
19	Sense (Fully Exonic)	IGKC
21	Sense (includes Intronic)	NFATC1
22	Sense (Fully Exonic)	HMHA1
23	Sense (Fully Exonic)	FCGR1B
24	Sense (Fully Exonic)	EDA2R
25	Sense (Fully Exonic)	COL8A1
26	Sense (Fully Exonic)	COL12A1
27	Sense (Fully Exonic)	HLA-B
28	Sense	HLA-F
37	Sense (Fully Exonic)	EGR1

40	Sense (Fully Exonic)	SULF2
41	Sense (Fully Exonic)	CERCAM
42	Sense (Fully Exonic)	ATF3
43	Sense (Fully Exonic)	MIR21
45	Sense (Fully Exonic)	IFIT2
47	Sense (Fully Exonic)	IGLC3
48	Sense (Fully Exonic)	IGLC3
49	Sense (Fully Exonic)	IGLC3
50	Sense (Fully Exonic)	IGLC3
51	Sense (Fully Exonic)	IGLC3
54	Sense (Fully Exonic)	IGLC3
55	Sense (Fully Exonic)	ANGPTL2
56	Sense (Fully Exonic)	COL5A2
58	Sense (Fully Exonic)	THY1
59	Sense (Fully Exonic)	NDN
60	Sense (Fully Exonic)	RGS2
61	Sense (Fully Exonic)	MEIS3P2
62	Sense (Fully Exonic)	GBP2
65	Sense (Fully Exonic)	FAT1
66	Sense (Fully Exonic)	COL1A1
68	Sense (Fully Exonic)	MMP11
69	Sense (Fully Exonic)	GADD45B
71	Sense (Fully Exonic)	MMP14
72	Sense (Fully Exonic)	IGHG4
80	Sense (Fully Exonic)	HCLS1
83	No Transcript match	
84	Sense (Fully Exonic)	JAM3
86	Sense (Fully Exonic)	TMEM49
87	Sense (Fully Exonic)	LTBP2
88	Sense (Fully Exonic)	IRS1
90	Sense (Fully Exonic)	C17orf91
91	Sense (Fully Exonic)	GPNMB
92	Sense (Fully Exonic)	FAM198B
95	Sense (Fully Exonic)	CHST15
97	Sense (Fully Exonic)	DCN
98	Sense (Fully Exonic)	VCAM1
105	Sense (Fully Exonic)	CIITA
106	Sense (Fully Exonic)	GAS7
107	Sense (Fully Exonic)	COL3A1

110	Sense (Fully Exonic)	ITGB2
111	Sense (Fully Exonic)	ELN
112	Sense (Fully Exonic)	CMTM3
113	Sense (Fully Exonic)	ANTXR1
118	Sense (Fully Exonic)	IL4I1
119	Sense (Fully Exonic)	ANTXR2
120	Sense (Fully Exonic)	IGLC2 /// IGLC3
123	Sense (Fully Exonic)	IGLC3
124	Sense (Fully Exonic)	BST2
126	Sense (Fully Exonic)	COL10A1
127	Sense (Fully Exonic)	IGLC3
128	Sense (Fully Exonic)	FBP1
129	Sense (Fully Exonic)	RHOBTB3
131	Sense (Fully Exonic)	CD74
132	Sense (Fully Exonic)	ISM1
135	Sense (Fully Exonic)	CSRNP1
138	Sense (Fully Exonic)	DCN
139	Sense (Fully Exonic)	IGFBP4
143	Sense (Fully Exonic)	CCDC80
148	Sense (Fully Exonic)	COL3A1
150	Sense (Fully Exonic)	ZFP36
151	Sense (Fully Exonic)	MMP11
152	Sense (Fully Exonic)	COL1A2
153	Sense (Fully Exonic)	HLA-DPA1
154	Sense (Fully Exonic)	TWIST1
155	Sense (Fully Exonic)	ZNF154
157	Sense (Fully Exonic)	IGLC3
159	Sense (Fully Exonic)	IGKC
160	Sense (Fully Exonic)	IGHG1
162	Sense (Fully Exonic)	COL1A2
163	Sense (Fully Exonic)	APOC1
167	AntiSense	EGR1
171	Sense (Fully Exonic)	KIAA0146
174	Sense (Fully Exonic)	TPM1
176	Sense (includes Intronic)	DMD
180	No Transcript match	
181	Sense (Fully Exonic)	DUSP1
182	Sense (Fully Exonic)	GBP1
185	Sense (includes Intronic)	PDGFC
186	Sense (includes Intronic)	MSN
188	Sense (includes Intronic)	TPM1
189	Sense (Fully Exonic)	EMB

191	Sense (Fully Exonic)	FOS
195	Sense (includes Intronic)	DPYSL3
197	AntiSense	EGR1
198	AntiSense	NRP2
201	Sense (Fully Exonic)	MMP2
204	Sense (Fully Exonic)	CTGF
211	Sense (Fully Exonic)	ACTA2
213	Sense (Fully Exonic)	LOXL1
216	Sense (Fully Exonic)	CDH11
218	Sense (Fully Exonic)	LUM
219	Sense (Fully Exonic)	NNMT
222	Sense (Fully Exonic)	GJA1
225	AntiSense	CTHRC1
229	Sense (Fully Exonic)	CTSB
232	Sense (Fully Exonic)	PLAU
233	Sense (Fully Exonic)	PDGFRA
242	Sense (Fully Exonic)	VCAN
243	AntiSense	--
244	Sense (Fully Exonic)	IGHG4 /// IGHG2 /// IGHG1 ///I GHGP
245	Sense (Fully Exonic)	IGHG2
246	Sense (includes Intronic)	C3orf26
247	AntiSense	ATF3
248	AntiSense	ATF3
250	Sense (Fully Exonic)	FN1
251	AntiSense	CALD1
252	AntiSense	CALD1
256	AntiSense	EGR1
261	AntiSense	TWIST1
262	AntiSense	TWIST1
263	AntiSense	BATF2
264	AntiSense	NFKBIZ
265	Sense (includes Intronic)	C3orf26
266	AntiSense	LOXL1
267	Sense (includes Intronic)	--
269	AntiSense	FN1
270	AntiSense	COL1A1
272	Sense (Fully Exonic)	TREH
274	AntiSense	APOL1
281	Sense (Fully Exonic)	COL10A1
282	Sense (Fully Exonic)	GAL3ST4

284	Sense (Fully Exonic)	TAGLN
285	Sense (Fully Exonic)	TWIST1
286	Sense (Fully Exonic)	HCLS1
288	Sense (Fully Exonic)	ITGB2
290	Sense (Fully Exonic)	HLA-B
291	Sense (Fully Exonic)	C17orf91
296	Sense (Fully Exonic)	FBLIM1
297	Sense (Fully Exonic)	COL15A1
298	Sense (Fully Exonic)	AQP7P3
299	AntiSense	IGFBP5
300	Sense (Fully Exonic)	FANK1
301	AntiSense	INS
302	Sense (Fully Exonic)	COL27A1
303	Sense (Fully Exonic)	COL5A1
304	Sense (Fully Exonic)	PRICKLE2
305	Sense (Fully Exonic)	N/A
306	Sense (Fully Exonic)	GXYLT2
307	Sense (includes Intronic)	KLF12
308	No Transcript match	
309	Sense (Fully Exonic)	FBXO32
310	No Transcript match	
311	Sense (Fully Exonic)	ASAH2B
312	AntiSense	PPFIBP1
313	AntiSense	XIST
314	Sense (Fully Exonic)	IGFBP6
315	Sense (Fully Exonic)	ROBO1
316	Sense (Fully Exonic)	TPM1
317	AntiSense	N/A
318	AntiSense	PLEKHG1
319	Sense (Fully Exonic)	NR2F1
320	Sense (Fully Exonic)	NPDC1
321	AntiSense	INS
322	Sense (Fully Exonic)	TRAF5
323	Sense (Fully Exonic)	CALD1
324	Sense (includes Intronic)	CHRM3
325	Sense (Fully Exonic)	AMOTL1
326	Sense (includes Intronic)	COL12A1
327	Sense (Fully Exonic)	PLXNA4
328	Sense (includes Intronic)	TMEM43

329	Sense (includes Intronic)	RORA
330	AntiSense	INS
331	Sense (Fully Exonic)	TSPAN18
332	No Transcript match	
333	Sense (Fully Exonic)	TNC
334	Sense (Fully Exonic)	TYRO3
335	AntiSense	EFNA5
336	Sense (Fully Exonic)	MYL9
337	Sense (Fully Exonic)	MIR198
338	Sense (includes Intronic)	N/A
339	Sense (includes Intronic)	PLA2R1
340	Sense (Fully Exonic)	COL14A1
341	Sense (Fully Exonic)	NRP1
342	Sense (Fully Exonic)	FSCN1
343	Sense (includes Intronic)	PDGFD
344	No Transcript match	
345	Sense (includes Intronic)	DOCK4
346	Sense (Fully Exonic)	TRIM13
347	Sense (Fully Exonic)	IGFBP5
348	Sense (Fully Exonic)	C19orf63
349	AntiSense	KLF6
350	AntiSense	TRIO
351	Sense (Fully Exonic)	COL4A1
352	Sense (Fully Exonic)	EPDR1
353	Sense (Fully Exonic)	FNDC1
354	Sense (Fully Exonic)	IL1R1
355	Sense (Fully Exonic)	CES4
356	Sense (Fully Exonic)	GPR176
357	Sense (includes Intronic)	GXYLT2
358	AntiSense	WHSC1L1
359	Sense (Fully Exonic)	N/A
360	Sense (Fully Exonic)	RGN
361	Sense (includes Intronic)	CA3
362	Sense (Fully Exonic)	TIMP3
363	Sense (Fully Exonic)	EFNA5
364	Sense (Fully Exonic)	RASGRF2
365	Sense (includes Intronic)	RELL1
366	AntiSense	ACSS3
367	Sense (Fully Exonic)	STMN3

368	Sense (Fully Exonic)	N/A
369	AntiSense	C7orf29
370	Sense (Fully Exonic)	HOXC6
371	Sense (Fully Exonic)	KLF8
372	Sense (includes Intronic)	SERINC5
373	Sense (Fully Exonic)	AKT3
374	Sense (Fully Exonic)	TGFB2
375	AntiSense	WNT5A
376	No Transcript match	
377	No Transcript match	
378	AntiSense	IGFBP7
379	No Transcript match	
380	Sense (includes Intronic)	SULT1C4
381	Sense (Fully Exonic)	AASS
382	Sense (Fully Exonic)	HEPH
383	Sense (Fully Exonic)	ADH5
384	Sense (Fully Exonic)	TIMP2
385	Sense (Fully Exonic)	EMP1
386	Sense (Fully Exonic)	CXCL14
387	Sense (Fully Exonic)	ZNF548
388	Sense (Fully Exonic)	SGCB
389	Sense (includes Intronic)	ASH2L
390	Sense (includes Intronic)	SERINC5
391	No Genome match	
392	Sense (Fully Exonic)	TMEM159
393	Sense (includes Intronic)	RBMS3
394	Sense (Fully Exonic)	TMEM49
395	Sense (includes Intronic)	RORA
396	No Transcript match	
397	AntiSense	ZNF608
398	No Genome match	
399	Sense (Fully Exonic)	ADAMTS2
400	Sense (Fully Exonic)	APCDD1
401	AntiSense	GXYLT2
402	Sense (Fully Exonic)	XIST
403	Sense (Fully Exonic)	MBNL2
404	Sense (Fully Exonic)	SHF
405	Sense (includes Intronic)	APBB2
406	No Transcript match	

407	Sense (Fully Exonic)	COL14A1
408	Sense (Fully Exonic)	IGFBP5
409	Sense (Fully Exonic)	CREB5
410	AntiSense	INS
411	Sense (Fully Exonic)	BAHCC1
412	Sense (Fully Exonic)	RFXAP
413	Sense (Fully Exonic)	INS
414	Sense (Fully Exonic)	DDR2
415	Sense (Fully Exonic)	CA12
416	Sense (Fully Exonic)	RHOB
417	Sense (Fully Exonic)	N/A
418	Sense (Fully Exonic)	SNORD116-4
419	Sense (Fully Exonic)	MEG3
420	Sense (Fully Exonic)	WNT4
421	Sense (Fully Exonic)	FBLN2
422	AntiSense	DAAM1
423	No Transcript match	
424	Sense (Fully Exonic)	CHN1
425	Sense (includes Intronic)	APBB2
426	Sense (Fully Exonic)	PTRF
427	AntiSense	IGF1
428	Sense (Fully Exonic)	UST
429	Sense (Fully Exonic)	SMARCA1
430	Sense (includes Intronic)	N/A
431	Sense (Fully Exonic)	IGLC3
432	AntiSense	INS
433	Sense (Fully Exonic)	KANK4
434	AntiSense	IGF1
435	Sense (Fully Exonic)	CYP27A1
436	AntiSense	EIF2B5
437	No Transcript match	
438	Sense (Fully Exonic)	SNRNP25
439	Sense (Fully Exonic)	SETD7
440	Sense (Fully Exonic)	MSX1
441	Sense (Fully Exonic)	HOPX
442	Sense (Fully Exonic)	NID2
443	Sense (Fully Exonic)	IGF1
444	Sense (Fully Exonic)	PSD3
445	Sense (Fully Exonic)	FGFR1

446	Sense (Fully Exonic)	ETV1
447	Sense (Fully Exonic)	ZNF655
448	No Genome match	
449	AntiSense	INS
450	Sense (Fully Exonic)	SFRP2
451	Sense (Fully Exonic)	SPAG16
452	AntiSense	NR2F2
453	Sense (includes Intronic)	SYNPO2
454	Sense (Fully Exonic)	FAM101B
455	AntiSense	IGF2
456	Sense (Fully Exonic)	CA3
457	Sense (Fully Exonic)	XIST
458	No Transcript match	
459	Sense (Fully Exonic)	WNT7A
460	Sense (includes Intronic)	N/A
461	Sense (Fully Exonic)	FGFR1
462	AntiSense	FXVD6
463	Sense (Fully Exonic)	FGFR1
464	Sense (includes Intronic)	IGFBP7
465	Sense (Fully Exonic)	TIMP2
466	Sense (Fully Exonic)	DUSP1
467	Sense (includes Intronic)	SERINC5
468	No Transcript match	
469	Sense (Fully Exonic)	ABLIM1
470	Sense (Fully Exonic)	ARL4A
471	AntiSense	SH3TC2
472	AntiSense	NR2F2
473	Sense (Fully Exonic)	ENG
474	Sense (Fully Exonic)	MGP
475	Sense (Fully Exonic)	MEG3
476	AntiSense	FAM115A
477	Sense (Fully Exonic)	EGR1
478	Sense (Fully Exonic)	SNORD116-3
479	Sense (Fully Exonic)	AEBP1
480	Sense (includes Intronic)	SDK1
481	Sense (Fully Exonic)	ENC1
482	Sense (Fully Exonic)	SNORD116-7
483	Sense (Fully Exonic)	N/A
484	Sense (Fully Exonic)	APOD

485	AntiSense	N/A
486	AntiSense	GAS1
487	Sense (Fully Exonic)	VPS36
488	No Transcript match	
489	Sense (Fully Exonic)	SPHK2
490	Sense (Fully Exonic)	SNORD116-8
491	Sense (Fully Exonic)	MYO10
492	Sense (Fully Exonic)	HOXC6
493	Sense (Fully Exonic)	RNF149
494	Sense (Fully Exonic)	BTG2
495	Sense (includes Intronic)	MAP3K1
496	Sense (Fully Exonic)	SNORD116-23
497	Sense (includes Intronic)	ACSL4
498	Sense (Fully Exonic)	CYP27C1
499	Sense (includes Intronic)	COL12A1
500	Sense (Fully Exonic)	IGFBP5
501	Sense (Fully Exonic)	DUSP4
502	Sense (Fully Exonic)	PFKFB3
503	Sense (Fully Exonic)	SDC2
504	AntiSense	FXVD6
505	Sense (Fully Exonic)	COL5A1
506	Sense (Fully Exonic)	MARCKS
507	Sense (Fully Exonic)	IRS2
508	Sense (Fully Exonic)	N/A
509	AntiSense	FSCN1
510	Sense (Fully Exonic)	FYN
511	Sense (Fully Exonic)	IGFBP5
512	Sense (Fully Exonic)	NUDT4P1
513	Sense (Fully Exonic)	NFKBIZ
514	Sense (Fully Exonic)	N/A
515	Sense (Fully Exonic)	C7orf41
516	Sense (Fully Exonic)	MEG3
517	Sense (Fully Exonic)	N/A
518	Sense (Fully Exonic)	PLEKHG1
519	Sense (Fully Exonic)	ZNF827
520	Sense (Fully Exonic)	ZNF175
521	Sense (Fully Exonic)	XIST
522	Sense (includes Intronic)	GSN
523	Sense (includes Intronic)	RORA

524	Sense (Fully Exonic)	CA13
525	AntiSense	TMX4
526	Sense (Fully Exonic)	KIT
527	Sense (includes Intronic)	WDR78
528	Sense (Fully Exonic)	ECEL1
529	Sense (Fully Exonic)	XIST
530	Sense (Fully Exonic)	PROCR
531	Sense (Fully Exonic)	C9orf167
532	Sense (Fully Exonic)	MUC6
533	Sense (includes Intronic)	P4HA2
534	Sense (Fully Exonic)	FAM69C
535	Sense (Fully Exonic)	NOX4
536	Sense (includes Intronic)	N/A
537	No Transcript match	
538	Sense (Fully Exonic)	SMOX
539	Sense (Fully Exonic)	KIAA0922
540	No Transcript match	
541	Sense (Fully Exonic)	XIST
542	Sense (Fully Exonic)	NPAS2
543	Sense (Fully Exonic)	NAV1
544	Sense (includes Intronic)	N/A
545	Sense (Fully Exonic)	HLA-A
546	Sense (Fully Exonic)	FAM46C
547	Sense (Fully Exonic)	N/A
548	Sense (Fully Exonic)	SLAMF7
549	Sense (Fully Exonic)	FCER1G
550	Sense (Fully Exonic)	C1S
551	Sense (Fully Exonic)	NUPR1
552	AntiSense	C1QC
553	AntiSense	SAT1
554	Sense (Fully Exonic)	SOD2
555	Sense (Fully Exonic)	IRF1
556	Sense (Fully Exonic)	SFN
557	AntiSense	LTB
558	Sense (Fully Exonic)	ARID5A
559	Sense (Fully Exonic)	BST2
560	Sense (Fully Exonic)	HLA-F
561	Sense (Fully Exonic)	XAF1
562	Sense (Fully Exonic)	TCOF1

563	Sense (Fully Exonic)	RPL23AP1
564	Sense (Fully Exonic)	IL1RN
565	Sense (Fully Exonic)	IFIT5
566	Sense (Fully Exonic)	B2M
567	AntiSense	GBP1
568	Sense (Fully Exonic)	HLA-F
569	Sense (Fully Exonic)	DGKA
570	Sense (Fully Exonic)	XBP1
571	Sense (Fully Exonic)	PLCG2
572	Sense (Fully Exonic)	FAM46C
573	No Genome match	
574	Sense (Fully Exonic)	TREM2
575	Sense (Fully Exonic)	LGALS9
576	Sense (Fully Exonic)	HLA-DPB1
577	AntiSense	ODF3B
578	Sense (Fully Exonic)	MX1
579	Sense (Fully Exonic)	STAT1
580	Sense (Fully Exonic)	CTSB
581	Sense (Fully Exonic)	FAM26F
582	Sense (includes Intronic)	PARP14
583	AntiSense	SAT1
584	Sense (Fully Exonic)	CTSS
585	No Transcript match	
586	Sense (Fully Exonic)	CTSB
587	Sense (Fully Exonic)	ADAM8
588	Sense (includes Intronic)	B2M
589	Sense (Fully Exonic)	FLVCR2
590	Sense (Fully Exonic)	TYROBP
591	AntiSense	SAMD9L
592	Sense (Fully Exonic)	SAMD9L
593	Sense (Fully Exonic)	SIGLEC1
594	Sense (Fully Exonic)	MMP7
595	Sense (Fully Exonic)	APOL1
596	Sense (Fully Exonic)	CYLD
597	Sense (Fully Exonic)	HLA-B
598	Sense (Fully Exonic)	SAT1
599	Sense (Fully Exonic)	C1QB
600	Sense (Fully Exonic)	HLA-DMB
601	Sense (Fully Exonic)	NLRC5

602	Sense (Fully Exonic)	FAM20A
603	AntiSense	N/A
604	Sense (Fully Exonic)	STAT1
605	Sense (includes Intronic)	STAT1
606	Sense (Fully Exonic)	STAT1
607	AntiSense	N/A
608	Sense (Fully Exonic)	DERL3
609	Sense (Fully Exonic)	HLA-F
610	Sense (Fully Exonic)	MAFB
611	Sense (Fully Exonic)	CD4
612	Sense (Fully Exonic)	HLA-A
613	Sense (Fully Exonic)	UBE2L6
614	Sense (Fully Exonic)	C1QC
615	Sense (Fully Exonic)	CD163
616	Sense (Fully Exonic)	LRMP
617	Sense (Fully Exonic)	C11orf17
618	Sense (Fully Exonic)	XAF1
619	Sense (Fully Exonic)	GLRX
620	Sense (Fully Exonic)	IFIH1
621	Sense (Fully Exonic)	CD44
622	Sense (Fully Exonic)	LITAF
623	Sense (Fully Exonic)	CCDC69
624	Sense (Fully Exonic)	GBP5
625	Sense (Fully Exonic)	PML
626	Sense (Fully Exonic)	SAMD9
627	Sense (Fully Exonic)	CBR3
628	Sense (Fully Exonic)	RASGRP2
629	Sense (Fully Exonic)	FCGR2A
630	Sense (Fully Exonic)	BST2
631	Sense (Fully Exonic)	HLA-A

Table 1C: Angiogenesis and immune response cluster genes of Figs 11A and 11B

SEQ No.	ER group	Gene Symbol	Orientation
632	ER pos	STAT1	Sense (Fully Exonic)
709	ER pos	STAT1	Sense (Fully Exonic)
803	ER neg	HOXD3	Sense (includes Intronic)
804	ER neg	LCP1	Sense (Fully Exonic)
875	ER neg	SPON1	Sense (Fully Exonic)

633	ER pos	IGF1	Sense (Fully Exonic)
805	ER neg	FHL1	Sense (Fully Exonic)
806	ER neg	MS4A1	Sense (Fully Exonic)
876	ER neg	FN1	Sense (Fully Exonic)
710	ER pos	FN1	Sense (Fully Exonic)
634	ER pos	HLA-DPA1	Sense (Fully Exonic)
877	ER neg	ADAM12	Sense (Fully Exonic)
711	ER pos	ITGBL1	Sense (Fully Exonic)
712	ER pos	POSTN	Sense (Fully Exonic)
635	ER pos	IGKV3-20 /// IGKV3D-20	AntiSense
748	ER neg,ER pos	DDX58	Sense (Fully Exonic)
636	ER pos	SLAMF7	Sense (Fully Exonic)
878	ER neg	AGPAT4	Sense (Fully Exonic)
959	ER neg,ER pos	FAM46C	Sense (Fully Exonic)
713	ER pos	GXYLT2	Sense (includes Intronic)
714	ER pos	SNX5	Sense (Fully Exonic)
637	ER pos		No Genome match
879	ER neg	PRICKLE1	Sense (Fully Exonic)
922	ER neg,ER pos	IL7R	Sense (Fully Exonic)
750	ER neg,ER pos	CMPK2	Sense (Fully Exonic)
638	ER pos	KLHL36	Sense (Fully Exonic)
807	ER neg	CD274	Sense (Fully Exonic)
880	ER neg	NRP2	AntiSense
924	ER neg,ER pos	POSTN	Sense (includes Intronic)
639	ER pos	CAMK2N1	AntiSense
881	ER neg	COL1A2	Sense (Fully Exonic)
715	ER pos	N/A	AntiSense
716	ER pos		No Transcript match
717	ER pos	COL12A1	Sense (Fully Exonic)
640	ER pos	MIR143	Sense (Fully Exonic)
808	ER neg		No Genome match
960	ER neg,ER pos	DNM3	AntiSense
718	ER pos	BNC2	Sense (includes Intronic)

641	ER pos	BCL11B	Sense (includes Intronic)
809	ER neg	CYBB	Sense (Fully Exonic)
882	ER neg	COL12A1	Sense (Fully Exonic)
642	ER pos	OR2I1P	AntiSense
752	ER neg,ER pos	EPSTI1	Sense (Fully Exonic)
926	ER neg,ER pos	GXYLT2	Sense (Fully Exonic)
643	ER pos	SAMD9L	Sense (Fully Exonic)
810	ER neg	SLC2A3	Sense (Fully Exonic)
927	ER neg,ER pos	IGKJ3 /// IGKJ4	Sense (Fully Exonic)
644	ER pos	THBS1	Sense (Fully Exonic)
811	ER neg	GLUL	Sense (Fully Exonic)
812	ER neg		No Transcript match
813	ER neg	THSD7A	Sense (includes Intronic)
928	ER neg,ER pos	COL11A1	Sense (Fully Exonic)
645	ER pos		No Transcript match
814	ER neg	SPP1	AntiSense
815	ER neg	TIMP3	Sense (Fully Exonic)
883	ER neg	FBN1	Sense (Fully Exonic)
646	ER pos	IGFBP5	Sense (Fully Exonic)
816	ER neg	IKZF1	Sense (Fully Exonic)
817	ER neg	CTGF	AntiSense
884	ER neg	COL5A2	AntiSense
647	ER pos	PALMD	Sense (Fully Exonic)
818	ER neg	IGKV4-1	Sense (Fully Exonic)
756	ER neg,ER pos	N/A	Sense (Fully Exonic)
648	ER pos	NLRC3	Sense (Fully Exonic)
819	ER neg	TNFRSF13B	Sense (Fully Exonic)
885	ER neg	APOC1	Sense (Fully Exonic)
649	ER pos	ELN	Sense (Fully Exonic)
757	ER neg,ER pos		No Genome match
650	ER pos	ELN	Sense (Fully Exonic)
758	ER neg,ER pos	IGKC	Sense (Fully Exonic)
651	ER pos	CIITA	Sense (Fully Exonic)

788	ER neg,ER pos	CCR7	Sense (Fully Exonic)
719	ER pos	STAT1	Sense (Fully Exonic)
720	ER pos	SDC1	Sense (Fully Exonic)
721	ER pos	ISG15	Sense (Fully Exonic)
722	ER pos	APOC1	Sense (Fully Exonic)
652	ER pos	INS /// IGF2	Sense (Fully Exonic)
820	ER neg	LPL	Sense (Fully Exonic)
962	ER neg,ER pos	IFI27	Sense (Fully Exonic)
723	ER pos	CTSK	Sense (Fully Exonic)
724	ER pos	PLEK	Sense (Fully Exonic)
725	ER pos	MIR198	Sense (Fully Exonic)
759	ER neg,ER pos	IGJ	AntiSense
653	ER pos	PXDN	Sense (Fully Exonic)
790	ER neg,ER pos	ENO2	Sense (Fully Exonic)
726	ER pos	CILP	Sense (Fully Exonic)
726	ER neg,ER pos	GBP4	Sense (Fully Exonic)
654	ER pos	GBP1	Sense (Fully Exonic)
886	ER neg	SULF1	Sense (Fully Exonic)
655	ER pos	EFEMP1	Sense (Fully Exonic)
761	ER neg,ER pos	MX1	Sense (Fully Exonic)
656	ER pos	CD109	Sense (Fully Exonic)
887	ER neg		No Transcript match
762	ER neg,ER pos	CXCL10	Sense (Fully Exonic)
657	ER pos	FYB	Sense (Fully Exonic)
791	ER neg,ER pos	IFI44	Sense (Fully Exonic)
727	ER pos	COL5A1	Sense (Fully Exonic)
658	ER pos	TIMP3	Sense (Fully Exonic)
888	ER neg	CADM1	AntiSense
659	ER pos	STAT1	AntiSense
889	ER neg	MXRA5	AntiSense
660	ER pos	CCDC152	Sense (Fully Exonic)
821	ER neg	MX1	AntiSense
890	ER neg	C1QC	AntiSense

792	ER neg,ER pos	N/A	Sense (includes Intronic)
728	ER pos	FNDC1	AntiSense
661	ER pos	HOXC5 /// HOXC10	AntiSense
822	ER neg	GABBR1 /// UBD	AntiSense
823	ER neg	CYP1B1	AntiSense
824	ER neg	SPP1	Sense (Fully Exonic)
824	ER neg,ER pos	FYB	Sense (Fully Exonic)
662	ER pos		No Transcript match
825	ER neg	GBP5	Sense (Fully Exonic)
937	ER neg,ER pos	IGHA1	Sense (Fully Exonic)
663	ER pos	CAMK2N1	Sense (Fully Exonic)
826	ER neg	SASH3	Sense (Fully Exonic)
827	ER neg	COL14A1	Sense (Fully Exonic)
793,	ER neg,ER pos	CD79A /// ARHGEF1	Sense (Fully Exonic)
729	ER pos	LAIR1	Sense (Fully Exonic)
664	ER pos	APOBEC3G	Sense (Fully Exonic)
828	ER neg	GPX8	Sense (Fully Exonic)
829	ER neg	RTP4	Sense (Fully Exonic)
830	ER neg	IFIH1	Sense (Fully Exonic)
891	ER neg	IFI6	Sense (Fully Exonic)
730	ER pos	IFI6	Sense (Fully Exonic)
665	ER pos	C1orf113	Sense (Fully Exonic)
831	ER neg	FAM26F	Sense (Fully Exonic)
832	ER neg	PARP9	Sense (Fully Exonic)
833	ER neg	ARHGAP9	Sense (Fully Exonic)
765	ER neg,ER pos	FNDC1	Sense (Fully Exonic)
666	ER pos	C13orf33	Sense (Fully Exonic)
766	ER neg,ER pos	GBP5	Sense (Fully Exonic)
667	ER pos	VNN2	Sense (Fully Exonic)
892	ER neg	RSAD2	Sense (Fully Exonic)
668	ER pos	PTPRC	Sense (Fully Exonic)
893	ER neg	LRRC15	Sense (Fully Exonic)
731	ER pos	CTHRC1	Sense (Fully Exonic)
669	ER pos	SMARCA1	Sense (Fully Exonic)

894	ER neg	STAT1	Sense (Fully Exonic)
767	ER neg,ER pos	IGJ	Sense (Fully Exonic)
670	ER pos	DACT3	Sense (Fully Exonic)
834	ER neg	PHLDB2	Sense (Fully Exonic)
967	ER neg,ER pos	IL2RG	Sense (Fully Exonic)
732	ER pos	C1orf162	Sense (Fully Exonic)
768	ER neg,ER pos	CECR1	Sense (Fully Exonic)
671	ER pos	BTN3A2 /// BTN3A3	Sense (Fully Exonic)
835	ER neg	CES1 /// CES4	Sense (Fully Exonic)
836	ER neg	TBC1D10C	Sense (Fully Exonic)
837	ER neg	CCDC80	Sense (Fully Exonic)
895	ER neg	GAS7	Sense (Fully Exonic)
672	ER pos	LPL	Sense (Fully Exonic)
896	ER neg	CD163	Sense (Fully Exonic)
795	ER neg,ER pos	LYZ	Sense (Fully Exonic)
733	ER pos	NAPSB	Sense (Fully Exonic)
673	ER pos	OAS2	Sense (Fully Exonic)
769	ER neg,ER pos	ZNF469	Sense (Fully Exonic)
674	ER pos	KIF26A	Sense (Fully Exonic)
770	ER neg,ER pos	IGHG1 /// IGHG2 /// IGHG3	Sense (Fully Exonic)
675	ER pos	N/A	Sense (Fully Exonic)
838	ER neg	DDX60L	Sense (Fully Exonic)
839	ER neg	SCD5	Sense (Fully Exonic)
840	ER neg	ANPEP	Sense (Fully Exonic)
841	ER neg	FABP4	Sense (Fully Exonic)
771	ER neg,ER pos	IL10RA	Sense (Fully Exonic)
676	ER pos	CXCL10	Sense (Fully Exonic)
897	ER neg	APOC1	Sense (Fully Exonic)
677	ER pos	APOD	Sense (Fully Exonic)
842	ER neg	APOD	Sense (Fully Exonic)
843	ER neg	DST	Sense (Fully Exonic)
772	ER neg,ER pos	CD2	Sense (Fully Exonic)
678	ER pos	CD22	Sense (Fully Exonic)

844	ER neg	CD52	Sense (Fully Exonic)
898	ER neg	CTSK	Sense (Fully Exonic)
773,	ER neg,ER pos	CCR7	Sense (Fully Exonic)
679	ER pos	CTGF	Sense (Fully Exonic)
899	ER neg	EDN2	Sense (Fully Exonic)
680	ER pos	EGR1	Sense (Fully Exonic)
845	ER neg	ENO2	Sense (Fully Exonic)
900	ER neg	IFI6	Sense (Fully Exonic)
681	ER pos	HLA-DOA	Sense (Fully Exonic)
846	ER neg	TNC	Sense (Fully Exonic)
847	ER neg	IDO1	Sense (Fully Exonic)
848	ER neg	ID1	Sense (Fully Exonic)
901	ER neg	IRF1	Sense (Fully Exonic)
774,	ER neg,ER pos	ITGAL	Sense (Fully Exonic)
682	ER pos	KRT81	Sense (Fully Exonic)
902	ER neg	LUM	Sense (Fully Exonic)
734	ER pos	MFAP2	Sense (Fully Exonic)
683	ER pos	CXCL9	Sense (Fully Exonic)
775,	ER neg,ER pos	MMP13	Sense (Fully Exonic)
684	ER pos	MSX1	Sense (Fully Exonic)
903	ER neg	MX1	Sense (Fully Exonic)
685	ER pos	TWIST1	Sense (Fully Exonic)
904	ER neg	OAS2	Sense (Fully Exonic)
686	ER pos	PIK3CG	Sense (Fully Exonic)
905	ER neg	PLAU	Sense (Fully Exonic)
735	ER pos	COL10A1	Sense (Fully Exonic)
687	ER pos	PSMB9	Sense (Fully Exonic)
849	ER neg	FBP1	Sense (Fully Exonic)
850	ER neg	PTN	Sense (Fully Exonic)
776	ER neg,ER pos	RAC2	Sense (Fully Exonic)
688	ER pos	CCL5	Sense (Fully Exonic)
851	ER neg	CCL5	Sense (Fully Exonic)
852	ER neg	CCL21	Sense (Fully Exonic)
906	ER neg	THBS2	Sense (Fully Exonic)
689	ER pos	TAP1	Sense (Fully Exonic)

853	ER neg	IGFBP5	Sense (Fully Exonic)
854	ER neg	IGF2	Sense (Fully Exonic)
855	ER neg	SELL	Sense (Fully Exonic)
777,	ER neg,ER pos	GJB2	Sense (Fully Exonic)
690	ER pos	F2RL2	Sense (Fully Exonic)
907	ER neg	VCAN	Sense (Fully Exonic)
691	ER pos	ALDH1A3	Sense (Fully Exonic)
856	ER neg	EGR3	Sense (Fully Exonic)
796	ER neg,ER pos	MMP2	Sense (Fully Exonic)
736	ER pos	MMP2	Sense (Fully Exonic)
778	ER neg,ER pos	SPOCK1	Sense (Fully Exonic)
797	ER neg,ER pos	SPOCK1	Sense (Fully Exonic)
737	ER pos	COL1A1	Sense (Fully Exonic)
692	ER pos	SPARCL1	Sense (Fully Exonic)
857	ER neg	CD3D	Sense (Fully Exonic)
798	ER neg,ER pos	CD3E	Sense (Fully Exonic)
738	ER pos	COL3A1	Sense (Fully Exonic)
693	ER pos	CXCL14	Sense (Fully Exonic)
908	ER neg	ADAMTS4	Sense (Fully Exonic)
779	ER neg,ER pos	NCKAP1L	Sense (Fully Exonic)
694	ER pos	CALCOCO2	Sense (Fully Exonic)
909	ER neg	MMP11	Sense (Fully Exonic)
695	ER pos	TRIM22	Sense (Fully Exonic)
910	ER neg	OAS3	Sense (Fully Exonic)
739	ER pos	OAS3	Sense (Fully Exonic)
696	ER pos	POU2AF1	Sense (Fully Exonic)
780	ER neg,ER pos	GABBR1 /// UBD	Sense (Fully Exonic)
697	ER pos	FOSB	Sense (Fully Exonic)
781	ER neg,ER pos	IFI44L	Sense (Fully Exonic)
698	ER pos	PIM2	Sense (Fully Exonic)
858	ER neg	KLRK1	Sense (Fully Exonic)
859	ER neg	TAGLN	Sense (Fully Exonic)
860	ER neg	CD36	Sense (Fully Exonic)

861	ER neg	CYP27C1	Sense (Fully Exonic)
862	ER neg	PDLIM3	Sense (Fully Exonic)
911	ER neg	RNF144A	Sense (Fully Exonic)
782	ER neg,ER pos	SPOCK2	Sense (Fully Exonic)
699	ER pos	FAM19A5	Sense (Fully Exonic)
863	ER neg	ABI3BP	Sense (Fully Exonic)
912	ER neg	TMEM158	Sense (Fully Exonic)
700	ER pos	CCDC69	Sense (Fully Exonic)
913	ER neg	C1QA	Sense (Fully Exonic)
701	ER pos	ETV7	Sense (Fully Exonic)
914	ER neg	N/A	Sense (Fully Exonic)
702	ER pos	USP18	Sense (Fully Exonic)
915	ER neg	XAF1	Sense (Fully Exonic)
703	ER pos	PARP14	Sense (Fully Exonic)
916	ER neg	SAMD9	Sense (Fully Exonic)
740	ER pos	ASPN	Sense (Fully Exonic)
704	ER pos	FAM46C	Sense (Fully Exonic)
864	ER neg	PINX1	Sense (Fully Exonic)
865	ER neg	GIMAP4	Sense (Fully Exonic)
866	ER neg	N/A	Sense (includes Intronic)
917	ER neg	COL3A1	Sense (Fully Exonic)
741	ER pos	COL1A2	Sense (Fully Exonic)
799	ER neg,ER pos	IGHG1	AntiSense
742	ER pos	FN1	AntiSense
800	ER neg,ER pos	RAC2	Sense (Fully Exonic)
743	ER pos	GLRX	Sense (Fully Exonic)
744	ER pos	BIRC3	AntiSense
783	ER neg,ER pos	TAP1	Sense (Fully Exonic)
957	ER neg,ER pos	POSTN	Sense (Fully Exonic)
705	ER pos	THBS1	AntiSense
867	ER neg	TNFAIP8	AntiSense
958	ER neg,ER pos	N/A	Sense (Fully Exonic)
974	ER neg,ER pos	IGJ	Sense (Fully Exonic)

745	ER pos	ADAM12	Sense (Fully Exonic)
706	ER pos	COL14A1	Sense (Fully Exonic)
868	ER neg		No Transcript match
869	ER neg	CD53	Sense (Fully Exonic)
918	ER neg	MIR1245	Sense (Fully Exonic)
707	ER pos		No Genome match
919	ER neg		No Transcript match
708	ER pos	TNFSF10	Sense (Fully Exonic)
870	ER neg	NLRC5	Sense (Fully Exonic)
871	ER neg	WWC2	Sense (includes Intronic)
872	ER neg	RORA	AntiSense
873	ER neg	IGKV4-1	AntiSense
874	ER neg		No Genome match
975	ER neg,ER pos	MIAT	Sense (Fully Exonic)
746	ER pos	COL8A1	Sense (Fully Exonic)
747	ER neg,ER pos	IFI44	Sense (Fully Exonic)

In certain exemplary embodiments, all or a portion of the biomarkers recited in Table 1A, Table 1B and Table 1C, may be used in an expression signature. For example, expression signatures comprising the biomarkers in Table 1A, Table 1B, and Table 1C can be generated using the methods provided herein and can comprise between one, and all of the markers set forth in Tables 1A, 1B, 1C and each and every combination in between (e.g., four selected markers, 16 selected markers, 74 selected markers, etc.). In some embodiments, the expression signature comprises at least 5, 10, 20, 40, 60, 100, 150, 200, or 300 or more markers. In other embodiments, the predictive biomarker panel comprises no more than 5, 10, 20, 40, 60, 100, 150, 200, 300, 400, 500, 600 or 700 markers. In one exemplary embodiment, the expression signature includes a plurality of markers listed in Table 1A. In another exemplary embodiment, the expression signature includes a plurality of biomarkers listing in Table 1B. In another exemplary embodiment, the expression signature includes a plurality of biomarkers listed in Table 1C. In yet another exemplary embodiment, the expression signature includes a plurality of biomarkers listed in Table 1A, Table 1B, and Table 1C. In some embodiments the expression signature includes at least about 1%, about 5%, about 10%, about 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, about 90%, about 95%, about 96%, about 97%, about 98%, or about 99% of the markers listed in Table 1A, Table 1B, Table 1C, or a combination thereof. Selected expression signatures can be assembled from the biomarkers

provided using methods described herein and analogous methods known in the art. In one embodiment, the expression signature contains all 250 genes or gene products in Table 1A. In another exemplary embodiment, the expression signature contains all 486 genes or gene products in Table 1B. In another exemplary embodiment, the expression signature contains all 343 genes or gene products in Table 1C.

4. Mathematical Models

[0076] The following methods may be used to derive expression signatures for distinguishing between subjects that are responsive or non-responsive to anti-angiogenic therapeutics, or as prognostic indicators of certain cancer types, including expression signatures derived from the biomarkers disclosed above. In certain other exemplary embodiments, the expression signature is derived using a decision tree (Hastie *et al.* The Elements of Statistical Learning, Springer, New York 2001), a random forest (Breiman, 2001 Random Forests, Machine Learning 45:5), a neural network (Bishop, Neural Networks for Pattern Recognition, Clarendon Press, Oxford 1995), discriminant analysis (Duda *et al.* Pattern Classification, 2nd ed., John Wiley, New York 2001), including, but not limited to linear, diagonal linear, quadratic and logistic discriminant analysis, a Prediction Analysis for Microarrays (PAM, (Tibshirani *et al.*, 2002, Proc. Natl. Acad. Sci. USA 99:6567-6572)) or a Soft Independent Modeling of Class Analogy analysis. (SIMCA, (Wold, 1976, Pattern Recogn. 8:127-139)).

[0077] Biomarker expression values may be defined in combination with corresponding scalar weights on the real scale with varying magnitude, which are further combined through linear or non-linear, algebraic, trigonometric or correlative means into a single scalar value via an algebraic, statistical learning, Bayesian, regression, or similar algorithms which together with a mathematically derived decision function on the scalar value provide a predictive model by which expression profiles from samples may be resolved into discrete classes of responder or non-responder, resistant or non-resistant, to a specified drug, drug class, or treatment regimen. Such predictive models, including biomarker membership, are developed by learning weights and the decision threshold, optimized for sensitivity, specificity, negative and positive predictive values, hazard ratio or any combination thereof, under cross-validation, bootstrapping or similar sampling techniques, from a set of representative expression profiles from historical patient samples with known drug response and/or resistance.

[0078] In one embodiment, the biomarkers are used to form a weighted sum of their signals, where individual weights can be positive or negative. The resulting sum ("expression score") is compared with a pre-determined reference point or value. The comparison with the reference point or value may be used to diagnose, or predict a clinical condition or outcome.

[0079] As described above, one of ordinary skill in the art will appreciate that the biomarkers included in the classifier provided in Tables 1A, 1B, and Table 1C will carry unequal weights in a classifier for responsiveness or resistance to a therapeutic agent. Therefore, while as few as one sequence may be used to diagnose or predict an outcome such as responsiveness to therapeutic agent, the specificity and sensitivity or diagnosis or prediction accuracy may increase using more sequences.

[0080] As used herein, the term “weight” refers to the relative importance of an item in a statistical calculation. The weight of each biomarker in a gene expression classifier may be determined on a data set of patient samples using analytical methods known in the art. As used herein the term “bias” or “offset” refers to a constant term derived using the mean expression of the signature genes in a training set and is used to mean-center the each gene analyzed in the test dataset.

[0081] In certain exemplary embodiments, the expression signature is defined by a decision function. A decision function is a set of weighted expression values derived using a linear classifier. All linear classifiers define the decision function using the following equation:

$$f(x) = w' \cdot x + b = \sum w_i \cdot x_i + b \quad (1)$$

[0082] All measurement values, such as the microarray gene expression intensities x_i , for a certain sample are collected in a vector x . Each intensity is then multiplied with a corresponding weight w_i to obtain the value of the decision function $f(x)$ after adding an offset term b . In deriving the decision function, the linear classifier will further define a threshold value that splits the gene expression data space into two disjoint halves. Exemplary linear classifiers include but are not limited to partial least squares (PLS), (Nguyen *et al.*, Bioinformatics 18 (2002) 39-50), support vector machines (SVM) (Schölkopf *et al.*, Learning with Kernels, MIT Press, Cambridge 2002), and shrinkage discriminant analysis (SDA) (Ahdesmäki *et al.*, Annals of applied statistics 4, 503-519 (2010)). In one exemplary embodiment, the linear classifier is a PLS linear classifier.

[0083] The decision function is empirically derived on a large set of training samples, for example from patients showing responsiveness or resistance to a therapeutic agent. The threshold separates a patient group based on different characteristics such as, but not limited to, responsiveness/non-responsiveness to treatment. The interpretation of this quantity, i.e. the cut-off threshold responsiveness or resistance to a therapeutic agent, is derived in the development phase (“training”) from a set of patients with known outcome. The corresponding weights and the responsiveness/resistance cut-off threshold for the decision score are fixed *a priori* from training data by methods known to those skilled in the art. In one exemplary embodiment, Partial Least Squares Discriminant Analysis (PLS-DA) is used for determining the weights. (L.

Ståhle, S. Wold, J. Chemom. 1 (1987) 185-196; D. V. Nguyen, D.M. Rocke, Bioinformatics 18 (2002) 39-50).

[0084] Effectively, this means that the data space, i.e. the set of all possible combinations of biomarker expression values, is split into two mutually exclusive groups corresponding to different clinical classifications or predictions, for example, one corresponding to responsiveness to a therapeutic agent and the other to non-responsiveness. In the context of the overall classifier, relative over-expression of a certain biomarker can either increase the decision score (positive weight) or reduce it (negative weight) and thus contribute to an overall decision of, for example, responsiveness or resistance to a therapeutic agent.

[0085] In certain exemplary embodiments of the invention, the data is transformed non-linearly before applying a weighted sum as described above. This non-linear transformation might include increasing the dimensionality of the data. The non-linear transformation and weighted summation might also be performed implicitly, for example, through the use of a kernel function. (Schölkopf *et al.* Learning with Kernels, MIT Press, Cambridge 2002).

[0086] In certain exemplary embodiments, the patient training set data is derived by isolated RNA from a corresponding cancer tissue sample set and determining expression values by hybridizing the isolated RNA to a microarray. In certain exemplary embodiments, the microarray used in deriving the expression signature is a transcriptome array. As used herein a “transcriptome array” refers to a microarray containing probe sets that are designed to hybridize to sequences that have been verified as expressed in the diseased tissue of interest. Given alternative splicing and variable poly-A tail processing between tissues and biological contexts, it is possible that probes designed against the same gene sequence derived from another tissue source or biological context will not effectively bind to transcripts expressed in the diseased tissue of interest, leading to a loss of potentially relevant biological information. Accordingly, it is beneficial to verify what sequences are expressed in the disease tissue of interest before deriving a microarray probe set. Verification of expressed sequences in a particular disease context may be done, for example, by isolating and sequencing total RNA from a diseased tissue sample set and cross-referencing the isolated sequences with known nucleic acid sequence databases to verify that the probe set on the transcriptome array is designed against the sequences actually expressed in the diseased tissue of interest. Methods for making transcriptome arrays are described in United States Patent Application Publication No. 2006/0134663, which is incorporated herein by reference. In certain exemplary embodiments, the probe set of the transcriptome array is designed to bind within 300 nucleotides of the 3' end of a transcript. Methods for designing transcriptome arrays with probe sets that bind within 300 nucleotides of the 3' end of target transcripts are disclosed in United States Patent Application

Publication No. 2009/0082218, which is incorporated by reference herein. In certain exemplary embodiments, the microarray used in deriving the gene expression profiles of the present invention is the Almac Ovarian Cancer DSA™ microarray (Almac Group, Craigavon, United Kingdom).

[0087] An optimal linear classifier can be selected by evaluating a linear classifier's performance using such diagnostics as "area under the curve" (AUC). AUC refers to the area under the curve of a receiver operating characteristic (ROC) curve, both of which are well known in the art. AUC measures are useful for comparing the accuracy of a classifier across the complete data range. Linear classifiers with a higher AUC have a greater capacity to classify unknowns correctly between two groups of interest (e.g., ovarian cancer samples and normal or control samples). ROC curves are useful for plotting the performance of a particular feature (e.g., any of the biomarkers described herein and/or any item of additional biomedical information) in distinguishing between two populations (e.g., individuals responding and not responding to a therapeutic agent). Typically, the feature data across the entire population (e.g., the cases and controls) are sorted in ascending order based on the value of a single feature. Then, for each value for that feature, the true positive and false positive rates for the data are calculated. The true positive rate is determined by counting the number of cases above the value for that feature and then dividing by the total number of cases. The false positive rate is determined by counting the number of controls above the value for that feature and then dividing by the total number of controls. Although this definition refers to scenarios in which a feature is elevated in cases compared to controls, this definition also applies to scenarios in which a feature is lower in cases compared to the controls (in such a scenario, samples below the value for that feature would be counted). ROC curves can be generated for a single feature as well as for other single outputs, for example, a combination of two or more features can be mathematically combined (e.g., added, subtracted, multiplied, etc.) to provide a single sum value, and this single sum value can be plotted in a ROC curve. Additionally, any combination of multiple features, in which the combination derives a single output value, can be plotted in a ROC curve. These combinations of features may comprise a test. The ROC curve is the plot of the true positive rate (sensitivity) of a test against the false positive rate (1-specificity) of the test.

[0088] In one exemplary embodiment an angiogenesis expression signature is directed to the 25 biomarkers detailed in Table 2A with corresponding ranks, weights and associated bias detailed in the table or alternative rankings, weightings and bias, depending, for example, on the disease setting. In another exemplary embodiment, an angiogenesis expression signature is directed to the 45 biomarkers detailed in Table 2B with corresponding ranks, weights and

associated bias detailed in the table or alternative rankings, weightings and bias, depending, for example, on the disease setting. In another exemplary embodiment, a non-angiogenesis expression signature is directed to the 63 biomarkers detailed in Table 2C with corresponding ranks, and weights and associated bias detailed in the table or alternative rankings, and weightings and bias, depending, for example, on the disease setting. Tables 2A, 2B and 2C rank the biomarkers in order of absolute decreasing weight, in an example classifier, in the compound decision score function.

Table 2A

25 Biomarker Signature			
Rank	Gene Symbol	Weight	Bias
1	CCDC80	0.0584	5.9594
2	INHBA	0.0508	3.8146
3	THBS2	0.0504	3.4342
4	SFRP2	0.0437	4.3293
5	MMP2	0.0367	5.3319
6	PLAU	-0.0323	8.3844
7	FAP	0.0300	3.4689
8	FN1	0.0277	10.0610
9	COL8A1	-0.0248	5.1984
10	RAB31	0.0244	5.6121
11	FAM38B	0.0242	5.0883
12	VCAN	0.0230	4.4460
13	GJB2	0.0223	5.8677
14	ITGA5	0.0216	5.4455
15	CRISPLD2	0.0192	6.5088
16	C17orf91	0.0167	6.4830
17	BGN	-0.0142	5.5396
18	TIMP3	0.0130	4.6739
19	ALPK2	0.0123	7.3709
20	LUM	0.0104	8.3279
21	NKD2	-0.0098	5.4448
22	LOX	-0.0082	8.2117
23	MIR1245	0.0059	4.9959
24	LOXL1	0.0052	2.9463
25	CXCL12	0.0048	9.7132

Table 2B

45 Biomarker Signature			
Rank	Gene Symbol	Weight	Bias
1	TMEM200A	0.0595	3.6813
2	GJB2	0.0560	4.4798
3	MMP13	0.0383	3.7241
4	GFPT2	0.0380	4.8602
5	POSTN	-0.0355	4.3599
6	BICC1	0.0304	3.6982
7	CDH11	0.0283	4.9968
8	MRV11	0.0256	5.0761
9	PMP22	0.0240	5.5645
10	COL11A1	-0.0237	3.5002
11	IGFL2	0.0222	3.3104
12	LUM	-0.0220	8.3363
13	NTM	-0.0218	4.2302
14	BGN	0.0211	10.1524
15	COL3A1	-0.0210	8.3236
16	COL10A1	0.0197	6.3538
17	RAB31	0.0180	5.3171
18	ANGPTL2	0.0166	5.6396
19	PLAU	0.0166	5.8488
20	COL8A1	0.0164	6.4193
21	MIR1245	0.0153	5.4552
22	POLD2	0.0146	9.3878
23	NKD2	0.0145	7.3717
24	FZD1	0.0143	4.1519
25	COPZ2	0.0139	5.1039
26	ITGA5	0.0136	8.3663
27	VGLL3	0.0125	4.5019
28	INHBA	-0.0118	4.6843
29	MMP14	0.0110	10.0841
30	VCAN	0.0100	5.5518
31	THBS2	-0.0087	8.1309
32	RUNX2	0.0083	4.7345
33	TIMP3	0.0081	6.4983
34	SFRP2	-0.0079	5.6017
35	COL1A2	0.0078	6.0100
36	COL5A2	-0.0072	3.5671
37	SERPINF1	0.0068	10.8334
38	KIF26B	-0.0052	4.9782
39	TNFAIP6	0.0050	5.3618
40	MMP2	0.0040	5.3622
41	FN1	0.0031	4.9840
42	ALPK2	0.0024	3.5136
43	CTSK	0.0015	5.7322
44	LOXL1	-0.0014	9.5939
45	FAP	0.0000	5.2254

Table 2C

63 Biomarker Signature			
Rank	Gene Symbol	Weight	Bias
1	IGF2	-0.01737	9.8884
2	SOX11	-0.01457	4.5276
3	INS	-0.01409	7.0637
4	CXCL17	0.012568	4.8478
5	SLC5A1	0.012426	4.8920
6	TMEM45A	-0.0124	6.1307
7	CXCR2P1	0.011427	3.1478
8	MFAP2	-0.01039	9.0516
9	MATN3	-0.01028	3.7313
10	RTP4	0.010052	4.9852
11	COL3A1	-0.01002	8.4130
12	CDR1	-0.00916	8.1778
13	RARRES3	0.009056	6.8964
14	TNFSF10	0.008876	6.2325
15	NUAK1	-0.0087	6.6771
16	SNORD114-14	-0.00864	5.6385
17	SRPX	-0.00862	5.0850
18	SPARC	-0.00848	6.0135
19	GJB1	0.008445	5.8142
20	TIMP3	-0.00823	6.5937
21	ISLR	-0.0079	8.9876
22	TUBA1A	-0.00754	9.6540
23	DEXI	0.007271	5.5913
24	BASP1	-0.00724	8.4396
25	PXDN	-0.00724	7.7570
26	GBP4	0.007226	3.1119
27	SLC28A3	0.007201	4.2125
28	HLA-DRA	0.007197	8.3089
29	TAP2	0.007189	4.8464
30	ACSL5	0.007155	6.8703
31	CDH11	-0.00708	4.9925
32	PSMB9	0.006962	4.1122
33	MMP14	-0.00683	10.1689
34	CD74	0.006825	9.2707
35	LOXL1	-0.00676	9.6429
36	CIITA	0.006623	5.5396
37	ZNF697	-0.00658	7.0319
38	SH3RF2	0.006549	5.0029
39	MIR198	-0.00654	5.1935
40	COL1A2	-0.00645	6.0427
41	TNFRSF14	0.006421	9.0366
42	COL8A1	-0.00642	6.4565
43	C21orf63	0.006261	5.9811
44	TAP1	0.006215	8.6458
45	PDPN	-0.00612	5.3198
46	RHOBTB3	-0.00597	3.5609

47	BCL11A	0.005943	4.3818
48	HLA-DOB	0.005851	4.6075
49	XAF1	0.005742	7.9229
50	ARHGAP26	0.005632	4.3991
51	POLD2	-0.00558	9.4183
52	DPYSL2	-0.00533	8.3469
53	COL4A1	-0.0052	7.0317
54	ID3	-0.00516	7.5673
55	CFB	0.005077	5.7951
56	NID1	-0.00494	4.7186
57	FKBP7	-0.00489	2.9437
58	TIMP2	-0.00468	7.5253
59	RCBTB1	-0.00458	7.4491
60	ANGPTL2	-0.00448	5.6807
61	ENTPD7	-0.00442	7.3772
62	SHISA4	-0.00403	6.0601
63	HINT1	0.003651	6.0724

[0089] In one exemplary embodiment, an expression signature comprises all or a portion of the following biomarkers: CCDC80, INHBA, THBS2, SFRP2, MMP2, PLAU, FAP, FN1, COL8A1, RAB31, FAM38B, VCAN, GJB2, ITGA5, CRISPLD2, C17, f91, BGN, TIMP3, ALPK2, LUM, NKD2, LOX, MIR1245, LOXL1, and CXCL12.

[0090] In another exemplary embodiment, an expression signature comprises CCDC80, INHBA, THBS2 and SFRP2 and at least N additional biomarkers selected from the list of biomarkers in Table 2A, wherein N equals 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or 21.

[0091] In another exemplary embodiment, the expression signature comprises CCDC80 and at least N additional biomarkers selected from the list of biomarkers in Table 2A, wherein N equals 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, or 24.

[0092] In another exemplary embodiment, the expression signature comprises INHBA and at least N additional biomarkers selected from the list of biomarkers in Table 2A, wherein N equals 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, or 24.

[0093] In another exemplary embodiment, the expression signature comprises THBS2 and at least N additional biomarkers selected from the list of biomarkers in Table 2A, wherein N equals 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, or 24.

[0094] In another exemplary embodiment, the expression signature comprises SFRP2 and at least N additional biomarkers selected from the list of biomarkers in Table 2A, wherein N equals 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, or 24.

[0095] In another example embodiment, an example expression signatures comprises the biomarkers and the corresponding biomarker weighted values listed in Table 2A. In another

exemplary embodiment, an example expression signature consists of the biomarkers and the corresponding biomarker weighted values listed in Table 2A

[0096] In a further aspect, the methods of the present invention comprise conducting an assay on a biological sample from an individual to determine the expression levels of one or more biomarkers in a biomarker panel, the biomarker panel comprising CCDC80, INHBA, THBS2 and SFRP2 and at least N additional biomarkers selected from the list of biomarkers in Table 2A, wherein N equals 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or 21.

[0097] In a further aspect, the methods of the present invention comprise conducting an assay on a biological sample from an individual to determine the expression levels of one or more biomarkers in a biomarker panel, the biomarker panel comprising CCDC80 and at least N additional biomarkers selected from the list of biomarkers in Table 2A, wherein N equals 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23 or 24.

[0098] In a further aspect, the methods of the present invention comprise conducting an assay on a biological sample from an individual to determine the expression levels of one or more biomarkers in a biomarker panel, the biomarker panel comprising INHBA and at least N additional biomarkers selected from the list of biomarkers in Table 2A, wherein N equals 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23 or 24.

[0099] In a further aspect, the methods of the present invention comprise conducting an assay on a biological sample from an individual to determine the expression levels of one or more biomarkers in a biomarker panel, the biomarker panel comprising THBS2 and at least N additional biomarkers selected from the list of biomarkers in Table 2A, wherein N equals 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23 or 24.

[00100] In a further aspect, the methods of the present invention comprise conducting an assay on a biological sample from an individual to determine the expression levels of one or more biomarkers in a biomarker panel, the biomarker panel comprising SFRP2 and at least N additional biomarkers selected from the list of biomarkers in Table 2A, wherein N equals 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23 or 24.

[00101] In another exemplary embodiment, an expression signature comprises all or a portion of the following biomarkers; TMEM200A, GJB2, MMP13, GFPT2, POSTN, BICC1, CDH11, MRVI1, PMP22, COL11A1, IGFL2, LUM, NTM, BGN, COL3A1, COL10A1, RAB31, ANGPTL2, PLAU, COL8A1, MIR1245, POLD2, NKD2, FZD1, COPZ2, ITGA5, VGLL3, INHBA, MMP14, VCAN, THBS2, RUNX2, TIMP3, SFRP2, COL1A2, COL5A2, SERPINF1, KIF26B, TNFAIP6, MMP2, FN1, ALPK2, CTSK, LOXL1 and FAP.

[0100] In another exemplary embodiment, an expression signature comprises TMEM200A, GJB2, MMP13 and GFPT2 and at least N additional biomarkers selected from the list of biomarkers in Table 2B, wherein N equals 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, or 41.

[0101] In another exemplary embodiment, an expression signature comprises TMEM200A and at least N additional biomarkers selected from the list of biomarkers in Table 2B, wherein N equals 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43 or 44.

[0102] In another exemplary embodiment, an expression signature comprises GJB2 and at least N additional biomarkers selected from the list of biomarkers in Table 2B, wherein N equals 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43 or 44.

[0103] In another exemplary embodiment, an expression signature comprises MMP13 and at least N additional biomarkers selected from the list of biomarkers in Table 2B, wherein N equals 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43 or 44.

[0104] In another exemplary embodiment, an expression signature comprises GFPT2 and at least N additional biomarkers selected from the list of biomarkers in Table 2B, wherein N equals 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43 or 44.

[0105] In another exemplary embodiment, an example expression signature comprises the biomarkers and the corresponding biomarker weighted values listed in Table 2B. In another exemplary embodiment, the expression signature consists of the biomarkers and corresponding biomarker weighted values listed in Table 2B.

[0106] In a further aspect, the methods of the present invention comprise conducting an assay on a biological sample from an individual to determine the expression levels of one or more biomarkers in a biomarker panel, the biomarker panel comprising TMEM200A, GJB2, MMP13 and GFPT2 and at least N additional biomarkers selected from the list of biomarkers in Table 2B, wherein N equals 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40 or 41.

[0107] In a further aspect, the methods of the present invention comprise conducting an assay on a biological sample from an individual to determine the expression levels of one or more biomarkers in a biomarker panel, the biomarker panel comprising TMEM200A and at least N additional biomarkers selected from the list of biomarkers in Table 2B, wherein N equals 1, 2,

3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 29, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43 or 44.

[0108] In a further aspect, the methods of the present invention comprise conducting an assay on a biological sample from an individual to determine the expression levels of one or more biomarkers in a biomarker panel, the biomarker panel comprising GJB2 and at least N additional biomarkers selected from the list of biomarkers in Table 2a, wherein N equals 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 29, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43 or 44.

[0109] In a further aspect, the methods of the present invention comprise conducting an assay on a biological sample from an individual to determine the expression levels of one or more biomarkers in a biomarker panel, the biomarker panel comprising MMP13 and at least N additional biomarkers selected from the list of biomarkers in Table 2B, wherein N equals 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 29, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43 or 44.

[0110] In a further aspect, the methods of the present invention comprise conducting an assay on a biological sample from an individual to determine the expression levels of one or more biomarkers in a biomarker panel, the biomarker panel comprising GFPT2 and at least N additional biomarkers selected from the list of biomarkers in Table 2B, wherein N equals 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 29, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43 or 44.

[0111] In another exemplary embodiment, an expression signature comprises all or a portion of the following biomarkers; IGF2, SOX11, INS, CXCL17, SLC5A1, TMEM45A, CXCR2P1, MFAP2, MATN3, RTP4, COL3A1, CDR1, RARRES3, TNFSF10, NUAKE1, SNORD114-14, SRPX, SPARC, GJB1, TIMP3, ISLR, TUBA1A, DEXI, BASP1, PXDN, GBP4, SLC28A3, HLA-DRA, TAP2, ACSL5, CDH11, PSMB9, MMP14, CD74, LOXL1, CIITA, ZNF697, SH3RF2, MIR198, COL1A2, TNFRSF14, COL8A1, C21orf63, TAP1, PDPN, RHOBTB3, BCL11A, HLA-DOB, XAF1, ARHGAP26, POLD2, DPYSL2, COL4A1, ID3, CFB, NID1, FKBP7, TIMP2, RCBTB1, ANGPTL2, ENTPD7, SHISA4, and HINT1,

[0112] In another exemplary embodiment, an expression signature comprises IGF2, SOX11, INS, and CXCL17 and at least N additional biomarkers selected from the list of biomarkers in Table 2C, wherein N equals 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, or 59.

[0113] In another exemplary embodiment, an expression signature comprises IGF2 and at least N additional biomarkers selected from the list of biomarkers in Table 2C, wherein N equals

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, or 62.

[0114] In another exemplary embodiment, an expression signature comprises SOX11 and at least N additional biomarkers selected from the list of biomarkers in Table 2C, wherein N equals 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, or 62.

[0115] In another exemplary embodiment, an expression signature comprises INS and at least N additional biomarkers selected from the list of biomarkers in Table 2C, wherein N equals 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, or 62.

[0116] In another exemplary embodiment, an expression signature comprises CXCL17 and at least N additional biomarkers selected from the list of biomarkers in Table 2C, wherein N equals 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, or 62.

[0117] In another exemplary embodiment, an example expression signature comprises the biomarkers and corresponding biomarker weighted values listed in Table 2C. In another exemplary embodiment, an example expression signature consists of the biomarkers and corresponding biomarker weighted values listed in Table 2C.

[0118] In a further aspect, the methods of the present invention comprise conducting an assay on a biological sample from an individual to determine the expression levels of one or more biomarkers in a biomarker panel, the biomarker panel comprising all or a portion of the biomarkers listed in Table 2C.

[0119] In a further aspect, the methods of the present invention comprise conducting an assay on a biological sample from an individual to determine the expression levels of one or more biomarkers in a biomarker panel, the biomarker panel comprising IGF2, SOX11, INS, and CXCL17 and at least N additional biomarkers selected from the list of biomarkers in Table 2C, wherein N equals 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, or 59.

[0120] In a further aspect, the methods of the present invention comprise conducting an assay on a biological sample from an individual to determine the expression levels of one or

more biomarkers in a biomarker panel, the biomarker panel comprising IGF2 and at least N additional biomarkers selected from the list of biomarkers in Table 2C, wherein N equals 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, or 62.

[0121] In a further aspect, the methods of the present invention comprise conducting an assay on a biological sample from an individual to determine the expression levels of one or more biomarkers in a biomarker panel, the biomarker panel comprising SOX11 and at least N additional biomarkers selected from the list of biomarkers in Table 2C, wherein N equals 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, or 62.

[0122] In a further aspect, the methods of the present invention comprise conducting an assay on a biological sample from an individual to determine the expression levels of one or more biomarkers in a biomarker panel, the biomarker panel comprising INS and at least N additional biomarkers selected from the list of biomarkers in Table 2C, wherein N equals 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, or 62.

[0123] In a further aspect, the methods of the present invention comprise conducting an assay on a biological sample from an individual to determine the expression levels of one or more biomarkers in a biomarker panel, the biomarker panel comprising CXCL17 and at least N additional biomarkers selected from the list of biomarkers in Table 2C, wherein N equals 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, or 62.

[0124] In one exemplary embodiment, the expression signature comprises all or a portion of the following biomarkers; ALPK2, BGN, COL8A1, FAP, FN1, GJB2, INHBA, ITGA5, LOXL1, LUM, MIR1245, MMP2, NKD2, PLAU, RAB31, SFRP2, THBS2, TIMP3 and VCAN.

[0125] In another exemplary embodiment, the expression signature comprises ALPK2, BGN, COL8A1, FAP and at least N additional biomarkers selected from FN1, GJB2, INHBA, ITGA5, LOXL1, LUM, MIR1245, MMP2, NKD2, PLAU, RAB31, SFRP2, THBS2, TIMP3 and VCAN, wherein N equals 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or 15.

[0126] In a further aspect, the methods of the present invention comprise conducting an assay on a biological sample from an individual to determine the expression levels of one or more biomarkers in a biomarker panel, the biomarker panel comprising ALPK2, BGN, COL8A1 and FAP at least N additional biomarkers selected from FN1, GJB2, INHBA, ITGA5, LOXL1, LUM, MIR1245, MMP2, NKD2, PLAU, RAB31, SFRP2, THBS2, TIMP3 and VCAN, wherein N equals 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or 15.

[0127] In a further aspect, the methods of the present invention comprise conducting an assay on a biological sample from an individual to determine the expression levels of one or more biomarkers in a biomarker panel, the biomarker panel comprising ALPK2 and at least N additional biomarkers selected from the list of biomarkers BGN, COL8A1, FAP, FN1, GJB2, INHBA, ITGA5, LOXL1, LUM, MIR1245, MMP2, NKD2, PLAU, RAB31, SFRP2, THBS2, TIMP3 and VCAN wherein N equals 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or 15.

[0128] In a further aspect, the methods of the present invention comprise conducting an assay on a biological sample from an individual to determine the expression levels of one or more biomarkers in a biomarker panel, the biomarker panel comprising BGN and at least N additional biomarkers selected from the list of biomarkers ALPK2, COL8A1, FAP, FN1, GJB2, INHBA, ITGA5, LOXL1, LUM, MIR1245, MMP2, NKD2, PLAU, RAB31, SFRP2, THBS2, TIMP3 and VCAN, wherein N equals 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or 15.

[0129] In a further aspect, the methods of the present invention comprise conducting an assay on a biological sample from an individual to determine the expression levels of one or more biomarkers in a biomarker panel, the biomarker panel comprising COL8A1 and at least N additional biomarkers selected from the list of biomarkers ALPK2, BGN, , FAP, FN1, GJB2, INHBA, ITGA5, LOXL1, LUM, MIR1245, MMP2, NKD2, PLAU, RAB31, SFRP2, THBS2, TIMP3 and VCAN, wherein N equals 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or 15.

[0130] In a further aspect, the methods of the present invention comprise conducting an assay on a biological sample from an individual to determine the expression levels of one or more biomarkers in a biomarker panel, the biomarker panel comprising FAP and at least N additional biomarkers selected from the list of biomarkers ALPK2, BGN, COL8A1, FN1, GJB2, INHBA, ITGA5, LOXL1, LUM, MIR1245, MMP2, NKD2, PLAU, RAB31, SFRP2, THBS2, TIMP3 and VCAN, wherein N equals 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or 15.

[0131] In another exemplary embodiment, an expression signature comprises all or a portion of the following biomarkers; GJB2, INHBA, THBS2, SFRP2, PLAU and at least N additional biomarkers from Table 1A-1C, wherein N is 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 29, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43

or 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, or 70.

[0132] In another exemplary embodiment, an expression signature comprises all GJB2 and at least N additional biomarkers from Table 1A-1C, wherein N is 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 29, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43 or 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, or 74.

[0133] In another exemplary embodiment, an expression signature comprises all INHBA and at least N additional biomarkers from Table 1A-1C, wherein N is 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 29, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43 or 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, or 74.

[0134] In another exemplary embodiment, an expression signature comprises all THBS2 and at least N additional biomarkers from Table 1A-1C, wherein N is 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 29, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43 or 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, or 74.

[0135] In another exemplary embodiment, an expression signature comprises all SFRP2 wherein N is 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 29, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43 or 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, or 74.

[0136] In another exemplary embodiment, an expression signature comprises all PLAUI and at least N additional biomarkers from Table 1A-1C, wherein N is 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 29, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43 or 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, or 70.

[0137] In another exemplary embodiment, an expression signature comprises all GJB2, INHBA, THBS2, SFRP2, PLAUI and at least about 1%, about 5%, about 10%, about 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, about 90%, about 95%, or about 99% of the biomarkers listed in Table 1A and Table 1B or a combination thereof.

Classifying New Test Samples using an Expression Signature

[0138] To classify new test samples using an expression signature, such as those described above, the relative expression levels of biomarkers in a cancer tissue are measured to form a test sample expression profile. In certain exemplary embodiments, the test sample expression profile is summarized in the form of a compound decision score ("expression score") and

compared to a threshold score that is mathematically derived from a training set of patient data. The score threshold separates a patient group based on different characteristics such as, but not limited to, responsiveness/non-responsiveness to treatment. The patient training set data is preferably derived from cancer tissue samples having been characterized by prognosis, likelihood of recurrence, long term survival, clinical outcome, treatment response, diagnosis, cancer classification, or personalized genomics profile. Expression profiles, and corresponding decision scores from patient samples may be correlated with the characteristics of patient samples in the training set that are on the same side of the mathematically derived score decision threshold. The threshold of the linear classifier scalar output is optimized to maximize the sum of sensitivity and specificity under cross-validation as observed within the training dataset.

[0139] The overall expression data for a given sample is normalized using methods known to those skilled in the art in order to correct for differing amounts of starting material, varying efficiencies of the extraction and amplification reactions, etc.

[0140] In one embodiment, the biomarker expression profile of a patient tissue sample is evaluated by a linear classifier. As used herein, a linear classifier refers to a weighted sum of the individual biomarker intensities into a compound decision score (“decision function”). The decision score is then compared to a pre-defined cut-off score threshold, corresponding to a certain set-point in terms of sensitivity and specificity which indicates if a sample is above the score threshold (decision function positive) or below (decision function negative).

[0141] Using a linear classifier on the normalized data to make a diagnostic or prognostic call (e.g. responsiveness or resistance to therapeutic agent) effectively means to split the data space, i.e. all possible combinations of expression values for all genes in the classifier, into two disjoint halves by means of a separating hyperplane. This split is empirically derived on a large set of training examples, for example from patients showing responsiveness or resistance to a therapeutic agent. Without loss of generality, one can assume a certain fixed set of values for all but one biomarker, which would automatically define a threshold value for this remaining biomarker where the decision would change from, for example, responsiveness or resistance to a therapeutic agent. Expression values above this dynamic threshold would then either indicate resistance (for a biomarker with a negative weight) or responsiveness (for a biomarker with a positive weight) to a therapeutic agent. The precise value of this threshold depends on the actual measured expression profile of all other biomarkers within the classifier, but the general indication of certain biomarkers remains fixed, i.e. high values or “relative over-expression” always contributes to either a responsiveness (genes with a positive weight) or resistance (genes with a negative weights). Therefore, in the context of the overall gene expression classifier,

relative expression can indicate if either up- or down-regulation of a certain biomarker is indicative of responsiveness or resistance to a therapeutic agent.

[0142] There are a number of suitable methods for measuring expression profiles of test samples depending on the type of biomarker to be assayed. Measuring mRNA in a biological sample may be used as a surrogate for detection of the level of the corresponding protein in the biological sample. Thus, any of the biomarkers or biomarker panels described herein can also be detected by detecting the appropriate RNA. Methods of gene expression profiling include, but are not limited to, microarray, RT-PCT, qPCR, NGS, northern blots, SAGE, mass spectrometry.

[0143] mRNA expression levels are measured by reverse transcription quantitative polymerase chain reaction (RT-PCR followed with qPCR). RT-PCR is used to create a cDNA from the mRNA. The cDNA may be used in a qPCR assay to produce fluorescence as the DNA amplification process progresses. By comparison to a standard curve, qPCR can produce an absolute measurement such as number of copies of mRNA per cell. Northern blots, microarrays, Invader assays, and RT-PCR combined with capillary electrophoresis have all been used to measure expression levels of mRNA in a sample. See *Gene Expression Profiling: Methods and Protocols*, Richard A. Shimkets, editor, Humana Press, 2004.

[0144] miRNA molecules are small RNAs that are non-coding but may regulate gene expression. Any of the methods suited to the measurement of mRNA expression levels can also be used for the corresponding miRNA. Recently many laboratories have investigated the use of miRNAs as biomarkers for disease. Many diseases involve widespread transcriptional regulation, and it is not surprising that miRNAs might find a role as biomarkers. The connection between miRNA concentrations and disease is often even less clear than the connections between protein levels and disease, yet the value of miRNA biomarkers might be substantial. Of course, as with any RNA expressed differentially during disease, the problems facing the development of an in vitro diagnostic product will include the requirement that the miRNAs survive in the diseased cell and are easily extracted for analysis, or that the miRNAs are released into blood or other matrices where they must survive long enough to be measured. Protein biomarkers have similar requirements, although many potential protein biomarkers are secreted intentionally at the site of pathology and function, during disease, in a paracrine fashion. Many potential protein biomarkers are designed to function outside the cells within which those proteins are synthesized.

[0145] Gene expression may also be evaluated using mass spectrometry methods. A variety of configurations of mass spectrometers can be used to detect biomarker values. Several types of mass spectrometers are available or can be produced with various configurations. In general, a mass spectrometer has the following major components: a sample inlet, an ion source, a mass

analyzer, a detector, a vacuum system, and instrument-control system, and a data system. Difference in the sample inlet, ion source, and mass analyzer generally define the type of instrument and its capabilities. For example, an inlet can be a capillary-column liquid chromatography source or can be a direct probe or stage such as used in matrix-assisted laser desorption. Common ion sources are, for example, electrospray, including nanospray and microspray or matrix-assisted laser desorption. Common mass analyzers include a quadrupole mass filter, ion trap mass analyzer and time-of-flight mass analyzer. Additional mass spectrometry methods are well known in the art (see Burlingame *et al.*, Anal. Chem. 70:647 R-716R (1998); Kinter and Sherman, New York (2000)).

[0146] Protein biomarkers and biomarker values can be detected and measured by any of the following: electrospray ionization mass spectrometry (ESI-MS), ESI-MS/MS, ESI-MS/(MS)_n, matrix-assisted laser desorption ionization time-of-flight mass spectrometry (MALDI-TOF-MS), surface-enhanced laser desorption/ionization time-of-flight mass spectrometry (SELDI-TOF-MS), desorption/ionization on silicon (DIOS), secondary ion mass spectrometry (SIMS), quadrupole time-of-flight (Q-TOF), tandem time-of-flight (TOF/TOF) technology, called ultraflex III TOF/TOF, atmospheric pressure chemical ionization mass spectrometry (APCI-MS), APCI-MS/MS, APCI-(MS).sup.N, atmospheric pressure photoionization mass spectrometry (APPI-MS), APPI-MS/MS, and APPI-(MS).sup.N, quadrupole mass spectrometry, Fourier transform mass spectrometry (FTMS), quantitative mass spectrometry, and ion trap mass spectrometry.

[0147] Sample preparation strategies are used to label and enrich samples before mass spectroscopic characterization of protein biomarkers and determination biomarker values. Labeling methods include but are not limited to isobaric tag for relative and absolute quantitation (iTRAQ) and stable isotope labeling with amino acids in cell culture (SILAC). Capture reagents used to selectively enrich samples for candidate biomarker proteins prior to mass spectroscopic analysis include but are not limited to aptamers, antibodies, nucleic acid probes, chimeras, small molecules, an F(ab')₂ fragment, a single chain antibody fragment, an Fv fragment, a single chain Fv fragment, a nucleic acid, a lectin, a ligand-binding receptor, affybodies, nanobodies, ankyrins, domain antibodies, alternative antibody scaffolds (e.g. diabodies etc) imprinted polymers, avimers, peptidomimetics, peptoids, peptide nucleic acids, threose nucleic acid, a hormone receptor, a cytokine receptor, and synthetic receptors, and modifications and fragments of these.

[0148] The foregoing assays enable the detection of biomarker values that are useful in methods for predicting responsiveness of a cancer therapeutic agent, where the methods comprise detecting, in a biological sample from an individual, at least N biomarker values that

each correspond to a biomarker selected from the group consisting of the biomarkers provided in Tables 1A, 1B, 2A, 2B or Groups I and II, wherein a classification, as described in detail below, using the biomarker values indicates whether the individual will be responsive to a therapeutic agent. While certain of the described predictive biomarkers are useful alone for predicting responsiveness to a therapeutic agent, methods are also described herein for the grouping of multiple subsets of the biomarkers that are each useful as a panel of two or more biomarkers. Thus, various embodiments of the instant application provide combinations comprising N biomarkers, wherein N is at least three biomarkers. It will be appreciated that N can be selected to be any number from any of the above-described ranges, as well as similar, but higher order, ranges. In accordance with any of the methods described herein, biomarker values can be detected and classified individually or they can be detected and classified collectively, as for example in a multiplex assay format.

b) Microarray methods

[0149] In one embodiment, the present invention makes use of "oligonucleotide arrays" (also called herein "microarrays"). Microarrays can be employed for analyzing the expression of biomarkers in a cell, and especially for measuring the expression of biomarkers of cancer tissues.

[0150] In one embodiment, biomarker arrays are produced by hybridizing detectably labeled polynucleotides representing the mRNA transcripts present in a cell (e.g., fluorescently-labeled cDNA synthesized from total cell mRNA or labeled cRNA) to a microarray. A microarray is a surface with an ordered array of binding (e.g., hybridization) sites for products of many of the genes in the genome of a cell or organism, preferably most or almost all of the genes. Microarrays can be made in a number of ways known in the art. However produced, microarrays share certain characteristics. The arrays are reproducible, allowing multiple copies of a given array to be produced and easily compared with each other. Preferably the microarrays are small, usually smaller than 5 cm², and they are made from materials that are stable under binding (e.g., nucleic acid hybridization) conditions. A given binding site or unique set of binding sites in the microarray will specifically bind the product of a single gene in the cell. In a specific embodiment, positionally addressable arrays containing affixed nucleic acids of known sequence at each location are used.

[0151] It will be appreciated that when cDNA complementary to the RNA of a cell is made and hybridized to a microarray under suitable hybridization conditions, the level of hybridization to the site in the array corresponding to any particular gene will reflect the prevalence in the cell of mRNA transcribed from that gene/biomarker. For example, when detectably labeled (e.g., with a fluorophore) cDNA or cRNA complementary to the total cellular

mRNA is hybridized to a microarray, the site on the array corresponding to a gene (i.e., capable of specifically binding the product of the gene) that is not transcribed in the cell will have little or no signal (e.g., fluorescent signal), and a gene for which the encoded mRNA is prevalent will have a relatively strong signal. Nucleic acid hybridization and wash conditions are chosen so that the probe "specifically binds" or "specifically hybridizes" to a specific array site, i.e., the probe hybridizes, duplexes or binds to a sequence array site with a complementary nucleic acid sequence but does not hybridize to a site with a non-complementary nucleic acid sequence. As used herein, one polynucleotide sequence is considered complementary to another when, if the shorter of the polynucleotides is less than or equal to 25 bases, there are no mismatches using standard base-pairing rules or, if the shorter of the polynucleotides is longer than 25 bases, there is no more than a 5% mismatch. Preferably, the polynucleotides are perfectly complementary (no mismatches). It can be demonstrated that specific hybridization conditions result in specific hybridization by carrying out a hybridization assay including negative controls using routine experimentation.

[0152] Optimal hybridization conditions will depend on the length (e.g., oligomer vs. polynucleotide greater than 200 bases) and type (e.g., RNA, DNA, PNA) of labeled probe and immobilized polynucleotide or oligonucleotide. General parameters for specific (i.e., stringent) hybridization conditions for nucleic acids are described in Sambrook *et al.*, supra, and in Ausubel *et al.*, "Current Protocols in Molecular Biology", Greene Publishing and Wiley-interscience, NY (1987), which is incorporated in its entirety for all purposes. When the cDNA microarrays are used, typical hybridization conditions are hybridization in 5xSSC plus 0.2% SDS at 65°C for 4 hours followed by washes at 25 °C in low stringency wash buffer (1xSSC plus 0.2% SDS) followed by 10 minutes at 25 °C in high stringency wash buffer (0.1SSC plus 0.2% SDS) (see Shena *et al.*, Proc. Natl. Acad. Sci. USA, Vol. 93, p. 10614 (1996)). Useful hybridization conditions are also provided in, e.g., Tijessen, Hybridization With Nucleic Acid Probes", Elsevier Science Publishers B.V. (1993) and Kricka, "Nonisotopic DNA Probe Techniques", Academic Press, San Diego, Calif. (1992).

c) Immunoassay methods

[0153] Immunoassay methods are based on the reaction of an antibody to its corresponding target or analyte and can detect the analyte in a sample depending on the specific assay format. To improve specificity and sensitivity of an assay method based on immunoreactivity, monoclonal antibodies are often used because of their specific epitope recognition. Polyclonal antibodies have also been successfully used in various immunoassays because of their increased affinity for the target as compared to monoclonal antibodies Immunoassays have been designed

for use with a wide range of biological sample matrices Immunoassay formats have been designed to provide qualitative, semi-quantitative, and quantitative results.

[0154] Quantitative results may be generated through the use of a standard curve created with known concentrations of the specific analyte to be detected. The response or signal from an unknown sample is plotted onto the standard curve, and a quantity or value corresponding to the target in the unknown sample is established.

[0155] Numerous immunoassay formats have been designed. ELISA or EIA can be quantitative for the detection of an analyte/biomarker. This method relies on attachment of a label to either the analyte or the antibody and the label component includes, either directly or indirectly, an enzyme. ELISA tests may be formatted for direct, indirect, competitive, or sandwich detection of the analyte. Other methods rely on labels such as, for example, radioisotopes (I^{125}) or fluorescence. Additional techniques include, for example, agglutination, nephelometry, turbidimetry, Western blot, immunoprecipitation, immunocytochemistry, immunohistochemistry, flow cytometry, Luminex assay, and others (see *ImmunoAssay: A Practical Guide*, edited by Brian Law, published by Taylor & Francis, Ltd., 2005 edition).

[0156] Exemplary assay formats include enzyme-linked immunosorbent assay (ELISA), radioimmunoassay, fluorescent, chemiluminescence, and fluorescence resonance energy transfer (FRET) or time resolved-FRET (TR-FRET) immunoassays. Examples of procedures for detecting biomarkers include biomarker immunoprecipitation followed by quantitative methods that allow size and peptide level discrimination, such as gel electrophoresis, capillary electrophoresis, planar electrochromatography, and the like.

[0157] Methods of detecting and/or quantifying a detectable label or signal generating material depend on the nature of the label. The products of reactions catalyzed by appropriate enzymes (where the detectable label is an enzyme; see above) can be, without limitation, fluorescent, luminescent, or radioactive or they may absorb visible or ultraviolet light. Examples of detectors suitable for detecting such detectable labels include, without limitation, x-ray film, radioactivity counters, scintillation counters, spectrophotometers, colorimeters, fluorometers, luminometers, and densitometers.

[0158] Any of the methods for detection can be performed in any format that allows for any suitable preparation, processing, and analysis of the reactions. This can be, for example, in multi-well assay plates (e.g., 96 wells or 384 wells) or using any suitable array or microarray. Stock solutions for various agents can be made manually or robotically, and all subsequent pipetting, diluting, mixing, distribution, washing, incubating, sample readout, data collection and analysis can be done robotically using commercially available analysis software, robotics, and detection instrumentation capable of detecting a detectable label.

Kits

[0159] Reagents, tools, and/or instructions for performing the methods described herein can be provided in a kit. For example, the kit can contain reagents, tools, and instructions for determining an appropriate therapy for a cancer patient. Such a kit can include reagents for collecting a tissue sample from a patient, such as by biopsy, and reagents for processing the tissue. The kit can also include one or more reagents for performing a gene or gene product expression analysis, such as reagents for performing nucleic acid amplification (e.g RT-PCR, qPCR), sequencing (e.g. next generation sequencing), northern blot, proteomic analysis, or immunohistochemistry to determine expression levels of gene or gene product markers in a sample of a patient. For example, primers for performing RT-PCR, probes for performing northern blot analyses, and/or antibodies for performing proteomic analysis such as Western blot, immunohistochemistry and ELISA analyses can be included in such kits. Appropriate buffers for the assays can also be included. Detection reagents required for any of these assays can also be included. The appropriate reagents and methods are described in further detail below. The kits may include suitable primers and/or probes to detect the expression levels of at least one (up to all) of the biomarkers of in Table 2A and/or 2B and/or 2C. Where expression is determined at the protein level the kit may contain binding reagents specific for the proteins of interest. The binding reagents may comprise antibodies to include all fragments and derivatives thereof. In the context of the various embodiments of the present invention the term “antibody” includes all immunoglobulins or immunoglobulin-like molecules with specific binding affinity for the relevant protein (including by way of example and without limitation, IgA, IgD, IgE, IgG and IgM, combinations thereof, and similar molecules produced during an immune response in any vertebrate, for example, in mammals such as humans, goats, rabbits and mice). Specific immunoglobulins useful in the various embodiments of the invention include IgG isotypes. The antibodies useful in the various embodiments of the invention may be monoclonal or polyclonal in origin, but are typically monoclonal antibodies. Antibodies may be human antibodies, non-human antibodies, or humanized versions of non-human antibodies, or chimeric antibodies. Various techniques for antibody humanization are well established and any suitable technique may be employed. The term “antibody” also refers to a polypeptide ligand comprising at least a light chain or heavy chain immunoglobulin variable region which specifically recognizes and binds an epitope of an antigen, and it extends to all antibody derivatives and fragments that retain the ability to specifically bind to the relevant protein. These derivatives and fragments may include Fab fragments, F(ab')₂ fragments, Fv fragments, single chain antibodies, single domain antibodies, Fc fragments etc. The term antibody encompasses antibodies comprised of both heavy and light chains, but also heavy chain (only) antibodies (which may be derived from

various species of cartilaginous fish or camelids). In specific embodiments, the antibodies may be engineered so as to be specific for more than protein, for example bi-specific to permit binding to two different target proteins as identified herein (see Tables 2A, 2B and 2C).

[0160] In some embodiments, the kits may also contain the specific anti-angiogenic therapeutic agent to be administered in the event that the test predicts responsiveness. This agent may be provided in a form, such as a dosage form, that is tailored to the specific treatment. The kit may be provided with suitable instructions for administration according to an appropriate treatment regimen.

[0161] The kits featured herein can also include an instruction sheet describing how to perform the assays for measuring gene or gene product expression. The instruction sheet can also include instructions for how to determine a reference cohort, including how to determine expression levels of gene or gene product markers in the reference cohort and how to assemble the expression data to establish a reference for comparison to a test patient. The instruction sheet can also include instructions for assaying gene or gene product expression in a test patient and for comparing the expression level with the expression in the reference cohort to subsequently determine the appropriate chemotherapy for the test patient. Methods for determining the appropriate chemotherapy are described above and can be described in detail in the instruction sheet.

[0162] Informational material included in the kits can be descriptive, instructional, marketing or other material that relates to the methods described herein and/or the use of the reagents for the methods described herein. For example, the informational material of the kit can contain contact information, e.g., a physical address, email address, website, or telephone number, where a user of the kit can obtain substantive information about performing a gene expression analysis and interpreting the results, particularly as they apply to a human's likelihood of having a positive response to a specific therapeutic agent.

[0163] The kits featured herein can also contain software necessary to infer a patient's likelihood of having a positive response to a specific therapeutic agent from the gene product marker expression.

Therapeutic agents

[0164] As described above, the methods described herein permit the classification of a patient as responsive or non-responsive to a therapeutic agent that targets angiogenic processes and signaling within tumors. Some current such therapeutics used to treat cancer include, but are not limited to, the following agents; VEGF pathway-targeted therapeutic agent, including multi-targeted pathway inhibitors (VEGF/PDGF/FGF/EGFT/FLT-3/c-KIT), Angiopoietin-TIE2 pathway inhibitors, endogenous angiogenic inhibitors, immunomodulatory Agents. VEGF

specific inhibitors include, but are not limited to, Bevacizumab (Avastin), Afibercept (VEGF Trap), IMC-1121B (Ramucirumab). Multi-targeted pathway inhibitors include, but are not limited to, Imatinib (Gleevec), Sorafenib (Nexavar), Gefitinib (Iressa), Sunitinib (Sutent), Erlotinib, Tivozinib, Cediranib (Recentin), Pazopanib (Votrient), BIBF 1120 (Vargatef), Dovitinib, Semaxanib (Sugen), Axitinib (AG013736), Vandetanib (Zactima), Nilotinib (Tasigna), Dasatinib (Sprycel), Vatalanib, Motesanib, ABT-869, TKI-258. Angiopoietin-TIE2 pathway inhibitors include, but are not limited to, AMG-386, PF-4856884 CVX-060, CEP-11981, CE-245677, MEDI-3617, CVX-241, Trastuzumab (Herceptin). Endogenous angiogenic inhibitors include, but are not limited to, Thrombospondin, Endostatin, Tumstatin, Canstatin, Arrestin, Angiostatin, Vasostatin, Interferon alpha. Immunomodulatory Agents include, but are not limited to, Thalidomide and Lenalidomide.

[0165] The invention is further defined with reference to the following numbered clauses:

1. A method of predicting a subject's responsiveness to an anti-angiogenic therapeutic agent comprising:

measuring expression levels of one or more biomarkers in a test sample of diseased tissue obtained from the subject to determine a sample expression score, wherein the biomarkers are defined by an expression signature;

comparing the sample expression score to a threshold expression score; and

classifying the subject as responsive or non-responsive, based on whether the sample expression score is above or below the threshold expression score.

2. The method of clause 1, wherein the diseased tissue is cancer tissue.

3. The method of clause 2, wherein the cancer is ovarian cancer, glioblastoma, lung cancer, colon cancer, prostate cancer, or breast cancer.

4. The method of any one of clauses 1 to 3, wherein the sample expression value is determined by measuring an expression level for each biomarker and multiplying it by a corresponding weight, wherein the weight for each biomarker is determined by the expression signature.

5. The method of clause 4, wherein the expression signature is derived by a method comprising:

isolating total RNA from a sample set of diseased tissue;

hybridizing the isolated total RNA to a microarray to obtain a sample expression data set;

selecting those probes on the microarray with a variability above a defined significance threshold to form a preliminary biomarker set;

generating clusters of biomarkers within the preliminary biomarker set having a similar expression profile using a clustering algorithm;

identifying the biological processes or biological pathways for each cluster of biomarkers;

selecting the cluster corresponding to the biological process or biological pathway of interest; and

defining an expression signature by analysing the expression levels of the biomarkers in the selected cluster in a the sample set of diseased tissue using a supervised or unsupervised training algorithm.

6. The method of clause 5, wherein the microarray is a transcriptome array comprising probe sets that binds to RNA transcripts verified as expressed in a test sample set by isolating and sequencing RNA transcripts from the test sample set and cross-validating the isolated RNA transcript sequences to known RNA transcript sequences, wherein the test sample set comprises the same tissue as the patient test sample

7. The method of clause 6, wherein the probe set comprises probes that bind within 300 nucleotides of the 3' end of each RNA transcript.

8. The method of any one of clauses 5 to 7, wherein RNA transcripts comprising coding and non-coding transcripts that include messenger RNAs (mRNA), alternatively spliced mRNAs, ribosomal RNAs (rRNA), transfer RNAs (tRNA), small nuclear RNAs (snRNA), microRNAs (miRNAs) and antisense RNAs.

9. The method of any one of clauses 5 to 8, wherein the expression signature is defined using a PLS classifier, a SVM classifier, a SDA classifier, or a DSDA classifier.

10. The method of clause 9, wherein the expression signature is defined using a PLS classifier.

11. The method of any one of clauses 1 to 10, wherein the expression signature comprises two or more genes from Table 1A, Table 1B, or Table 2C.
12. The method of any one of clauses 1 to 10, wherein the expression signature comprises two or more genes from Table 2A, 2B, or 2C.
13. The method of any one of clauses 1 to 10, wherein the expression signature comprises ALPK2, BGN, COL8A1, FAP, FN1, GJB2, INHBA, ITGA5, LOXL1, LUM, MIR1245, MMP2, NKD2, PLAU, RAB31, SFRP2, THBS2, TIMP3, VCAN.
14. The method of any one of clauses 1 to 10, wherein the expression signature comprises CCDC80, INHBA, THBS2, SFRP2, and MMP2.
15. The method of any one of clauses 1 to 10, wherein the expression signature comprises TMEM200A, GJB2, MMP13, GFPT2, and POSTN.
16. The method of any one of clauses 1 to 10, wherein the expression signature comprises IGF2, SOX11, INS, CSCL17, and SLC5A1.
17. The method of any one of clauses 1 to 10, wherein the expression signatures comprises the genes listed in Table 2A.
18. The method of any one of clauses 1 to 10, wherein the expression signature comprises the genes listed in Table 2B.
19. The method of any one of clauses 1 to 10, wherein the expression signature comprises the genes listed in Table 2C.
20. The method of any one of clauses 1 to 10,, wherein the expression signature comprises GJB2, INHBA, THBS2, SFRP2, and PLAU.
21. The method of any one of clauses 1 to 20, wherein the anti-angiogenic therapeutic agent is a VEGF-pathway-targeted therapeutic agent, an angiopoietin-TIE2 pathway inhibitor, endogenous angiogenic inhibitors, and immunomodulatory agents.

22. The method of clause 21, wherein the VEGF pathway-targeted therapeutic agents include Bevacizumab (Avastin), Afibercept (VEGF Trap), IMC-1121B (Ramucirumab), Imatinib (Gleevec), Sorafenib (Nexavar), Gefitinib (Iressa), Sunitinib (Sutent), Erlotinib, Tivozinib, Cediranib (Recentin), Pazopanib (Votrient), BIBF 1120 (Vargatef), Dovitinib, Semaxanib (Sugen), Axitinib (AG013736), Vandetanib (Zactima), Nilotinib (Tasigna), Dasatinib (Sprycel), Vatalanib, Motesanib, ABT-869, TKI-258 or a combination thereof.
23. The method of clause 21, wherein the angiopoietin-TIE2 pathway inhibitor includes AMG-386, PF-4856884 CVX-060, CEP-11981, CE-245677, MEDI-3617, CVX-241, Trastuzumab (Herceptin) or a combination thereof.
24. The method of clause 21, wherein the endogenous angiogenic inhibitors include Thombospondin, Endostatin, Tumstatin, Canstatin, Arrestin, Angiostatin, Vasostatin, Interferon alpha or a combination thereof.
25. The method of clause 21, wherein the immunomodulatory agents include thalidomide and lenalidomide or a combination thereof.

26. A method of diagnosing a subject as having a cancer or being susceptible to developing the cancer response to anti-angiogenic therapeutics comprising:

measuring expression levels of biomarkers in a test sample of a diseased tissue obtained from the subject to determine obtain a sample expression score, wherein the biomarkers are defined by an expression signature;

comparing the sample expression value to a threshold score; and

classifying the subject as responsive or non-responsive based on whether the expression score is above or below the threshold score.

27. The method of clause 26, wherein the cancer is ovarian cancer, breast cancer, prostate cancer, lung cancer, colon cancer or a glioblastoma.

28. The method of any one of clauses 26 to 27, wherein the reference expression value is determined by calculating an expression value for each biomarker and multiplying it by a corresponding weight, wherein the weight for each biomarker is determined by the expression signature.

29. The method of clause 26, wherein the expression signature is derived by a method comprising:

isolating total RNA from a sample set of the diseased tissue;

hybridizing the isolated total RNA to a microarray to obtain a set of expression values;

selecting those probes on the microarray with the variability above a defined significance threshold to form a preliminary biomarker set;

generating clusters of biomarkers within the preliminary biomarker set having a similar gene expression profile using a clustering algorithm;

identifying the biological process or biological pathway for each cluster of biomarkers;

selecting the cluster corresponding to the biological processes or biological pathways of interest; and

deriving the expression signature by analysing the expression levels of the biomarkers in the selected cluster in a the sample set of cancer tissue using a supervised or unsupervised training algorithm, wherein the expression value defines a set of biomarkers, corresponding weights for each biomarker and the reference expression value.

30. The method of clause 29, wherein the microarray is a transcriptome array comprising a probe set that binds to RNA transcripts verified as expressed in a sample set of cancer tissue by isolating and sequencing RNA transcripts from the cancer tissue and cross-validating the isolated RNA transcript sequences to known RNA transcript sequences.
31. The method of clause 30, wherein the probe set comprises probes that bind within 300 nucleotides of the 3' end of each RNA transcript.
32. The method of any one of clauses 29 to 31, wherein RNA transcripts comprising coding and non-coding transcripts that include messenger RNAs (mRNA), alternatively spliced mRNAs, ribosomal RNAs (rRNA), transfer RNAs (tRNA), small nuclear RNAs (snRNA), microRNAs (miRNAs) and antisense RNA.
33. The method of any one of clauses 27 to 32, wherein the expression signature is defined using a PLS classifier, a SVM classifier, a SDA classifier, or a DSDA classifier.
34. The method of clause 33, wherein the expression signature is defined using a PLS classifier.
35. The method of any one of clauses 26 to 34, wherein the expression signature comprises two or more genes from Table 1A, Table 1B, or Table 1C.
36. The method of any one of clauses 26 to 34, wherein the expression signature comprises two or more genes from Table 2A, Table 2B, or Table 2C.
37. The method of any one of clauses 26 to 34, wherein the expression signature comprises ALPK2, BGN, COL8A1, FAP, FN1, GJB2, INHBA, ITGA5, LOXL1, LUM, MIR1245, MMP2, NKD2, PLAU, RAB31, SFRP2, THBS2, TIMP3, VCAN.
38. The method of any one of clauses 26 to 34, wherein the expression signature comprises CCDC80, INHBA, THBS2, SFRP2, MMP2.
39. The method of any one of clauses 26 to 34, wherein the expression signature comprises TMEM200A, GJB2, MMP13, GFPT2, and POSTN.

40. The method of any one of clauses 26 to 34, wherein the expression signature comprises IGF2, SOX11, INS, CSCL17, and SLC5A1.
41. The method of any one of clauses 26 to 34, wherein the expression signature comprises the genes listed in Table 2A.
42. The method of any one of clauses 26 to 34, wherein the expression signature comprises the genes listed in Table 2B.
43. The method of any one of clauses 26 to 34, wherein the expression signature comprises the genes listed in Table 2C.
44. The method of any one of clauses 26 to 34, wherein the expression signature comprises GJB2, INHBA, THBS2, SFRP2, and PLAU.
45. The method of any one of clauses 26 to 44, wherein the anti-angiogenic agent is a VEGF-pathway-targeted therapeutic agent, an angiopoietin-TIE2 pathway inhibitor, endogenous angiogenic inhibitors, and immunomodulatory agents.
46. The method of clause 45, wherein the VEGF pathway-targeted therapeutic agents include Bevacizumab (Avastin), Afibercept (VEGF Trap), IMC-1121B (Ramucirumab), Imatinib (Gleevec), Sorafenib (Nexavar), Gefitinib (Iressa), Sunitinib (Sutent), Erlotinib, Tivozinib, Cediranib (Recentin), Pazopanib (Votrient), BIBF 1120 (Vargatef), Dovitinib, Semaxanib (Sugen), Axitinib (AG013736), Vandetanib (Zactima), Nilotinib (Tasigna), Dasatinib (Sprycel), Vatalanib, Motesanib, ABT-869, and TKI-258.
47. The method of clause 45, wherein the angiopoietin-TIE2 pathway inhibitor includes AMG-386, PF-4856884, CVX-060, CEP-11981, CE-245677, MEDI-3617, CVX-241, Trastuzumab (Herceptin).
48. The method of clause 45, wherein the endogenous angiogenic inhibitors include Thrombospondin, Endostatin, Tumorstatin, Canstatin, Arrestin, Angiostatin, Vasostatin, Interferon alpha.

49. The method of clause 45, wherein the immunomodulatory agents include thalidomide and lenalidomide.
50. A method of determining a prognosis of a subject with cancer comprising:
measuring expression levels of one or more biomarkers in a test sample of diseased tissue obtained from the subject to determine a sample expression score, wherein the biomarkers are defined by an expression signature;
comparing the sample expression score to a threshold expression score; and
classifying the subject as responsive or non-responsive, based on whether the sample expression score is above or below the threshold expression score.
47. The method of clause 46, wherein the diseased tissue is cancer tissue.
48. The method of clause 47, wherein the cancer is ovarian cancer, lung cancer, colon cancer, prostate cancer, glioblastoma, or breast cancer.
49. The method of any one clauses 46 to 48, wherein the sample expression value is determined by measuring an expression level for each biomarker and multiplying it by a corresponding weight, wherein each weight for each biomarker is determined by the expression signature.
50. The method of clause 49, wherein the expression signature is derived by a method comprising:
isolating total RNA from a sample set of diseased tissue;
hybridizing the isolated total RNA to a microarray to obtain a sample expression data set;
selecting those probes on the microarray with a variability above a defined significance threshold to form a preliminary biomarker set;
generating clusters of biomarkers within the preliminary biomarker set having a similar expression profile using a clustering algorithm;
identifying the biological processes or biological pathways for each cluster of biomarkers;
selecting the cluster corresponding to the biological process or biological pathway of interest; and

defining an expression signature by analysing the expression levels of the biomarkers in the selected cluster in a the sample set of diseased tissue using a supervised or unsupervised training algorithm.

51. The method of clause 50, wherein the microarray is a transcriptome array comprising probe sets that binds to RNA transcripts verified as expressed in a test sample set by isolating and sequencing RNA transcripts from the test sample set and cross-validating the isolated RNA transcript sequences to known RNA transcript sequences, wherein the test sample set comprises the same tissue as the patient test sample

52. The method of clause 51, wherein the probe set comprises probes that bind within 300 nucleotides of the 3' end of each RNA transcript.

53. The method of any one of clauses 50 to 57, wherein RNA transcripts comprising coding and non-coding transcripts that include messenger RNAs (mRNA), alternatively spliced mRNAs, ribosomal RNAs (rRNA), transfer RNAs (tRNA), small nuclear RNAs (snRNA), microRNAs (miRNAs) and antisense RNAs.

54. The method of any one of clauses 50 to 53, wherein the expression signature is defined using a PLS classifier, a SVM classifier, a SDA classifier, or a DSDA classifier.

55. The method of clause 46 to 54, wherein the expression signature is defined using a PLS classifier.

56. The method of any one of clauses 46 to 55, wherein the expression signature comprises two or more genes from Table 1A, Table 1B, or Table 1C.

57. The method of any one of clauses 46 to 55, wherein the expression signature comprises two or more genes from Table 2A, 2B, or 2C.

58. The method of any one of clauses 46 to 55, wherein the expression signature comprises ALPK2, BGN, COL8A1, FAP, FN1, GJB2, INHBA, ITGA5, LOXL1, LUM, MIR1245, MMP2, NKD2, PLAU, RAB31, SFRP2, THBS2, TIMP3, VCAN.

59. The method of any one of clauses 46 to 55, wherein the expression signature comprises CCDC80, INHBA, THBS2, SFRP2, and MMP2.
60. The method of any one of clauses 46 to 55, wherein the expression signature comprises TMEM200A, GJB2, MMP13, GFPT2, and POSTN.
61. The method of any one of clauses 46 to 55, wherein the expression signature comprises IGF2, SOX11, INS, CSCL17, and SLC5A1.
62. The method of any one of clauses 46 to 55, wherein the expression signatures comprises the genes listed in Table 2A.
63. The method of any one of clauses 46 to 55, wherein the expression signature comprises the genes listed in Table 2B.
64. The method of any one of clauses 46 to 55, wherein the expression signature comprises the genes listed in Table 2C.
65. The method of any one of clauses 46 to 55, wherein the expression signature comprises GJB2, INHBA, THBS2, SFRP2, and PLAU.
66. A method for determining a course of treatment for a subject with cancer comprising:
measuring expression levels of one or more biomarkers in a test sample of diseased tissue obtained from the subject to determine a sample expression score using a non-angiogenesis expression signature, wherein the biomarkers are defined by the expression signature
determining a prognosis for the subject by comparing the sample expression score from the non-angiogenesis signature to a threshold score, wherein a sample expression score greater than the threshold score indicates a good prognosis and a sample expression score below the the threshold scored indicates a poor prognosis;
measuring expression levels of one or more biomarkers in a test sample of diseased tissue obtained from the subject to determine a sample expression score using an angiogenesis expression signature, wherein the biomarkers are defined by the angiogenesis expression signature;

determining the subject's responsiveness to a therapeutic agent by comparing the sample expression score to a threshold score, wherein a sample expression score greater than the threshold value indicates responsiveness to the therapeutic agent and a sample expression score less than the threshold value indicates non-responsiveness to the therapeutic agent.

67. The method of clause 66, wherein the non-angiogenesis signature comprises two or more biomarkers listed in Table 2C

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68. The method of clause 66, wherein the non-angiogenesis signature consists of the biomarkers listed in Table 2C.

69. The method of clause 66, wherein the angiogenesis signature comprises two or more biomarkers listed in Table 2A, Table 2B, or a combination thereof.

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71. The method of clause 66, wherein the angiogenesis signature consists of the biomarkers listed in Table 1A.

72. The method of clause 66, wherein the angiogenesis signature consists of the biomarkers listed in Table 1B.

73. The method of clause 66, wherein the cancer is ovarian cancer, breast cancer, colon cancer, prostate cancer, lung cancer, or glioblastoma.

74. The method of clause 66, wherein the therapeutic agent is an anti-angiogenic therapeutic agent.

75. The method of clause 74, wherein the anti-angiogenic therapeutic agent is a VEGF-pathway-targeted therapeutic agent, an angiopoietin-TIE2 pathway inhibitor, endogenous angiogenic inhibitors, and immunomodulatory agents.

76. The method of clause 75, wherein the VEGF pathway-targeted therapeutic agents include Bevacizumab (Avastin), Afibercept (VEGF Trap), IMC-1121B (Ramucirumab), Imatinib (Gleevec), Sorafenib (Nexavar), Gefitinib (Iressa), Sunitinib (Sutent), Erlotinib, Tivozinib, Cediranib (Recentin), Pazopanib (Votrient), BIBF 1120 (Vargatef), Dovitinib,

Semaxanib (Sugen), Axitinib (AG013736), Vandetanib (Zactima), Nilotinib (Tasigna), Dasatinib (Sprycel), Vatalanib, Motesanib, ABT-869, TKI-258 or a combination thereof.

77. The method of clause 75, wherein the angiopoietin-TIE2 pathway inhibitor includes AMG-386, PF-4856884 CVX-060, CEP-11981, CE-245677, MEDI-3617, CVX-241, Trastuzumab (Herceptin) or a combination thereof.

78. The method of clause 75, wherein the endogenous angiogenic inhibitors include Thrombospondin, Endostatin, Tumstatin, Canstatin, Arrestin, Angiostatin, Vasostatin, Interferon alpha or a combination thereof.

79. The method of clause 75, wherein the immunomodulatory agents include thalidomide and lenalidomide or a combination thereof.

[0166] For the avoidance of doubt, the scope of the invention is defined by the appended claims.

[0167] This invention is further illustrated by the following examples, which are not to be construed in any way as imposing limitations upon the scope thereof. On the contrary, it is to be clearly understood that resort may be had to various other embodiments, modifications, and equivalents thereof which, after reading the description herein, may suggest themselves to those skilled in the art without departing from the spirit of the present invention and/or scope of the appended claims.

EXAMPLES

Example 1: Tissue processing, hierarchical clustering, subtype identification and classifier development

Tumor Material.

[0168] Exemplary expression signatures were identified from gene expression analysis of a cohort of macrodissected epithelial serous ovarian tumor FFPE tissue samples sourced from the NHS Lothian and University of Edinburgh.

[0169] The protocol for histological classification of epithelial ovarian cancer to define serous, endometrioid, clear cell and mucinous histologies has recently been updated. One of the consequences of this is that many tumors that would previously been classified as endometrioid are now being classified as serous. (McCluggage, W.G. "Morphological subtypes of ovarian carcinoma: a review with emphasis on new developments and pathogenesis," PATHOLOGY 2011 Aug;43(5):420-32). Serous samples that were used in this study were among a larger set of epithelial ovarian cancer samples of all histologies that were harvested between 1984 and 2006.

Pathology to assign histology status was performed by the pathologists at each of the centers at the time of harvesting. During March and April 2012, 357 of these epithelial ovarian samples were reviewed for histology classification by two independent consultant ovarian cancer pathologists according to the revised protocol. This resulted in a reclassification of several of these samples as indicated Table 3.

Table 3: results of pathology review of 357 epithelial ovarian cancer samples.

(Original histological status is presented in rows, and updated histological status is presented in columns)

Original/Updated	CLEAR CELL	ENDOMETRIOID	MUCINOUS	SEROUS	TOTAL
CLEAR CELL	19	1	0	5	25
ENDOMETRIOID	2	33	0	38	73
MUCINOUS	0	1	8	1	10
OTHER MIXED	3	5	0	8	16
SEROUS	1	3	1	193	198
SEROUS/ENDO	0	2	0	25	27
UNCLASSIFIED	0	0	0	4	4
UNDIFFERENTIATED	1	0	0	3	4
TOTAL	26	45	9	277	357

The original three serous subtypes identified below, and consequently a 25 gene signature (Table 2A) described in the example below (Figure1) were identified from 199 samples that were classified as serous according to the original pathologist reports. Bioinformatic analysis was similarly performed on the 277 samples classified as stage III and IV high grade serous ovarian cancer using the updated pathology classification method. This analysis identified the updated serous subgroups detailed in Figure 6 and consequently used to define a 45 gene “angiogenesis” signature (Table 2B) and a 63 gene “non-angiogenesis” signature (Table 2C)

Gene Expression Profiling from FFPE

[0170] Total RNA was extracted from macrodissected FFPE tissue using the High Pure RNA Paraffin Kit (Roche Diagnostics GmbH, Mannheim, Germany). RNA was converted into

complementary deoxyribonucleic acid (cDNA), which was subsequently amplified and converted into single-stranded form using the SPIA® technology of the WT-Ovation™ FFPE RNA Amplification System V2 (NuGEN Technologies Inc., San Carlos, CA, USA). The amplified single-stranded cDNA was then fragmented and biotin labeled using the FL-Ovation™ cDNA Biotin Module V2 (NuGEN Technologies Inc.). The fragmented and labeled cDNA was then hybridized to the Almac Ovarian Cancer DSA™. Almac's Ovarian Cancer DSA™ research tool has been optimised for analysis of FFPE tissue samples, enabling the use of valuable archived tissue banks. The Almac Ovarian Cancer DSA™ research tool is an innovative microarray platform that represents the transcriptome in both normal and cancerous ovarian tissues. Consequently, the Ovarian Cancer DSA™ provides a comprehensive representation of the transcriptome within the ovarian disease and tissue setting, not available using generic microarray platforms. Arrays were scanned using the Affymetrix Genechip® Scanner 7G (Affymetrix Inc., Santa Clara, CA).

Data preparation

[0171] Quality Control (QC) of profiled samples was carried out using MAS5 pre-processing algorithm. Different technical aspects were addressed: average noise and background homogeneity, percentage of present call (array quality), signal quality, RNA quality and hybridization quality. Distributions and Median Absolute Deviation of corresponding parameters were analyzed and used to identify possible outliers.

[0172] Almac's Ovarian Cancer DSA™ contains probes that primarily target the area within 300 nucleotides from the 3' end. Therefore standard Affymetrix RNA quality measures were adapted – for housekeeping genes intensities of 3' end probe sets with ratios of 3' end probe set intensity to the average background intensity were used in addition to usual 3'/5' ratios. Hybridization controls were checked to ensure that their intensities and present calls conform to the requirements specified by Affymetrix.

[0173] Pre-processing of the raw data generated from expression profiling of the epithelial serous ovarian cancer training set was performed in Expression Console v1.1 with Robust Multi-array Analysis (RMA).

Hierarchical Clustering and Functional Analysis

a. Hierarchical clustering analysis

[0174] Hierarchical clustering techniques were applied to microarray data from the epithelial serous ovarian tumors analysed using the Ovarian Cancer DSA™ (disease specific array) platform. Raw expression data was preprocessed using the standard Robust Multichip Algorithm (RMA) procedure. Non-biological systematic variance in the data set was identified and

removed. Those probe sets whose expression levels varied significantly from tumor to tumor were identified. These probe sets formed the intrinsic list.

[0175] Two dimensional cluster analysis (tumor, probe set) was performed to establish tumor relationships based on the intrinsic list. Hierarchical agglomerative clustering was applied (Pearson correlation – Original analysis – or Euclidean distance – updated analysis – and Ward’s linkage). Optimal partition number was selected using the GAP index (Tibshirani *et al.*, 2002, J. R. Stat. Soc., 63:411-423). All probe sets available in the cluster subgroups were mapped to genes names.

b. Functional analysis of gene clusters

[0176] To establish the functional significance of the probe set clusters, probe sets were mapped to genes (Entrez gene ID) and an enrichment analysis was performed. Enrichment significance was calculated based on the hypergeometric function (False Discovery Rate applied (Benjamini and Hochberg, 1995, J. R. Stat. Soc. 57:289:300)). Over-representation of biological processes and pathways were analysed for each gene group generated by the hierarchical clustering for the epithelial serous ovarian cancer samples using Almac Diagnostics’ proprietary Functional Enrichment Tool (FET). Antisense probe sets were excluded from the analysis. Hypergeometric p-values were assessed for each enriched functional entity class. Functional entity classes with the highest p-values were selected as representative of the group and a general functional category representing these functional entities was assigned to the gene clusters based on significance of representation (i.e. p-value).

[0177] To generate an angiogenesis classifier using the original 199 epithelial serous ovarian tumors, genes in clusters enriched for angiogenesis, vasculature development and immune response general functional terms were grouped into a putative angiogenesis gene group and used for the signature generation. The sample clusters presenting high expression for the genes involved in angiogenesis, vasculature development and immune response general functional terms were selected for classification and labeled as ‘angiogenesis’. Those not showing high expression for the genes involved in these functional terms were labeled as ‘non-angiogenesis’.

[0178] To generate an angiogenesis classifier using the reclassified 265 epithelial serous ovarian tumors, genes in clusters enriched for angiogenesis and vasculature development general functional terms were grouped into a putative angiogenesis gene group and used for the signature generation. The sample clusters presenting high expression for the genes involved in angiogenesis and vasculature development general functional terms were selected for classification and labeled as ‘angiogenesis’. Those not showing high expression for the genes involved in these functional terms were labeled as ‘others ‘others’ (Figure 6 top label identifying “angiogenesis” samples (red) plus “others” (grey)).

[0179] To generate a “non-angiogenesis classifier” using the reclassified 265 epithelial serous ovarian tumors the sample clusters presenting low expression for the genes involved in angiogenesis and vasculature development general functional terms were selected for classification and labeled as “non-angiogenesis.” Those not showing low expression for the genes involved in these functional terms were labeled as ‘others’ (Figure 6 bottom label identifying “non-angiogenesis” samples plus “others”).

Classifier development at a gene level

[0180] To facilitate validation of the classifier across multiple array platforms, the angiogenesis classifier was generated at the gene level. The following steps outline the procedures that were taken for gene level signature development (each step performed over internal cross validation using 10 repeats of 5-fold cross-validation):

Gene level signature development

- Pre-processing:
 - RMA background correction.
 - Reference set of genes are those genes (sense probe sets only) unique to the ovarian DSA platform.
 - Gene level summarization was performed in two steps; first probes to probe set summarization was performed by calculating the median expression of the probes in a probe set; secondly, median expression of the (sense only) probe sets mapping to each gene in the reference distribution is calculated, yielding a “gene level” expression matrix.
 - Quantile normalization was performed on the full gene expression data matrix and a reference quantile derived from the training data was used to normalize the test samples within each round of cross validation.
- Feature selection: Filtering 75% of genes by variance, intensity and correlation to cDNA concentration, followed by either recursive feature elimination (RFE) or filter feature selection (FFS) based on CAT scores.
- Classification algorithms: Partial Least Squares (PLS), SDA (Shrinkage Discriminate Analysis) and DSDA (Diagonal SDA).

Model selection

[0181] The criteria used for model selection were AUC and/or hazard ratio (HR) over internal cross-validation and feature elimination. Functional enrichment of the signatures over cross validation using FET based on the gene ontologies, interim validation sets which included two sets of technical replicates for which standard deviation in signature scores for repeated

samples was evaluated over cross-validation and feature elimination and an assessment of the independence to clinical and technical factors over cross validation (factors listed in Table 4).

[0182] It should be noted, since the subgroup (i.e. class label) derivation was performed using microarray expression from the same sample cohort that was used for signature development, there was an expected positive bias in any performance estimates based on AUC. This highlights the importance of widening the criteria used for model selection, by including additional metrics such as the hazard ratio, functional enrichment and assessing the independence to clinical and technical factors.

Table 4 List of clinical and technical factors investigated

Clinical factors:	Technical factors:	Sample processing factors:
Debulking	Hospital	Post Amp operator
	Block age	
	RNA concentration	
	cDNA yield	

Calculating classifier scores for validation data sets

[0183] All datasets were background corrected using RMA. For each validation set, the probe sets that map to the classifier genes were determined, excluding anti-sense probe sets (if applicable). Annotation for Affymetrix Plus 2.0 and U133A arrays are available from the Affymetrix website. The median intensity over all probes mapping to each gene in the classifier was calculated and the quantile normalization model from the training set was applied to normalize the testing samples one at a time, resulting in a gene intensity matrix. The classifier was then applied to this data matrix to produce a classifier score/prediction for each sample.

Univariate and Multivariate analysis

[0184] Univariate and multivariate analysis may be carried out in relation to the glioblastoma dataset to assess respectively the association between the angiogenesis subtype classifier and survival, and to determine if the association, if any, was independent to known clinical predictors. The p-values for univariate analysis were calculated using logistic regression in MATLAB. For the multivariate analysis we used a likelihood ratio test from logistic regression was used, where the p-values represent the drop in the log-likelihood when comparing the model with the clinical covariates and the predictions to a reduced model with clinical covariates only. The likelihood ratio test measures the importance of the gene predictor in modeling survival, and highlights its independence as a predictor relative to the clinical predictors. In both univariate and multivariate analysis, a p-value < 0.05 was used as the

criterion for significance. Furthermore, samples with unknown clinical factors were excluded in this assessment.

Results

Identification of subgroups and generation of signature from original and updated histology classification

Hierarchical Clustering Analysis

[0185] Feature selection resulted in the selection of 1200 probe sets from the original epithelial serous ovarian cancer data set (199 samples) and 1400 PS from the reclassified epithelial serous ovarian cancer data set (265 samples). The GAP analysis revealed three sample clusters and three probe set cluster groups within both sample sets (Figure 1, Figure 6).

Classification of tumors into ‘angiogenesis’ or ‘non-angiogenesis’ sample groups

[0186] The classification of samples as ‘angiogenesis’ or ‘non-angiogenesis’ was based upon the results of the functional analysis of the epithelial serous ovarian cancer dataset (Figure 1 Figure 6). The objective of this study was to characterize at a transcriptomic level a set of genes that would be capable of determining responsiveness or resistance of a pathogenic cell to anti-angiogenic agents and potentially identify patients who could benefit from anti-angiogenic therapy. With this in mind, those samples within the epithelial serous ovarian cancer datasets that best represented this biology were to be selected and compared to the remaining samples for classifier generation (see next section). It was decided that the samples from the sample angiogenesis cluster within the original epithelial serous ovarian cancer sample set (199 samples) (Figure 1) were the most relevant samples for this selection as these samples demonstrated an up-regulation of genes involved in signaling related to angiogenic and immune response processes and pathways as defined by functional analysis (Figure 2A and 2B). It was decided that the samples from sample cluster three within the reclassified epithelial serous ovarian cancer sample set (265 samples) (Figure 6) were the most relevant samples for this selection as these samples demonstrated an up-regulation of genes involved in signaling related to angiogenic processes and pathways as defined by functional analysis (Figure 2A and 2B).

[0187] It was decided that the samples from sample cluster 1 within the reclassified epithelial serous ovarian cancer sample set (265 samples) (Figure 6) were the most relevant samples for selection to represent the “non-angiogenic” subgroup as these samples demonstrated a down-regulation of genes involved in signaling related to angiogenic processes and pathways as defined by functional analysis (Figure 2A and 2B).

[0188] An identical hierarchical clustering approach was applied to 105 breast cancer samples. The dominant biology in Breast cancer is ER status and therefore in order to identify the structure in the biology of the samples this cohort was divided into 2 populations for cluster

analysis. We identified angiogenesis and vasculature development subtypes (Figure 11A and 11B) demonstrating the expositing of an angiogenesis subtype from breast cancer samples.

Development and validation of the angiogenesis subtype classifier models

[0189] For ease of reference, the following steps are detailed in reference to expression signatures derived from Table 1A or Table 1B. Following the identification of a class of tumors, that form the putative ‘angiogenesis’ subgroup, computational classification of these tumors versus all others in the tumor cohort with reference to the functional ‘angiogenesis’ (angiogenesis, vasculature development, immune response) gene list (Table 1A or Table 1B) was performed to identify a refined gene classification model, which classifies the ‘angiogenesis’ subtype.

[0190] The classification pipeline was used to derive a model using the set of epithelial serous ovarian cancer samples. The classification pipeline has been developed in accordance with commonly accepted good practice (MAQC Consortium, *Nat Biotechnol* 2010). The process will, in parallel: 1) derive gene classification models from empirical data; and 2) assess the classification performance of the models, both under cross-validation. The performance and success of the classifier generation depends on a number of parameters that can be varied, for instance the choice of classification method or probe set filtering. Taking this into account, two feature sets were evaluated (i) the full feature list with 75% variance/intensity filtering (with forced inclusion of the angiogenesis gene list, Table 1A) and (ii) the angiogenesis gene list only; and three classification algorithms were evaluated, namely PLS; SDA and DSDA. Two feature elimination methods were adopted: (i) Recursive Feature Elimination (RFE) which is an iterative procedure removing a fraction of the lowest-ranked features at each iteration; stopping when only a minimum number of features remain; (ii) Filter Feature Selection (FFS) which pre-ranks the features based on correlation adjusted t-scores (CAT-scores) (ref) and removes the lowest ranking features at each round of feature elimination. The Area Under the Receiver Operator Characteristic Curve (AUC) was used to assess the classification performance, as this measure is independent of cut-off between groups and prevalence rates in the data. It is also one of the recognized measurements of choice for classification performance. As such, the best number of features for each model was chosen based on the average AUC under cross-validation.

[0191] From the analysis described above, the PLS FFS model was deemed to be the most suitable classifier model. Weights were calculated for each gene using PLS regression, resulting in the final gene classifier models (25-gene classifier model for the original approach, and a 45-gene classifier for samples reclassified reflecting recent changes to standard histology protocols) that may be used for validation on external data sets from different array platforms. The gene

signature development process was focused upon identification of the ontological processes and pathways relevant to angiogenesis to ensure biological relevance of any signature developed. As such, functional analysis was performed upon both signatures to qualify their relevance to angiogenesis and related processes. The significance processes in FIGURE 3 and FIGURE 8 are related to angiogenesis and vasculature development.

Example 2: *In silico* validation of the angiogenesis subtype and angiogenesis classifier models

[0192] The performance of both the 25-gene (original approach) and 45-gene (reclassification approach) angiogenesis classifier models were validated by the Area Under the ROC (Receiver Operator Characteristic) Curve (AUC) within the original Almac epithelial serous ovarian cancer dataset and two independent datasets. The AUC is a statistic calculated on the observed disease scale and is a measure of the efficacy of prediction of a phenotype using a classifier model (Wray *et al.*, PLoS Genetics Vol 6, 1-9). An AUC of 0.5 is typical of a random classifier, and an AUC of 1.0 would represent perfect separation of classes. Therefore, in order to determine if the angiogenesis subtype classifier model is capable of predicting response to, and selecting patients for anti-angiogenic ovarian cancer therapeutic drug classes either as single agent or in combination with standard of care therapies, the hypothesis is that the AUCs following application within these datasets should be above 0.5 with the lowest confidence interval also above 0.5.

Application of the classifier models to an independent prostate cancer cell-line dataset

[0193] To assess the predictive power of the 25-gene and 45-gene classifier models, they were applied to a dataset of 16 prostate cell-lines following treatment with Dasatanib. The cell-lines were defined as being either a 'responder' or 'non-responder' based upon cell-proliferation assays. This analysis revealed that the 25-gene classifier model is associated with response to Dasatanib, with an AUC of 0.8364 (CI = 0.5255 – 1.0000), indicating that the 25-gene classifier is predictive of response to Dasatanib. The analysis revealed that the 45-gene classifier model is associated with response to the same compound, with an AUC of 0.9455 (CI = 0.7949 – 1.0000) indicating that the 45-gene classifier is also predictive of response to Dasatanib.

Example 3: Identification of and *in silico* validation of a “non-angiogenic subgroup of ovarian cancer

Classification of tumors into ‘non -angiogenesis’ sample groups

[0194] The expression of angiogenesis genes in probe set cluster 2 is down regulated in all samples in sample Cluster 1 of hierarchical clustering of 265 samples newly classified as serous (Figure 6 bottom labelled Blue bar)). These samples in sample cluster 2 have a better prognosis than the rest of the serous samples in samples from cluster 1 and 3 combined together as

demonstrated in Figure 10. This indicated that this group is defined by down regulation of expression of the angiogenesis genes identified in Table 1B. Patients with downregulation of genes involved in angiogenesis and therefore this subgroup is termed a “non-angiogenesis” group. This phenotype has also been identified in ER+ and ER- breast cancer as can be see the middle sample group in Figure 11A and the second sample group in Figure 11B.

Development and validation of the non-angiogenesis subtype classifier models

[0195] Following the identification of a class of tumors, within the 265 samples newly classified as serous, that form the putative ‘non-angiogenesis’ subgroup, computational classification of these tumors versus all others in the tumor cohort with reference to the functional ‘angiogenesis’ (angiogenesis, vasculature development, immune response) gene list (Table 1A or Table 1B) was performed to identify a refined gene classification model, which classifies the ‘non-angiogenesis’ subtype.

[0196] The classification pipeline was used to derive a model using the set of epithelial serous ovarian cancer samples. The methods are analogous to those described above in Example 1.

[0197] Applying the analysis described in Example 1, the PLS FFS model was deemed to be the most suitable classifier model. Weights were calculated for each gene using PLS regression, resulting in the final gene classifier model (63-gene classifier model) that may be used for validation on external data sets from different array platforms.

Application of non-angiogenesis classifier model to the discovery data and an independent microarray dataset

[0198] The performance of the 63-gene non-angiogenesis classifier model was validated using hazard ratio (HR) within the original Almac epithelial serous ovarian cancer dataset and one independent dataset. The hazard ratio is the ratio of the hazard rates corresponding to the conditions described by two sets of explanatory variables. For example, a treated population may die at twice the rate per unit time as the control population. The hazard ratio would be 2, indicating higher hazard of death from the treatment. Therefore, in order to determine if the non-angiogenesis subtype classifier model is capable of predicting non-response to, and selecting patients that should not be treated with anti-angiogenic cancer therapeutic drug classes, either as single agent or in combination with standard of care therapies, it is expected that the HRs should be below 1.0 with a p-value less than 0.05.

[0199] To assess the prognostic power of the 63-gene classifier models, it was applied first to the discovery data of 265 epithelial serous ovarian samples and then to a dataset of 275 epithelial serous and endometrioid ovarian samples (14). Within both datasets the samples were taken at the time of initial surgical resection from patients without prior therapy.

[0200] This analysis revealed that the 63-gene classifier model was independently associated with prognosis in both ovarian cancer datasets. In the discovery set the non-angiogenesis group was associated with significantly better survival compared to the other samples (FIGURE 12); Hazard Ratio = 0.4842, $p = 1.307 \times 10^{-5}$). Similarly in the independent microarray dataset the non-angiogenesis group demonstrated significantly better survival compared to the other samples (FIGURE 13) Hazard Ratio = 0.62 [0.41-0.95], $p = 0.029$ and OS (multivariable analysis; HR=0.32 [0.19-0.54], $p=0.00001$). This validates the fact that the 63-gene classifier is an independent prognostic biomarker of survival in ovarian serous and endometrioid cancer samples.

[0201] The International Collaboration on Ovarian Neoplasms 7 (ICON7) trial is a Gynecologic Cancer Intergroup phase 3 trial that assessed the effects of adding bevacizumab, concurrently and as a continuation, to standard chemotherapy with carboplatin and paclitaxel in patients with primary peritoneal carcinoma, fallopian tube carcinoma, and epithelial ovarian carcinoma (Perren TJ, Swart AM, Pfisterer J, Ledermann JA, Pujade-Lauraine E, Kristensen G, et al. A phase 3 trial of bevacizumab in ovarian cancer. *N Engl J Med.* 365(26): 2484-96, Aghajanian C, Blank SV, Goff BA, Judson PL, Teneriello MG, Husain A, et al. OCEANS: A randomized, double-blind, placebo-controlled phase III trial of chemotherapy with or without bevacizumab in patients with platinum-sensitive recurrent epithelial ovarian, primary peritoneal, or fallopian tube cancer. *Journal of Clinical Oncology.* 2012; 30(17): 2039-45).

[0202] Patient characteristics, progression-free survival, toxicity, and preliminary overall survival data and a summary of quality-of-life (QoL) data have been reported from ICON7. In the standard chemotherapy group, 696 (91%) of 764 women received 18 weeks of chemotherapy by protocol. In the bevacizumab group, 719 (94%) of 764 women received 18 weeks of chemotherapy and bevacizumab and 472 (62%) continued bevacizumab to protocol completion at 54 weeks. The hazard ratio for progression-free survival with standard chemotherapy and bevacizumab was 0.81 (95% CI 0.70–0.94, $p=0.004$). In patients at high risk of progression, defined as International Federation of Gynecology and Obstetrics (FIGO) stage IV disease or stage III disease with greater than 1.0 cm of residual disease after debulking surgery, the hazard ratio for death in the bevacizumab group was 0.64 (95% CI 0.48–0.85; $p=0.002$).

[0203] Access was obtained to the ICON7 trial samples via the Medical Research Council (MRC). An honest broker holds the associated clinical data from the MRC. A randomization strategy for profiling the samples has been performed based on clinical factors. All reagents, arrays, and reference samples were previously tested and passed qualification criteria.

[0204] Total RNA was extracted from macrodissected FFPE tissue using the High Pure RNA Paraffin Kit (Roche Diagnostics GmbH, Mannheim, Germany). RNA is converted into

complementary deoxyribonucleic acid (cDNA), which is subsequently amplified and converted into single-stranded form using the SPIA® technology of the WT-Ovation™ FFPE RNA Amplification System V2 (NuGEN Technologies Inc., San Carlos, CA, USA). The amplified single-stranded cDNA is then fragmented and biotin labeled using the FL-Ovation™ cDNA Biotin Module V2 (NuGEN Technologies Inc.). The fragmented and labeled cDNA was then hybridized to the Almac Ovarian Cancer DSA, on this the signature was developed. Arrays are scanned using the Affymetrix Genechip® Scanner 7G (Affymetrix Inc., Santa Clara, CA).

[0205] Control UHR and a pooled clinical reference sample are processed in each post RNA extraction batch. QC is performed at several steps of the process, from RNA Extraction QC to array QC.

[0206] Quality Control (QC) of profiled samples is carried out using the RMA pre-processing algorithm. Different technical aspects are assessed: average noise and background homogeneity, percentage of present call (array quality), signal quality, RNA quality and hybridization quality. Distributions and Median Absolute Deviation of corresponding parameters are analyzed and used to identify possible outliers.

[0207] Almac's Ovarian Cancer DSA™ contains probes that primarily target the area within 300 nucleotides from the 3' end. Therefore standard Affymetrix RNA quality measures were adapted – for housekeeping genes intensities of 3' end probe sets with ratios of 3' end probe set intensity to the average background intensity were used in addition to usual 3'/5' ratios. Hybridization controls were checked to ensure that their intensities and present calls conform to the requirements specified by Affymetrix.

[0208] Samples that pass QC metrics will be deemed suitable for inclusion in subsequent analysis, and signature scores will be calculated (per sample) using the following:

- Background correction
- RefRMA model to pre-process the data, one sample at a time
- The signature score is calculated as a weighted sum of the expression of the

genes in the signature:

$$SignatureScore = \sum_i w_i \times (ge_i - b_i) + k$$

where w_i is a weight for each gene, b_i is a gene-specific bias (Supplementary Table S5), ge_i is the observed gene expression level after pre-processing, and $k = 0.2953$ is a constant offset.

[0209] Sample IDs and corresponding signature scores will be sent to the honest broker to evaluate the predictive performance of the Ovarian Immune signature to predict resistance to Avastin in the treatment arm of the study.

Application of angiogenesis classifier model to the discovery data and an independent microarray dataset

[0210] Class labels were assigned to samples based upon expression of the angiogenesis-related genes and a 25 and 45 gene expression signatures were developed to identify the pro-angiogenic molecular subgroup of high grade serous (HGS) carcinoma.

[0211] Angiogenesis is central to the process of cancer growth and metastasis and has a role in the progression and prognosis of ovarian cancer. VEGF is an important promoter of angiogenesis produced by normal and neoplastic cells. Bevacizumab (Avastin, Riche) is a recombinant humanised version of a murine anti-human VEGF monoclonal antibody and has been studied in the management of many tumours. The International Collaboration on Ovarian Neoplasms 7 (ICON7) trial is a Gynecologic Cancer Intergroup phase 3 trial that assessed the effects of adding bevacizumab, concurrently and as a continuation, to standard chemotherapy with carboplatin and paclitaxel in patients with primary peritoneal carcinoma, fallopian tube carcinoma, and epithelial ovarian carcinoma (Perren TJ, Swart AM, Pfisterer J, Ledermann JA, Pujade-Lauraine E, Kristensen G, et al. A phase 3 trial of bevacizumab in ovarian cancer. *N Engl J Med.* 365(26): 2484-96, Aghajanian C, Blank SV, Goff BA, Judson PL, Teneriello MG, Husain A, et al. OCEANS: A randomized, double-blind, placebo-controlled phase III trial of chemotherapy with or without bevacizumab in patients with platinum-sensitive recurrent epithelial ovarian, primary peritoneal, or fallopian tube cancer. *Journal of Clinical Oncology.* 2012; 30(17): 2039-45).

[0212] Patient characteristics, progression-free survival, toxicity, and preliminary overall survival data and a summary of quality-of-life (QoL) data have been reported from ICON7. In the standard chemotherapy group, 696 (91%) of 764 women received 18 weeks of chemotherapy by protocol. In the bevacizumab group, 719 (94%) of 764 women received 18 weeks of chemotherapy and bevacizumab and 472 (62%) continued bevacizumab to protocol completion at 54 weeks. The hazard ratio for progression-free survival with standard chemotherapy and bevacizumab was 0.81 (95% CI 0.70–0.94, $p=0.004$). In patients at high risk of progression, defined as International Federation of Gynecology and Obstetrics (FIGO) stage IV disease or stage III disease with greater than 1.0 cm of residual disease after debulking surgery, the hazard ratio for death in the bevacizumab group was 0.64 (95% CI 0.48–0.85; $p=0.002$).

[0213] HGS patients with the angiogenic subgroup may benefit from anti-angiogenic targeted therapies. Access to the ICON7 trial samples was obtained via the MRC, and are being profiled on Ovarian DSAs in order to validate this hypothesis.

[0214] H & E Sections of FFPE material from ICON7 trial samples have been pathology reviewed, marked for tumour content and the tumour material macro dissected.

[0215] An honest broker obtained and holds the associated clinical data from the MRC. They have also performed the randomisation strategy, based on clinical factors, for profiling the samples. All reagents, arrays and reference samples were previously tested and passed qualification criteria.

[0216] Total RNA was extracted from macrodissected FFPE tissue using the High Pure RNA Paraffin Kit (Roche Diagnostics GmbH, Mannheim, Germany). RNA is converted into complementary deoxyribonucleic acid (cDNA), which is subsequently amplified and converted into single-stranded form using the SPIA® technology of the WT-Ovation™ FFPE RNA Amplification System V2 (NuGEN Technologies Inc., San Carlos, CA, USA). The amplified single-stranded cDNA is then fragmented and biotin labeled using the FL-Ovation™ cDNA Biotin Module V2 (NuGEN Technologies Inc.). The fragmented and labeled cDNA was then hybridized to the Almac Ovarian Cancer DSA, on this the signature was developed. Arrays are scanned using the Affymetrix Genechip® Scanner 7G (Affymetrix Inc., Santa Clara, CA).

[0217] Control UHR and a pooled clinical reference sample are processed in each post RNA extraction batch. QC is performed at several steps of the process, from RNA Extraction QC to array QC.

[0218] Quality Control (QC) of profiled samples is carried out using the RMA pre-processing algorithm. Different technical aspects are assessed: average noise and background homogeneity, percentage of present call (array quality), signal quality, RNA quality and hybridization quality. Distributions and Median Absolute Deviation of corresponding parameters are analyzed and used to identify possible outliers.

[0219] Almac's Ovarian Cancer DSATM contains probes that primarily target the area within 300 nucleotides from the 3' end. Therefore standard Affymetrix RNA quality measures were adapted – for housekeeping genes intensities of 3' end probe sets with ratios of 3' end probe set intensity to the average background intensity were used in addition to usual 3'/5' ratios. Hybridization controls were checked to ensure that their intensities and present calls conform to the requirements specified by Affymetrix.

[0220] Samples that pass QC metrics will be deemed suitable for inclusion in subsequent analysis, and signature scores will be calculated (per sample) using the following:

Background correction

[0221] RefRMA model to pre-process the data, one sample at a time

[0222] The signature score is calculated as a weighted sum of the expression of the genes in the signature:

$$SignatureScore = \sum_i w_i \times (ge_i - b_i) + k$$

[0223]

[0224] where w_i is a weight for each gene, b_i is a gene-specific bias (Supplementary Table S5), ge_i is the observed gene expression level after pre-processing, and $k = 0.2953$ is a constant offset.

[0225] Sample IDs and corresponding signature scores will be sent to the honest broker to evaluate the predictive performance of the pro-angiogenic signature to predict benefit from Avastin in the treatment arm of the study.

Application of classifier model combination to identify three molecular subgroups

[0226] As a secondary endpoint, analysis of the combined signature approach (see Figure 17) will be evaluated. This approach utilizes the 63 gene signature to identify 2 groups, one with a better survival i.e. the group with reduced activation of angiogenic processes, and the other with poorer survival. The 45 gene signature will be applied to the group with poorer survival outcome to identify a further 2 groups, one with elevated activation of angiogenic processes and the other with indifferent angiogenic activation. It is hypothesised that the group identified with elevated angiogenic activity should respond to Avastin in the treatment arm of the study.

Example 4: Predictive utility of non-angiogenesis signature in colorectal cancer.

[0227] A public array data set obtained from the Gene Expression Omnibus database for a cohort of recurrent or metastatic colorectal cancer responders and non-responders to Bevacizumab on plus 2 arrays (E-GEOD-19862) was obtained and analyzed using the example 63 gene signature of Table 2C. The 63 gene ovarian immune signatures predicts response to bevacizumab with an AUC: 0.86 (0.60-1.00). See Figure 14.

Example 5: Predictive utility of the 25 and 45 angiogenesis gene signatures in colorectal cancer

[0228] In a public array data set obtained from the Gene Expression Omnibus database from a cohort of recurrent or metastatic colorectal cancer responders and non-responders to Bevacizumab on plus 2 arrays (E-GEOD-19862), the 25 gene and 45 gene angiogenic signatures both predict response to bevacizumab – see Figures 18 and 19 respectively.

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CLAIMS

We claim:

1. A method for predicting a subject's responsiveness to an anti-angiogenic therapeutic agent comprising:
 - obtaining a test sample from a subject;
 - measuring expression levels of a biomarker panel from the test sample obtained from the subject, wherein the biomarker panel comprises one or more biomarkers selected from Table 2C;
 - determining a sample expression score for the biomarker panel;
 - comparing the sample expression score to a threshold score; and
 - classifying the subject as responsive or non-responsive to the anti-angiogenic therapeutic agent based on whether the sample expression score is above or below the threshold expression score.
2. The method of claim 1, wherein the biomarker panel comprises one or more of IGF2, SOX11, INS, CXCL17, SLC5A1, TMEM45A, CXCR2P1, MFAP2, MATN3, or RTP4.
3. The method of claim 1, wherein the biomarker panel comprises the biomarkers listed in Table 2C.
4. The method of any one of claims 1 to 3, wherein the sample expression score is determined by measuring an expression level for each biomarker and multiplying it by a corresponding weight, wherein an expression signature defines the weight for each biomarker.
5. The method of any one of claims 1 to 4, wherein the expression level of each biomarker in the biomarker panel is measured using a microarray, quantitative PCR, or an immunoassay.

6. The method of claim 4, wherein the expression signature is derived by a method comprising:

isolating total RNA from a sample set of diseased tissue;

hybridizing the isolated total RNA to a microarray to obtain a sample expression data set;

selecting those probes on the microarray with a variability above a defined significance threshold to form a preliminary biomarker set;

generating clusters of biomarkers within the preliminary biomarker set having a similar expression profile using a clustering algorithm;

identifying the biological processes or biological pathways for each cluster of biomarkers;

selecting the cluster corresponding to the biological process or biological pathway of interest; and

defining an expression signature by analyzing the expression levels of the biomarkers in the selected cluster in a the sample set of diseased tissue using a supervised or unsupervised training algorithm.

7. The method of claim 6, wherein the expression signature is defined using a PLS classifier, a SVM classifier, a SDA classifier, or a DSDA classifier.

8. The method of any one of claims 1 to 7, wherein the diseased tissue is cancer tissue.

9. The method of claim 8, wherein the cancer is ovarian cancer, prostate, breast cancer, colon cancer, or colorectal cancer.

10. The method of any one of claims 1 to 8, wherein the anti-angiogenic therapeutic agent is a VEGF-pathway-targeted therapeutic agent, an angiopoietin-TIE2 pathway inhibitor, an endogenous angiogenic inhibitor, or an immunomodulatory agent.

11. The method of claim 10, wherein the VEGF pathway-targeted therapeutic agents include Bevacizumab (Avastin), Afibercept (VEGF Trap), IMC-1121B (Ramucirumab), Imatinib (Gleevec), Sorafenib (Nexavar), Gefitinib (Iressa), Sunitinib (Sutent), Erlotinib, Tivozinib, Cediranib (Recentin), Pazopanib (Votrient), BIBF 1120 (Vargatef), Dovitinib, Semaxanib (Sugen), Axitinib (AG013736), Vandetanib (Zactima), Nilotinib (Tasigna), Dasatinib (Sprycel), Vatalanib, Motesanib, ABT-869, TKI-258 or a combination thereof.

12. The method of claim 10, wherein the angiopoietin-TIE2 pathway inhibitor includes AMG-386, PF-4856884 CVX-060, CEP-11981, CE-245677, MEDI-3617, CVX-241, Trastuzumab (Herceptin) or a combination thereof.

13. The method of claim 10, wherein the endogenous angiogenic inhibitors include Thrombospondin, Endostatin, Tumstatin, Canstatin, Arrestin, Angiostatin, Vasostatin, Interferon alpha or a combination thereof.

14. The method of claim 10, wherein the immunomodulatory agents include thalidomide and lenalidomide.

15. The method of any one of claims 1 to 14, further comprising determining the subject's prognosis, wherein a classification as responsive to the anti-angiogenic therapeutic agent indicates a good prognosis, the good prognosis indicating at least an increased expected survival time as compared to a classification as non-responsive to the anti-angiogenic therapeutic agent.

16. A method for predicting subject responsiveness to anti-angiogenic therapeutic agents and providing treatment prognosis, the method comprising:

obtaining a test sample from a subject with a disease or disorder;

measuring expression levels of a first biomarker panel from the test sample of diseased tissue obtained from the subject, wherein the biomarker panel comprises one or more biomarkers selected from Table 2C;

determining a first sample expression score for the first biomarker panel;

comparing the first sample expression score to a first threshold score

classifying the subject as having a good prognosis or bad prognosis based on whether the first sample expression score is above or below the first threshold score, wherein a good prognosis indicates at least an increased expected survival time as compared to a bad prognosis and wherein, in the event of a bad prognosis; measuring expression levels of a second biomarker panel from the test sample of diseased tissue obtained from the subject, wherein the second biomarker panel comprises one or more biomarkers selected from Table 2A or Table 2B;

determining a second sample expression score for the second biomarker panel;

comparing the second sample expression score to a second threshold score; and

classifying the subject as responsive or non-responsive to an anti-angiogenic therapeutic agent based on whether the second sample expression score is above or below the second threshold expression score.

17. The method of claim 16, wherein the first biomarker panel comprises one or more of IGF2, SOX11, INS, CXCL17, SLC5A1, TMEM45A, CXCR2P1, MFAP2, MATN3, or RTP4, and the second biomarker panel comprises one or more of CCDC80, INHBA, THBS2, SFRP2, MMP2, PLAU, FAP, FN1, COL8A1, and RAB31.

18. The method of claim 16, wherein the first biomarker panel comprises one or more of IGF2, SOX11, INS, CXCL17, SLC5A1, TMEM45A, CXCR2P1, MFAP2, MATN3, or RTP4, and the second biomarker panel comprises one or more of TMEM200A, GJB2, MMP13, GFPT2, POSTN, BICC1, CDH11, MRVI1, PMP22, and COL11A1.

19. The method of claim 16, wherein the first biomarker panel consists of the biomarkers in Table 2C, and the second biomarker panel consists of the biomarkers in Table 2A or 2B.

20. The method of any one of claims 16 to 19, wherein the expression level of each biomarker in the biomarker panel is measured using a microarray, quantitative PCR, or an immunoassay.

21. A method for diagnosing a subject as having a cancer, or being susceptible to developing a cancer, that is responsive to an anti-angiogenic therapeutic, the method comprising;

obtaining a test sample from a subject having or suspected of having a cancer;

measuring expression levels of a biomarker panel from the test sample obtained from the subject, wherein the biomarker panel comprises one or more biomarkers selected from Table 2C;

determining a sample expression score for the biomarker panel;

comparing the sample expression score to a threshold score; and

diagnosing the subject as having a cancer, or being susceptible to developing a cancer that is responsive to an anti-angiogenic therapeutic based on whether the sample expression score is above or below the threshold expression score.

22. The method of claim 21, wherein the biomarker panel comprises one or more of IGF2, SOX11, INS, CXCL17, SLC5A1, TMEM45A, CXCR2P1, MFAP2, MATN3, or RTP4.

23. The method of claim 21, wherein the biomarker panel comprises the biomarkers listed in Table 2C.

24. The method of any one of claims 21 to 23, wherein the sample expression score is determined by measuring an expression level for each biomarker and multiplying it by a corresponding weight, wherein an expression signature defines the weight for each biomarker.

25. The method of claim 24, wherein the expression signature is defined using a PLS classifier, a SVM classifier, a SDA classifier, or a DSDA classifier.

26. The method of any one of claims 21 to 25, wherein the cancer is ovarian cancer, glioblastoma, breast cancer, prostate cancer, colorectal cancer or colon cancer.

27. The method of any one of claims 21 to 26, wherein the expression level of each biomarker in the biomarker panel is measured using a microarray, quantitative PCR, or an immunoassay.

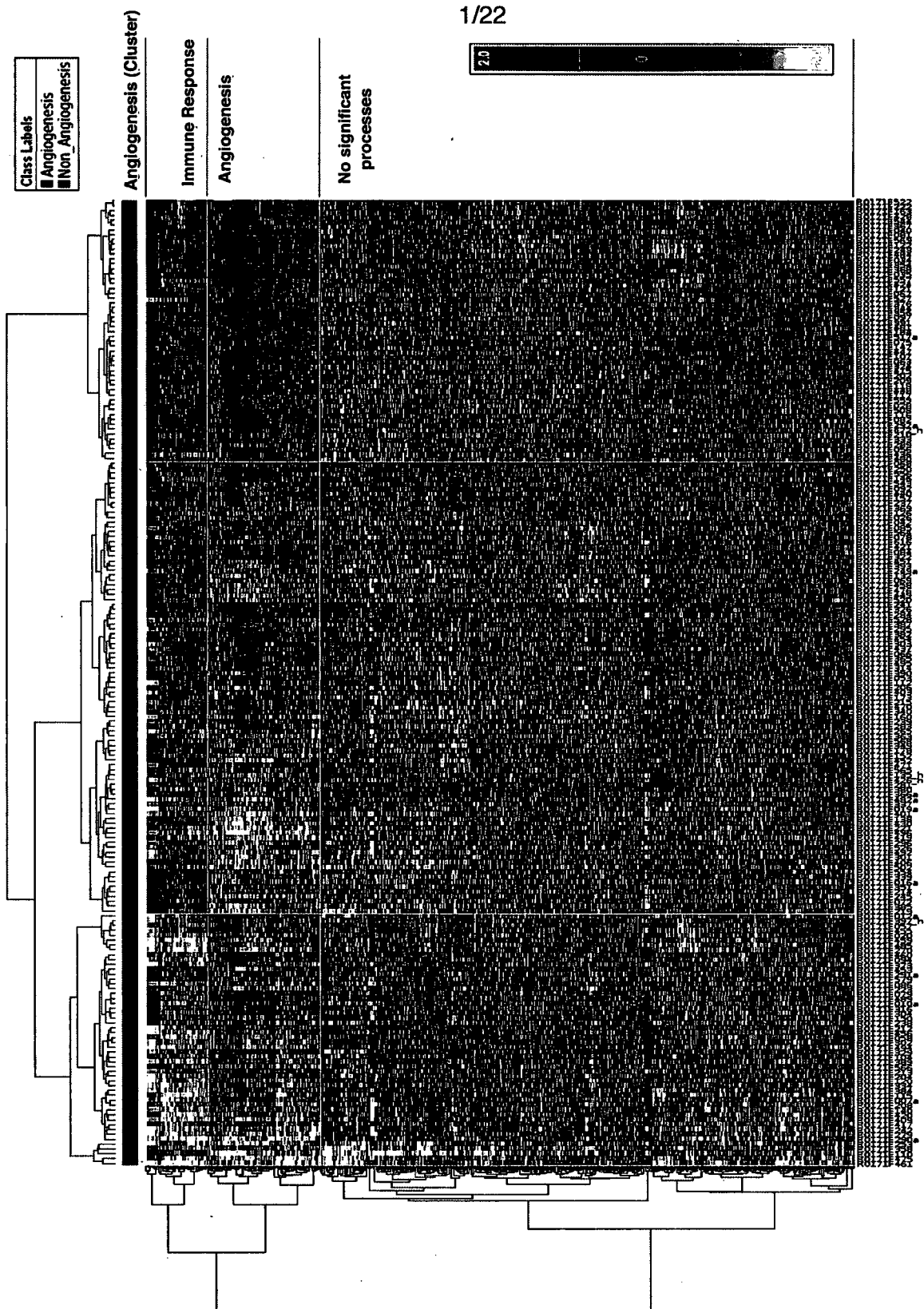


Figure 1

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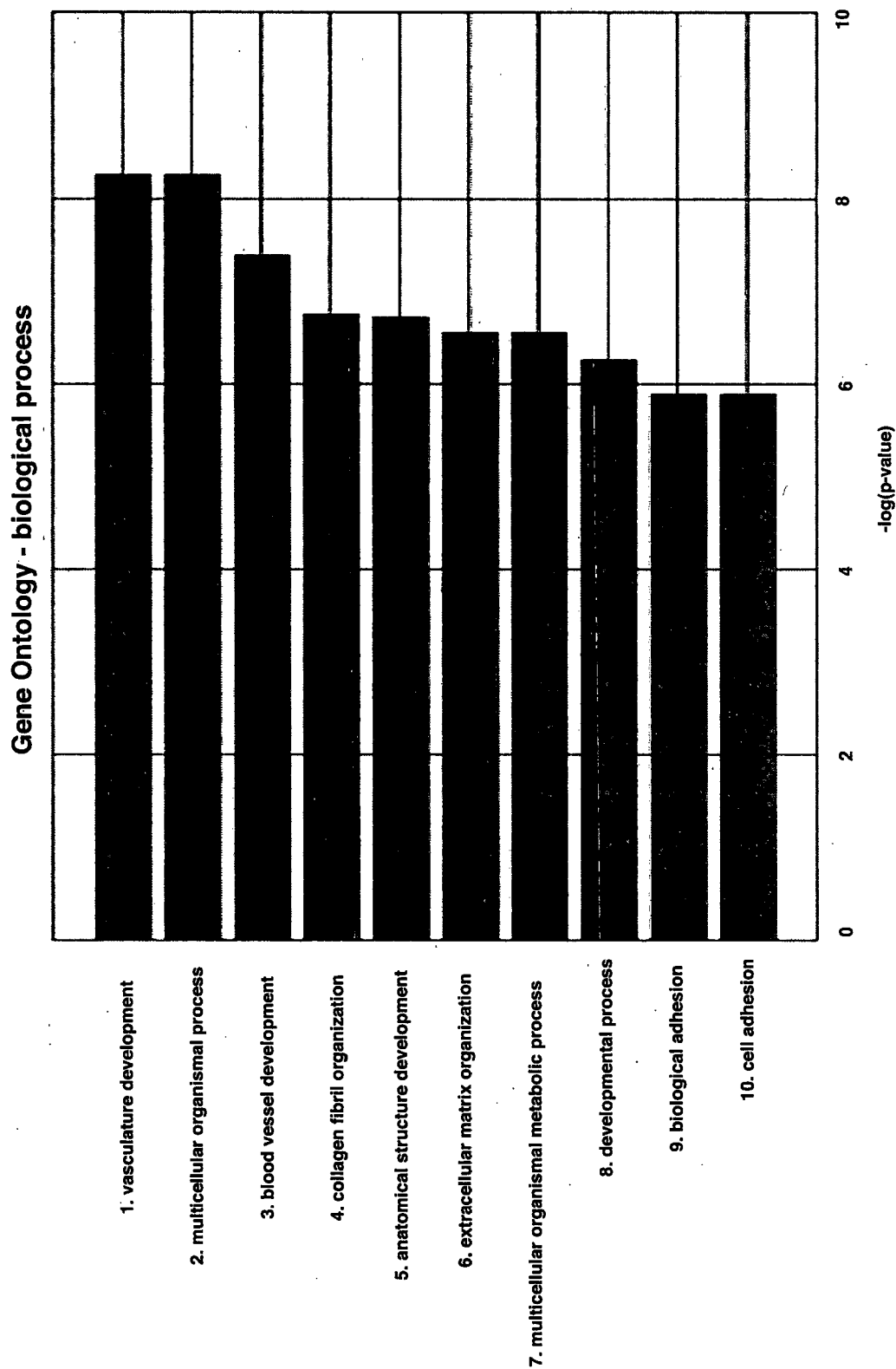


Figure 2

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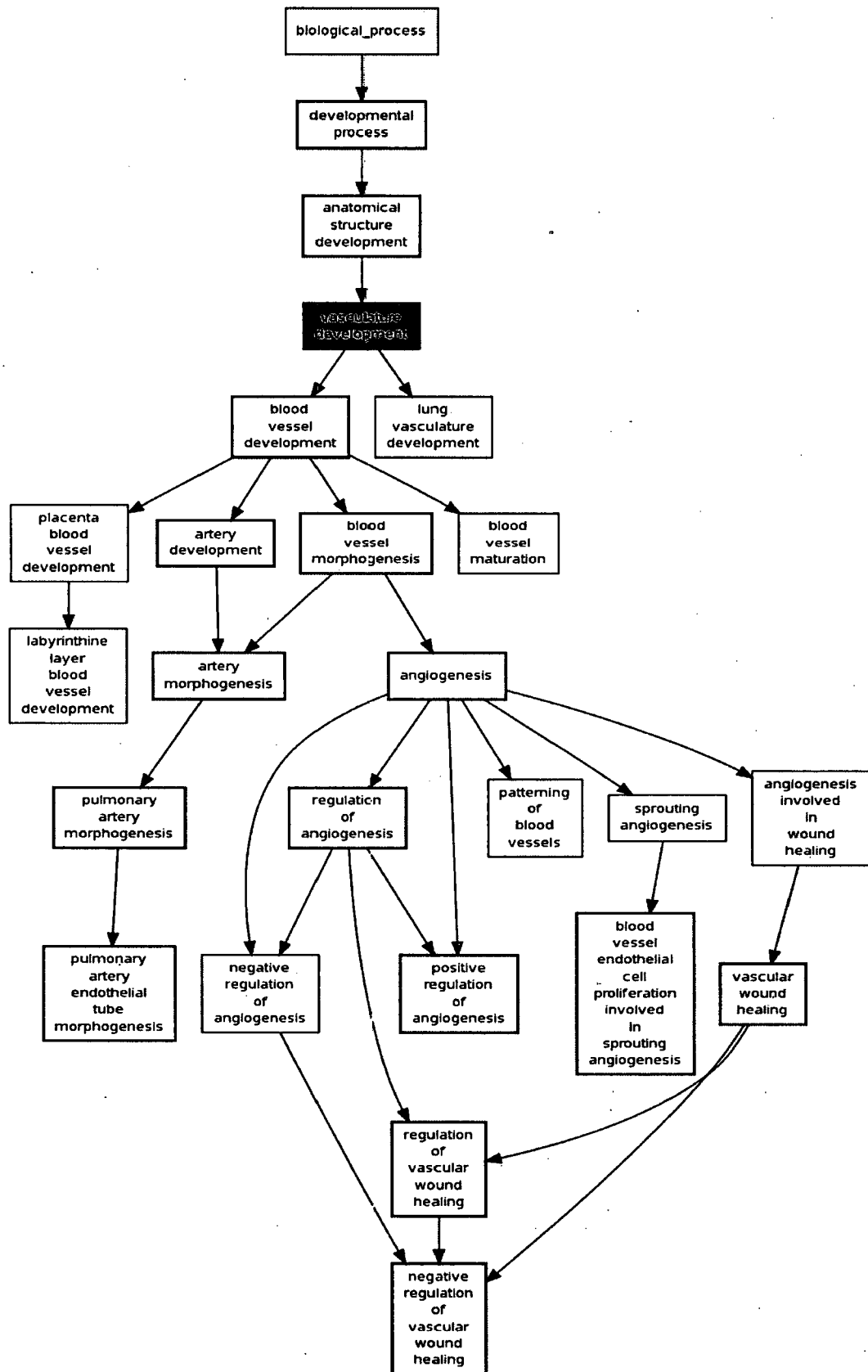


Figure 2B

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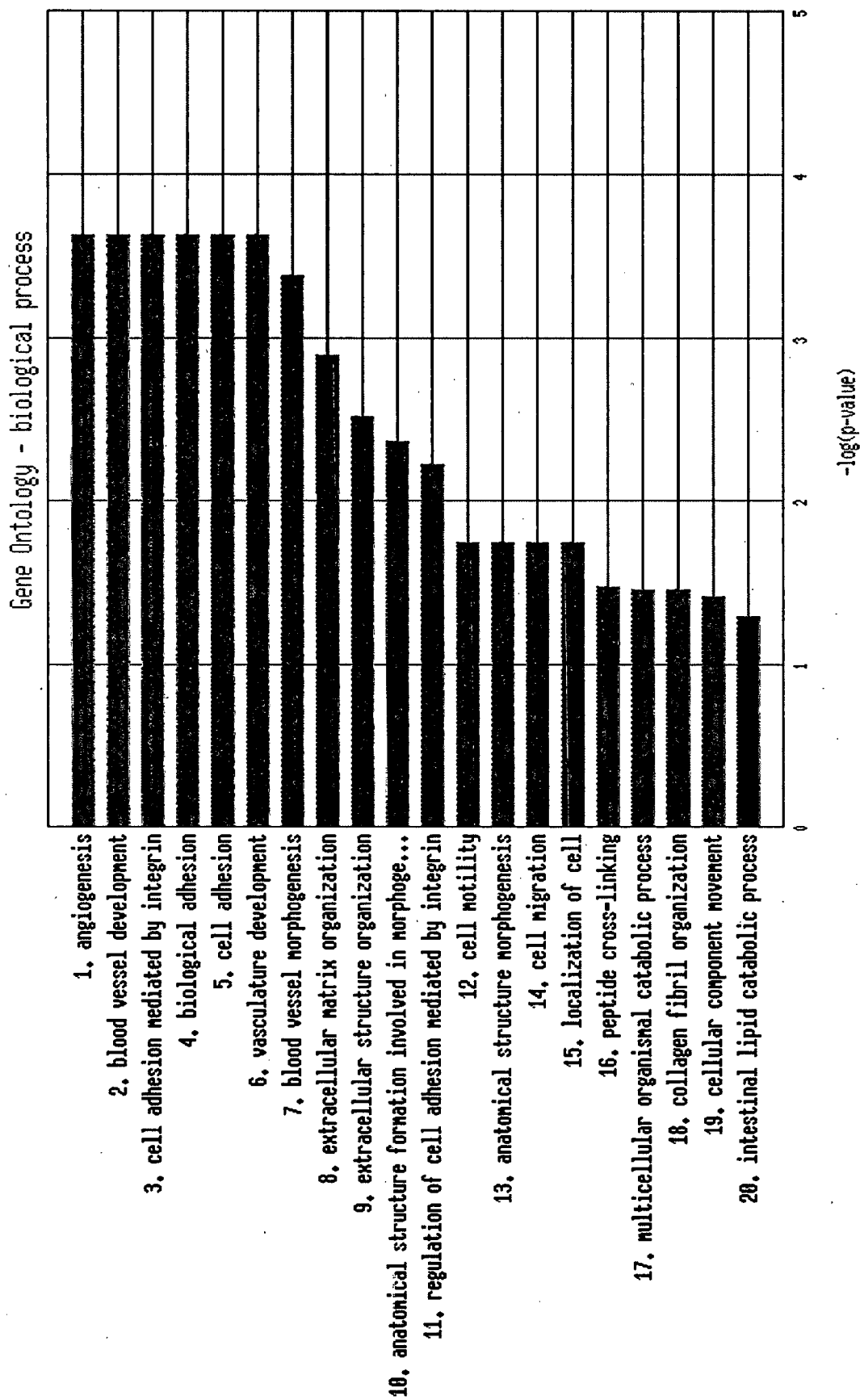


Figure 3

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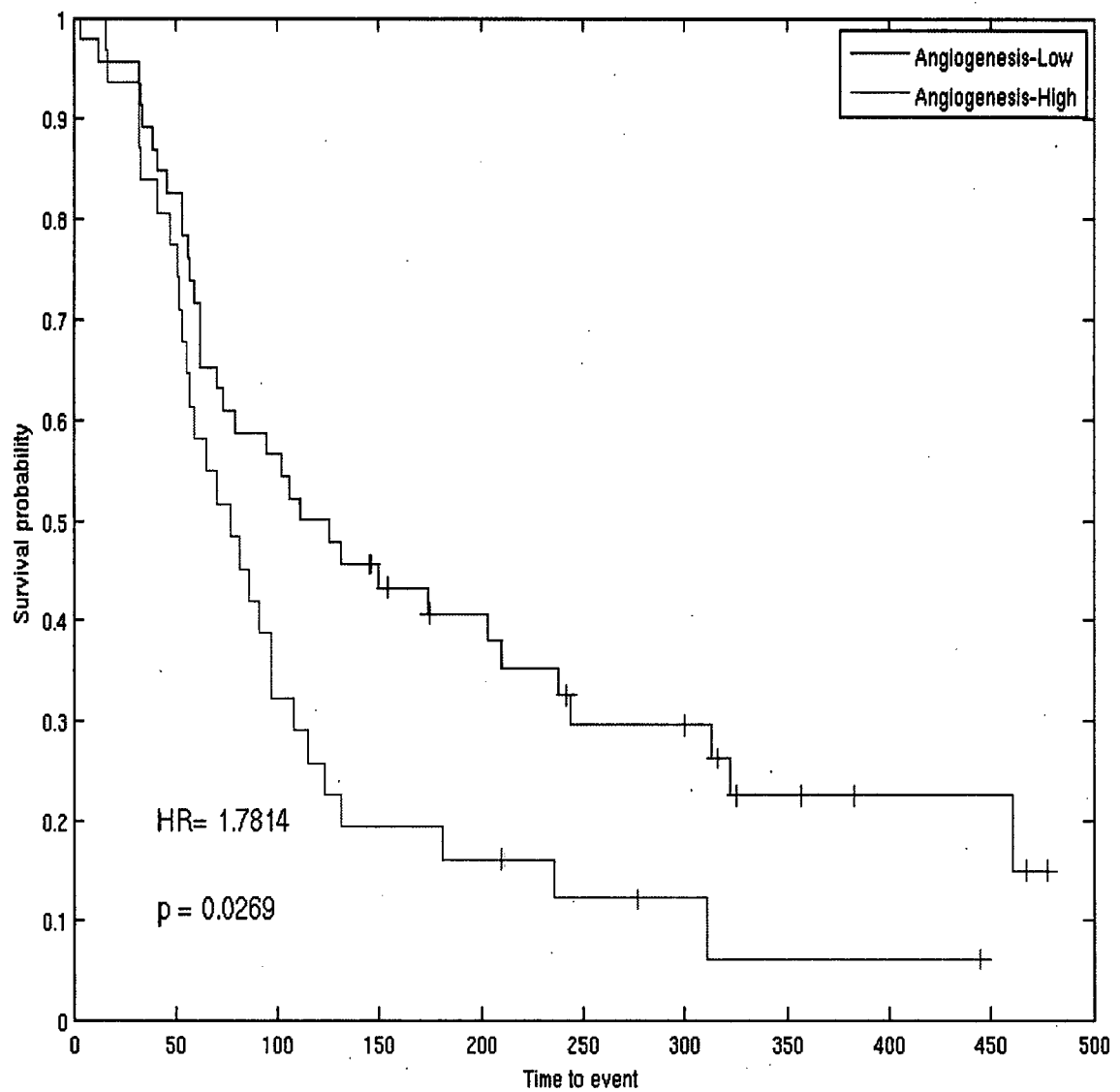
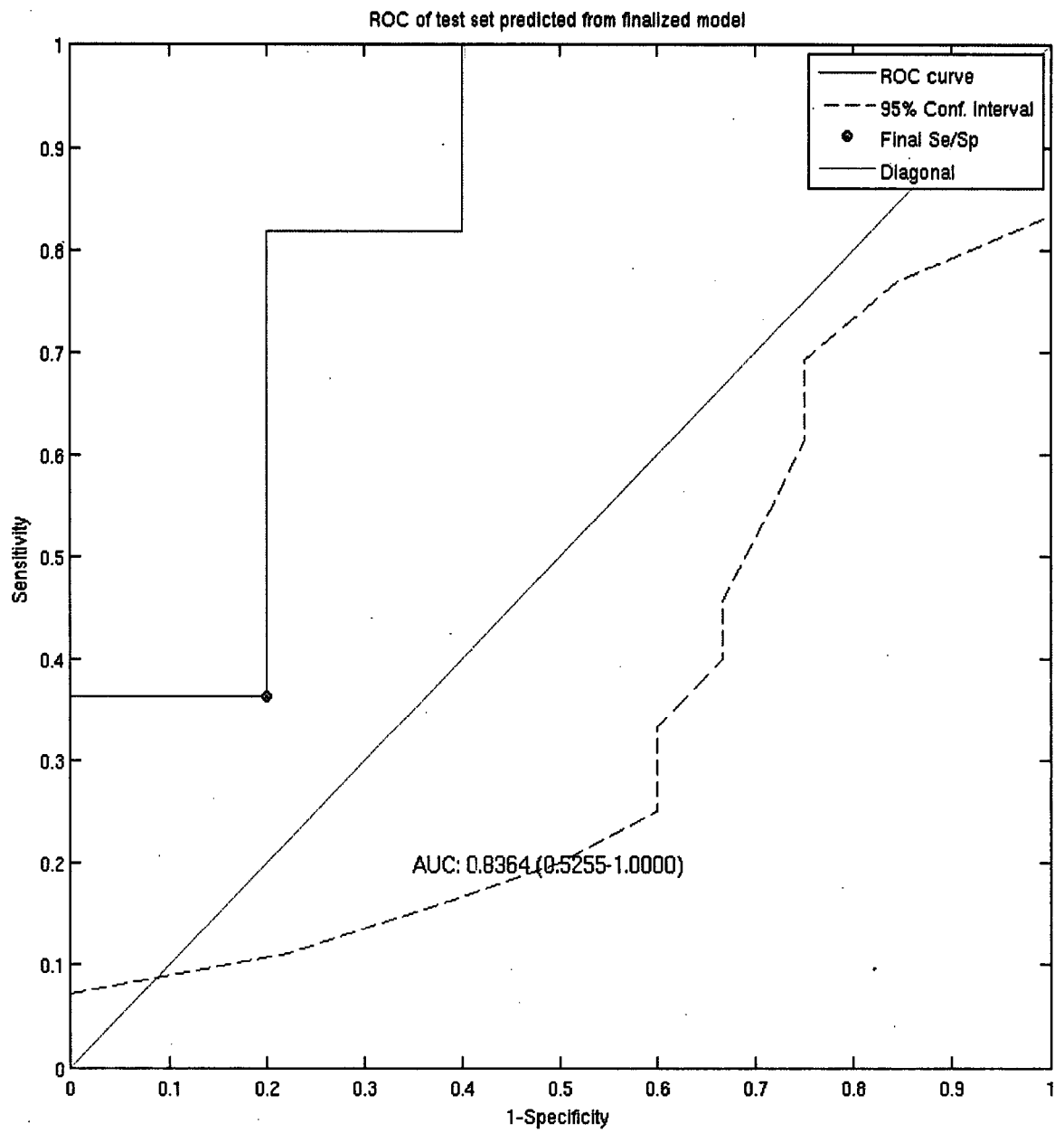


Figure 4

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**Figure 5**

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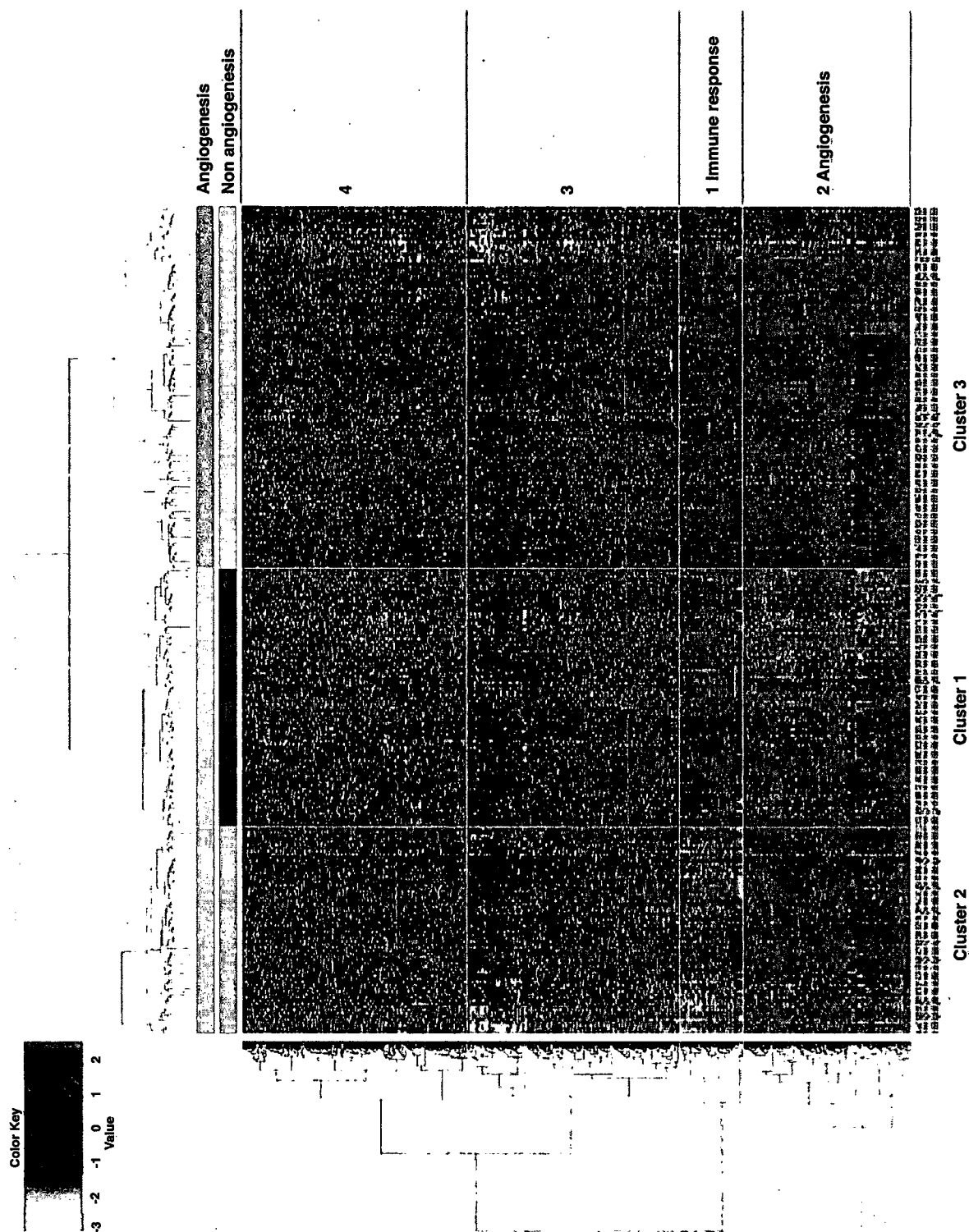


Figure 6

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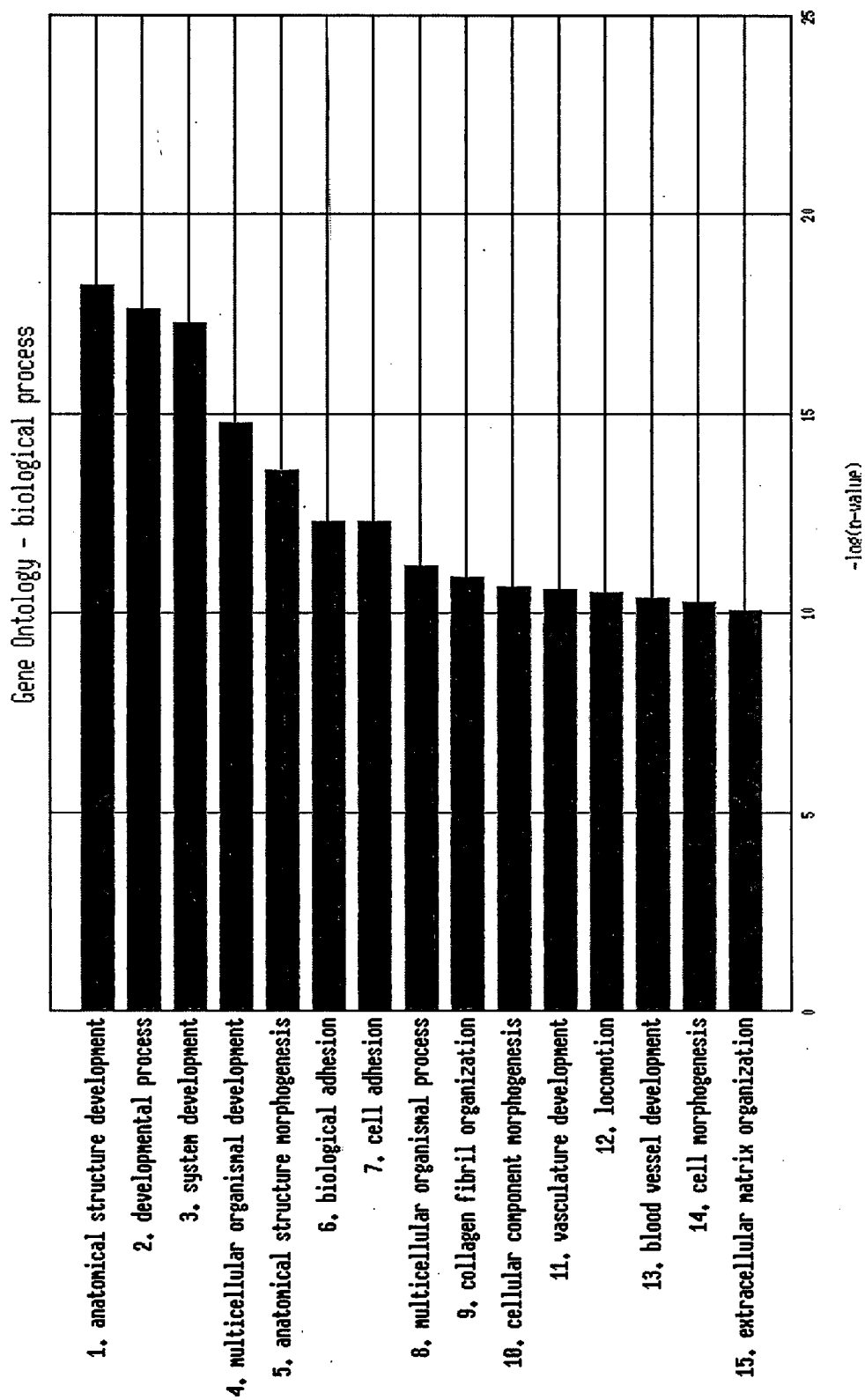


Figure 7A

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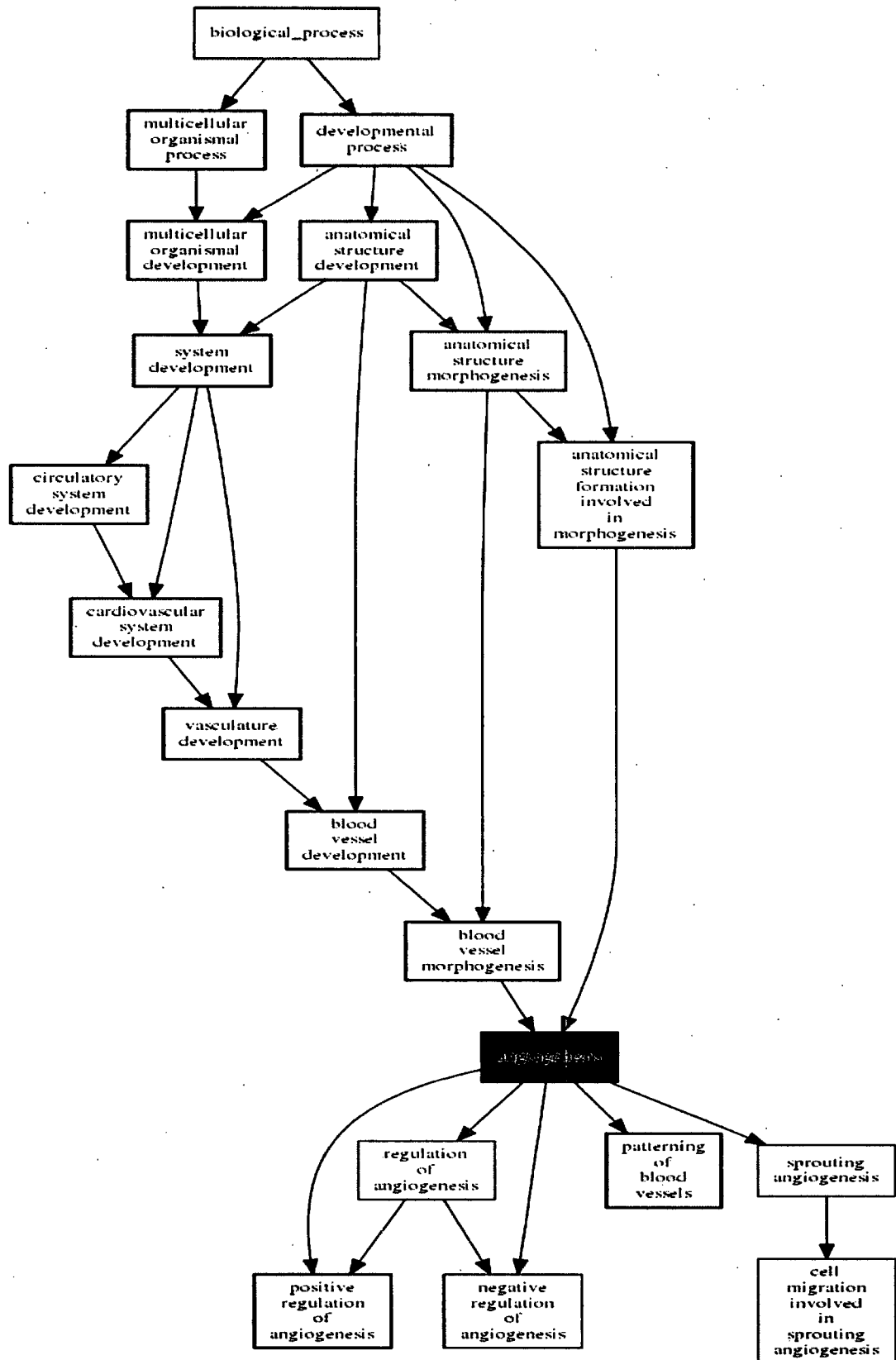


Figure 7B

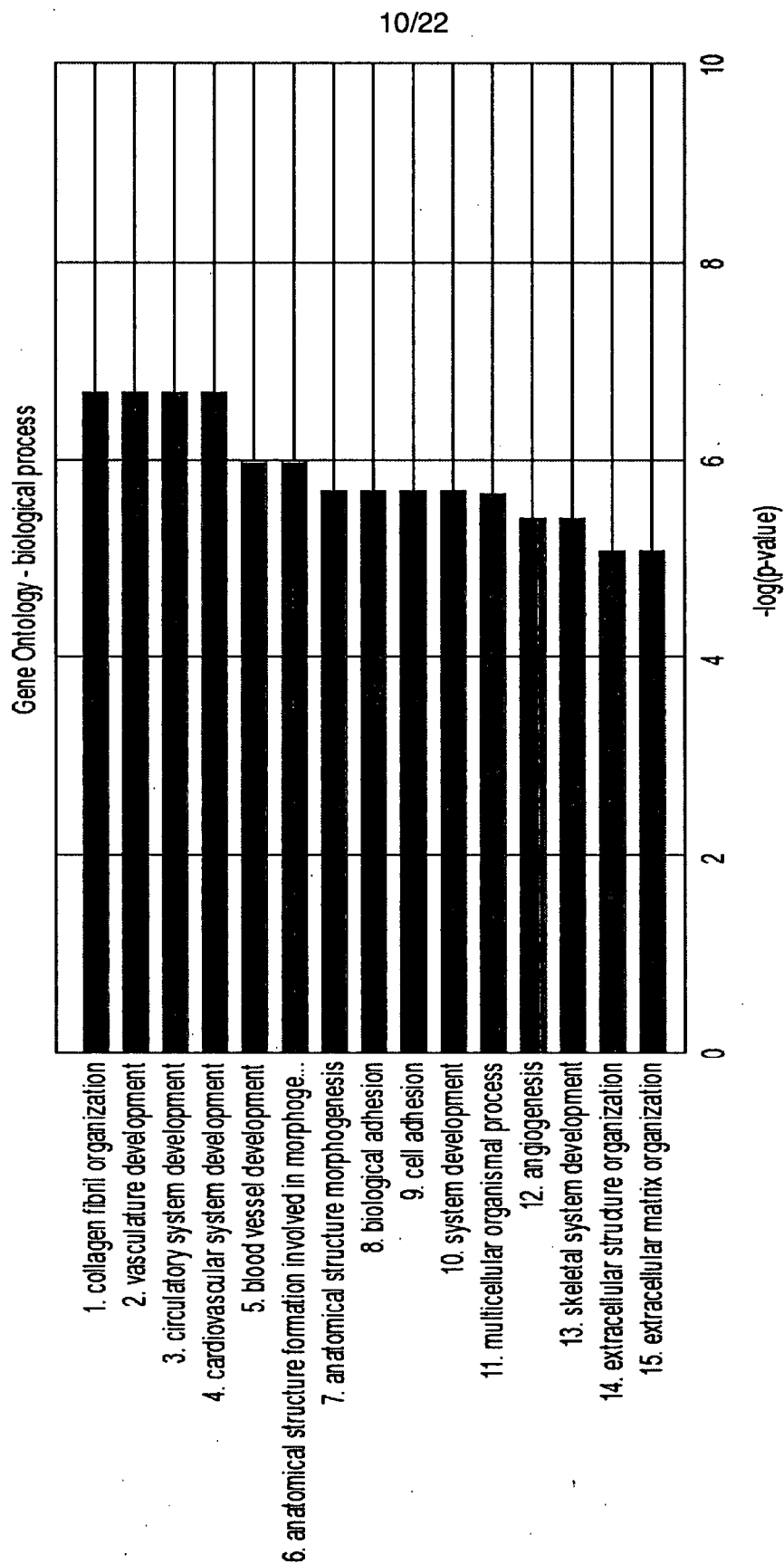


Figure 8

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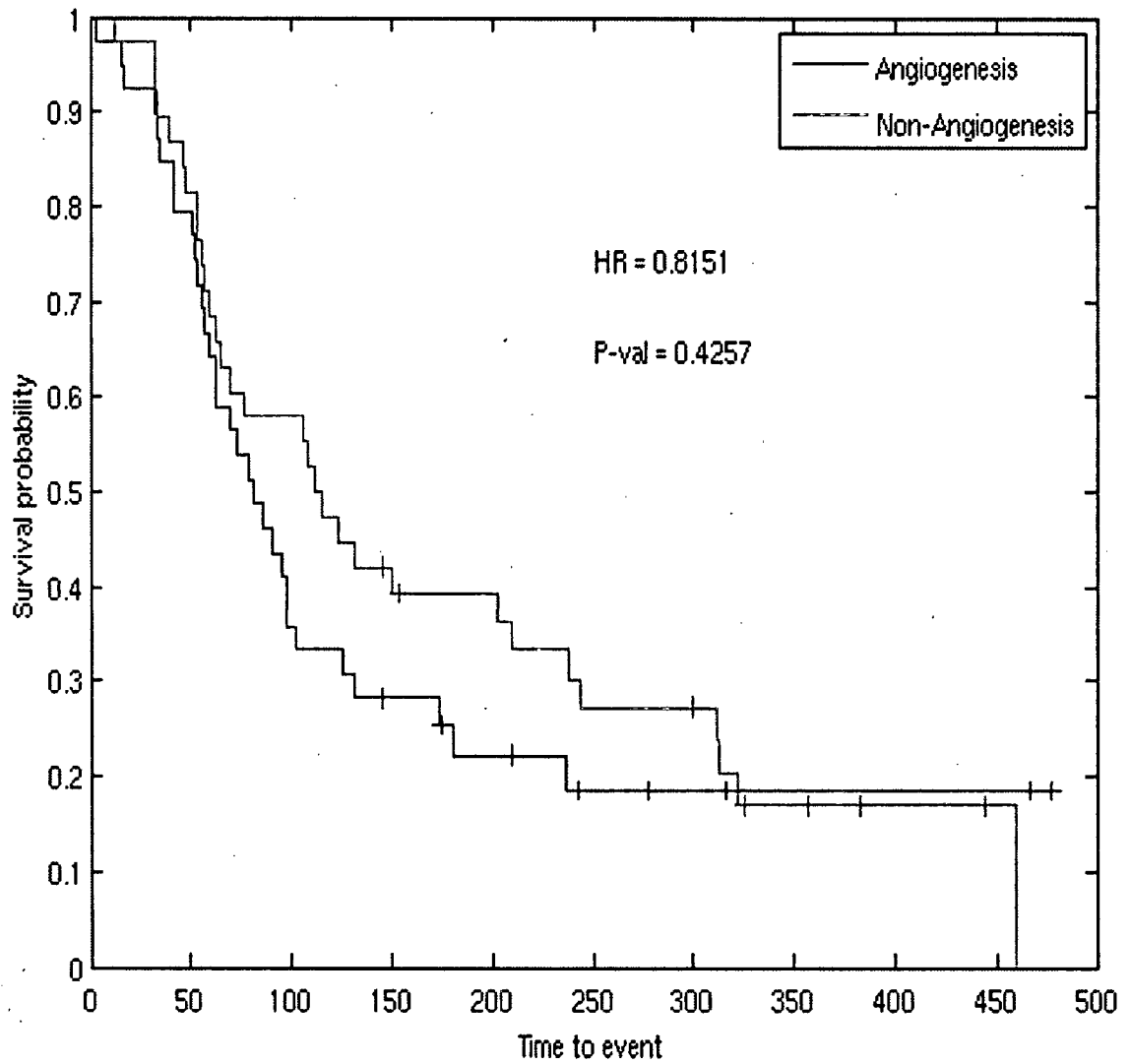


Figure 9

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Non Angiogenesis - PFS Distributions

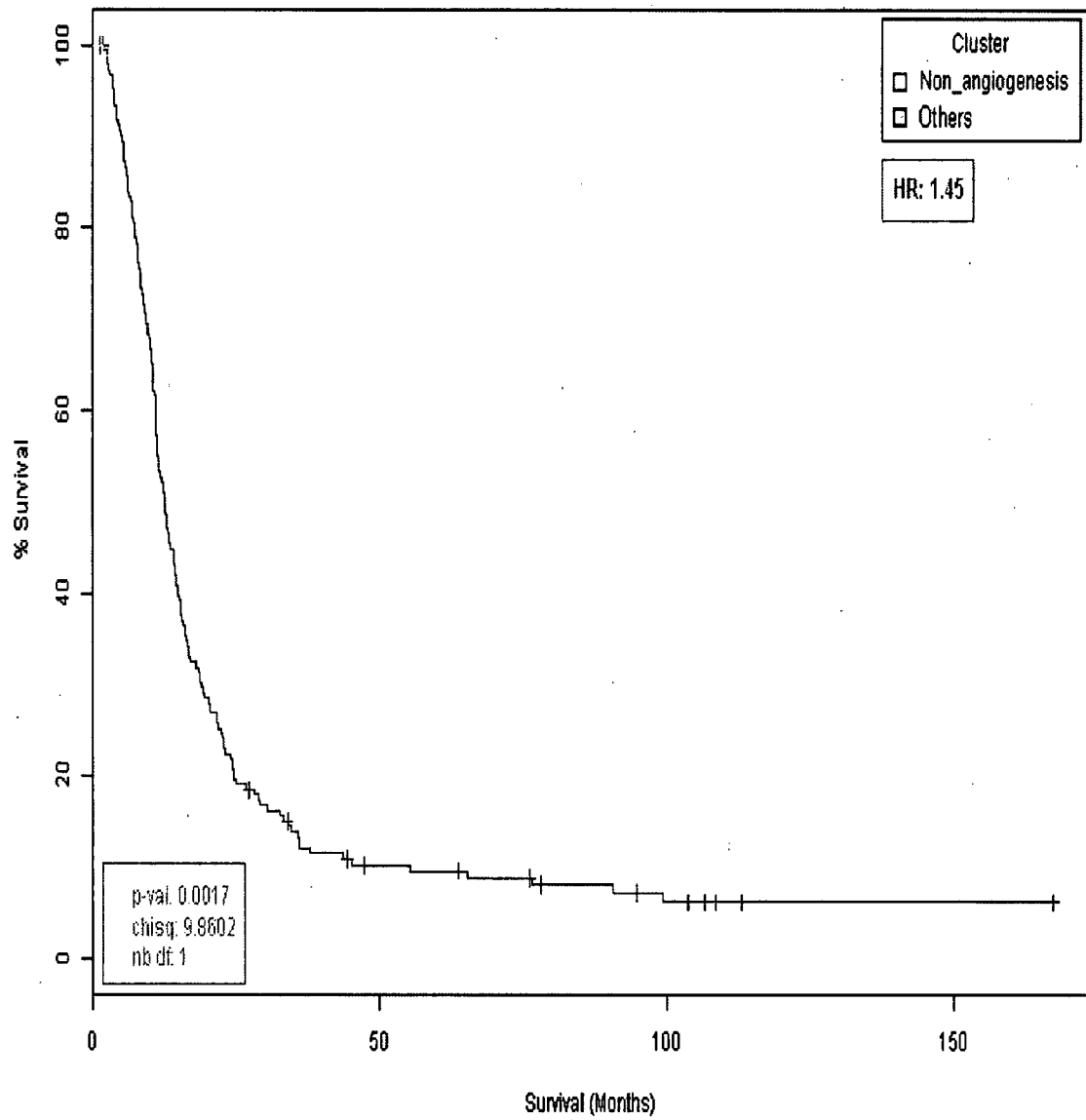


Figure 10

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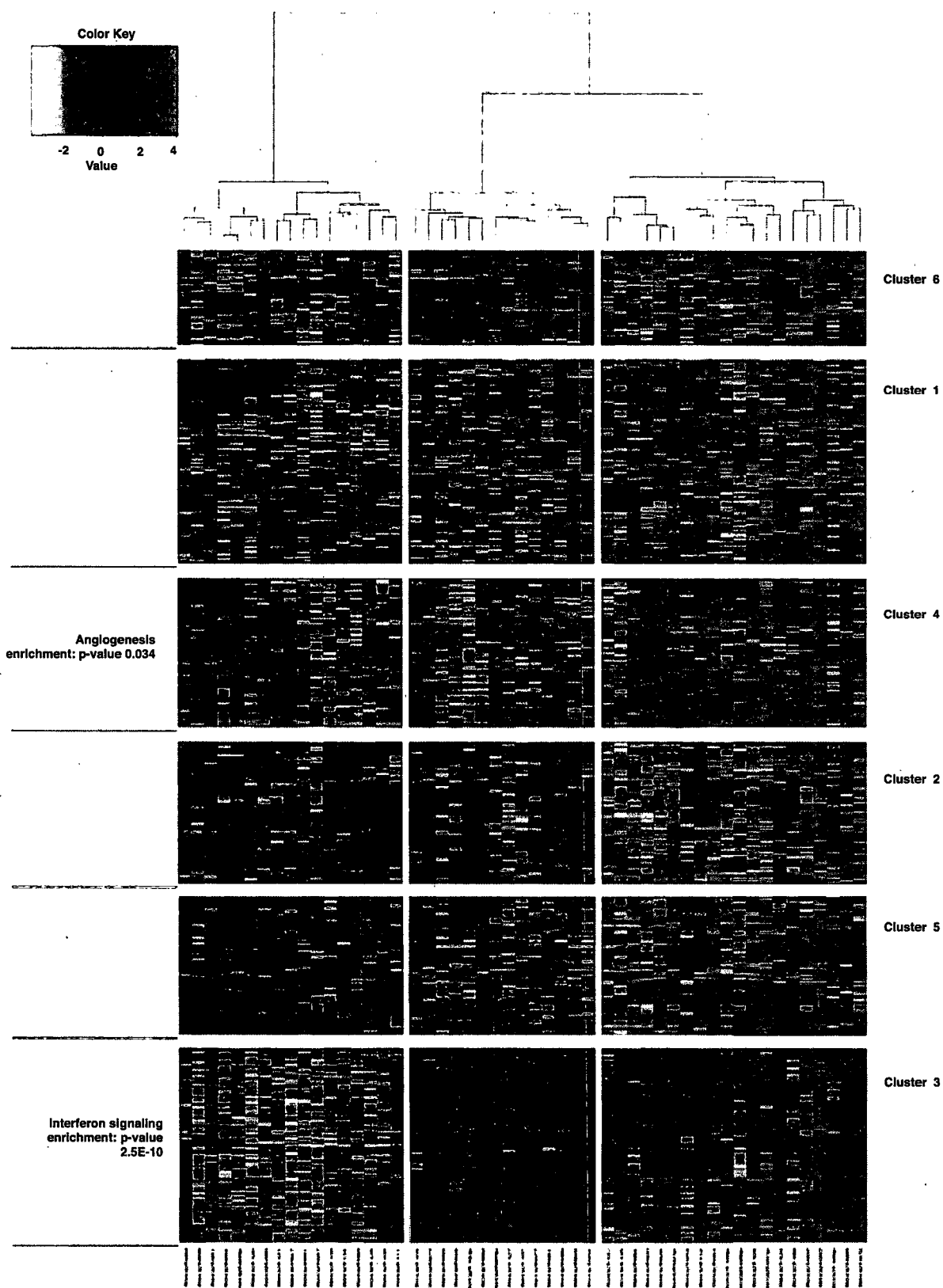


Figure 11A

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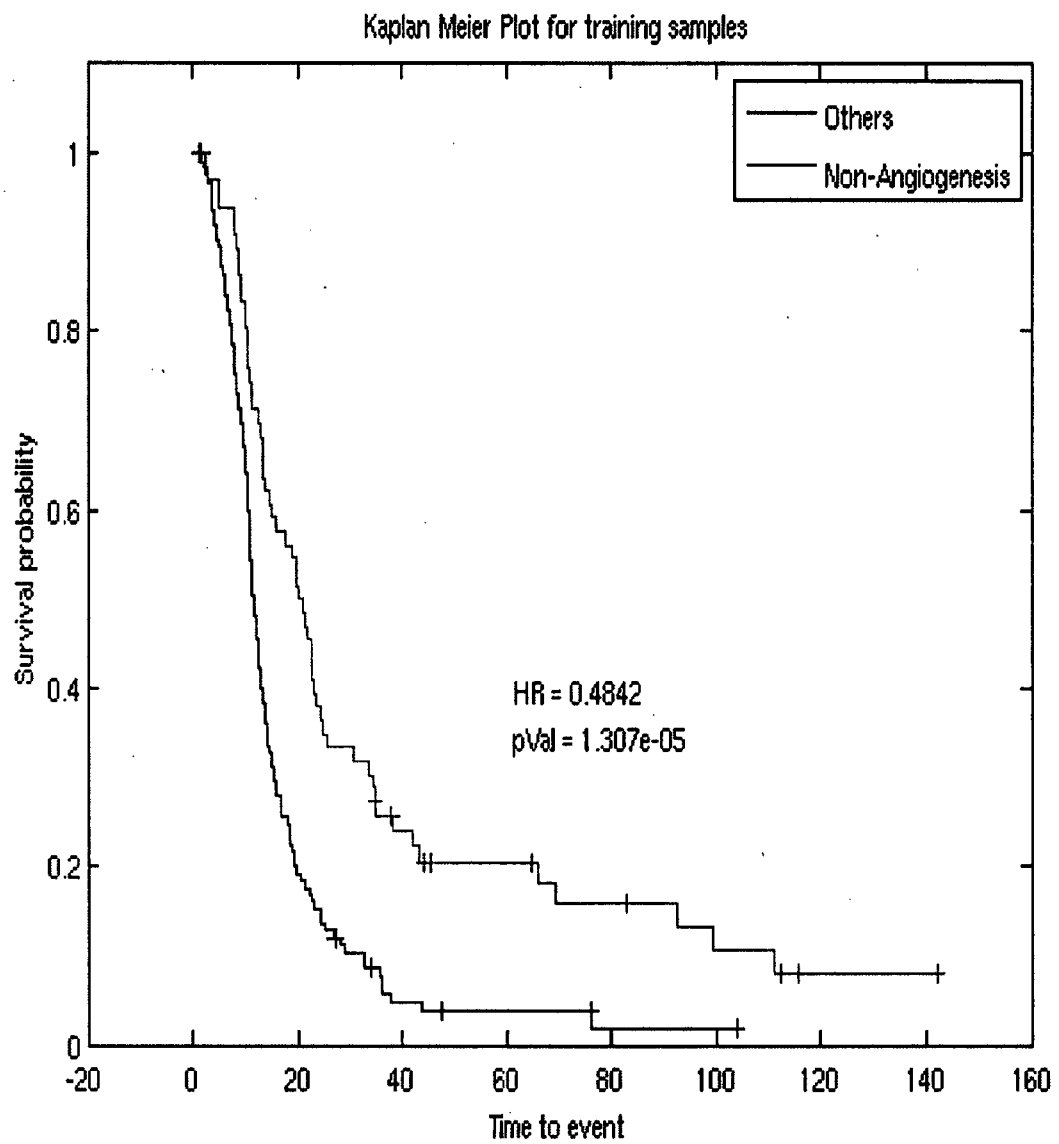


Figure 12

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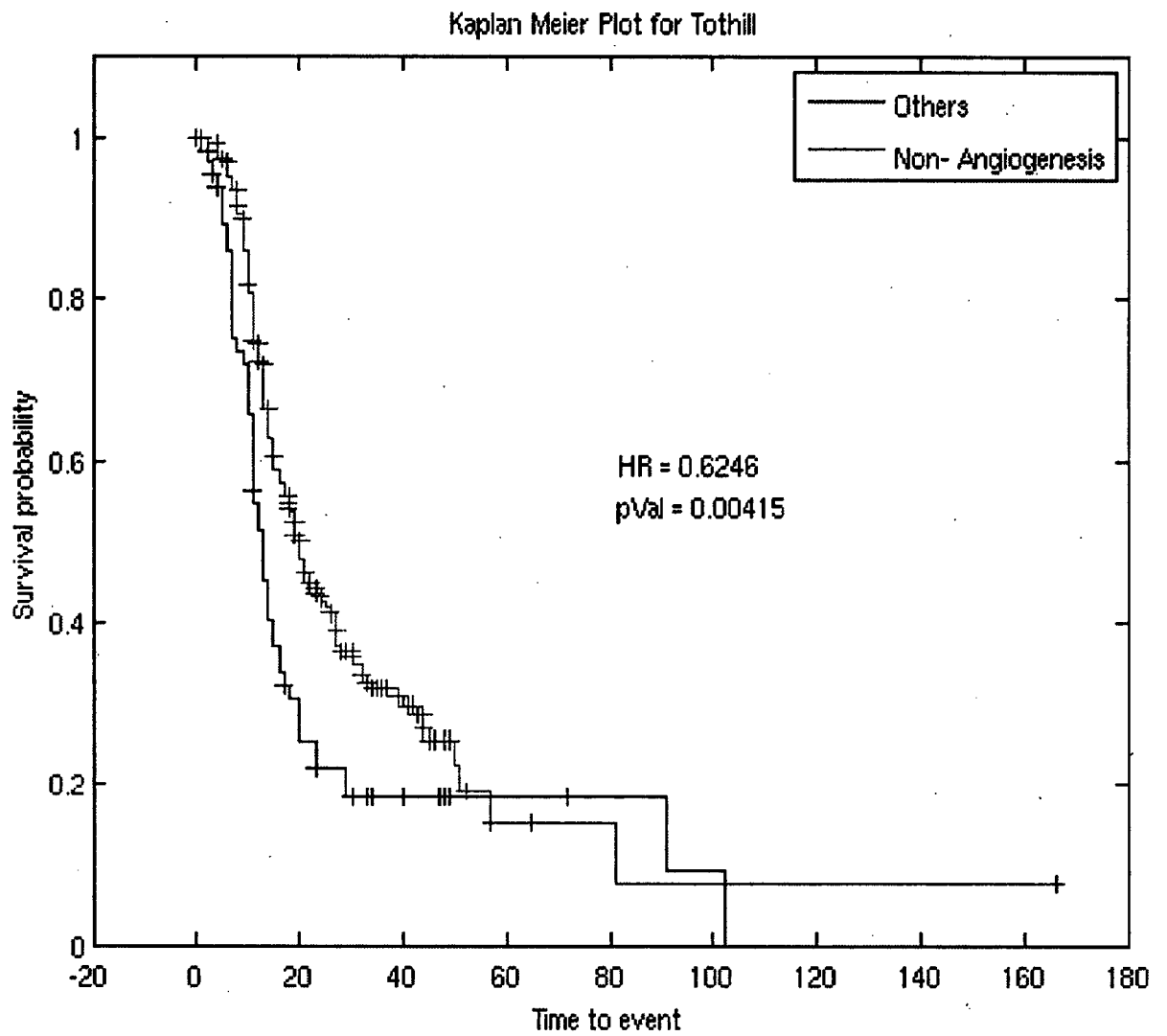


Figure 13

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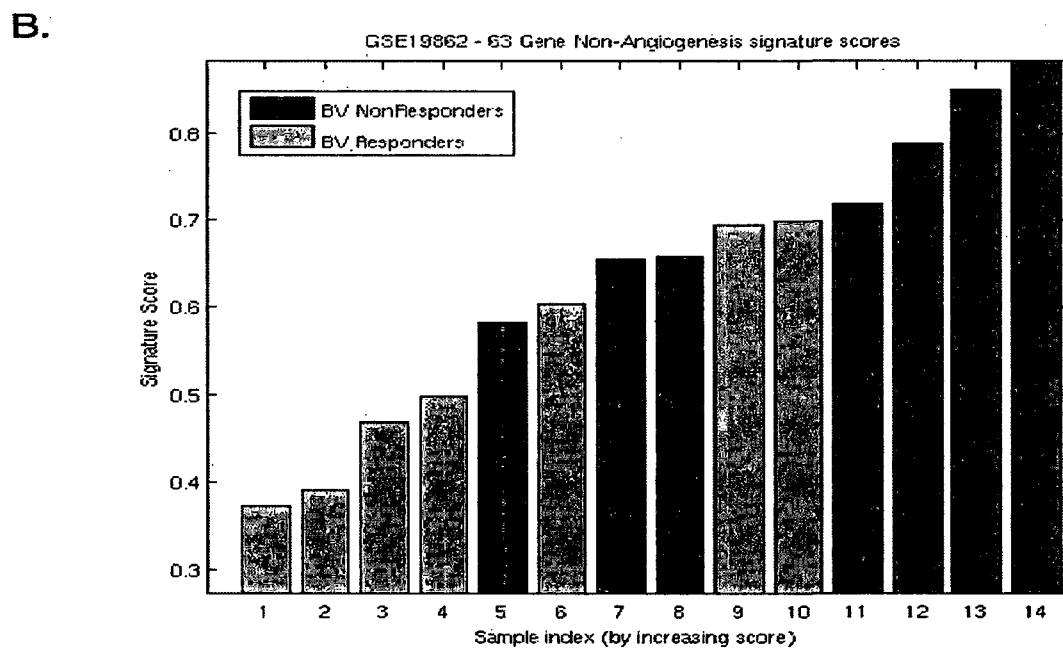
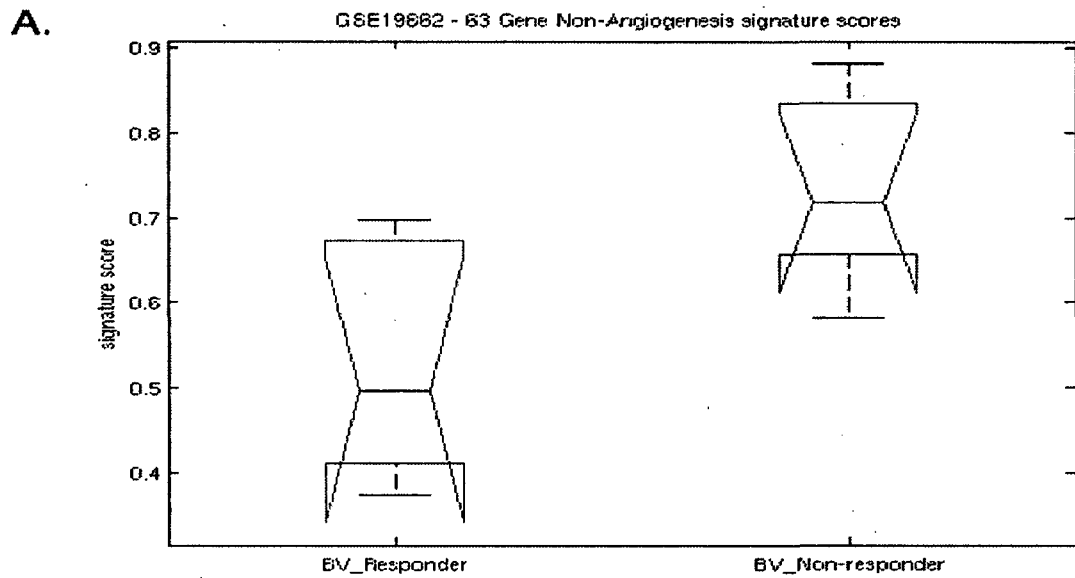


Figure 14

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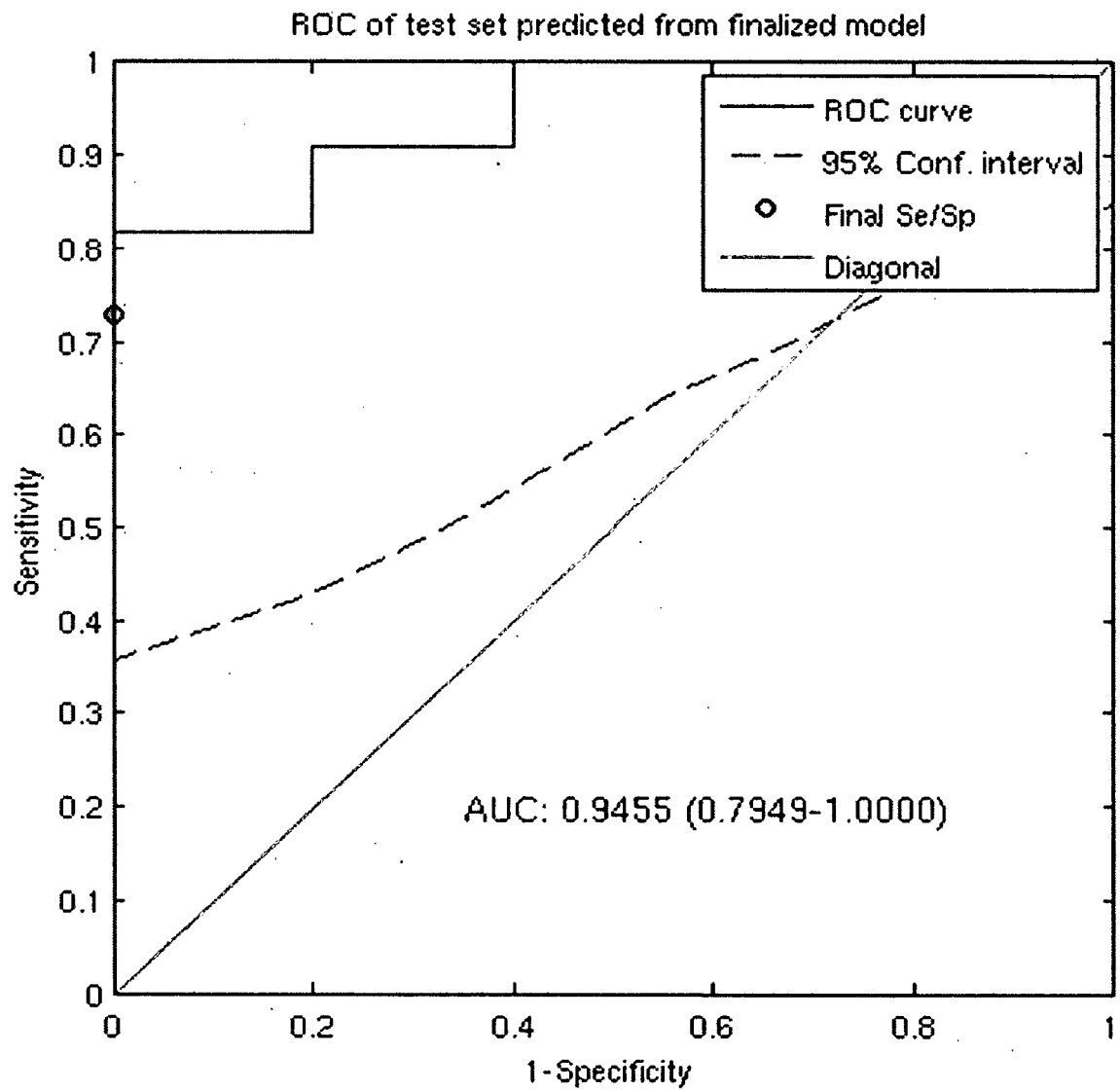


Figure 15

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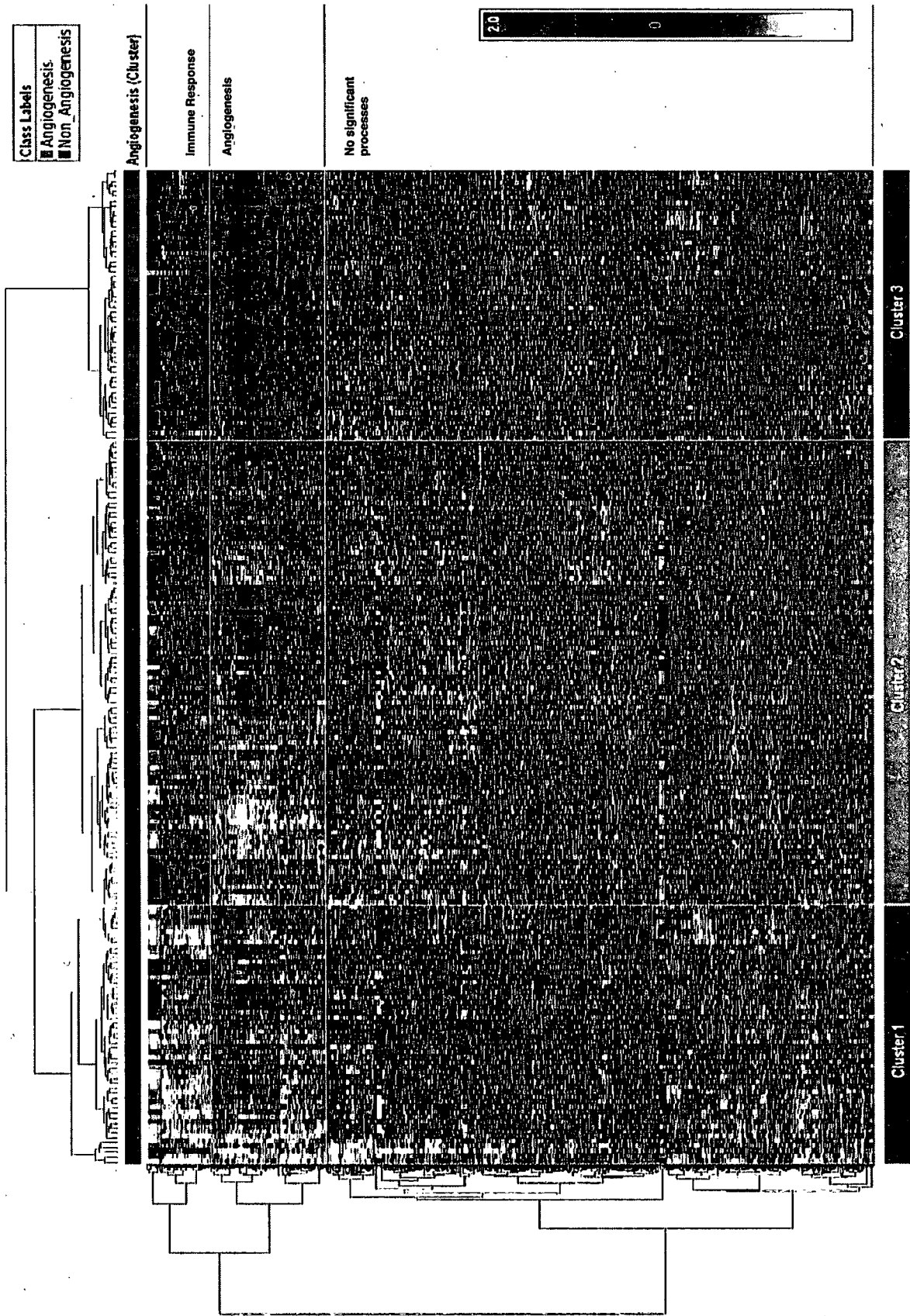


Figure 16

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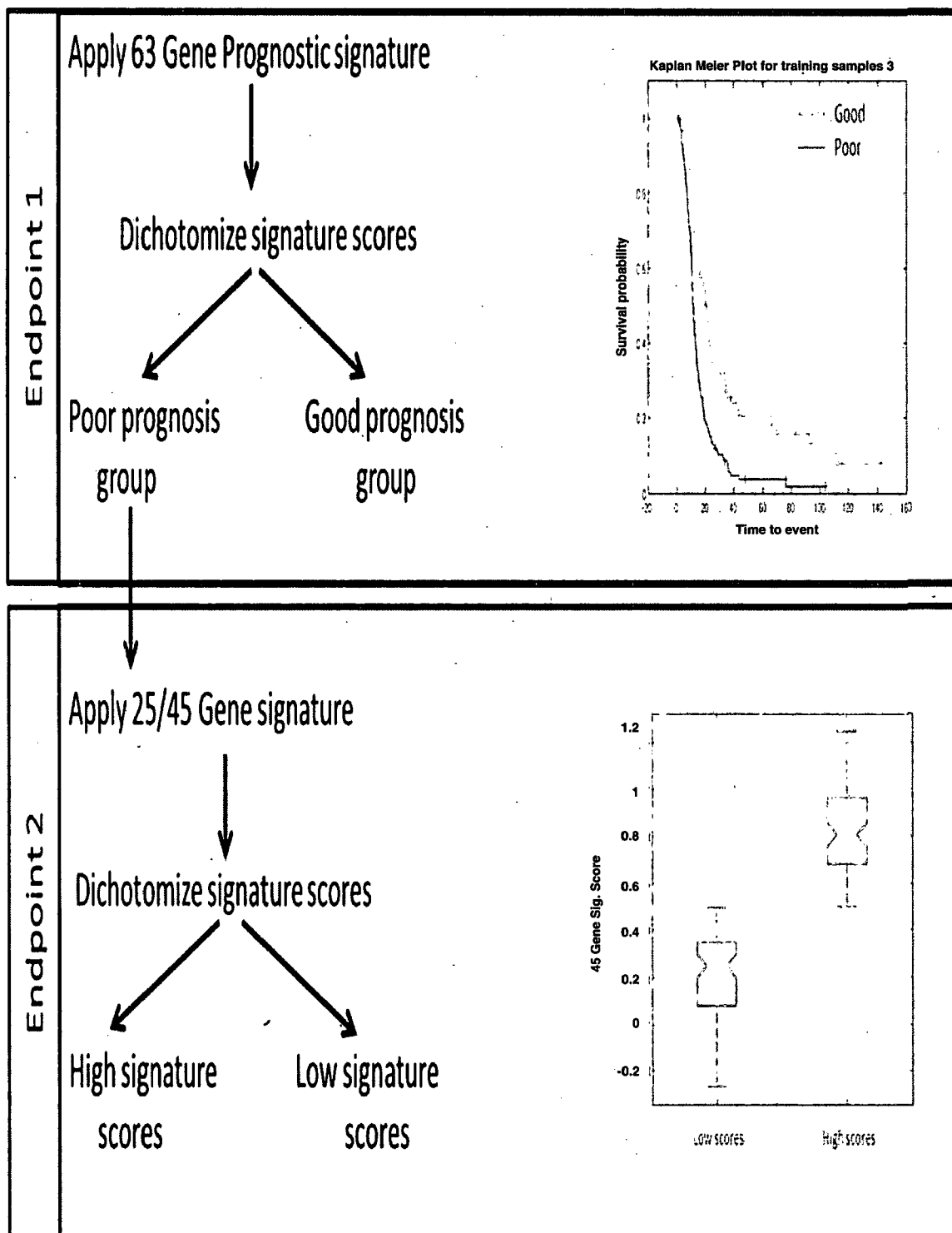
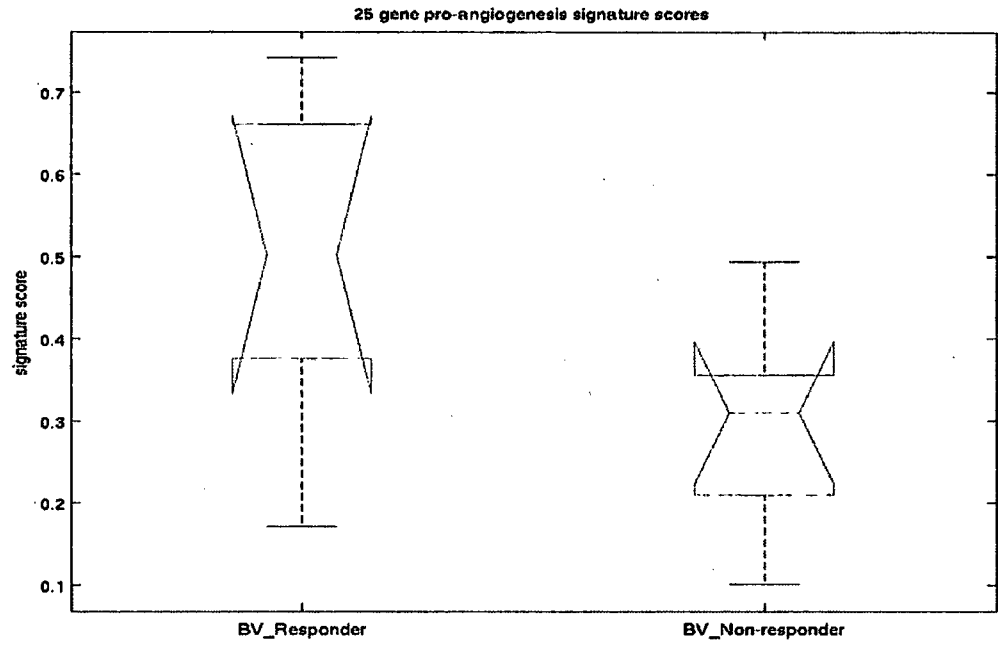


Figure 17

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A



B

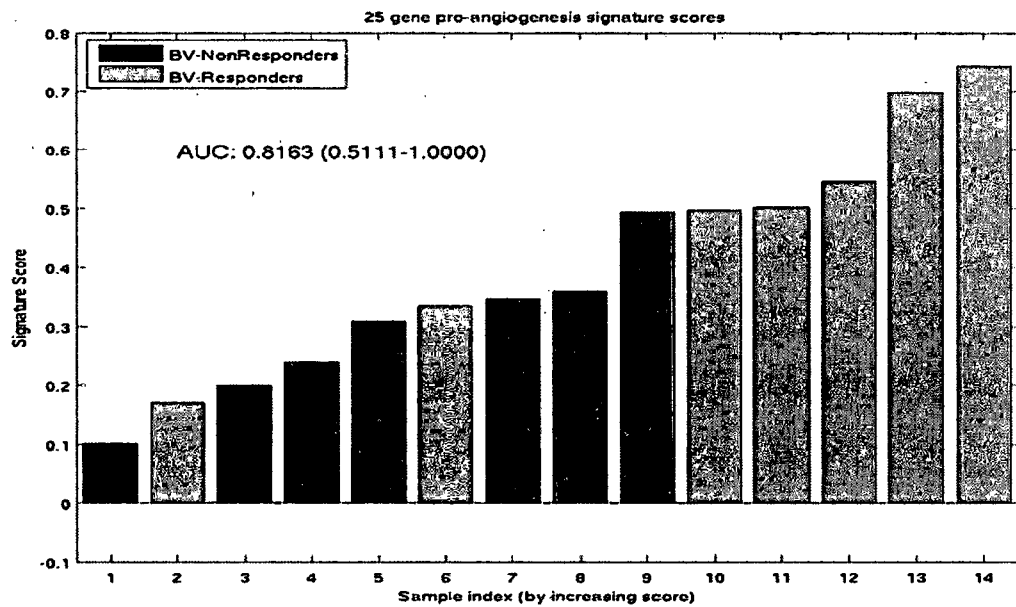
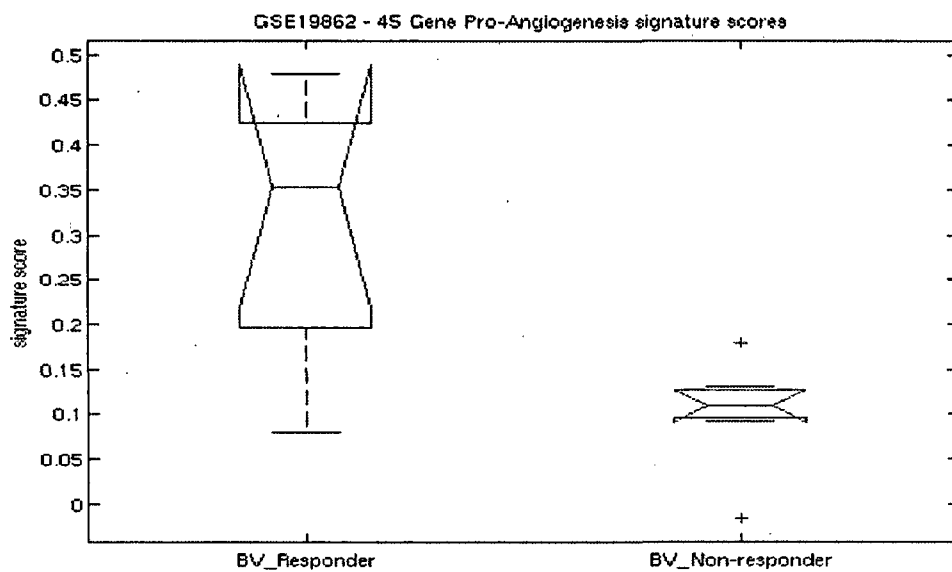


Figure 18

22/22

A



B

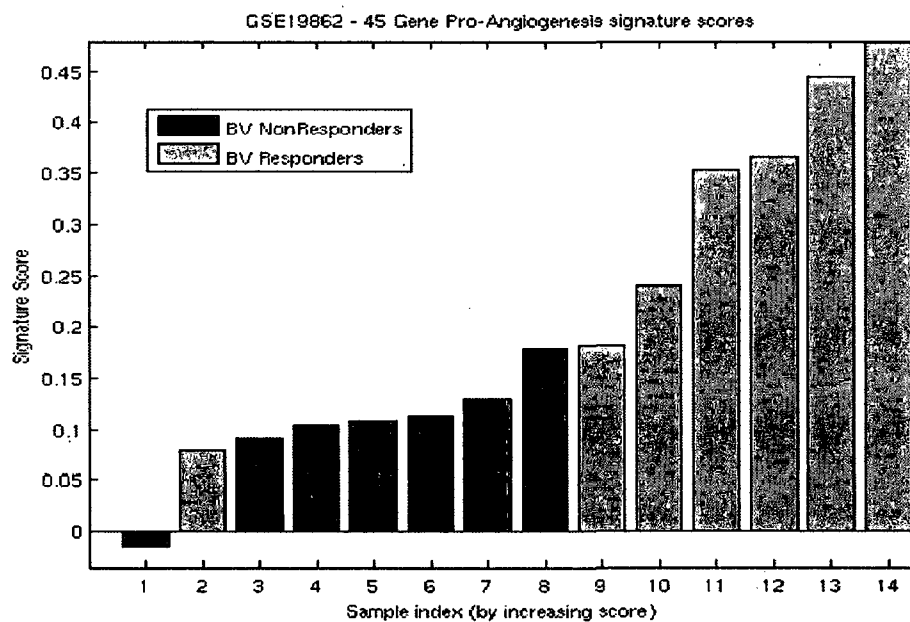


Figure 19

INTERNATIONAL SEARCH REPORT

International application No
PCT/GB2013/053202

A. CLASSIFICATION OF SUBJECT MATTER INV. C12Q1/68 ADD.		
According to International Patent Classification (IPC) or to both national classification and IPC		
B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) C12Q		
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched		
Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) EPO-Internal, BIOSIS, EMBASE, WPI Data, Sequence Search		
C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	US 2006/127928 A1 (BACUS SARAH S [US] ET AL) 15 June 2006 (2006-06-15) paragraphs [0014], [0083], [0108] - [0109]	1,2,5,6, 8-10,12, 15,21, 22,26,27
X	LU Y ET AL: "INSULIN-LIKE GROWTH FACTOR-I RECEPTOR SIGNALING AND RESISTANCE TO TRASTUZUMAB (HERCEPTIN)", JOURNAL OF THE NATIONAL CANCER INSTITUTE, OXFORD UNIVERSITY PRESS, GB, vol. 93, no. 24, 19 December 2001 (2001-12-19), pages 1852-1857, XP008009958, ISSN: 0027-8874, DOI: 10.1093/JNCI/93.24.1852 page 1856	1,2,5, 8-10,12, 21,22, 26,27
☒ Further documents are listed in the continuation of Box C. ☒ See patent family annex.		
* Special categories of cited documents : "A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier application or patent but published on or after the international filing date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filing date but later than the priority date claimed "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art "&" document member of the same patent family		
Date of the actual completion of the international search 12 February 2014		Date of mailing of the international search report 24/04/2014
Name and mailing address of the ISA/ European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016		Authorized officer Schmitt, Anja

INTERNATIONAL SEARCH REPORT

International application No

PCT/GB2013/053202

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	ANTOINE ITALIANO ET AL: "Patterns of deregulation of insulin growth factor signalling pathway in paediatric and adult gastrointestinal stromal tumours", EUROPEAN JOURNAL OF CANCER, vol. 48, no. 17, 1 November 2012 (2012-11-01), pages 3215-3222, XP055101499, ISSN: 0959-8049, DOI: 10.1016/j.ejca.2012.05.021 the whole document	1,2,5,8, 10,11, 21,22,27
Y	----- WO 2011/005273 A1 (AVEO PHARMACEUTICALS INC [US]; LIN JIE [US]; ROBINSON MURRAY [US]; FEN) 13 January 2011 (2011-01-13) claims 1-5 the whole document	1-27
Y	----- WO 2009/061800 A2 (GENENTECH INC [US]; CHEN DANIEL S [US]; LE COUTER JENNIFER [US]; WU TH) 14 May 2009 (2009-05-14) claims 2-6	1-27
X,P	----- WO 2012/167278 A1 (ALMAC DIAGNOSTICS LTD [GB]; HARKIN DENNIS PAUL [GB]; MCDYER FIONNUALA) 6 December 2012 (2012-12-06) claims 1-68; examples 1-4; tables 1a, 1b, 2a, 2b; sequences 45,455,853	1,2, 4-15,21, 22,24-27 3,16-20, 23
Y,P		
X,P	----- DATABASE Geneseq [Online] 17 January 2013 (2013-01-17), "Human expression signature biomarker DNA, SEQ ID: 853.", XP002720107, retrieved from EBI accession no. GSN:BAH85778 Database accession no. BAH85778 sequence	1,2, 4-15,21, 22,24-27
A	----- WO 2004/108896 A2 (UNIV ARKANSAS [US]) 16 December 2004 (2004-12-16) claim 11 -----	1-27

INTERNATIONAL SEARCH REPORT

International application No.
PCT/GB2013/053202

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fees, this Authority did not invite payment of additional fees.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

3, 19, 23(completely); 1, 2, 4-18, 20-22, 24-27(partially)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.
- ☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. claims: 3, 19, 23(completely); 1, 2, 4-18, 20-22, 24-27(partially)

Method for predicting a subject's responsiveness to an anti-angiogenic therapeutic agent, said method further providing treatment prognosis, and method for diagnosing a subject as having a cancer, or being susceptible to developing a cancer, that is responsive to an anti-angiogenic therapeutic, said methods comprising measuring the expression levels of a biomarker panel in a subject's sample, wherein the biomarker panel comprises one or more biomarkers selected from Table 2C; determining a sample expression score for the biomarker panel; comparing the sample expression score to a threshold score; and classifying the subject as responsive or non-responsive to the anti-angiogenic therapeutic agent (as having a good or bad prognosis; or as having or being susceptible to developing said cancer) based on whether the sample expression score is above or below the threshold expression score; wherein said at least one marker selected from Table 2C is IGF2 ; or wherein said biomarker panel comprises the biomarkers listed in Table 2C.

- 2-10. claims: 1, 2, 4-18, 20-22, 24-27(all partially)

Method for predicting a subject's responsiveness to an anti-angiogenic therapeutic agent, said method further providing treatment prognosis, and method for diagnosing a subject as having a cancer, or being susceptible to developing a cancer, that is responsive to an anti-angiogenic therapeutic, said methods comprising measuring the expression levels of a biomarker panel in a subject's sample, wherein the biomarker panel comprises one or more biomarkers selected from Table 2C; determining a sample expression score for the biomarker panel; comparing the sample expression score to a threshold score; and classifying the subject as responsive or non-responsive to the anti-angiogenic therapeutic agent (as having a good or bad prognosis; or as having or being susceptible to developing said cancer) based on whether the sample expression score is above or below the threshold expression score; wherein said at least one marker selected from Table 2C is SOX11 (INS, CXCL17, SLC5A1, TMEM45A, CXCR2P1, MFAP2, MATN3, or RTP4).

- 11-63. claims: 1, 4-16, 20, 21, 24-27(all partially)

Method for predicting a subject's responsiveness to an anti-angiogenic therapeutic agent, said method further providing treatment prognosis, and method for diagnosing a

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

subject as having a cancer, or being susceptible to developing a cancer, that is responsive to an anti-angiogenic therapeutic, said methods comprising measuring the expression levels of a biomarker panel in a subject's sample, wherein the biomarker panel comprises one or more biomarkers selected from Table 2C; determining a sample expression score for the biomarker panel; comparing the sample expression score to a threshold score; and classifying the subject as responsive or non-responsive to the anti-angiogenic therapeutic agent (as having a good or bad prognosis; or as having or being susceptible to developing said cancer) based on whether the sample expression score is above or below the threshold expression score; wherein said at least one marker selected from Table 2C is the 11th (12th, 13th, ... 63rd) marker listed in said Table 2C.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No

PCT/GB2013/053202

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
US 2006127928 A1	15-06-2006	NONE	
WO 2011005273 A1	13-01-2011	AU 2009349657 A1 CA 2767246 A1 CN 102471799 A EP 2451967 A1 JP 2012531925 A KR 20120034778 A US 7615353 B1 WO 2011005273 A1	02-02-2012 13-01-2011 23-05-2012 16-05-2012 13-12-2012 12-04-2012 10-11-2009 13-01-2011
WO 2009061800 A2	14-05-2009	AU 2008324782 A1 CA 2703258 A1 CN 101910416 A EP 2222874 A2 JP 2011502513 A KR 20100095571 A RU 2010123381 A US 2009123930 A1 US 2011151468 A1 WO 2009061800 A2	14-05-2009 14-05-2009 08-12-2010 01-09-2010 27-01-2011 31-08-2010 20-12-2011 14-05-2009 23-06-2011 14-05-2009
WO 2012167278 A1	06-12-2012	CA 2838086 A1 EA 201391805 A1 EP 2715348 A1 SG 195208 A1 WO 2012167278 A1	06-12-2012 31-03-2014 09-04-2014 30-12-2013 06-12-2012
WO 2004108896 A2	16-12-2004	US 2005037389 A1 WO 2004108896 A2	17-02-2005 16-12-2004

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<110> Almac Diagnostics Limited

Harkin, Dennis Paul

Patterson, Fionnuala

Trinder, Claire

O'Brien, Eamonn J.

Michie, Caroline

Gourley, Charlie

Hill, Laura A.

Keating, Katherine E.

O'Donnell, Jude

Bylesjo, Max

Deharo, Steve

Proutski, Vitali

Kennedy, Richard

Davison, Timothy

Winter, Andreas

McCavigan, Andrena

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<211> 114

<212> DNA

<213> Homo sapiens

<400> 33

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<210> 34

<211> 112

<212> DNA

<213> Homo sapiens

<400> 34

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<210> 35

<211> 274

<212> DNA

<213> Homo sapiens

<400> 35

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gccgcgtgcg tgagaaccgc gccggtgtcc ccagagacca ggctgtgtcc ctcttctctt 180

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<210> 36

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<213> Homo sapiens

<400> 36

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gagacaactt cccaaagcac aaagcagttt ttccccctag gggtgggagg aagcaaaaga 180

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<210> 37

<211> 151

<212> DNA

<213> Homo sapiens

<400> 37

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<210> 38

<211> 201

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<213> Homo sapiens

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ggagttaggt cctcacttgg g 201

<210> 39

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<212> DNA

<213> Homo sapiens

<400> 39

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taatatcaag attactaaaa atgggggaaa ggacttttaa tctttttttc ataatatctt 120

tgacacatat tacagaag 138

<210> 40

<211> 205

<212> DNA

<213> Homo sapiens

<400> 40

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tgttatgtcc cagaactgat gttttttttt taaggtactg aaaagaaatg aagttgatgt 180

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<210> 41

<211> 269

<212> DNA

<213> Homo sapiens

<400> 41

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ctcagcaccc tccccagct tgatgtttgg gtctccccag caccctcctc cctggccggt 180

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cctcaataaa agccatttgc actttaaat 269

<210> 42

<211> 169

<212> DNA

<213> Homo sapiens

<400> 42

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tctgtgaaat tctcagagtg ttttaattgta ctcaatggta tcattacaat tttctgtaag 120

agaaaatatt acttatttat cctagtattc ctaacctgtc agaataata 169

<210> 43

<211> 234

<212> DNA

<213> Homo sapiens

<400> 43

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ttcagctgtt cgtgccttcc tttcttgtat ccaccaaagt ggagacaaat acatgatttc 120

aaagatacac agtacctact taattccagc tgatgggaga ccaaagaatt tgcaagtgga 180

tggtttggta tcactgtaaa taaaaagagg gcctgggaat tcttgcgatt ccat 234

<210> 44

<211> 168

<212> DNA

<213> Homo sapiens

<400> 44

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tttcctctcc agatattttt gggagtgaca aacattcttt catcctactt agcctaccta 120

gatttttcat gacgagttaa tgcattgtccg tggttgggtg cacctgta 168

<210> 45

<211> 232

<212> DNA

<213> Homo sapiens

<400> 45

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cctgttgga ttaatttaag cttaagtata tatcaacatt attttattgt gcaattaaaa 120

caatacaaat tcatggtttt ttaaagttaa aaattttaac cactgtaaca acagtttttg 180

tgttattttc tgtattaaac atcttgttgc acgcatttga ggatcatcagg gt 232

<210> 46

<211> 234

<212> DNA

<213> Homo sapiens

<400> 46

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tgattagttt tattttttta tttttacagg cttatcagtc tcactgttgg ctgtcattgt 120

gacaaagtca aataaacccc caaggacgac acacagtatg gatcacatat tgtttgacat 180

taagcttttg ccagaaaatg ttgcatgtgt ttacctcga cttgctaaaa tcga 234

<210> 47

<211> 147

<212> DNA

<213> Homo sapiens

<400> 47

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cctcaatata tattctcatt gtcaatc 147

<210> 48

<211> 149

<212> DNA

<213> Homo sapiens

<400> 48

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ggggaggggt ctctcctccc accccaaggc atcaagccct tctccctgca ctcaataaac 120

cctcaataaa tattctcatt gtcaatcag

149

<210> 49

<211> 152

<212> DNA

<213> Homo sapiens

<400> 49

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ggggaggggt ctctcctccc accccaaggc atcaagccct tctccctgca ctcaataaac 120

cctcaataaa tattctcatt gtcaatcagc aa 152

<210> 50

<211> 150

<212> DNA

<213> Homo sapiens

<400> 50

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aggggagggg tctctcctcc caccccaagg catcaagccc ttctccctgc actcaataaa 120

ccctcaataa atattctcat tgtcaatcag

150

<210> 51

<211> 151

<212> DNA

<213> Homo sapiens

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gggaggggtc tctctccca cccaaggca tcaagccctt ctccctgcac tcaataaacc 120

ctcaataaat attctcattg tcaatcagca a 151

<210> 52

<211> 147

<212> DNA

<213> Homo sapiens

<400> 52

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<211> 150

<212> DNA

<213> Homo sapiens

<400> 53

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gggaggggtc tctctcccca tccaagtca tccagccctt ctccctgcac tcatgaaacc 120

ccaataaata tcctcattga caaccagcaa 150

<210> 54

<211> 254

<212> DNA

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tcacgcatga agggagcacc gtggagaaga cagtggcccc tacagaatgt tcataggttc 120

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tcattgtcaa tcag 254

<210> 55

<211> 239

<212> DNA

<213> Homo sapiens

<400> 55

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ttccgaagtc actgcagcgg atgatggaac tgaatcgata cggtgttttc tgtccctcct 120

actttccttc acaccagaca gccccctcatg tctccaggac aggacaggac tacagacaac 180

tctttcttta aataaattaa gtctttacaa taaaaacaca actgcaaagt accttcata 239

<210> 56

<211> 270

<212> DNA

<213> Homo sapiens

<400> 56

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ttgtaatact tgcattgcttc ttagaccaga acatgtaggt ccccttgtgt ctcaatactt 120

tttttttctt aattgcattt gttggctcta ttttaatttt tttcttttaa aataaacagc 180

tgggaccatc ccaaagaca agccatgcat acaactttgg tcatgtatct ctgcaaagca 240

tcaaattaaa tgcacgcttt tgtcatgtca 270

<210> 57

<211> 147

<212> DNA

<213> Homo sapiens

<400> 57

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catttgaaac aatccatttt gtaactgaac cttatgaaat atatgtatct catggtacgt 120

attctctagc acagtctgag caattaa 147

<210> 58

<211> 97

<212> DNA

<213> Homo sapiens

<400> 58

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<210> 59

<211> 213

<212> DNA

<213> Homo sapiens

<400> 59

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ccaagaaaag tcaaggccct tcatgacctt gctgggcaca gaaaacaccc tcgtggagta 120

cactaatttg aactggactg gtctcagtgt gagcacttgg cacactttac taaacacata 180

tacaaccca ccgtgagtca actttaagt aaa 213

<210> 60

<211> 151

<212> DNA

<213> Homo sapiens

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atgagtgcta tgggtgttgaa aactgcagtg tccgttatga gtgccaaaaa tttgtcttga 120

aggcagctac actttgaagt ggtctttgaa t 151

<210> 61

<211> 116

<212> DNA

<213> Homo sapiens

<400> 61

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<210> 62

<211> 220

<212> DNA

<213> Homo sapiens

<400> 62

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atatgggata tccagatgag aagcaaata ttggagccaa tatgtaacat actttaaaag 120

tccaaggagc aaaatttgcc tgtccagctc cctctcccca agaaacaaca tgaatgagca 180

acttcagagt gtcaaacaac tgccattaaa cttaactcaa 220

<210> 63

<211> 262

<212> DNA

<213> Homo sapiens

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acccctccca ccccatact ggtactgctg taatgagcca agtggcagct aaaagttggg 120

ggtgttctgc ccagtccgt cattctgggc tagaaggcag gggaccttgg catgtggctg 180

gccacaccaa gcaggaagca caaactcccc caagctgact catcctaact aacagtcacg 240

ccgtgggatg tctctgtcca ca 262

<210> 64

<211> 72

<212> DNA

<213> Homo sapiens

<400> 64

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<210> 65

<211> 232

<212> DNA

<213> Homo sapiens

<400> 65

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tattggaaa tgtaacgggg accttttgca tacctgttta gaacaaaac caccatgaca 180

cagtttttat agtgtctgta tttttgtgat gcaatggtct tgtaaaggtt tt 232

<210> 66

<211> 53

<212> DNA

<213> Homo sapiens

<400> 66

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<210> 67

<211> 76

<212> DNA

<213> Homo sapiens

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aaaattgttc agtcca 76

<210> 68

<211> 132

<212> DNA

<213> Homo sapiens

<400> 68

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tgctatcctc ca 132

<210> 69

<211> 287

<212> DNA

<213> Homo sapiens

<400> 69

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tgggagctgg ggctgaagtt gctctgtacc catgaactcc cagtttgcga attatagaga 180

caatctatatt tggttacttgc acttggttatt cgaaccactg agagcgagat gggaagcata 240

gatatctata tttttatatt tactatgagg gccttgtaat aaatttc 287

<210> 70

<211> 36

<212> DNA

<213> Homo sapiens

<400> 70

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<211> 157

<212> DNA

<213> Homo sapiens

<400> 71

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aaggacaatt ttgaccttgt tcaacctttc cacaaag 157

<210> 72

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atgagtgcga cggccggcaa gccccgctc cccaggctct cggggtcgcg cgaggatgct 120

tggcacgtac cccgtgtaca tacttcccgg gcgcccagca tggaaataaa gcacccagcg 180

ctgccctggg cccctgcgca actttcttgt ac 212

<210> 73

<211> 225

<212> DNA

<213> Homo sapiens

<400> 73

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aactgcaagt gatttaaaaa ttagagaata taatttttaa agctattgaa agtttcaacc 120

agaaaacctc aagtgaattt tgtatgtaaa tgaaattttg aatgtaagtt ctgtgattct 180

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<210> 74

<211> 287

<212> DNA

<213> Homo sapiens

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tagaagcaaa caaaatactt ttaccactt aaaaagagaa tataacattt tatgtcacta 120

taatcttttg tttttaagt tagtgtatat ttgtttgtga ttatcttttt gtggtgtgaa 180

taaatctttt atcttgaatg taataagaat ttggtggtgt caattgctta tttgttttcc 240

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<210> 75

<211> 276

<212> DNA

<213> Homo sapiens

<400> 75

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<211> 222

<212> DNA

<213> Homo sapiens

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atgtTTTTta ctccaattca taaatctatt cataagTctt tggtacaagT ttacatgata 180

aaaagaaTg tgattTgtct tccTtctTt gcactTtTga aa 222

<210> 77

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<213> Homo sapiens

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aacagataat agcaacttgg gaaatgctta tgttacaggt tacgtgagaa caatcatgta 120

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tt 182

<210> 78

<211> 212

<212> DNA

<213> Homo sapiens

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tgctaactcc ccgcgtctcc tgaatttcag tcattcatgt acccgctcg aaatttttgc 180

aatatctgtg taccaactgt ccatttactt aa 212

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<211> 238

<212> DNA

<213> Homo sapiens

<400> 79

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gtagctggga ccataggctc acaacaccac acctggcaaa ttgattttt ttttttttcc 180

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cactttcctt ccctgaagaa atatctgtga accttctttc tgttcagtcc taaaattcga 240

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<210> 81

<211> 129

<212> DNA

<213> Homo sapiens

<400> 81

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atatgtatgt atgtgttggtg tacacgatgt tttagtgtga aaaatatgta aaagagctct 120

acttggctt 129

<210> 82

<211> 178

<212> DNA

<213> Homo sapiens

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aacaatataa tatttttaaaa tgtataaata attatgaatt ttgttttaga acaaagagga 120

ttactgatat ttgtttccct atgaatggca aaaggtttag ctactactg catttctg 178

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<211> 135

<212> DNA

<213> Homo sapiens

<400> 83

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ccgagaaaaa taaat 135

<210> 84

<211> 235

<212> DNA

<213> Homo sapiens

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gttgctgtac acagatgcta cagacttgta ctaacacacc gtaatttggc atttg 235

<210> 85

<211> 177

<212> DNA

<213> Homo sapiens

<400> 85

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ctttcccatc ctcaaaaaag ggccatttta tgatgcattg cacaccctct ggggaaattg 120

atctttaaat tttagacag tataaggaaa atctggttgg tgtcttaca gtgagct 177

<210> 86

<211> 236

<212> DNA

<213> Homo sapiens

<400> 86

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cttttccaac ctgtatcaat ttttacaact tttttcctga aagcagttta gtccatactt 120

tgactgaca tactttttcc ttctgtgcta aggtaaggta tccaccctcg atgcaatcca 180

ccttggtgtt tcttaggggtg gaatgtgatg ttcagcagca aacttgcaac agactg 236

<210> 87

<211> 243

<212> DNA

<213> Homo sapiens

<400> 87

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cctgcccttt cccttcagaa aacgatggca ggcattcctt tgagttttaca agcagagact 180

cactccaacc caaactagct gggagttcag aaccatggtg gaataaagaa atgtgcatct 240

ggt 243

<210> 88

<211> 221

<212> DNA

<213> Homo sapiens

<400> 88

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tcaaattgtca gcttaaaatt ggtaattgaa tggaagcaaa attataagaa gaggaaatta 120

aagtcttcca ttgcatgtat tgtaaacaga aggagatggg tgattccttc aattcaaaag 180

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<210> 89

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<400> 89

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cttcagaata tttatcttac ttacaatcct caagttttaaa ttgattttaaa atattttttca 180

atacaacagt ttaggtttaaa gatgaccaat gacaatgacc acctttgcag aaagtaaact 240

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<211> 225

<212> DNA

<213> Homo sapiens

<400> 90

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aaatatgggt gtatgcttgt atacgttagag cagataaaaa agacggaagg cataactaaaa 180

aatgttgagt gggttatcttt gtatgggtgga acaaagtcac tgtaa 225

<210> 91

<211> 182

<212> DNA

<213> Homo sapiens

<400> 91

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aaatcatata ttaagacttt ccaaagatga ggtccctggt ttttcatggc aacttgatca 120

gtaaggattt cacctctgtt tgtaactaaa accatttact atatgttaga catgacattc 180

tt 182

<210> 92

<211> 157

<212> DNA

<213> Homo sapiens

<400> 92

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agagtcaaga attttgttgg attgtgtttg tgtgtgcata tatttgatat catcattata 120

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pctgb2013053202-seq1.txt

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<211> 201

<212> DNA

<213> Homo sapiens

<400> 93

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gccacacgga accctgtatt ttgcacacag caaaacaaac aatgttttagc tttatttatg 180

gtattttgatg ctgtaaattgg a 201

<210> 94

<211> 35

<212> DNA

<213> Homo sapiens

<400> 94

atattatttg attatggttc ctgaaggtca ttaaa 35

<210> 95

<211> 249

<212> DNA

<213> Homo sapiens

<400> 95

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cagaataggt tccgttttgg gcggtgggtc tcgagcctgc cattcaaac caaagcaaata 120

tggagcattt ctcaacaat ggtattgaag ttcctttttg ttctcaaaag ttgtgaccgt 180

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ttttattaa 249

<210> 96

<211> 203

<212> DNA

<213> Homosapiens

<400> 96

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ttgaaaaagt tccatgactc gaatatctga aatgaagaaa acaaaccgac tcacaaacct 180

ccaagtagct ccaaagcaa ttt 203

<210> 97

<211> 73

<212> DNA

<213> Homo sapiens

<400> 97

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tgtattaatc ccc 73

<210> 98

<211> 123

<212> DNA

<213> Homo sapiens

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cgaagtttgt tcatcagact cctgtgcaac tttcccaatg tggcctaaaa atgcaacttc 120

ttt 123

<210> 99

<211> 132

<212> DNA

<213> Homo sapiens

<400> 99

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attataaaaa gtatttgaaa tttgcacatt taattgtccc taatagaaag ccacctattc 120

tttgttgga tt 132

<210> 100

<211> 189

<212> DNA

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acccccctccc ccaccacct ctctggcttc catgctccgc ctgtaaaatg ggggcgctat 120

tgcttcagct gctgaaggga gggggctggc tttgagagcc ccaggactgg ctgccccgtg 180

acacatgct 189

<210> 101

<211> 265

<212> DNA

<213> Homo sapiens

<400> 101

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tccgcctgta aaatgggggc gctattgctt cagctgctga agggaggggg ctggctttga 180

gagccccagg actggctgcc ccgtgacaca tgctttaaga agctcgtttt ttagacctct 240

tcctggaata aacatctgtg tctgt 265

<210> 102

<211> 174

<212> DNA

<213> Homo sapiens

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aaggggtcccc ctgctgactg gagagctggg aatatggcat ttggacactt catttgtaaa 120

tagtgtacat tttaaacatt ggctcgaaac ttcagagata agtcatggag agga 174

<210> 103

<211> 239

<212> DNA

<213> Homo sapiens

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aattgcagat tattttgcag agaggggaatt gcatgtttgt gttgtatatt tagtatgaac 120

ttttttcaga atataatatt ttttagttat caaaagtagt tggaaaacat ttgcaagact 180

atgaacatag aattgctgct tttatatattt aactgcagat tgtgaatttc actgcctta 239

<210> 104

<211> 110

<212> DNA

<213> Homo sapiens

<400> 104

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ttaaaagttt agggttttct cttggttgta gaggggccca gaattgcatt 110

<210> 105

<211> 292

<212> DNA

<213> Homo sapiens

<400> 105

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acagggaggt gaccccaggt ttctatgtgt agggcgggag gatgttttgg gacacagttc 180

aattctcatt tgtcacacac tttggctatt agagatcaac cccttcgctc ctgtgtcttg 240

caatggcagc cttggcaaac gctaaatgaa aatcgtgaca acacttgtgt ta 292

<210> 106

<211> 223

<212> DNA

<213> Homo sapiens

<400> 106

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ataatttata agtaacactg ttgaaaccct gatcccagtg gaggctgtaa cccacctgcc 180

cccgaccac cccctgacc cctgttaccg catttgtgtg tat 223

<210> 107

<211> 275

<212> DNA

<213> Homo sapiens

<400> 107

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agaacataaa tgcacaaaat ctgtacatgt ctcccatcag aaagattcat tggcatgcca 120

caggggattt tcctccttca tcctgtaaag gtcaacaata aaaaccaaat tatggggctg 180

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cttttgtcac actagcatag agaatgtggt gaaatttaac ttgtgaagct tgtatgtggt 240

tggtgatctt ttttttcctt acagacaccc ataata 275

<210> 108

<211> 196

<212> DNA

<213> Homo sapiens

<400> 108

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acagtactca ctttttccaa atgacaccta taattgccta gaaatatctt tttcttacct 120

gttatattatc aatttttccc agtatatttta tacggaaaaa attgtattga aaacacttag 180

tatgcagttg ataaga 196

<210> 109

<211> 129

<212> DNA

<213> Homo sapiens

<400> 109

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agaccctcgg cacctgctac ttaccaactg gaaaatttta tgcattccat gaagcccaga 120

tacacaaaa 129

<210> 110

<211> 296

<212> DNA

<213> Homo sapiens

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ggccggccgg gtgcttttgg gggctcgtcg gggggacagc tccactttga ctggcacagt 120

ctttgcatgg agacttgagg agggagggct tgaggttggt gaggttaggt gcgtgtttcc 180

tgtgcaagtc aggacatcag ttgattaaa ggtggtgcca atttatttac atttaaactt 240

gtcagggtat aaaatgacat cccattaatt atattgttaa tcaatcacgt gtatag 296

<210> 111

<211> 108

<212> DNA

<213> Homo sapiens

<400> 111

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cattcctgcc ccgccccatct ttttgtgtct cgctgtgata gatcaata 108

<210> 112

<211> 243

<212> DNA

<213> Homo sapiens

<400> 112

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gtgaatcttt taccctgaaa aaaagccata atgaattaag ccagactgac cacttgcttg 120

gagtgtgtgc ttgaaaaaac cagagcaata ctgttgggta ttgtatcagg cttcagtaca 180

aactggtaac accaatgtgg atcctgacag ctttcagttt tagcaaaaat acacgtgaaa 240

tct 243

<210> 113

<211> 52

<212> DNA

<213> Homo sapiens

<400> 113

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<210> 114

<211> 294

<212> DNA

<213> Homo sapiens

<400> 114

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gttttacccc tattcaagca actagaggcc agaaaatggg caaattatca ctaacaggtc 120

tttgactcag gttccagtag ttcattttta tgcctagatt cttttgtggt tgttgctggc 180

ccaatgagtc cctagtcaca tcccctgcc gagggagttt tttttttgtg agagacactg 240

taaacgacac aagagaacaa gaataaaaca ataactgtgt gtgttttggc tgag 294

<210> 115

<211> 277

<212> DNA

<213> Homo sapiens

<400> 115

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catggcggtt gtggcagctg gggagggttg gcccacacag ccctcctgtg cctgcttccc 120

tgtgtgtcgg ggtcctccag ggagctgacc cagaggtgga ggccacggag gcagggtctc 180

tggggactgt cgggggggtac agaggagaa ggctctgcaa gagctccctg gcaatacccc 240

cttgtgtaat tgctttgtgt gcgacaggga ggaagtt 277

<210> 116

<211> 173

<212> DNA

<213> Homo sapiens

<400> 116

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agagtcctgg agccacagtt ttttttgctt tgcattgtag gagagggaat aagtgctaga 120

gactatgtcg ctttcctgag ctaccgagag cgctcgtgaa ctggaatcaa ctg 173

<210> 117

<211> 217

<212> DNA

<213> Homo sapiens

<400> 117

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ttttcactgc tgaatatgat gttaactatg aactttttat acatgtatatt actatgttga 120

ggtaattttcc ttttactcct ggtttaagtg ttttttgttt ttttttgttt tttttttttt 180

ttaaatcatg gaaggacttg ggttttatca aatgtct 217

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<211> 286

<212> DNA

<213> Homo sapiens

<400> 118

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ccgaggggca cgcatttgac atggaggggc aggggcatgt gcatggggtg gccagcagcc 180

cctcgcatga cctggcaaag gaagaaggca gccaccctcc agtccaaggc cagttatctt 240

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<211> 168

<212> DNA

<213> Homo sapiens

<400> 119

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gtataattac cccatttgct cttttaatgg aaatttcaaa ggacgggagt attttgttgg 120

ttggtgtcca ggtttgtggc actgttccaa gaggccttac acacacac 168

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<211> 150

<212> DNA

<213> Homo sapiens

<400> 120

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aggggagggg tctctcctcc caccccaagg catcaagccc ttctccctgc actcaataaa 120

ccctcaataa atattctcat tgtcaatcaa 150

<210> 121

<211> 177

<212> DNA

<213> Homo sapiens

<400> 121

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gtagggtaga aaaagaggga gtcacttgat gctttcaggt taatcagagc tatgggtgct 120

acaggcttgt ctttctaagt gacatattct tatctaattc tcagatcagg ttttgaa 177

<210> 122

<211> 124

<212> DNA

<213> Homo sapiens

<400> 122

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acatttctct gtcttttttg atcagtgtcc tatacatcga aggtgtgcat atatgttgaa 120

tgac 124

<210> 123

<211> 64

<212> DNA

<213> Homo sapiens

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ggga 64

<210> 124

<211> 167

<212> DNA

<213> Homo sapiens

<400> 124

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cctctggagc aggtctggag gggccatggg gcagtcctgg gtgtggggac acagtcgggt 120

tgacccaggg ctgtctccct ccagagcctc cctccggaca atgagtc 167

<210> 125

<211> 36

<212> DNA

<213> Homo sapiens

<400> 125

caccactaaa agatcgagc ttgcctggtg cagtgg 36

<210> 126

<211> 129

<212> DNA

<213> Homo sapiens

<400> 126

aatgcatatg gaggtaggct gaaaagaatg taatTTTTAT tttctgaaat acagatttga 60

gctatcagac caacaaacct tccccctgaa aagtgagcag caacgtaaaa acgtatgtga 120

agcctctct 129

<210> 127

<211> 150

<212> DNA

<213> Homo sapiens

<400> 127

aatgttcata ggttctcatc cctcaccccc caccacggga gactagagct gcaggatccc 60

aggggagggg tctctcctcc caccccaagg catcaagccc ttctccctgc actcaataaa 120

ccctcaataa atattctcat tgtcaatcaa 150

<210> 128

<211> 83

<212> DNA

<213> Homo sapiens

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gccactggtg ttaagatata ttt

83

<210> 129

<211> 121

<212> DNA

<213> Homo sapiens

<400> 129

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tttcccttaa agatgtcctg ttgctttagt gatatttaga cccctctcag ttaagaaatg 120

c 121

<210> 130

<211> 257

<212> DNA

<213> Homo sapiens

<400> 130

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aaaatattgg ttcacgtaga gtgcaaatta gaactagaaa gttttatacg attatcattt 120

pctgb2013053202-seq1.txt

tgagatgtgt taaagtaggt tttcactgta aaatgtatta gtgtttctgc attgccatag 180

ggcctgggta aaactttctc ttaggtttca ggaagactgt cacatacagt aagctttttt 240

ccttctgact tataata 257

<210> 131

<211> 285

<212> DNA

<213> Homo sapiens

<400> 131

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agaccccagg ctggacatgc tgactgtcct ctcccctcca gcctttggcc ttggcttttc 120

tagcctatth acctgcaggc tgagccactc tcttcccttt cccagcatc actccccaag 180

gaagagccaa tgttttccac ccataatcct ttctgccgac ccctagttcc ctctgctcag 240

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<210> 132

<211> 105

<212> DNA

<213> Homo sapiens

<400> 132

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ggggtagaac ttaggaaaaa taaagttggt tcttattcaa tattt 105

<210> 133

<211> 205

<212> DNA

<213> Homo sapiens

<400> 133

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tctccttcct ctgaacttct ttaggagtca ctgcttgtgt ggcttcctggg acacttaacc 180

aatgccttct ggtactgcca ttctt 205

<210> 134

<211> 189

<212> DNA

<213> Homo sapiens

<400> 134

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tataaaaagc aaaagtatct atagacacag acacttgcct atacagagac ataaccacac 120

acactcagag gatagtgaac aaatctgtct ttgacttacg acccattttg caagacttaa 180

agccggaag 189

<210> 135

<211> 248

<212> DNA

<213> Homo sapiens

<400> 135

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aatgtttaat tttgcatcat aatttctaca ttgtccctga gtgtcagaac tataatttat 120

tccatttctc tctgtgtctg tgccaagaaa cgcaggctct gggcctgccc cttgccagg 180

aggccttgcc agcctgtgtg cttgtgggaa caccttgtag ctgagcttac aggtaccaat 240

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<210> 136

<211> 99

<212> DNA

<213> Homo sapiens

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tgcacctcat tccaactcct accgcgatac agaccaca 99

<210> 137

<211> 250

<212> DNA

<213> Homo sapiens

<400> 137

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ctcatagagg tacagtgcc atagatattc aaatgttgca tgttgaccag agggatttta 180

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ataaaaactgt 250

<210> 138

<211> 55

<212> DNA

<213> Homo sapiens

<400> 138

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<210> 139

<211> 237

<212> DNA

<213> Homo sapiens

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ggcacagcc atgaagtcac cgggatgaac ctatccttcc agtggctcgc tccctgtagc 120

tctgcctccc tctccatata tccttcccct acacctccct cccacacct cctactccc 180

ctgggcatct tctggcttga ctggatggaa ggagacttag gaacctacca gttggcc 237

<210> 140

<211> 216

<212> DNA

<213> Homo sapiens

<400> 140

gaggcagagg cttgggtaaa ctcatccac aaaccctatg ggggctgcca cgtcacaggc 60

ccaaaggact cttcttcagc agcatctttg caaaatgtct ttctctcaat gaagagcata 120

tctggacgac tgtgcaatgc tgtgtgctcc cgggatcagt aacccttcg ctgttcctga 180

aataaccttt cataaagtgc tttgggtgcc attcca 216

<210> 141

<211> 156

<212> DNA

<213> Homo sapiens

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ccccaggaaa aggaagaggt cgaaccaacc ctgcggaagg agcatggttt caggagttta 120

ttttaagact gctgggaagg aaacaggccc cathtt 156

<210> 142

<211> 151

<212> DNA

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<400> 142

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gtagatTTTT acaatctgta tctttgacaa ttctgggtgc gagtgtgaga gtgtgagcag 120

ggcttgctcc tgccaaccac aattcaatga a 151

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<211> 151

<212> DNA

<213> Homo sapiens

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gccagctcca ttcttccaca ctgctacta catttcctgc ctttttcttt cagtgttttt 120

ctaagactaa ataaatagca aactttcacc t 151

<210> 144

<211> 132

<212> DNA

<213> Homo sapiens

<400> 144

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attgacaacc aa 132

<210> 145

<211> 80

<212> DNA

<213> Homo sapiens

<400> 145

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aactttttgga ttgtaataaa 80

<210> 146

<211> 94

<212> DNA

<213> Homo sapiens

<400> 146

ctgggcttgg gtgcccataat aggaggtctg tatgttcacc aacagtgcgg aggggtcaca 60

cattgcaaaa cactgcccag aacagtaaaa agag 94

<210> 147

<211> 264

<212> DNA

<213> Homo sapiens

<400> 147

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aaggaatatt gaagttagat acaattactt acctttgagg gaaataattg ttggtaatga 180

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gatgtgatgt ttctcctgcc acctggaaac aaagcattga agtctgcagt tgaaaagccc 240

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<211> 286

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<213> Homo sapiens

<400> 148

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ttggcatgcc acaggggatt ctctccttc atcctgtaaa ggtcaacaat aaaaacaaaa 180

ttatggggct gcttttgtca cactagcata gagaatgtgt tgaaatttaa ctttgtaagc 240

ttgtatgtgg ttgttgatct tttttttcct tacagacacc cataat 286

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<400> 149

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42

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<211> 189

<212> DNA

<213> Homo sapiens

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cctttattta tgacgacttt atttattcta atatgatttt atagtattta tatatattgg

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180

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189

<210> 151

<211> 211

<212> DNA

<213> Homo sapiens

<400> 151

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ttctccagaa tccaggccaa aaagttcaca gtcaaattggg gaggggtatt cttcatgcag 120

gagaccccag gccctggagg ctgcaacata cctcaatcct gtcccaggcc ggatcctcct 180

gaagcccttt tcgcagcact gctatcctcc a 211

<210> 152

<211> 211

<212> DNA

<213> Homo sapiens

<400> 152

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catttcttct gcacatctac ttgcttaaatt tgtgggcaaa agagaaaaag aaggattgat 120

cagagcattg tgcaatacag tttcattaac tccttcccc gctcccccaa aaatttgaat 180

ttttttttca acactcttac acctgttatg g 211

<210> 153

<211> 89

<212> DNA

<213> Homo sapiens

<400> 153

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ttagtaaagt ttccaacaaa tagaaatta 89

<210> 154

<211> 162

<212> DNA

<213> Homo sapiens

<400> 154

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tgggatcaaa ctggcctgca aaaccatagt cagttaattc tt 162

<210> 155

<211> 86

<212> DNA

<213> Homo sapiens

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tatactcccg gatatcatat tatttta 86

<210> 156

<211> 233

<212> DNA

<213> Homo sapiens

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ttggccaaca atcctttctg cccacttccc cttccccaat tactattccc ttgacttca 180

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<211> 146

<212> DNA

<213> Homo sapiens

<400> 157

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ctcaataaat attctcattg tcaagg 146

<210> 158

<211> 265

<212> DNA

<213> Homo sapiens

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ctgggaccag aggaagaagc aacacattgt cttctccaaa ctccaagaat gaaaaggctc 120

tgggccgcaa aataaactcc tgggaatcat caaggagtgg gcattcattc ctgagcaact 180

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<211> 186

<212> DNA

<213> Homo sapiens

<400> 159

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cacagg 186

<210> 160

<211> 41

<212> DNA

<213> Homo sapiens

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tacaagacca cgcctcccgt gctggactcc gacggctcct t 41

<210> 161

<211> 45

<212> DNA

<213> Homo sapiens

<400> 161

aacagaaaag aaactgtaga ccttgggaca atcaacattt aaata 45

<210> 162

<211> 211

<212> DNA

<213> Homo sapiens

<400> 162

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catttcttct gcacatctac ttgcttaaata tgtgggcaaa agagaaaaag aaggattgat 120

cagagcattg tgcaatacag tttcattaac tccttccttc gtcccccaa aaatttgaat 180

ttttttttca acactcttac acctgttatg g 211

<210> 163

<211> 105

<212> DNA

<213> Homo sapiens

<400> 163

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gctgaggact ccctccatgt ggccccaggt gccaccaata aaaat 105

<210> 164

<211> 175

<212> DNA

<213> Homo sapiens

<400> 164

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tctctgtgta agtcttttcc ttaaggtaat aaaccatcag caaagtcaca tactggagtt 120

ggtggctttt tttgtacagg cagttgttat gagacaatga tggagcattg agcat 175

<210> 165

<211> 65

<212> DNA

<213> Homo sapiens

<400> 165

ttaactccat atgtgttcct cttgttttaa ttttgtcaac cagtgcaggt gaccgacaaa 60

attcc 65

<210> 166

<211> 114

<212> DNA

<213> Homo sapiens

<400> 166

aaggagctga cacacggaga gtcacaggct atacagctgc ttcgagcagc gggaatgttt 60

gtcttgggat tagatgctga cgtgtggtga aatgttacag agagcccaga ggaa 114

<210> 167

<211> 100

<212> DNA

<213> Homo sapiens

<400> 167

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caaggcgcac cacacaaaag gcaccaagac gtgaaacttt 100

<210> 168

<211> 273

<212> DNA

<213> Homo sapiens

<400> 168

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attgaagtgg aatgtgtaaa agctgaatct gcacaggctt cagcaaaaat ggtggaggaa 120

atgcaaataa agtatcagca gatgatggaa gagaaagaga agagttatca agaacatgtg 180

aaacaattga ctgagaagat ggagaggag agggcccagt tgctggaaga gcaagagaag 240

accctcacta gtaaacttca ggtatccaaa tgc 273

<210> 169

<211> 36

<212> DNA

<213> Homo sapiens

<400> 169

agcaggatca agggccggaa ataaaggctg ttgtaa 36

<210> 170

<211> 109

<212> DNA

<213> Homo sapiens

<400> 170

agaattattg catttgagct ccgctcccct tccgaaccaa ggtataaaag taaatcaagc 60

cccttcctcg gggccgagag aattttggaa agtcaagcct tctcttggc 109

<210> 171

<211> 115

<212> DNA

<213> Homo sapiens

<400> 171

gcatgctcag tcttttcctc ttatctacaa tacaaagggt ttgtctgaaa agtctggttt 60

tttttctttt tacaaatgta ccttagctgc atcaacagga gtaagatgta gaaaa 115

<210> 172

<211> 175

<212> DNA

<213> Homo sapiens

<400> 172

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gtgcaatgca aggaagtttt ggggggtgatg aactgtcctg tatcccgatt gtggtggcag 120

ttacatgaat ctatatttgt gttaagatct atagatctgt actccctcaa aaagt 175

<210> 173

<211> 279

<212> DNA

<213> Homo sapiens

<400> 173

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gcacggtcag gtagggctg gacagatgag gaagagctag caaagggggc ttgaggagca 120

gtggccacta agacaggagt gtgacatttt agaagccaaa agaagaccat gtaattcaag 180

ggagaggtat gatttgctgg gtcagatcta aaaataaatc acacgttttt ttaaactgta 240

gtaattaacc actgaaaact tatgagtgat ccaatatta 279

<210> 174

<211> 74

<212> DNA

<213> Homo sapiens

<400> 174

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aatgtaataa actc 74

<210> 175

<211> 48

<212> DNA

<213> Homo sapiens

<400> 175

gccgagatcg tgctagggtg actggagcaa aacccttca agaaaaga 48

<210> 176

<211> 164

<212> DNA

<213> Homo sapiens

<400> 176

gtgtggatgc taaggtgttt gttttgtttt gtatatttat gtagcgctg ggtattgtgc 60

ctagaaatga agtcattatt agggatttaa atatgcaact catggagtgg atgagaccag 120

ctagaaagat aatagagtgt gaagaggaga tcggaaattc aata 164

<210> 177

<211> 34

<212> DNA

<213> Homo sapiens

<400> 177

attccaggac tttggcgctt tcaccgggag catg 34

<210> 178

<211> 32

<212> DNA

<213> Homo sapiens

<400> 178

cacaaagctc tgtcaataag tgatacatgt tt 32

<210> 179

<211> 141

<212> DNA

<213> Homo sapiens

<400> 179

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cttttagtggt agaatgacag aacttaggga tcccttgacg gctagaacaa agttctgacc 120

cttagaccaa atctttatgt t 141

<210> 180

<211> 211

<212> DNA

<213> Homo sapiens

<400> 180

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gatactgagc tttctctgtg ttcttgccgt taaccattgc cggtttgtgg gagattaaga 120

agtcgatgag ttttatggag aattaattta ttttgatata gacagatgga cgggtcatga 180

aaatttggtg acatacttta ctaaactgct a 211

<210> 181

<211> 127

<212> DNA

<213> Homo sapiens

<400> 181

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atggcat 127

<210> 182

<211> 251

<212> DNA

<213> Homo sapiens

<400> 182

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atacaggatc tccagacgaa aatgagacga cgaaaggcat gtaccataag ctaaagacca 120

gagccttcct gtcaccccta accaaggcat aattgaaaca attttagaat ttggaacaag 180

cgtcactaca ttgataata attagatctt gcatcataac accaaaagtt tataaaggca 240

tgtggtacaa t 251

<210> 183

<211> 248

<212> DNA

<213> Homo sapiens

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gtgtcctccc acagtcccgc tgtttcctgt gcattcgtga cccgcttccc tcccaccctg 180

tctcctgtct ccatcgttgg attatctttg aacccccttg tgtggatcat tttagccgc 240

ctggcctt 248

<210> 184

<211> 71

<212> DNA

<213> Homo sapiens

<400> 184

tattgcccgg ctcctagaat ttattttattt cctgacttac agcaagcgag ttatcgtctt 60

ctgtattttg t 71

<210> 185

<211> 163

<212> DNA

<213> Homo sapiens

<400> 185

ctttcattgg aagttcatca ctgttaggcg ttatcttgag tattataaca aagcaaattc 60

acaagtattc aatataagat taggaaaaaa attcctgcga tactttgttg tcaaactt 120

gccactgata gacgttattt tagcttttaa ggcctgtcac att 163

<210> 186

<211> 258

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (61)..(61)

<223> n is a, c, g, or t

<400> 186

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natTTTTatg cagattgact gaaacctgaa tcaaattgga aggagagggc tgaattttga 120

tagactggaa gtattagaga attttctata ctttgactca aggaatggtc aacttttagg 180

aaaagcaact atattatgtc tgttaagatc atagaatctt aacctgaaag ggaccttgga 240

gactatttag tacaactc 258

<210> 187

<211> 89

<212> DNA

<213> Homo sapiens

<400> 187

ttttgaatga actctgagtc agttgaaata gggtaccatc taggtcagtt taagaagagt 60

cagctcagag aaagcaagca taagggaaa

89

<210> 188

<211> 193

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (120)..(125)

<223> n is a, c, g, or t

<220>

<221> misc_feature

<222> (127)..(127)

<223> n is a, c, g, or t

<400> 188

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60

gggtcttgac cctcccaaaa tgccttggtta tttatatctc tgcttttaga taacagatgn

120

nnnnntntct atgggcttgt accggcagag gcaacagcag gtccttaaga ctccccaggt

180

gccatgatga aaa 193

<210> 189

<211> 173

<212> DNA

<213> Homo sapiens

<400> 189

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aatatacatt tgtttgtctc tctcttggat tattttgttt ctttgtcctg taactaccac 120

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<210> 190

<211> 265

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (41)..(41)

<223> n is a, c, g, or t

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tcataagttt attttattca acagaagcaa aatctaatat aatggaaaaa ataaagatct 120

gtgataaatc tgatctgtgt ggataaacac aattagaaag atttaaagat taagtattga 180

aacaaactac caaaatattt taatactgat ttgtaaaaat ttcagtacat ttttcttctt 240

tgcttaattc tactgggtcc tgttt 265

<210> 191

<211> 217

<212> DNA

<213> Homo sapiens

<400> 191

gttcccagtg acacttcaga gagctggtag ttagtagcat gttgagccag gcctgggtct 60

gtgtctcttt tctctttctc cttagtcttc tcatagcatt aactaatcta ttgggttcat 120

tattggaatt aacctgggtgc tggatatttt caaattgtat ctagtgcagc tgattttaac 180

aataactact gtgttcctgg caatagtgtg ttctgat 217

<210> 192

<211> 168

<212> DNA

<213> Homo sapiens

<400> 192

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ctgagggtgga aggatcactt gagtttgaaa ccagcctggg caacatagtg agaccccgtc 120

tctacaaaaa gtaggaaaaa aaaaatagcg aggtgttgtg gtacacgc 168

<210> 193

<211> 115

<212> DNA

<213> Homo sapiens

<400> 193

ttctagtaat tatcaattgt cctgggtctgg ctgcttagag tatcagtttg ctcaaaattg 60

cttgaatcat taaagcaaact actaattgtg agcattgacc agatcttaag ttaaa 115

<210> 194
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 <212> DNA
 <213> Homo sapiens

<220>
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 <223> n is a, c, g, or t

<220>
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 <222> (164)..(164)
 <223> n is a, c, g, or t

<400> 194
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 ttgtagcctg caagcctaga gtatttacta tctggatttc tacaaaaaaaa aaaaaaaaaa 120
 aatttggggg gggcccgtaa cccaatncgc ccctatagtg agtngtatta caatccacct 180
 ggccgcgttt tac 193

<210> 195
<211> 233
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (35)..(35)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (53)..(53)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (60)..(60)
<223> n is a, c, g, or t

<400> 195
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tagaagaagg gacaaatgca atccgacctt tggatctaca cattcctctt gcttcaatgg 120

gtgtcattta agaattagag gaaaatatta ggagatggag aactagagtt gaggaaccca 180

aaagaagagg agtcacagaa aaccagctct ctctgtgcaa ggcatttga aag 233

<210> 196

<211> 139

<212> DNA

<213> Homo sapiens

<400> 196

caatattaaa aaaggctctg tatgcatggg ggggctatgt aagtactctt taaaactatg 60

gccctattaa tcttacaagt gttacttatg ggtcaagcaa tgtaaactgt ataaatgtaa 120

aaacaacccc tccacacac 139

<210> 197

<211> 178

<212> DNA

<213> Homo sapiens

<400> 197

ctttggatag aggtgaagaa cttggacatg gctgtttcag gcagctgaag tcaaaggga 60

tagtaattgg ggaaggggaa gtgggcagaa aggattgttg gccaatatac cttccactcc 120

agtagagagg gaggacttgg ctctgagaac ctccatctga cctaagagga accctcct 178

<210> 198

<211> 163

<212> DNA

<213> Homo sapiens

<400> 198

ctgcaaaagc cgagatgggt tccatgcagt tctccagtgg gacatcagtg cttatccgaa 60

tgatcatcaat ggcaatctct ccggaacgtc ctttccttat cactccctcg aacacaatct 120

ggtactccat gtcgtagctg ggcaggatga tccgcccgtg ctt 163

<210> 199

<211> 104

<212> DNA

<213> Homo sapiens

<400> 199

ttcagcaagg actggtcttt ctatctcttg tactacactg aattcacccc cactgaaaaa 60

gatgagtatg cctgccgtgt gaaccatgtg actttgtcac agcc 104

<210> 200

<211> 222

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (93)..(93)

<223> n is a, c, g, or t

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taagaagtat aataaccttt tcaaaaccca cantgcagct tagttttcct ttatttattt 120

gtggtcatga agactatccc catttctcca taaaatcctc cctccatact gctgcattat 180

ggcacaaaaag actctaagtg ccaccagaca gaaggaccag ag 222

<210> 201

<211> 267

<212> DNA

<213> Homo sapiens

<400> 201

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tgcatttcct gacagaagga ctcaggttgt ctgaagtcac tgcacagtgc atctcagccc 120

acatagtgat gggtcccctg ttcactctac ttagcatgtc cctaccgagt ctcttctcca 180

ctggatggag gaaaaccaag ccgtggcttc ccgctcagcc ctccctgccc ctcccttcaa 240

ccattcccca tgggaaatgt caacaag 267

<210> 202

<211> 108

<212> DNA

<213> Homo sapiens

<400> 202

ggatggaagac cagtaattgc tggaagactg gatttgctgg aagacttgat ttactggaag 60

acttgagct tcttggaaga catggattgt ccggaagaca tggattgt 108

pctgb2013053202-seq1.txt

<210> 203

<211> 209

<212> DNA

<213> Homo sapiens

<400> 203

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ctagcagttg tggtcacgga agctgtgggc gctgctgtga tgtgtaggag gaagagctca 120

ggtggaaaag gagggagcta ctctcaggct gcgtgcagcg acagtgccca gggctctgat 180

gtgtctctca cagcttgaaa agcctgaga 209

<210> 204

<211> 146

<212> DNA

<213> Homo sapiens

<400> 204

gctttgatat ttcaatgtta gcctcaattt ctgaacacca taggtagaat gtaaagcttg 60

tctgatcgtt caaagcatga aatggatact tatatggaaa ttctgctcag atagaatgac 120

agtcctgcaa aacagattgt ttgcaa 146

<210> 205

<211> 48

<212> DNA

<213> Homo sapiens

<400> 205

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<210> 206

<211> 150

<212> DNA

<213> Homo sapiens

<400> 206

gtgtcatgta agattactgc ttgcctctct aaggaaggtc gtgactgttt aaatagacgg 60

gcaaggtgga accttttgaa agatgagctt ttgaatataa gttgtctgct agatcatggt 120

ttgtattgaa ctaacaaggt ttgcagatct 150

<210> 207

<211> 186

<212> DNA

<213> Homo sapiens

<400> 207

tattcctgca ccaactgacc tgaagttcac tcaggtcaca cccacaagcc tgagcgccca 60

gtggacacca cccaatgttc agctcactgg atatcgagtg cgggtgaccc ccaaggagaa 120

gaccggacca atgaaagaag tcaaccttgc tcctgacagc tcatccgtgg ttgtatcagg 180

acttat 186

<210> 208

<211> 276

<212> DNA

<213> Homo sapiens

<400> 208

aacaatgtca gattttaact atgaaaacga cattaccttg tgcattttta tattgattcc 60

tatttttttt ttaagattaa agtttaaag ttttcacta gtcatttcac ttctaacttg 120

gtataggaag ctagctctc tacataccta tcatgtgcc tgtatcacag aagattcagg 180

aaaaatgcac ttgggaatca aagaaaatgg aacttctttt tgaaaagaca agcaaccatg 240

ttaactgtat tgacacatcc tcaataaaac ctgttg 276

<210> 209

<211> 158

<212> DNA

<213> Homo sapiens

<400> 209

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attaacatgg ttataatacg tacaatcctt ccctcatc 158

<210> 210

<211> 225

<212> DNA

<213> Homo sapiens

<400> 210

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aaccagaag tgatggagag aaaccaaaa gagatctcga accctgtcta gaaggaatgt 120

atttggtgct aaatttcgta gcactgttta cagttttcct ccatgttatt tatgaatttt 180

atattccgtg aatgtatatt gtcttgtaat gttgcataat gttca 225

<210> 211

<211> 174

<212> DNA

<213> Homo sapiens

<400> 211

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aaacactttc ctgctcctct ctgtctctag cacacaactg tgaatgtcct gtggaattat 120

gccttcagtt cttttcaaaa tcattcctag ccaaagctct gactcggtac ctat 174

<210> 212

<211> 168

<212> DNA

<213> Homo sapiens

<400> 212

atattttaca gggtaggagtg tactatatac tattaccttt gaatgtgttt gcagagctag 60

tggatgtgtt tgtctacaag tatgattgct gttacataac accccaaatt aactcccaa 120

ttaaaacaca gttgtgctgt caataacctca tactgcttta cttttttt 168

<210> 213

<211> 165

<212> DNA

<213> Homo sapiens

<400> 213

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cttcactttt ctctacagt ttgttttggt gttgttggtt tttatttttt atactttggc 120

cataccacag agctagattg cccaggtctg ggctgaataa aacaa 165

<210> 214

<211> 208

<212> DNA

<213> Homo sapiens

<400> 214

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ccaaacactg acattaccta cacttccact acccaaagac aaaatgtgcc cactgtgtgc 60

ttttgagtgt attttctttt agtttgtttt ttgttgggtg catatttatg ataataacaa 120

tgatggactt caattgtact cactgttcta ttgttggttt taattagcag caagttgtga 180

tcactttccc aggtgaataa atcatttc 208

<210> 215

<211> 245

<212> DNA

<213> Homo sapiens

<400> 215

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atgatagtct tttctaattc ttaacactca tacttgaaat ctttccgagt ttccccagaa 120

gagaatatgg gatttttttt gacatttttg acccatttaa taatgctctt gtgtttacct 180

agtatatgta gactttgtct tatgtgtcaa aagtcctagg aaagtggttg atgtttctta 240

tagca 245

<210> 216

<211> 257

<212> DNA

<213> Homo sapiens

<400> 216

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ccagatataa ctgtcttggt tcagtggagag acgccctatt tctatgtcat ttttaatgta 120

tctatttgta caattttaaa gttcttattt tagtatacgt ataaatatca gtattctgac 180

atgtaagaaa atgttacggc atcacactta tattttatga acattgtact gttgctttaa 240

tatgagcttc aatataa 257

<210> 217

<211> 174

<212> DNA

<213> Homo sapiens

<400> 217

tttcaaattcc ttcattcatgt cagttccaat gaggtgggga tggagaagac aattgttgct 60

tatgaaagaa agcttttagct gtctctgttt tgtaagcttt aagcgcaaca tttcttggtt 120

ccaataaagc attttacaag atcttgcacg ctactcttag atagaagatg ggaa 174

<210> 218

<211> 191

<212> DNA

<213> Homo sapiens

<400> 218

taggtggtag atattgaggc caagaatatt gcaaaataca tgaagcttca tgcacttaaa 60

gaagtatttt tagaataaga atttgcatac ttacctagtg aaacttttct agaattattt 120

ttcactctaa gtcacgtatg tttctctttg attatttgca tgttatgttt aataagctac 180

tagcaaaata a 191

<210> 219

<211> 116

<212> DNA

<213> Homo sapiens

<400> 219

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ttccaccatg gccacaacg aaggactttt ctccctggtg gcgaggaagc tgagca 116

<210> 220

<211> 181

<212> DNA

<213> Homo sapiens

<400> 220

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tattcccaat taaaagtatg cagattattt gcccaaactt tcttcagatt cagcatttgt 120

tctttgccag tctcattttc atcttcttcc atggttccac agaagctttg tttcttgggc 180

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<210> 221

<211> 248

<212> DNA

<213> Homo sapiens

<400> 221

tgttttcaaa ttgccattgc tactattgct tgtcgggtgtt attttatttt attgtttttg 60

pctgb2013053202-seq1.txt

actttggaag agatgaactg tgtattttaac ttaagctatt gctcttaaaa ccaggagtc 120

agaatatatt tgtaagttaa atcattggtg ctaataataa atgtggattt tgtattaaaa 180

tatatagaag caatttctgt ttacatgtcc ttgctacttt taaaaacttg catttattcc 240

tcagattt 248

<210> 222

<211> 227

<212> DNA

<213> Homo sapiens

<400> 222

tatttgaact atatgttgaa gacatctacc agtttctcca aatgcctttt ttaaaactca 60

tcacagaaga ttggtgaaaa tgctgagtat gacacttttc ttcttgcatt catgtcagct 120

acataaacag ttttgtacaa tgaaaattac taatttgttt gacattccat gttaaactac 180

ggtcattgtc agcttcattg catgtaatgt agacctagtc catcaga 227

<210> 223

<211> 194

<212> DNA

<213> Homo sapiens

<400> 223

gaagtttaat tcatagtaat ttcactctct gcattgactt atgagataat taatgattaa 60

actattaatg ataaaaataa tgcatttgta ttgttcataa tatcatgtgc acttcaagaa 120

aatggaatgc tactcttttg tggtttacgt gtattatattt caatatctta ataccctaata 180

aaagagtcca taaa 194

<210> 224

<211> 217

<212> DNA

<213> Homo sapiens

<400> 224

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atggcataat tttctatcag cttcctactc agtcactata aacacagact tgaaatagta 120

ctttaaatgt ccaaatacct aaatgtgcta aactggaggt aactatttct aggtagttga 180

atTTTTgaaa gTcatgatca gccacacaac tgTTTTg 217

<210> 225

<211> 293

<212> DNA

<213> Homo sapiens

<400> 225

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caaggcataa taaaacccga ggtagcaaT gaaaattaaa gcattttattt tggtagttct 120

tcaataatga tgcgagaaac tgaattccat ccagtagaag catctccttt tgggtaatct 180

gaacaagtgc caaccagat agcaacatcc actaatccag caccaattcc ttcacaaagt 240

ccttccacag aagaagtgcg atgaatatta attgttgaat tcatttcagg gct 293

<210> 226

<211> 95

<212> DNA

<213> Homo sapiens

<400> 226

ctgtcaggaa ctcctcactg tttaaattatt tattttattgt gacaaatgga gctgggtttcc 60

tagatatgaa tgatgtttgc aatccccatt ttcct 95

<210> 227

<211> 210

<212> DNA

<213> Homo sapiens

<400> 227

gctgctgtag aatagcacag acgtggatga taaattatcc ccagaagcag catgacagaa 60

tgccctgggg agcacttgga agggaaattg cagttctgtt gaaatagagg aaaatccctt 120

ggtaaagaca cagcctgtta ggctcgtgtg ggcctccagt atgttcacca ggggaatggc 180

tgggatttct cggcactctg catcatccat 210

<210> 228

<211> 243

<212> DNA

<213> Homo sapiens

<400> 228

pctgb2013053202-seq1.txt

ttaatatatttg ttattctctc atgaatagaa atttatgtag aagcaaacaa aatactttta 60

cccacttaaa aagagaatat aacattttat gtcactataa tcttttgttt ttttaagttag 120

tgtatatattt gttgtgatta tctttttgtg gtgtgaataa atcttttatc ttgaatgtaa 180

taagaatttg gtgggtgcaa ttgcttattt gttttccac ggttgtccag caattaataa 240

aac 243

<210> 229

<211> 37

<212> DNA

<213> Homo sapiens

<400> 229

gatgcttaac aaaggttacc ataagccaca aattcat 37

<210> 230

<211> 264

<212> DNA

<213> Homo sapiens

<400> 230

pctgb2013053202-seq1.txt

aatgcaaact atcactgtat tttaatatatt gttattctct catgaataga aatttatgta 60

gaagcaaaca aaatactttt acccacttaa aaagagaata taacatttta tgtcactata 120

atcttttgtt tttaagtta gtgtatatatt tgttgtgatt atctttttgt ggtgtgaata 180

aatcttttat ctggaatgta ataagaattt ggtgggtgtca attgcttatt tgttttccca 240

cggttgtcca gcaattaata aaac 264

<210> 231

<211> 269

<212> DNA

<213> Homo sapiens

<400> 231

gcttatttga caacgtttca gcgactccgt tggccactcc gagaggtggg ccagtctgtg 60

gatcagagat gcaccaccaa gccaagggaa cctgtgtccg gtattcgata ctgcgacttt 120

ctgcctggag tgtatgactg cacatgactc ggggggtgggg aaaggggtcg gctgaccatg 180

ctcatctgct ggtccgtggg acggtgccca agccagaggc tgggttcatt tgtgtaacga 240

caataaacgg tacttgtcat ttcgggcaa 269

<210> 232

<211> 179

<212> DNA

<213> Homo sapiens

<400> 232

agaggttata ggtcactcct ggggcctctt ggggtcccca cgtgacagtg cctgggaatg 60

tattattctg cagcatgacc tgtgaccagc actgtctcag tttcactttc acatagatgt 120

ccctttcttg gccagttatc ccttcctttt agcctagtgc atccaatcct cactgggtg 179

<210> 233

<211> 220

<212> DNA

<213> Homo sapiens

<400> 233

ctgtatcact gccttcgttt atatTTTTTT aactgtgata atccccacag gcacattaac 60

tgttgacttt ttgaatgtcc aaaatttata ttttagaaat aataaaaaga aagatactta 120

catgttccca aaacaatggt gtggtgaatg tgtgagaaaa actaacttga tagggtctac 180

caatacaaaa tgtattacga atgcccctgt tcatgttttt 220

<210> 234

<211> 127

<212> DNA

<213> Homo sapiens

<400> 234

gggcccctaa tatcccagtt taatattcca ataccctaga agaaaacccg agggacagca 60

gattccacag gacacgaagg ctgcccctgt aaggtttcaa tgcatacaat aaaagagctt 120

tatccct 127

<210> 235

<211> 225

<212> DNA

<213> Homo sapiens

<400> 235

cccaaacctg tactgtcccg gaggaggttg ggaggtggag gcccagcatc ccgcgcagat 60

gacaccatca accgccagag tcccagacac cggttttcct agaagcccct cccccccact 120

ggcccactgg tggctaggtc tccccttatc cttctggtcc agcgcaagga ggggctgctt 180

ctgaggtcgg tggctgtctt tccattaaag aaacaccgtg caacg 225

<210> 236

<211> 41

<212> DNA

<213> Homo sapiens

<400> 236

ttaatctatg tgcaccgttg ggaccaatgc cttaattaaa g 41

<210> 237

<211> 160

<212> DNA

<213> Homo sapiens

<400> 237

cttctcactg gacagcacta gttttttgcc tgggaagtcg tggacagtaa cagtgactgg 60

aacatcccct tgcgcgtcgt gggcctccag caccatggtc tcctcgctct ccagccgcaa 120

gatgttgggg gtgatgatag agtacatggg actccccaga 160

<210> 238

<211> 179

<212> DNA

<213> Homo sapiens

<400> 238

gggtcagcac agtcttctca ctggacagca ctagtttttt gcctgggaag tcgtggacag 60

taacagtgac tggaacatcc ctttgcgcgt cgtgggcctc cagcaccatg gtctcctcgc 120

tctccagccg caagatgttg ggggtgatga tagagtacat gggactcccc agagccagg 179

<210> 239

<211> 164

<212> DNA

<213> Homo sapiens

<400> 239

gtagtgagtt ttccttggtc ggcgtttggc tgagaaggct gcaactggcc tgagacgagt 60

ctgggtcccga cgatgctgtg ctctgcctcc tcctgctgct gctgacaacc aagccctccc 120

agaatttaaa tgctgctgca gacatcctcc accaacacag ggag 164

<210> 240

<211> 167

<212> DNA

<213> Homo sapiens

<400> 240

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tgcccatgtc tcagccatgt gatgttgacc acaggaggaa agatgttgtc cacaagacag 120

atgaggatgt tgggctgacc cagtgtcacg ggagacttgg aaaacac 167

<210> 241

<211> 183

<212> DNA

<213> Homo sapiens

<400> 241

ggattataat atcctcactg gccacaatct gtaaaagtcg atactggcac tttttttgcc 60

ccctcaaagg aaatatgcta atagacagcc cctttgcaaa tataattcct ccttcccaac 120

ccttcaaatt gctaaggccc cactggtcag caccttcctt ttcgagtcca ggactactgt 180

tct 183

<210> 242

<211> 237

<212> DNA

<213> Homo sapiens

<400> 242

acaaaagctc ccctgatcca actagcacac tgtcaaatac agtgtcatat gagaggtcca 60

cagacggtag tttccaagac cgtttcaggg aattcgagga ttccacctta aaacctaaca 120

gaaaaaaacc cactgaaaat attatcatag acctggacaa agaggacaag gatttaatat 180

tgacaattac agagagtacc atccttgaaa ttctacctga gctgacatcg gataaaa 237

<210> 243

<211> 197

<212> DNA

<213> Homo sapiens

<400> 243

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pctgb2013053202-seq1.txt

agtgagagtg atgttggtgga gacagttgaa atgtcagtcg tagagcctct gtggtgtgaa 120

tgggcacgtt aggttggtgc attagaaagt gactgtttct gacagaaatt ttagctttg 180

tgcaaaactca cccacca 197

<210> 244

<211> 131

<212> DNA

<213> Homo sapiens

<400> 244

ctacttcccc gaaccggtga cgggtgctg gaactcaggc gccctgacca gcggcgtgca 60

caccttcccc gctgtcctac agtcctcagg actctactcc ctcagcagcg tggtagaccgt 120

gccctccagc a 131

<210> 245

<211> 95

<212> DNA

<213> Homo sapiens

<400> 245

ccagacctac acctgcaacg tagatcaciaa gccagcaac accaaagtgg acaagacagt 60

tgagcgcaaa tgttgtgtcg agtgcccacc gtgcc 95

<210> 246

<211> 131

<212> DNA

<213> Homo sapiens

<400> 246

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actttattgg ttgttttggt tagtgccccg ttaattaagc cttgagttcg gttatcctgc 120

agtgggtgctg a 131

<210> 247

<211> 38

<212> DNA

<213> Homo sapiens

<400> 247

tttccccac tgtctggaca ctggtgaatg acattaga 38

<210> 248

<211> 173

<212> DNA

<213> Homo sapiens

<400> 248

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tccccctttcc cccactgtct ggacactggg gaatgacatt agaagagacc cacccttctc 120

aagtccccctc actggctcct tttctcccca ctacaccact tccaaaatct gaa 173

<210> 249

<211> 298

<212> DNA

<213> Homo sapiens

<400> 249

tgactttgtc acaatgacag ccaacagtga gactgataag cctgtaaaaa taaaaaaata 60

agactaatca aatagacatg gcattttaat ctcaaagtcg aaaatcatct aactgaaaat 120

gacggcattg aaaaattcca gtggttaaaa atgaatcaaa acttcattac gcaggcagtg 180

gaagtgtgtt gaaagattta ccaggggtgt caagtttttag acactcagaa aggcaccatt 240

ctagccatct tgattggata acatgtatat acttatgtcc ctacgatatt caaaagat 298

<210> 250

<211> 145

<212> DNA

<213> Homo sapiens

<400> 250

gataccgact gaccgtgggc cttacccgaa gaggacagcc catgcagtac aatgtgggtc 60

cctctgtctt caagtaccca ctgaggaatc tgcagcctgc atctgagtac accgtattcc 120

tcgtggccat aaagggcaac caaga 145

<210> 251

<211> 111

<212> DNA

<213> Homo sapiens

<400> 251

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gtttacttgt ggttgcccta tcctatgctg cataaatcct tgaaaggaaa g 111

<210> 252

<211> 137

<212> DNA

<213> Homo sapiens

<400> 252

ttaagacatt ggagtgattt ctggaaatgt tttctttaag aaggctcacg tgatgtttgt 60

gtttacttgt ggttgcccta tcctatgctg cataaatcct tgaaaggaaa ggtttttagtt 120

agttgctttc tttcttc 137

<210> 253

<211> 203

<212> DNA

<213> Homo sapiens

<400> 253

tttttctttg ggctactgta ccctgcttcc agtgctgacc ccggcataag tccatctctg 60

cagaagccat ttcaggagta cctggaggct caacggcaca agcttcacca caaaagcgaa 120

atggacacac cacaggttaag actttaatcc ggtttcttct cccctctggg aagtttcggg 180

ctgaaattac attcacagct ctc 203

<210> 254

<211> 243

<212> DNA

<213> Homo sapiens

<400> 254

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ctgaccccgg cataagtcca tctctgcaga agccatttca ggagtacctg gaggctcaac 120

ggcacaagct tcaccacaaa agcgaaatgg acacaccaca ggtaagactt taatccggtt 180

tcttctcccc tctgggaagt ttcgggctga aattacattc acagctctca ctcacatttt 240

tag 243

<210> 255

<211> 292

<212> DNA

<213> Homo sapiens

<400> 255

cgcggtctga gtctcgtttg gaagctcgag gcataggaca gtctctgcct gggtagggaa 60

tgcagttagc tgaggaacca cggtagggtt taaaaaaaaa gactcgggga gagaaatagc 120

acattattta catgactgga caaggacaga aggtgggagg aagcccctgt cactccttgg 180

gacctgggat ctgagcacia agctgagtgg gaaacagtgg gggctccgaa gcgcccagca 240

gggccagcgc cctcctttct agaccccgac tgcccttggt cttctgccct tt 292

<210> 256

<211> 156

<212> DNA

<213> Homo sapiens

<400> 256

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aggcggaggc ggaggaggcc gctggagatg gtgctgagga cgaggaggcc ggtgggttgg 120

tcatgctcac taggccactg accaagctga agaggg 156

<210> 257
 <211> 249
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (142)..(142)
 <223> n is a, c, g, or t

<220>
 <221> misc_feature
 <222> (188)..(188)
 <223> n is a, c, g, or t

<400> 257
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 atacagaact cattcaatca tataaaaata aacacaaatt tacattgact catcaactat 120
 acaatttaaa aaggcacttg anaggggtat tgtattattg catttgtggt atgcatttga 180
 aatagtnta agtacattaa tgaaatttgt aagaattcct cttttgcact tattcccatc 240

tttaattaa

249

<210> 258

<211> 62

<212> DNA

<213> Homo sapiens

<400> 258

gtccccaat gaccacatg attcaaagtg caaatttact ccaacctgca agagaaaacg 60

aa

62

<210> 259

<211> 126

<212> DNA

<213> Homo sapiens

<400> 259

actagtctca gtaatacatt agtaaaaatc atgtcactta attaattgtg ttagaatcaa 60

agaaacatag agttgggcaa tatacttcat cctacccatc ccacccaaat cttactctac 120

tcatct

126

pctgb2013053202-seq1.txt

<210> 260

<211> 149

<212> DNA

<213> Homo sapiens

<400> 260

aaaaatttat ttactagtct cagtaatata ttagtaaaaa tcatgtcact taattaattg 60

tgtagaatc aaagaaacat agagttgggc aatatacttc atcctaccca tcccacccaa 120

atcttactct actcatctca ttctcatta 149

<210> 261

<211> 163

<212> DNA

<213> Homo sapiens

<400> 261

agaattaact gactatgggt ttgcaggcca gtttgatccc agtatTTTTA tttctaaagg 60

ggttcttata gttcctctga ttgttaccat tttaaaatag agaaagtcca tagtgatgcc 120

tttcctttca gtggctgatt ggcacgacct cttgagaatg cat 163

pctgb2013053202-seq1.txt

<210> 262

<211> 269

<212> DNA

<213> Homo sapiens

<400> 262

atttgcatTT taccatgggt cctcaataaa taaatagaat gttgtttttt gtattttaag 60

tttttttttg tttttcccct cagaggaagg atgaaaaaaaa gaattaactg actatggttt 120

tgcaggccag tttgatccca gtatttttat ttctaaaggg gttcttatag ttcctctgat 180

tgttaccatt ttaaaataga gaaagtccat agtgcgcct ttcctttcag tggctgattg 240

gcacgacctc ttgagaatgc atgcatgaa 269

<210> 263

<211> 105

<212> DNA

<213> Homo sapiens

<400> 263

atttccatca catatgtgcc aagacttggt ttctgtatcc aggagtgtgt tagatactaa 60

catagtgttt catttacatg tgtgtgaaac ctgggtgaag agcca 105

<210> 264

<211> 174

<212> DNA

<213> Homo sapiens

<400> 264

ccatcagttt ttccaatgtg aatggactgg ttcatatcac accatattta gagatacaag 60

gtgattataa ctaacgtgtc tacaagacat actgggtcaa acaatgtgat caatccaaag 120

ggtatctttt taaaaagaat ttaagtactc agctgcaaag ataagttcac taat 174

<210> 265

<211> 218

<212> DNA

<213> Homo sapiens

<400> 265

gtacatggtc tggagtaacc tttatatgaa gtggctgccc aggtgtgtgg cttaggacta 60

gatctccagg ttgcacaaag ttggcattgg gtttagtttg cttttttcca ttctgaagat 120

ggccctcctt ggatttcac caggaaatcc atagctttct gttaacagga catggagtag 180

actggctgca tttgaaggac agcacagatc cctcatca 218

<210> 266

<211> 103

<212> DNA

<213> Homo sapiens

<400> 266

aaaccttggt ttattcagcc cagacctggg agatctagct ctgtggtatg gccaaagtat 60

aaaaaataaa aaccaacaac aacaaaacaa cactgtagag aaa 103

<210> 267

<211> 194

<212> DNA

<213> Homo sapiens

<400> 267

tcaaactcag gtatgtgaca ctctacagtt caatgctagc acacctgtgt gaggcttaac 60

aacatgagga actgatagcc agtgatacac aaatccagca cttcctctcc atttactctg 120

tcaggctgta tatggggagc aacacatatg gctttgtggc agccagaaag tgaaggtctt 180

tttaggaggt gaca 194

<210> 268

<211> 61

<212> DNA

<213> Homo sapiens

<400> 268

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c 61

<210> 269

<211> 268

<212> DNA

<213> Homo sapiens

<400> 269

gtaaagcttt ggcacataca gtataaaaaa taatcaccca ccataattat accaaattcc 60

tcttatcaac tgcatactaa gtgttttcaa tacaattttt tccgtataaa aatactggga 120

aaaattgata aataacaggt aagagaaaga tatttctagg caattactag gatcatttgg 180

aaaaagtgag tactgtggat atttaaaata tcacagtaac aagatcatgc ttgttcctac 240

agtattgcgg gccagacact taagtgaa 268

<210> 270

<211> 37

<212> DNA

<213> Homo sapiens

<400> 270

tgggctggag ccgcacacgc tctcctccca tgttaaa 37

<210> 271

<211> 112

<212> DNA

<213> Homo sapiens

<400> 271

atagatgaca taagttacca tactcaaag taagataggg agaggtagaa gaaatagctg 60

agaacttgaa aagatgtact gttattgtca acaaaccaat gtcttctccc tt 112

pctgb2013053202-seq1.txt

<210> 272

<211> 158

<212> DNA

<213> Homo sapiens

<400> 272

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agtgttaagg cgtgaagggc gaggccagac agctggag 158

<210> 273

<211> 75

<212> DNA

<213> Homo sapiens

<400> 273

catctctgac tttaatggct taagcaagaa catggtttcc gtggctcccc ctggactgaa 60

tgctggagga tatat 75

<210> 274

<211> 182

<212> DNA

<213> Homo sapiens

<400> 274

tgagtaggtg agtttattgg gacttacaca caggtcaatc ctgggcggcg acaagacagc 60

tctagagatc tgagcttcct cccaatgcta aactgctttc atgctaattt tctgactggt 120

tacttaccgg gtaagagcga tgggactggt ttcattgggt ggttctcaca tactctctgg 180

ga 182

<210> 275

<211> 121

<212> DNA

<213> Homo sapiens

<400> 275

cctggatctc acagacgttg ggcttttcaa ctgcagactt caatgctttg tttccaggtg 60

gcaggagaaa catcacatct cattaccaac aattatttcc ctcaaaggta agtaattgta 120

t 121

<210> 276

<211> 177

<212> DNA

<213> Homo sapiens

<400> 276

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ttcaatgctt tgtttcagg tggcaggaga aacatcacat ctcattacca acaattattt 120

ccctcaaagg taagtaattg tatctaactt caatattcct ttcctggcc aaaaatt 177

<210> 277

<211> 237

<212> DNA

<213> Homo sapiens

<400> 277

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aagataaata atatccctgc attatcaaaa taaagtagca gaccttcaa ttcacaatga 120

gttaactgat aaaacaaaac agaagtcaga caatgtttta aattgaatga tcatgtaaat 180

attacacatc aaaccaatga catgggaaaa tgggagcttc taatgaggac aaacaaa 237

<210> 278

<211> 43

<212> DNA

<213> Homo sapiens

<400> 278

caatggttga gcccctgtca agtgccagtc atgatagtag taa 43

<210> 279

<211> 198

<212> DNA

<213> Homo sapiens

<400> 279

gggatttctt ggtttgtgaa aacaggagag gagaaatatc tcatacaagt gaaaggatac 60

tggagagaga aattacccat ttctaataaaa aaaccacact ctgtcgtatc tgtgttaatg 120

ttttctagca tgtactctgg tttcaacaga cacaatttta tatgttaacc cagttttctt 180

gccgttctgt aagtgttt 198

<210> 280

<211> 70

<212> DNA

<213> Homo sapiens

<400> 280

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tgattttaa 70

<210> 281

<211> 94

<212> DNA

<213> Homo sapiens

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gcctccatt caagtgaagt tataatttac actgagggtt tcaaaattcg actagaagtg 60

gagatatatt atttatttat gcactgtact gtat 94

<210> 282

<211> 165

<212> DNA

<213> Homo sapiens

<400> 282

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gagccacagg aagtttgggg cgtggtgagt tggaatgata cgtccatttc tctatgaaat 120

atttgctact agactgttca tttctctctg acatgtttgt tgaat 165

<210> 283

<211> 208

<212> DNA

<213> Homo sapiens

<400> 283

catccgccag ggcccacacc cccttcctac tcccagacac ccaccctcgc ttcagccaca 60

gtttcctcat ctgtccagtg ggtaggttgg actggaaaat ctctttttga ctcttgcaat 120

ccacaatctg acattctcag gaagcccca agttgatatt tctatttcct ggaatggttg 180

gatttttagtt acagctgtga tttggaag 208

<210> 284

<211> 227

<212> DNA

<213> Homo sapiens

<400> 284

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cacctctact gtctcctccc tgggctaagc aggggagaag cgggctgggg gtagcctgga 120

tgtgggccaa gtccactgtc ctccttggcg gcaaaagccc attgaagaag aaccagccca 180

gcctgcccc tatcttgtcc tggaatattt ttggggttgg aactcaa 227

<210> 285

<211> 57

<212> DNA

<213> Homo sapiens

<400> 285

tattgaggac ccatggtaaa atgcaaatag atccggtgtc taaatgcatt catattt 57

<210> 286

<211> 135

<212> DNA

<213> Homo sapiens

<400> 286

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tgagactatg gttca 135

<210> 287

<211> 247

<212> DNA

<213> Homo sapiens

<400> 287

caaactatTT ttccacctcc aaaagaaatt aacacatgga catTTTtaaag tctTTtagtat 60

aaagaaaatt tgtattcaat gtgttaagca ttaacatgta ttttatttgt gtatccactc 120

catctgattt ttctgagcca ttttgatttg ttccttcatt aaaaaaaatc tcttaaagtt 180

atttagtgtc taaaagtgac tgacttaaAT tatgtggtgc caatctgtaa tgtctttgaa 240

ttccttt 247

<210> 288

<211> 174

<212> DNA

<213> Homo sapiens

<400> 288

ttgcatggag acttgaggag ggagggcttg aggttggtga ggtaggtgc gtgtttcctg 60

tgcaagtcag gacatcagtc tgattaaagg tggcgccaat ttatttacat ttaaacttgt 120

caggtataa aatgacatcc cattaattat attgttaatc aatcacgtgt atag 174

<210> 289

<211> 126

<212> DNA

<213> Homo sapiens

<400> 289

ggatccaaga gctgactatg cctgcattgc tgagaacaaa cccacctgag caccacagac 60

accttcctca acccaggcgg gtggacaggg tccccctgtg gtccagccag taaaaaccat 120

gtcccc 126

pctgb2013053202-seq1.txt

<210> 290

<211> 132

<212> DNA

<213> Homo sapiens

<400> 290

acagcccacc cttgtgtcca ctgtgacccc tgttcccatg ctgacctgtg tttcctcccc 60

agtcacatctt cttgttccag agaggtgggg ctggatgtct ccatctctgt ctcaacttta 120

cgtgcactga gc 132

<210> 291

<211> 173

<212> DNA

<213> Homo sapiens

<400> 291

aaatgctcct tgaatattaa aaggttgtaa aaatagtgca tgttatgtga tttcaatttt 60

gttttttaaa atatgggtgt atgcttgat acgtagagca gataaaaaag acggaaggca 120

tactaaaaaa tgttgagtgg ttatctttgt atggtggaac aaagtcactg taa 173

pctgb2013053202-seq1.txt

<210> 292

<211> 274

<212> DNA

<213> Homo sapiens

<400> 292

ggcacgtggc ttcatgtcag taagcaagat gcttcttaat aaccacctt ctgccccact 60

ctattcctta tcctgctgcc cctgtagggg tcaagggcc tccgtctaca ccctcttctt 120

ctcctccatc ctttattcag agtcattctg cccttcccca tgggtggggg aacctgtgtt 180

tgtttgtgtg cacatgtaaa ttttaaata ttttaagcaga aagtccttac ctcctgtaac 240

acatcaataa agtacaatca ttgtgagccc tttc 274

<210> 293

<211> 185

<212> DNA

<213> Homo sapiens

<400> 293

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pctgb2013053202-seq1.txt

tggaacaaaca aaagtacatt gcttaaaata tatagtgaag aatgtcacta tatcttccca 120

tttaacattg tttttgtata ttgggtgtag atttctgaca tcaaaacttg gacccttgga 180

aaaca 185

<210> 294

<211> 42

<212> DNA

<213> Homo sapiens

<400> 294

tcatgacgag ttaatgcatg tccgtgggtg ggtgcacctg ta 42

<210> 295

<211> 250

<212> DNA

<213> Homo sapiens

<400> 295

gatttctcat gacgagttaa tgcattgccg tgggtgggtg cacctgtagt tctgtttatt 60

ggtcagtggg aatgaaaaaa aaaaaaaaaa aaagtctgcg ttcatgtcag ttccagtttc 120

pctgb2013053202-seq1.txt

tcttccattc tgtgtcacag acaccaacac accactcatt ggaaaatgga aaaaaaaaaac 180

aaaaaaaaaa caaaaaaatg tacaatggat gcattgaaat tatatgtaat tgtataaatg 240

gtgcaacagt 250

<210> 296

<211> 247

<212> DNA

<213> Homo sapiens

<400> 296

ggcaggcttc tctgtagaac ccagggggct tcggcccaga ccacagcgtc ttgccctgag 60

cctagagcag ggagtcccga acttctgcat tcacagacca cctccacaat tgttataacc 120

aaaggcctcc tgttctgtta tttcacttaa atcaacatgc tattttgttt tcactcactt 180

ctgactttag cctcgtgctg agccgtgtat ccatgcagtc atgttcacgt gctagttacg 240

tttttct 247

<210> 297

<211> 112

<212> DNA

<213> Homo sapiens

<400> 297

atttttagtat ggtgtctgtt tatgtaactc tgacttgctg gaaaagttga aactccaaat 60

aatctgaaac tagaaaagaa atagcacata attactacct tccccttggc gg 112

<210> 298

<211> 278

<212> DNA

<213> Homo sapiens

<400> 298

aaatggcttc cgatttccag cttgggcctg gggattggag atgtccccac tgagagtagg 60

gcacaagtga ggaaatggtt tggagaggaa gatgataagt tacatcatgg atgtgctgag 120

tctgagttgc ctatgggact tggaatgggg ggtggcaaaa ggtgtgtgat cttgagcaag 180

atattcaact cttctgggcc ttggtcttct catttgtaaa acggtgataa gaatattact 240

tcccatttgt gttgctgtga atattaaatg cgctacca 278

<210> 299

<211> 137

<212> DNA

<213> Homo sapiens

<400> 299

gtgggcagca cttagattcg gagccatgga tagtccggag tccaaggtct ctgggtgagc 60

agacagtcgg ccaaaggcca gcctggagtc aaagagacca gaccctgct tagattgcca 120

tactcgcacc attccaa 137

<210> 300

<211> 252

<212> DNA

<213> Homo sapiens

<400> 300

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tattagaaga aaggaaaaaa aagcagaggc caaagaagtt ttgtgtttgc tgatgagagc 120

cccactcatt tgcgaaacgc acgtaaaaca aagtgaaccg tgactgttaa actagggatg 180

ggaaattttg catcttgggg ggctgtacat ttatttattt agttgaagat tcactgatcc 240

cactttgaaa ta 252

<210> 301

<211> 106

<212> DNA

<213> Homo sapiens

<400> 301

gtgcatgtgt gtgctgtgtc tttgtgtgtg tgctgtgtgc tagtgtgtgt gctgtgtgtg 60

catgtgtgtg cgtgtgctgt gcgtttgtgt gctgtgtgct cgtgtg 106

<210> 302

<211> 294

<212> DNA

<213> Homo sapiens

<400> 302

tggaagcgg cgagatcctc gggctggggg tgcccacgtt tgctacctcc ccctgtgaaa 60

tcgctgggtgc tcacaattgt ctttcacagt gtatgtgatt tttttaagga aaaaaaaaaa 120

atccctattt aagattttga aggtgctacc attattttgc cacagacttt gaagaaactt 180

pctgb2013053202-seq1.txt

ttggatgtgg ggcacatcc gcatctttct ctctcctcca aatgacaaag tttggggaat 240

ttttgaattt tcctagcatc gcccttgtgc tcatcaggta atctgctaag gagg 294

<210> 303

<211> 238

<212> DNA

<213> Homo sapiens

<400> 303

acccatcctg ttcgtgaata ggtctcaggg gttgggggag ggactgccag atttggacac 60

tatatTTTTT tttaaattca acttgaagat gtgtatttcc cctgaccttc aaaaaatgtt 120

ccaaggtaag cctcgtaaag gtcacccac catcaccaaa gcctccgttt ttaacaacct 180

ccaacacgat ccatttagag gccaaatgtc attctgcagg tgccttcccg atggatta 238

<210> 304

<211> 258

<212> DNA

<213> Homo sapiens

<400> 304

cattctttcc tccacaggat tgctttgtcc atctcctgct ttcatttcaa gtgcataaac 60

aaaacctcaa agggcctggg aaggtgaggc aggccagagt ctgtgttctg tgttgagtgt 120

caagctatatt gttaagaagg ttgcaacag gcctttggtg tgggctttgc cagagactgt 180

tttgaacact ttgcttgaga tccgtgccct gtaaaatgga tatgatgttt tactgatgtc 240

tgtaatacat ttgtaaac 258

<210> 305

<211> 85

<212> DNA

<213> Homo sapiens

<400> 305

ttaagcgcac tagaaaacaa ttgtttgtaa tggaatcaaa gtgtttccct ggacagtttg 60

atgtgcttat gggtgagatt tataa 85

<210> 306

<211> 299

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (127)..(127)

<223> n is a, c, g, or t

<220>

<221> misc_feature

<222> (194)..(194)

<223> n is a, c, g, or t

<400> 306

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aaattgtaac acaaagaaat aaacatattg aatataattg ctattctgta agacatacag 120

tctgtgnaag atgtatctta ttacagaga cttttttgaa aattaaaata ttaaatactt 180

ttgtttatat aganacaatg atctggaagt ataaaaagaa aaatattatc ttgttgatgt 240

aaatatgata tccttatata tattagaatc caataagata tcatgggcgc aatattagc 299

<210> 307

<211> 229

<212> DNA

<213> Homo sapiens

<400> 307

gatggctggg agataagtcc ttgaatggag gaaccaagag gtgagttaga ggcataaact 60

aaggaatttc agttagtagg gtttaggagt gacagtctag aatgagtgga gactaggaga 120

ttcatcttga tgcaagcata cttagatcca tgttactcag gatagcatag gtgagagagg 180

agctggtaga attttaatgt catacctggg tagtacaact ggttattat 229

<210> 308

<211> 213

<212> DNA

<213> Homo sapiens

<400> 308

tattttccgg ttgacccag aattcattag atttttttaaa aaaacaattt caaaatagtt 60

gctgttttaa attagttgca tccagttcat atcaatgttt gcatgctttt tagtctttgt 120

tatttattga aaacctttgg tacctaaact taagtttgat tgtttcagtg tgtacttggt 180

aaatatgtca gtggcctttt aactaaacat caa 213

<210> 309

<211> 174

<212> DNA

<213> Homo sapiens

<400> 309

caccccagga ctttatcaac ttgttcaagt tctgaatccc agcacatgac aacacttcag 60

aaggggtcccc ctgctgactg gagagctggg aatatggcat ttggacactt catttgtaaa 120

tagtgtacat tttaaacatt ggctcgaaac ttcagagata agtcatggag agga 174

<210> 310

<211> 32

<212> DNA

<213> Homo sapiens

<400> 310

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<210> 311

<211> 166

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (101)..(101)

<223> n is a, c, g, or t

<400> 311

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aagcatgatt tcccttgaag tcttgggggt gtttaaagga nagtcccttc aatataaaac 120

ctctgaaata ttagtgagaa tggctcacta atgtgaacaa tgttta 166

<210> 312

<211> 213

<212> DNA

<213> Homo sapiens

<400> 312

tacaaagaat atttgggccc agtgctacag aaaaacatga actacatctt atcgtcacia 60

aatagccatt ataaaatgaa ttttgcagcc tctgtttttt tgaactttga aataaaatgt 120

tcagacaaat attcaacttt ttaaaaacct ccattcattg atagcctgag aaatgtacaa 180

tgaacatggt taggcagact gctagtattt tgc 213

<210> 313

<211> 225

<212> DNA

<213> Homo sapiens

<400> 313

cctccaccaa tcatactttg acatttatct atttccttct ccacttatgg atgtaattgg 60

cttgctatag aaactacagt tcagatgctt tgaatgtatg aactacaatg aacaataaag 120

tcctcttctt ttgaagcata ttttggcttc agctttaaga taatcttatg acaagaaggg 180

tcacactgat tcacttaata aattccattc ttacctaaca caagg 225

<210> 314

<211> 259

<212> DNA

<213> Homo sapiens

pctgb2013053202-seq1.txt

<400> 314

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cctcctgccc cactgggagt agcggctaaa gctgggggat agaggggctg cagggccact 120

ggaaggaaca tggagctgtc atcactcaac aaaaaaccga ggccctcaat ccaccttcag 180

gccccgcccc atggggcccct caccgctggt tggaaagagt gttggtgttg gctggggtgt 240

caataaagct gtgcttggg 259

<210> 315

<211> 217

<212> DNA

<213> Homo sapiens

<400> 315

gaccccagtg gaaaacaaag ccaaacaaaa ctgaaccaca aaaaaaaggc tgggtgttcac 60

caaaacaaaa ctgtgtcatt tagataattt gaaaaagttc catagaaaag gcgtgcagta 120

ctaagggaac aatccatgtg attaattgtt tcattatgtt catgtaagaa gcccttatt 180

tttagccata attttgcata ctgaaaatcc aataatc 217

<210> 316

<211> 243

<212> DNA

<213> Homo sapiens

<400> 316

gagtaaaaag aaccctttgc tgagtaacca agcctttaat tttgtgtttt tatgaaagga 60

attaaaatac ccacgataaa tatttaccac aacctgtgtc agataaatgg gaaattaaac 120

acagattgta caatgtgagc ttgggagtta atggcccaga ttttactgtt aggcagtaag 180

agttggagta ggtagtcttg ttatcatgag aagaaccttg aacagataca actaatttac 240

ata 243

<210> 317

<211> 172

<212> DNA

<213> Homo sapiens

<400> 317

aacacccata atcaatcaca gagataacca ctgttcataa ttccttccag tcttcttact 60

tgccacatat acatttgtct ttctttatat atgacatatg gatattttac aaagttagga 120

tcctactcta tgcactgctt ggtgatcgga tctattcaat gtacaaaata tt 172

<210> 318

<211> 100

<212> DNA

<213> Homo sapiens

<400> 318

ttttctaacc ttgattgacc atgggcaa at gaaactgcag aaagtgaaac tgcggatagg 60

ggggatgact gtattcaata gattccgaca ttatgtctgc 100

<210> 319

<211> 32

<212> DNA

<213> Homo sapiens

<400> 319

ttataatgag tgcgatatat gttgtcgagg ct 32

<210> 320

<211> 210

<212> DNA

<213> Homo sapiens

<400> 320

gttttgatgc tgtgtgcttt tggctgggcc tcgggctcca ggccctggga ccccttgcca 60

gggagacccc cgaacctttg tgccaggaca cctcctgggc ccctgcacct ttcctgttcg 120

gttttagacc ccaaactgga gggggcatgg agaaccgtag agcgcaggaa cgggtgggta 180

attttagaga caaaagccaa tttaaagtcca 210

<210> 321

<211> 115

<212> DNA

<213> Homo sapiens

<400> 321

ttcattgagg ttcgtgtgtg ctgtgttcgc gtgtgtgtgc tgtgtgtgca tgtgtgtgct 60

gtgtcttagt gtgtgtgctg tgtgctagtg tgtgtgctgt ggggtaccga gctcg 115

<210> 322

<211> 241

<212> DNA

<213> Homo sapiens

<400> 322

ttcatcatat ccaagttcac tctgtcttcc tgagcagtgg aagatcatat tgctgtaact 60

tcttttaagt agttgatgtg gaaaacattt taaagtgaat ttgtcaaaat gctggttttg 120

tgttttatcc aacttttgtg catatatata aagtatgtca tggcatgggtt tgcttaggag 180

ttcagagttc cttcatcatc gaaatagtga ttaagtgatc ccagaacaag gaataactaga 240

g 241

<210> 323

<211> 148

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (89)..(89)

<223> n is a, c, g, or t

<220>

<221> misc_feature

<222> (91)..(93)

<223> n is a, c, g, or t

<400> 323

gtcattgata cctgtagtaa gttgacaatg tggtgaaatt tcaaaattat atgtaacttc 60

tactagtttt actttctccc ccaagtctnt nnnaactcat gatTTTTtaca cacacaatcc 120

agaacttatt atatagcctc taagtctt 148

<210> 324

<211> 198

<212> DNA

<213> Homo sapiens

<400> 324

gattttcttt tgacacagct ccaaggccac cagctatgca aggccacaag ttatgcacta 60

tatgattaac tgcttttTgt ttacttttTgt aagtccactt ataaaaaccc tgctctgtct 120

ttgtttaatg ctCagctttt tggatttgaa tccactcagc cggtgcacac cttaaaataa 180

acatcctcct gtactctc 198

<210> 325

<211> 269

<212> DNA

<213> Homo sapiens

<400> 325

agacctagaa ggtttagat gggaaatcag gaatgatttg aactgataaa gatttcagac 60

tcataagaac acattttata aatgttaaac acaaaaacta catgactgaa gatagaagag 120

aatgcgatgg attttattac acatggtgga agagagaaga ggcgtgtagg ttgcaaaca 180

aagttaagaa ataggaaact gaatttttca ttgtacagaa aatgtatctc ttggggaggg 240

cctgtgtacc cccattctct gattataaa 269

<210> 326

<211> 243

<212> DNA

<213> Homo sapiens

<400> 326

ggattttttc ccctgtagta gtgaggtaac atgcttgaat gtcactgtga tattttatttc 60

ctctttgttc agttgttttt gaattcctgt taagtacatg ttttaatact ttgagcgatt 120

taagatactt ttctttttgc ccatcatttt cccaaggaa tgtaattcac ataaatccaa 180

agctcatttt tttttttatt gtacacaagt agtataatgt ttgcttttcc caataaacct 240

caa 243

<210> 327

<211> 178

<212> DNA

<213> Homo sapiens

<220>

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<222> (84)..(84)

<223> n is a, c, g, or t

<220>

<221> misc_feature

<222> (89)..(89)

<223> n is a, c, g, or t

<220>

<221> misc_feature

<222> (123)..(123)

<223> n is a, c, g, or t

<400> 327

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ctggtttgac tttaattggt gggngggtn g tttctgccgc tctgtttgct gcagtccccg 120

tgncctgctt ggggactgag aaatttgagc caggtatcca gagccacagc ccatcttg 178

<210> 328

<211> 238

<212> DNA

<213> Homo sapiens

<400> 328

agttggtgcc ctgattccat ttttctcaag ttgtagaaga aacaaactaa tttacggtag 60

gagaaattca aattcagatt ctccccatcc ccaccagtta cctttggttg gtggagaggg 120

ggagaattgg caggaaaggg gcacaaagaa actttttggg gtgatggaaa tattttgtac 180

cttgcttttag atgttgggtca gatggaatat acgtttgtgg aaacctgcca aactgtac 238

<210> 329

<211> 155

<212> DNA

<213> Homo sapiens

<400> 329

aaacattacc gggcatggta gcttgcacct gcagtcccag ctacttggga gactgaggtg 60

agaggatcac ctgagtgtag gaggtgaaag cctcaccgaa ctatgactga accactgcac 120

tccagcgtgg gcacttggca ccagagcaag attct 155

<210> 330

<211> 47

<212> DNA

<213> Homo sapiens

<400> 330

gggatgcata aagtatgagt gccttttagg atgggaattg agatgta 47

<210> 331
 <211> 235
 <212> DNA
 <213> Homo sapiens

<220>
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 <223> n is a, c, g, or t

<400> 331
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 tgcagagcta atttatcacg tttctctcct gtgaganccc cccttttata tgatatatcc 180
 agaggaagtt ttgtaatata aaacaggacg cccacactga tggttttgca ctggt 235

<210> 332
 <211> 38
 <212> DNA
 <213> Homo sapiens

<400> 332

tttggatttg aatccactca gccggtgcac accttaaa 38

<210> 333

<211> 265

<212> DNA

<213> Homo sapiens

<400> 333

tgttttagaa ccagccgtat ttacatgaa gctgtataat taattgtcat tttttttgtt 60

agcaaagatt aaatgtgtca ttggaagcca tccctttttt tacatttcat acaacagaaa 120

ccagaaaagc aatactgttt ccattttaag gatatgatta atattattaa tataataatg 180

atgatgatga tgatgaaaac taaggatttt tcaagagatc tttctttcca aaacattttt 240

ggacagtacc tgattgtatt ttttt 265

<210> 334

<211> 56

<212> DNA

<213> Homo sapiens

<400> 334

cacaatctga gcacgctacc aaatctcaaa atatcctaag actaacaaag gcagct 56

<210> 335

<211> 289

<212> DNA

<213> Homo sapiens

<400> 335

tcccaagtag tgctgactga ctctcctggg gacaggggtt tgtgtccgag cccctgcggt 60

caaggagtgt ggagcaaaac gtgggtacta ggggtgggagg cggggaaagg ccacagcaca 120

ctggcgctcc agcaaagcca aatcatgtct cctctggcca ctgcggtcct ctccttggtta 180

catgtcatcc cccagaggag tatccaaagc tattccacta tgcactcatc aaccctggct 240

tgtcagcctt ggggaaggct actttattca taaaaatgcc tctttgagt 289

<210> 336

<211> 212

<212> DNA

<213> Homo sapiens

<400> 336

cctgagtcct gggatcagac accccttcac gtgtatcccc acacaaatgc aagctcacca 60

aggtccccctt tcagtcccct tccctacacc ctgaccggcc actgccgcac acccaccag 120

agcacgccac ccgccatggg agtgtgctca ggagtcgcgg gcagcgtgga catctgtccc 180

agagggggca gaatctcaa tagaggactg ag 212

<210> 337

<211> 294

<212> DNA

<213> Homo sapiens

<400> 337

cagggttcct ttgcctgcta acaagcccac gtggaccagt ttgaatgtct ttcctttaca 60

cctatgtttt taagtagtca aacttcaaga aacaatttaa acaagttttt gttgcatatg 120

tgtttgtaa cttgtatttg tatttagtag gcttctatat tgcatttaac ttgtttttgt 180

aactcctgat ttttcctttt cggatactat tgatgaataa agaaattaaa gtgatagttt 240

tattggtttc ctttccccca attaaggcca aataaagtcg tgagaacatt accc 294

<210> 338

<211> 52

<212> DNA

<213> Homo sapiens

<400> 338

gaggccggtg ccagtgcagg tccttggtgt gctgtgtgcc ggtcccctgg gc 52

<210> 339

<211> 297

<212> DNA

<213> Homo sapiens

<400> 339

atggtaatgt aggatccttt cacagagtgc caggctaaag agctgaactt tgtggtggaa 60

gagacagacc ccctatgtgc tctgtagaca cctgtgatga agtagaactc atgaggatat 120

gaagagaaac atttgtaatt tgagtgatta aactaggaac gaaagaggag gggagaaata 180

ggaagagaga atcaccggcc ctgttgactg atttgagctg ggaatgaaga agaaaaccct 240

gcaggtgtgg gcaccaatgt ttgaaacccc cacagtgtga gtctcaactc tgtgtga 297

pctgb2013053202-seq1.txt

<210> 340

<211> 223

<212> DNA

<213> Homo sapiens

<400> 340

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aggatggatg ggcatctttc tccttgacca ccctactctc ccttcctccc ctgatcacct 180

cccctccctg ctctcccctg gtgatggact tctaacatga gat 223

<210> 341

<211> 238

<212> DNA

<213> Homo sapiens

<400> 341

actggtatat tattgcttca tgttttgtac catcataaga ttttgtgcag atttttttta 60

cagaaattat tattttttat gacaatatga cacttgtaaa ttgttgtttc aaaatgaaca 120

pctgb2013053202-seq1.txt

gcgaagcctt aactttaaat gacatttgta ttttcagaca ctgagtagca taaaaaccac 180

atagaactga actgtaactt aaattccaaa ctatgactac tacattccaa agaaacag 238

<210> 342

<211> 129

<212> DNA

<213> Homo sapiens

<400> 342

cgtccccaac atgcatctca ctctgggtgt cttggtcttt ttttttttgt aagtgtcatt 60

tgtataactc taaacgcca tgatagtagc ttcaaactgg aaatagcgaa ataaaataac 120

tcagtctgc 129

<210> 343

<211> 277

<212> DNA

<213> Homo sapiens

<400> 343

tggaggattc aagatgagca ggtatgtttt ctgctttcaa taactcattt tctgctgcag 60

agatagcctt gtaagcaagc aaaggaaaac tttgacattt ctctgcaaag ataatgcatt 120

acataataagg gtgtgtcttg gagggtagca ggtgcctgtc agcaaaagtt gcaaaaacag 180

cttgataagg gtattaagtg ggctgttg gaaaggcagg agtgtcaaat gtcggacaga 240

actccagaca gagaaatcca gatatccagt aggttag 277

<210> 344

<211> 231

<212> DNA

<213> Homo sapiens

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<222> (92)..(92)

<223> n is a, c, g, or t

<220>

<221> misc_feature

<222> (105)..(105)

<223> n is a, c, g, or t

<220>

<221> misc_feature

<222> (160)..(160)

<223> n is a, c, g, or t

<220>

<221> misc_feature

<222> (169)..(170)

<223> n is a, c, g, or t

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<221> misc_feature

<222> (172)..(176)

<223> n is a, c, g, or t

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<222> (178)..(180)

<223> n is a, c, g, or t

<220>

<221> misc_feature

<222> (182)..(182)

<223> n is a, c, g, or t

<220>

<221> misc_feature

<222> (186)..(187)

<223> n is a, c, g, or t

<400> 344

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tcaagttgag gatgtcattt attcttgaat tntgtttttt tactnagatg ctttcaatta 120

atagccctat atttttgtgc aggcgaactg tataacaggn ataaaaaann annnnnnnnn 180

antgannagg aggagaaatt ctcacagaac accatatgag ctttagacca a 231

<210> 345

<211> 262

<212> DNA

<213> Homo sapiens

<400> 345

gaggtgtgat tttaaggcat tgttatattt ttttttattt gtgagtgttt taaaattttg 60

tatttctttt aaacttttta ttttagaaaa atttccaaca tatatagaag tagactattg 120

taaggaaccc ttatgtaccc tccaccagct tcaacaacta tcaacaaaag tttgatcttg 180

ttttaaccac attcctttcc aatttttgtg tttaccccca gattattttg aagcaaattc 240

ctgacctcat aacattttca aa 262

<210> 346

<211> 187

<212> DNA

<213> Homo sapiens

<400> 346

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ccactttgtt acaatctact atctgtatat actatttgta tcttaattct tttatgagat 120

gttctgtaac atttttctca ctttgacaaa tgtttttaga ctgtacagtc aagatctggc 180

gcttggg 187

<210> 347

<211> 180

<212> DNA

<213> Homo sapiens

<400> 347

acagtgattc cccacgtgtg ttcatctgca cccaccgagc caggcagagg ccagccctcc 60

gtggtgcaca cagcacgcg ctcagtccat cccatttttag tcttttaaacc ctcaggaagt 120

cacagtctcc ggacaccaca ccacatgagc ccaacaggtc cacgatggat ccaccagtcc 180

<210> 348

<211> 55

<212> DNA

<213> Homo sapiens

<400> 348

cagatcgaca cgcagctagc ctcctgcatt gtatggttat aaatagcacc ctagt 55

<210> 349

<211> 207

<212> DNA

<213> Homo sapiens

<400> 349

aagtgttcta caaaagaatc cctgtgggta gcttactctt aggttagatc ttctaataag 60

gctgaaattc aaaatcaaaa ccttagtggtg tccgagtcca gcctggggttc cagcattctg 120

ttcaggccac ttctgaacgg ccgaagggtgc cccattccag acctgcccac ttgatggaca 180

gagcagacag cccggaacag attcaag

207

<210> 350

<211> 241

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (93)..(93)

<223> n is a, c, g, or t

<220>

<221> misc_feature

<222> (97)..(97)

<223> n is a, c, g, or t

<400> 350

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60

aatccaaatt ttccatcttt gaaattttcc atncttncag tcaatattag taatacctgg

120

gtcaaagggg agagtttagc ataccaatta atgatcatca gaaatgacat agtcctacaa

180

aagcaaagaa aatttagaga cactttctta aaaatacgac tcttggtact gttgaagaaa 240

a 241

<210> 351

<211> 261

<212> DNA

<213> Homo sapiens

<400> 351

agccgctgcc aagtctgtat gagaagaaca taatgaagcc tgactcagct aatgtcacao 60

catggtgcta cttcttcttc tttttgttaa cagcaacgaa ccctagaaat atattctgtg 120

tacctcactg tccaatatga aaaccgtaaa gtgccttata ggaatttgcg taactaacac 180

accctgcttc attgacctct acttgctgaa ggagaaaaag acagcgataa gctttcaata 240

gtggcatacc aaatggcact t 261

<210> 352

<211> 274

<212> DNA

<213> Homo sapiens

<400> 352

ggttgagttt gtccattgct agggagagac ttccagtaat aaaatttact attctagatg 60

cttctactgt tatgttttat ctgcccattt atctttctta gttaccagga gaaatgtgtg 120

acacctatat tataatgaaa acaatcttat tacttatagt ttatctatat taaacaaatt 180

taattgcatt ttaaagcatt ctttgatatt gttgcttttg caataaatat ggataatctt 240

ggttataagg gagttaaac aatgctgtaa taaa 274

<210> 353

<211> 179

<212> DNA

<213> Homo sapiens

<400> 353

tcatggaatg ctacatgctt tctgtttttt tcattttgga tttctccaaa actaactgaa 60

tttaagcttc aggtcccttt gtatgcagta gaaaggaatt attaaaaaca ccaccaaaga 120

aaataaatat atcctacttg aaatttactt tatggactta cccactgcta gaataaatg 179

pctgb2013053202-seq1.txt

<210> 354

<211> 249

<212> DNA

<213> Homo sapiens

<400> 354

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aataaaaggt attgagccat tttttaaatg acatttttga taaattatgt ttgtactagt 120

tgatgaagga gtttttttta acctgtttat ataattttgc agcagaagcc aaattttttg 180

tatattaaag caccaaattc atgtacagca tgcacacgg atcaatagac tgtacttatt 240

ttccaataa 249

<210> 355

<211> 64

<212> DNA

<213> Homo sapiens

<400> 355

ccatgaagga gcaagttttg tatttgtgac ctcagctttg ggaataaagg atcttttgaa 60

ggcc

64

<210> 356

<211> 57

<212> DNA

<213> Homo sapiens

<400> 356

atgaggcaga atctggttgg gtatgtttct tatatatgtt tgaagcagat ggctgac

57

<210> 357

<211> 141

<212> DNA

<213> Homo sapiens

<400> 357

atTTTTgcct ttccgtttct gtctatgatg taggcttctg aggagaacca agaagcttgg

60

ctttagtggt agaatgacag aacttaggga tcccttgacag gctagaacaa agttctgacc

120

cttagaccaa atctttatgt t

141

<210> 358

<211> 108

<212> DNA

<213> Homo sapiens

<400> 358

gaggaggtgg gcctcgttag actgctcaga ttactggaac ctcgttatca catcccattc 60

tacaagtttt tcactgaatg tttcctgaca tctataaatg agggtgcc 108

<210> 359

<211> 158

<212> DNA

<213> Homo sapiens

<400> 359

gttcaaatga tctacactta cattttgcaa atcttttttt tttaaattttt taaattttat 60

attttttttc cagccaactc aaggccaaaa aaaatttctt aatatagtta ttatgcgagg 120

ggagggggaag caaaggagca caggtagtcc acagaata 158

<210> 360

<211> 157

<212> DNA

<213> Homo sapiens

<400> 360

aggtggtttt gataacacac ttataaggct ttctgtaaaa ggtactatag aagggcgaag 60

aatcgttcaa ctgtcaatca gcctcttgat tctttgtaaa ttgccagggt gggtaggtac 120

atatctcttc ttgattctgc atttcatact taactat 157

<210> 361

<211> 273

<212> DNA

<213> Homo sapiens

<400> 361

gactgagtga gtaactgcaa gctacagggg gcagcttacg tatggcacac agggtagggc 60

tagcttggtt tcataggctc tctgtggatt ggatgattta aataattttg gtgggccctg 120

gggttaggg actgtcccta gttgtttggt gctaggtccc agggcagatt agggcagatg 180

tgagtgtgag agcatgataa ggaaagtctt caaggtgtgg aattactcaa ctgctggaga 240

aagggaattt atcagccttt agccagggcc tca 273

pctgb2013053202-seq1.txt

<210> 362

<211> 257

<212> DNA

<213> Homo sapiens

<400> 362

gaaagcctga gtttgcaacc agttgtaggg tttttgttgt gttttttttt tttttttgaa 60

ataaaactat aatataaatt ctctatttaa ataaaattat ttttaagtttt agtgtcaaaa 120

gtgagatgct gagagtaggt gataatgtat attttacaga gtggggggtg gcaggatggt 180

gacattgaac atgattgctc tctgtctctt ttttcagctt atgggtatatt atcttctatt 240

agtatttgta tcttcag 257

<210> 363

<211> 268

<212> DNA

<213> Homo sapiens

<400> 363

atgagtcaaa atccgctctc catgcttact cttgacaccc cattgaagcc actcattgtg 60

pctgb2013053202-seq1.txt

tgtgcgtctg ggtgtgaagt ccagctccgt gtggtcctgt gcttgactg ccctgctttg 120

cagttccttt gcacttactc atcgagtgcg gttttgaaat gctgacatta tataaacgta 180

aaagaaaatg taaaaaaaaa aaaccacac acaaacaac ccatacgatc tgtatttgta 240

tatacacgtg tccgtacaag tataacta 268

<210> 364

<211> 290

<212> DNA

<213> Homo sapiens

<400> 364

gaccaaattg attagactgt aaactgcaaa gtgctgtccg cacatgaggt catctgatta 60

ctgtcctcag atctcttttg tagaggattt caatgtattt ctttatcatt tgagtgtgtg 120

tgtgatggac gaatatgtgt gtgagtttga gaagcatatc gttcgtgtcc agttactttg 180

caaatttggtg gacatttggt attggacaga ggggtttgtg ctgtggccta acacttgcca 240

agtgaggtgt aggttatgcc tatatgcaaa ttaaacttca cttttcttga 290

pctgb2013053202-seq1.txt

<210> 365

<211> 205

<212> DNA

<213> Homo sapiens

<400> 365

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tttcaccatt tcgagtgca agtgtatattt taactgtctg gtttgtactt ttatgacttt 180

tgtactacca aagcggagtt aaaaa 205

<210> 366

<211> 278

<212> DNA

<213> Homo sapiens

<400> 366

ctatcaggta ctgtgctcat ctgaacaaca aacctcaaca acacgcaatt tatccatgta 60

attaacctgc acatgtaccc ccgaaaccta aaataaaaagt tcaaaaaaaaa cctgtggtat 120

ttaaataagg attgtgtcta aaaatgcatg ctatctaaaa atgtagtttt attgcactgt 180

ataagaatac gagaggttta aaatagacac tctaaaagtt ataagcccta atttacatat 240

attctctagc ctttctccac cttctatcta ccaaaaaa 278

<210> 367

<211> 41

<212> DNA

<213> Homo sapiens

<400> 367

tcctcatggt ggcagcgctc atagcgaaag cctactgtaa t 41

<210> 368

<211> 133

<212> DNA

<213> Homo sapiens

<400> 368

aatgcagaat attcctctga acacttcctc catacatcat tcaatattat aaattaaaca 60

caaagagcct ctccacttag atttttatca tgcacacctac attgtaatgt ctttactctt 120

ccatagaaaa ggt 133

<210> 369

<211> 74

<212> DNA

<213> Homo sapiens

<400> 369

ggtgcaatta ttatactgcg aaaatgaaaa tattgcatac taaacagtac ctagggtatg 60

atctcaatgt aaaa 74

<210> 370

<211> 172

<212> DNA

<213> Homo sapiens

<400> 370

aactgtgacc gtttctgtgt gaagatTTTT agctgtatTT gtggtctctg tatttatatt 60

tatgttttagc accgtcagtg ttcctatcca atttcaaaaa aggaaaaaaa agagggaaaa 120

ttacaaaaag agagaaaaaa agtgaatgac gtttgtttag ccagtaggag aa 172

<210> 371

<211> 258

<212> DNA

<213> Homo sapiens

<400> 371

actcaaggct gtgaacaaac atacgctgct ttattctttc caatTTTTct cttgttttct 60

agaactctta tccatatggt tttaaaataa gtacctaataa gtggtttgat agtgtcctaa 120

acgacttttt taacttccta aatggaaaga gcataacaat gtagttgatt ggtaagattt 180

acagggattt ggtttctgag tttagggcac attcccagtg aataagctga gtcccatacc 240

acactcaaaa ggttttaa 258

<210> 372

<211> 103

<212> DNA

<213> Homo sapiens

<400> 372

attaaagtac tcaagttagt tgttttgcag agatgttgcc ttcagatggt aatcaggtct 60

ctcaagtttc atggagtcta tgctgaccc ttaattgaca aat 103

<210> 373

<211> 258

<212> DNA

<213> Homo sapiens

<400> 373

ggatgaagtg gcacacactc taactgaaag cagagtatta aagaacacta gacatccctt 60

tttaacatcc ttgaaatatt ccttcagac aaaagaccgt ttgtgttttg tgatggaata 120

tgtaaatggg ggcgagctgt ttttccattt gtcgagagag cgggtgttct ctgaggaccg 180

cacacgtttc tatggtgcag aaattgtctc tgccttgac tatctacatt ccggaagat 240

tgtgtaccgt gatctcaa 258

<210> 374

<211> 252

<212> DNA

<213> Homo sapiens

<400> 374

ggttctgtaa ggtctttatt tcccataagt aaatattgcc atgggagggg ggtggaggtg 60

pctgb2013053202-seq1.txt

gcaaggaagg ggtgaagtgc tagtatgcaa gtgggcagca attatTTTTg tgTTaatcag 120

cagtacaatt tgatcgTTgg catggttaaa aaatggaata taagattagc tgTTTTgtat 180

TTtgatgacc aattacgctg tattTTtaaca cgatgtatgt ctgTTTTTgt ggtgctctag 240

tggtaaataa at 252

<210> 375

<211> 210

<212> DNA

<213> Homo sapiens

<400> 375

TTTcaagatc TTTtgctcac aattcactgc aactgagggg atgtgaatat cattatgcaa 60

Taaattaaga gccacagTTg gctgaggtga tatgaaagcc aacctgccta aggggggtat 120

gaaagatgtg tatctTTTcca aactTTTtaa acaacgtaag tctgagataa gaacatattt 180

gatggcactg TTTggaaaga ggtgtcctta 210

<210> 376

pctgb2013053202-seq1.txt

<211> 258

<212> DNA

<213> Homo sapiens

<400> 376

ctcaccagga ctcgtctctc cattccccgtc agagtttgct ttgatttccc tttcctttcc 60

ttctcgggga ccagttctta cttcctttta tttttagctt tgcactccat gtggtttcag 120

ggttcagttt gatccatcaa aaggttcttt ttttataatc ctttttgaaa atgataatca 180

aaggaagaga tgtggtgttt ggcatgtgg aaaactcaat gtataattta gacgtctgtc 240

aaaaatccga caaataaa 258

<210> 377

<211> 218

<212> DNA

<213> Homo sapiens

<400> 377

gtttcaattg attcacaact ttaaaaaata tccacagagg cgtaagagga gatattgtat 60

tgcaccacg aaccagtttt atgctgttta agaaaggac attcaagaaa caaaaaggga 120

gctttgggaa atttgaacaa taaataatag tagaataaaa aattcagaga aagtttggat 180

gataaatttg agccaatctc ccagtaagca gagcaaaa 218

<210> 378

<211> 267

<212> DNA

<213> Homo sapiens

<400> 378

atgactgtgc tagagccacc ctctcacttt agcctcctga gtagctggga ctacaggtgc 60

ttcccactgt gcctggccaa ttaacaattt catttttatt tttagtagag atgagatctc 120

actatgttgc ccaggctggg cctgaactcc tgagctcaag agatcctccc accttggcct 180

cccaaagtac tgggattaca aacaagagcc actgtgcctg accaggctct aagattgcta 240

atctggctat agaaggacta atgttag 267

<210> 379

<211> 230

<212> DNA

<213> Homo sapiens

<400> 379

aagccgaggg gcccgagact ctgcagcggg gccagaaaga gaagagtggg ggaggaggcc 60

gggagtgggtg catggaccag ggggtagagg gaggtgggtg tggacctggg gtcgggcgcc 120

agtcagcttg cagcctatga aggacggaag ggagggttac agagataggg gaagagtggg 180

gctgaggata gccagagcgg cttggcacac agtttttaggg taaaagcatc 230

<210> 380

<211> 196

<212> DNA

<213> Homo sapiens

<400> 380

tttatttata ccaagcctcc tcctgaaatt tctcttcctt tctttctacc tacccaagac 60

ataccacgtg cttcaataac cagtccttc ctctacaaa cactacaacc tggaaagcac 120

tcttgctttt ctgaagtcct ctatacttag tgtaactctt ctgtgatgaa gattaaagtg 180

tattatggca actctc 196

<210> 381

<211> 267

<212> DNA

<213> Homo sapiens

<400> 381

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ttttcttccc aggcaataca cctctgaaca tgtgtgtgat aaatgggttt gctaattgtgc 120

tgttttaaaag tataaaagcat aatatgtttt ggtaacaca atgtactttt tgaactataa 180

atctttatatt taatatggaa atgtttggaa caggagatgc aagccactaa cagagaactt 240

taataattct accctgtatt ttataaa 267

<210> 382

<211> 280

<212> DNA

<213> Homo sapiens

<400> 382

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gtattgggaa tccaaattga attttgattc tccttggcag tgaactactt tgaagaagtg 120

pctgb2013053202-seq1.txt

gtcaatgggt tggtgctgcc atgagcatgt acaacctttg gagctagaag ctcctcagga 180

aagccagttc tccaagtttt taacctgtgg cactgaaagg aatgttgagt tacctcttca 240

tgtttttagac agcaaaccct atccattaaa gtacttggtta 280

<210> 383

<211> 72

<212> DNA

<213> Homo sapiens

<400> 383

acatgagtat ggaatgggtgt tttattatga ctttagtttg cattttcctc aattctcggt 60

aaatccttca tt 72

<210> 384

<211> 260

<212> DNA

<213> Homo sapiens

<400> 384

gagtaggttc ggtctgaaag gtgtggcctt tatatttgat ccacacacgt tggtctttta 60

pctgb2013053202-seq1.txt

accgtgctga gcagaaaaca aaacaggtta agaagagccg ggtggcagct gacagaggaa 120

gccgctcaaa taccttcaca ataaatagtg gcaatatata tatagtttaa gaaggctctc 180

catttgcat cgtttaattt atatgttatg ttctaagcac agctctcttc tcctattttc 240

atcctgcaag caactcaaaa 260

<210> 385

<211> 222

<212> DNA

<213> Homo sapiens

<400> 385

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ggaatactca ctttttgta agaagttgaa ctatgactgg agtaaaccat gtattccctt 120

atcttttact ttttttctgt gacatttatg tctcatgtaa tttgcattac tctggtggat 180

tgttctagta ctgtattggg cttcttcgtt aatagattat tt 222

<210> 386

<211> 216

<212> DNA

<213> Homo sapiens

<400> 386

gcaatatatt tgtgattccc catgtaattc ttcaatgtta aacagtgcag tcctctttcg 60

aaagctaaga tgaccatgcg ccctttcctc tgtacatata cccttaagaa cgccccctcc 120

acacactgcc cccagtata tgccgcattg tactgctgtg ttatatgcta tgtacatgtc 180

agaaaccatt agcattgcat gcaggtttca tattct 216

<210> 387

<211> 35

<212> DNA

<213> Homo sapiens

<400> 387

ttggatagca gctatcttgt tggatgtgag gtgga 35

<210> 388

<211> 258

<212> DNA

<213> Homo sapiens

<400> 388

atgaaaggtg gaagttctac ctagatttga atgagtgttt ttttaaggga atgagaatgt 60

catggtgcta aacctgacaa ataagagatc attgaaatgc tgaaaatttt aacagttttt 120

ttaaaagtat tgagggggca aaaattacca attatggtat acaaaaataa gcctataaat 180

gtgtttcaca ttgctaactt gagtttcagt tgattcagtt tgtaataact agtaatgagc 240

ttctgtttac aataaaaa 258

<210> 389

<211> 275

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (195)..(195)

<223> n is a, c, g, or t

<400> 389

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ttcatcaact cctttgtttt ttccttcttt tttttttttt gagatgaggt ctcactatct 120

tgcccagact ggtttcgaat tgccctccag caattctccc acctcagcct tcagagtagc 180

tggcattgtg ggtangcacc actgtgccca gctcctgttt tataataaat aagccagagc 240

tctatctcca aatggtgcaa atcatcaatg ctatt 275

<210> 390

<211> 281

<212> DNA

<213> Homo sapiens

<400> 390

gggcccctgg tatttatagg gtccaagagg aggcacctgc ttttcaactg caccctcagt 60

gctgcctctt cacggcccct aaacgtttcc ctttgagggt gtgatgctgg gaatcacaga 120

cttcactctc tgcctgcacc cttccccgag gtctcatctt ttctgggtcc cacatctttg 180

taataatgtg aaaaagcaca atttgtctga tcacccccca ggtggttccc caccttatta 240

tcactacctg atccgagtta ctgcaataag tacggtgtcg c 281

<210> 391

<211> 274

<212> DNA

<213> Homo sapiens

<400> 391

tgctcagtgt catgctgtgt gtgcatgtgt gtgctgtgtg ttttgtgtgt gtgctgtgtt 60

catgtgtgct gtgcatgcgt gtgtgctgtg tgtgcctgtg tgtgcggtgt gctgtgtcct 120

tgtgtgtgct gtgtgtgcgt gtgctgtgtg catgtgtgtg ctgtgttatg tcgtgtgtgc 180

agtgtgtgct gtgtccgatg tgtgctgtgt acacatgaga gagcagagtg tacatgtgtg 240

tgctgagtct atcagaagat gtgtgtagct gcgg 274

<210> 392

<211> 89

<212> DNA

<213> Homo sapiens

<400> 392

tgtgcccagc ctaagccatt tcttaaaata aaaatgctaa aggactagta agtaaaaata 60

aaacttccta tgggatttcc cagtggaaa 89

<210> 393

<211> 72

<212> DNA

<213> Homo sapiens

<400> 393

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gtctttaaaa gc 72

<210> 394

<211> 177

<212> DNA

<213> Homo sapiens

<400> 394

gataacagtc ttgcatgttt atcatgttac aatttaatat tccatcctgc ccaacccttc 60

ctttcccatc ctcaaaaaag ggccatttta tgatgcattg cacaccctct ggggaaattg 120

atctttaaat ttgagacag tataaggaaa atctggttgg tgtcttacia gtgagct 177

<210> 395

<211> 117

<212> DNA

<213> Homo sapiens

<400> 395

ttaaacagtc tagagtgaag ggaatgtttt aaaatccaga ggcgatcaag tgaagccaac 60

ctttggaggc ccgtagaagt catttggagg aatttggact tcgtgcagta ggaaaga 117

<210> 396

<211> 164

<212> DNA

<213> Homo sapiens

<400> 396

cagggggggc tgagagtaac agtgaggatt atccaggtgc cctgagtgta acagtgagga 60

ttatccaggg gggccctgag tgtaacagcg aggattatcc agggggccct gaggcaaca 120

gtgaggatta tccagggggg cctgagtgta acagtgagga ttat 164

<210> 397

<211> 259

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (139)..(139)

<223> n is a, c, g, or t

<400> 397

caaaaatgag tcacaactct tgattccatc cacctccaaa atccaggtat tttccttaat 60

tctcattctt tcacaactcc acatatatcc atatcctcat tatctcagga caacgtgacc 120

atttcttgcc acttcccanc acttccatgc ctaccaaaga agcctatctt ctctcaccag 180

gaccactgaa aaagtcttgc aactgatttc cttgtcctc ttcttgctc tctacagtca 240

attctctata caacagtca 259

<210> 398

<211> 104

<212> DNA

<213> Homo sapiens

<400> 398

tgctgcggtc gcctctctca ggctcccccg ctccccggg cctccgcttc tcagccgggt 60

gctgtgcggt tgagtgtgtg ctgctgctcg ctgtgtgtgc tgtg 104

<210> 399

<211> 147

<212> DNA

<213> Homo sapiens

<400> 399

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ctcctgtatg acaggtagcc actatactga atcaaggtgc tgaactcaaa tcacaaaatt 120

ctggcttacc gatacaaaa ccaatac 147

<210> 400

<211> 208

<212> DNA

<213> Homo sapiens

<400> 400

ctctgagttt tatatgctgg aatccaatgc agagttgggt tgggactgtg atcaagacac 60

cttttattaa taaagaagag acacaggtgt agatatgtat atacaaaaag atgtacggtc 120

tggccaaacc accttcccag cttttatgca aaaaaagggg agaatcaaag ctttcatttc 180

agaaatgttg cgtggaaaag tatctgta 208

<210> 401

<211> 139

<212> DNA

<213> Homo sapiens

<400> 401

aaaaagagag aatatgtcct gtgttagctt gcttaggaaa taaagagaga gagagagagg 60

gagggagggga aagagagaaa gagagagaga gaaagagagt gagagaaaga gagagcaaga 120

gagcaagagt aagaaagaa 139

<210> 402

<211> 243

<212> DNA

<213> Homo sapiens

<400> 402

ggcagtagat agtcaaagtc aaatcatttc taatgtttta aaaatgtgct ggtcattttc 60

tttgaaattg acttaactat tttcctttga agagtctgta gcacagaaac agtaaaaaat 120

ttaacttcat gacctaattg aaaaaagagt gtttgaaggt ttacacaggt ccaggccttg 180

ctttgttacc attctgatgt tggactaatt gactaatcac ctacttatca gacaggaaac 240

ttg 243

<210> 403

<211> 298

<212> DNA

<213> Homo sapiens

<400> 403

agaggcccat gccaacagtc taatctaaga gattagtctt tcaaactcac catccagttg 60

cctgttacag aataactctt cttaactaaa aacctagtca aacaaggaag ctgtaggtga 120

ggagatctgt ataatatctt aatttaagta agtttgagtt tagtcactgc aaatttgact 180

gtgacttttaa tctaaattac tatgtaaaca aaaagtagat agtttcactt tttaaaaaat 240

ccattactgt tttgcatttc aaaagttgga ttaaagggtt gtaactgact acagcatg 298

<210> 404

<211> 193

<212> DNA

<213> Homo sapiens

<400> 404

agagggaact gtgcagtccc caggccgccc cggctccggg ctagaggcaa taaataaacc 60

cgatcctgcc gggcacagcc gcgcccgcgc ctccggcgcc gtccccgggc tgacggggga 120

gggagcggag aagcgagcgc agattctgcg tataaatcag ctctggagca gacacagccc 180

ggctgtgaaa agc 193

<210> 405

<211> 275

<212> DNA

<213> Homo sapiens

<400> 405

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gcacggtcag gttagggctg gacagatgag gaagagctag caaagggggc ttgaggagca 120

gtggccacta agacaggagt gtgacatttt agaagccaaa agaagaccat gtaattcaag 180

ggagaggat gatttgctgg gtcagatcta aaaataaatc acacgttttt ttaaactgta 240

gtaattaacc actgaaaact tatgagtgat ccaat 275

<210> 406

<211> 143

<212> DNA

<213> Homo sapiens

<400> 406

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gccaggctgg tcttgaactc cttccctcgc tccccaaaa atttgaattt ttttttcaac 120

acttttacac ctgttatgga aaa 143

<210> 407

<211> 263

<212> DNA

<213> Homo sapiens

<400> 407

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ctgaatttgg tagtttaaga aacagattta gtttttcagt ggttttaact catgtgaaat 120

aatgattttc caccagcttt gatgcaaaga gatataattt taatgaacga tttatccagc 180

agtttgttcc aggggttgcc tctccttatt tacggggatt actttgtaca tgcagataag 240

ttttcgcaaa cctattttcca ttt 263

<210> 408

<211> 300

<212> DNA

<213> Homo sapiens

<400> 408

gatgataatc ttactgggtg aaaaggatgg aaaaataaat caacaaatgc aaccagtttg 60

tgagaaaaaa aaaaaaaagc cgaaaaaa aaacaaacaa cctgaatgag gaagagctcg 120

gctcccgttt agcattttgt acttaaggaa ataaaaaacc aacaaaggat ctcacatttt 180

pctgb2013053202-seq1.txt

cttaaaaagt gaagattgct gtatactatt tattcaactt ataatttatg ttactccttg 240

atctttgtct tttgtcatga caaagcattt atttaataaa gttatgcatt cagttcccaa 300

<210> 409

<211> 238

<212> DNA

<213> Homo sapiens

<400> 409

agaattccag ataaacacac agcctttccc ataccttttt ttttcttact ataaaatatt 60

ataagatcca ttgatgtcca aataatacca ccgagcatct cttcacctct cctcctcttg 120

gtccacttgc taatgccag ttttcttctc catttccact ttttcttagg ctccctatatt 180

actattcatt ttgacttcct tctgttttat ttttttcct ttagcattgc atgtgaat 238

<210> 410

<211> 101

<212> DNA

<213> Homo sapiens

<400> 410

tgagtgtgct gtgctcgcgt gtgtgctgtg ttcatgcgtg tgctgtgtgt tgtgtgtgtg 60

tagctgcggg gatgcataaa gtatgagtcg tttttaggat g 101

<210> 411

<211> 34

<212> DNA

<213> Homo sapiens

<400> 411

tttatgaaca gcagactcta tgtaaaggca tttt 34

<210> 412

<211> 168

<212> DNA

<213> Homo sapiens

<400> 412

aggagggaataa ataatagccc agtgagagct gaatgaaaag ggactgaatt taaatatttg 60

taagaacttt gtgatgatga gtaattgtca gacgtgggat agataactga gaggctcaga 120

atctttacca aggatatttt ttaggataag gtagctgcct gttcatga 168

<210> 413

<211> 150

<212> DNA

<213> Homo sapiens

<400> 413

agggacccag taagaccaa ggaggggagg acagagcatg aaaacaaaa tccatgcaaa 60

tgaaatgtaa ttggcacgac ctcaccccc aaatcttaca tctcaattcc catcctaaaa 120

agcactcata ctttatgcat cccgcagct 150

<210> 414

<211> 124

<212> DNA

<213> Homo sapiens

<400> 414

ggctcaggtc ctccctacaa gacctaccac tcacccatgc ctatgccact ccatctggac 60

atttaatgaa actgagagac agaggcttgt ttgctttgcc ctcttttcct ggtcaccccc 120

actc 124

<210> 415

<211> 93

<212> DNA

<213> Homo sapiens

<400> 415

tggagaagca ctggtgtctg cagcaccct cagttcctgt gcctcagccc acaggccact 60

gtgataatgg tctgttttagc acttctgtat tta 93

<210> 416

<211> 76

<212> DNA

<213> Homo sapiens

<400> 416

ggaggatgcg ctgtgggggtt gtttttgcca taagcgaact ttgtgcctgt cctagaagtg 60

aaaattgttc agtcca 76

<210> 417

<211> 220

<212> DNA

<213> Homo sapiens

<400> 417

tctggtagat aaagccctag accttgtcca cactctcacc cccatcccca actttccctg 60

gaccggtgcc gccccactt gatgcttgct caaggccggg gactggagcg ggctacttgt 120

atatttcgtt gtcagtctgc agaatgtgtt tgatTTTTat tttccctcc ttctctgaca 180

tgtgtcaagg aataaagact ggatacaggt ccattacgtc 220

<210> 418

<211> 98

<212> DNA

<213> Homo sapiens

<400> 418

tggatcgatg atgagtcccc ccaaaaaaac attccttgga aaagctgaac aaaatgagtg 60

aaaactcata ccgtcgttct cagcggaact gaggtcca 98

<210> 419

<211> 97

<212> DNA

<213> Homo sapiens

<400> 419

ggccaaaaag tctacattgc gtgtgtggat ggatgaatga gcagtgggag tgcagcgcca 60

ggtgacaaga tgttgtgagg ggttttgagt catccag 97

<210> 420

<211> 87

<212> DNA

<213> Homo sapiens

<400> 420

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ccacctaccc caagagatac tggttgt 87

<210> 421

<211> 36

<212> DNA

<213> Homo sapiens

<400> 421

aaaaaagttc aactagtatg aaagggttat aaagta

36

<210> 422

<211> 116

<212> DNA

<213> Homo sapiens

<400> 422

gtgagtaaataat aatgtttctag tgcaacagga caaactactc tctccacagg aaaccaacc 60

acaacaggat caatagaaag aaaagagaaa acgttagccc ccaactacaa ataaat 116

<210> 423

<211> 264

<212> DNA

<213> Homo sapiens

<400> 423

tttcttcttt atgtccaatt ttgtgggtgg gaggaggatt tagtctcttc ctgatttcga 60

agagctcatt tactatttcg ggaaataaga tttggattgt caaccattat agctatTTTT 120

tacacacttt tcaactttgt ttttgttata agaatgtgta tgattgttac atgtccaagt 180

ataaccatgt tcgcttttat ggcttttgag tttcatgtca tttttggaaa gatatatata 240

ttgagtccat aaaacccttc acct 264

<210> 424

<211> 119

<212> DNA

<213> Homo sapiens

<400> 424

actttaataa aggttatcca taccaataaa aagtgtacaa cacagcattt tctgttaaatt 60

tattattggt tttcagttgt aatttggtat tttttctggc atgcgtttat taatttatt 119

<210> 425

<211> 279

<212> DNA

<213> Homo sapiens

<400> 425

gtaggtttgg gagtataacg gtcacccagg gaggggggtga agacggagaa gacttacata 60

gcacggtcag gttagggctg gacagatgag gaagagctag caaagggggc ttgaggagca 120

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gtggccacta agacaggagt gtgacatttt agaagccaaa agaagaccat gtaattcaag 180

ggagaggat gatttgctgg gtcagatcta aaaataaatc acacgttttt ttaaactgta 240

gtaattaacc actgaaaact tatgagtgat ccaatatta 279

<210> 426

<211> 130

<212> DNA

<213> Homo sapiens

<400> 426

gggacaaggt cccttggtgc tgatggcctg aaggggcctg agctgtgggc agatgcagtt 60

ttctgtgggc ttggggaacc tctcacgttg ctgtgtcctg gtgagcagcc cgaccaataa 120

acctgctttt 130

<210> 427

<211> 262

<212> DNA

<213> Homo sapiens

<400> 427

pctgb2013053202-seq1.txt

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gtccttcatt ttcctttttt gcctctgcat tcagcatttc tacttccaat ctccctcctc 120

tgctctttct tatttcctct gatctgcaga cttgcttctg tcccctcctt ctgttccctt 180

cctggatgtg tctttggcca acctttcctt ctctgagact tcgtgttctt gttggtagat 240

gggggctgat acttctgggt ct 262

<210> 428

<211> 140

<212> DNA

<213> Homo sapiens

<400> 428

ttattattat gaaccttcag cctactttct tgagtgccgt aaaagtgcct gttaaattttt 60

ttttttttta agaagaaaga aaaaaatggt gtttgacgtt gatggaaatt caaaaatata 120

tatggaactg aaacattaac 140

<210> 429

<211> 143

<212> DNA

<213> Homo sapiens

<400> 429

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ttgaaagaga acctagattc tatagttgta ttattgttgt ttcatacttt aaatttatat 120

ggctgtggaa aaacgaatta aaa 143

<210> 430

<211> 151

<212> DNA

<213> Homo sapiens

<400> 430

gtgtgtcaag gatttgacaa actgccattt ttctccagaa gtcaagcccc taagtgattg 60

tctagaggca agaatttttt gatatgttgt ctcaacaatg cttctcactt cgtcttcagg 120

tgccccaacc cgcaagtaca catactatgt a 151

<210> 431

<211> 150

<212> DNA

<213> Homo sapiens

<400> 431

aatgttcata ggttctcaac cctcaccccc caccacggga gactagagct gcaggatccc 60

aggggagggg tctctcctcc caccccaagg catcaagccc ttctccctgc actcaataaa 120

ccctcaataa atattctcat tgtcaatcaa 150

<210> 432

<211> 115

<212> DNA

<213> Homo sapiens

<400> 432

gatgggaatt gagatgtaag atttgggggt gagggtcgtg ccaattacat ttcatttgca 60

tggattttgg ttttcatgct ctgtcctccc ctcctttggt cttactgggt ccctc 115

<210> 433

<211> 223

<212> DNA

<213> Homo sapiens

pctgb2013053202-seq1.txt

<400> 433

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ttatgtgcat acaaatcacc tgggatcttg ttagaaggca gtaggtctgg ggtggggcct 120

gagattctgc atttctaacc aggtcctggg agatgctgat gctatcgagc cacaaccaca 180

ctttgagtag caagcctctg gcctatcctt attgtttggtt ata 223

<210> 434

<211> 272

<212> DNA

<213> Homo sapiens

<400> 434

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gtccttcatt ttcctttttt gcctctgcat tcagcatttc tacttccaat ctccctcctc 120

tgctctttct tatttcctct gatctgcaga cttgcttctg tcccctcctt ctgttcccct 180

cctggatgtg tctttggcca acctttcctt ctctgagact tcgtgttctt gttggtagat 240

gggggctgat acttctgggt cttgggcatg tc 272

<210> 435

<211> 221

<212> DNA

<213> Homo sapiens

<400> 435

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tttcagatga ggaggagag aaggaggccg ccagactcga gaggtgggag gaactccttg 120

cacacaccct gagcttttgc cacttttatc atttttgagc aactcccttt cagctaaaag 180

gccacccctt tatcgattg ctgtccttgg gtagaatata a 221

<210> 436

<211> 183

<212> DNA

<213> Homo sapiens

<400> 436

acaaaactct ccaataatga ctctgctcag ctcaggggca gcaggagtgg agtgtcgggg 60

gcccttggtg ctgagtgaag ataaattaaa aatcccaaca agccagtgac attatgtaca 120

ggaggaaagg ggtggggcctt ccaggacaga ggccgagggt ggcagggcag gacttggagt 180

ggc 183

<210> 437

<211> 237

<212> DNA

<213> Homo sapiens

<400> 437

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acctgaaata tgggactcaa tcatttttagt ccccttcttt ctataagtgt gtgtgtgcgg 120

atatgtgtgc tagatgttct tgctgtgtta ggaggtgata aacatttgtc catgttatat 180

aggtggaaag ggtcagacta ctaaattgtg aagacatcat ctgtctgcat ttattga 237

<210> 438

<211> 189

<212> DNA

<213> Homo sapiens

<400> 438

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aagaaacaag ttagaagggt atgacaggaa gtagtataat aaatgcccgg cagtacgagg 120

ggttcaacag aagtgaacaa ggcacaagaa agaggtctgt gttcaggaaa caggccagtc 180

cccacatgg 189

<210> 439

<211> 246

<212> DNA

<213> Homo sapiens

<400> 439

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gaaattaatg aaagatgttt acatgaataa tgtttgccct tactgtgtta tgaatgagtt 120

ttttgtagtg tgtctgggtg catgatgcaa gagagtagga aaaatgtttt tgaaacaaaa 180

cttgacaaat atttgtaatg aaagtaaatt taaagattgc tataattgcg ctatagaaac 240

aatgca 246

<210> 440

<211> 65

<212> DNA

<213> Homo sapiens

<400> 440

ttaacagtac atttgtgtgg ctctcaaaca tccctttgga agggattgtg tgtactatgt 60

aatat 65

<210> 441

<211> 120

<212> DNA

<213> Homo sapiens

<400> 441

tacaatgatg gttgagtga aatacagaag gggggtttga gtattcagat ttcataaaac 60

acttccttgg aatatagctg cattaacttg gaaagaagcc tgttgggcca gaagacagaa 120

<210> 442

<211> 156

<212> DNA

<213> Homo sapiens

<400> 442

aactgatggg aaaggaccaa ttatttatag tttcccaaca aaagttttaa gattttttac 60

ctttgcatca gtgcattttt atttatatca aaaggtgcta aaatgattca atttgcattt 120

tttgatcctg tagtgcctct atagaagtac ccacag 156

<210> 443

<211> 169

<212> DNA

<213> Homo sapiens

<400> 443

tgttaaactt tggaacacct accaaaaaat aagtttgata acatttaaaa gatgggcgtt 60

tcccccaatg aaatacacia gttaacattc caacattgtc tttaggagtg atttgcacct 120

tgcaaaaatg gtcctggagt tggtagattg ctgttgatct tttatcaat 169

<210> 444

<211> 87

<212> DNA

<213> Homo sapiens

<400> 444

aaatgacttt caactaacct tgtgaatctt ttgcagtgtgta ctgtgtgcaa taccaagggc 60

atagctccct gtaatttggg aaataca 87

<210> 445

<211> 96

<212> DNA

<213> Homo sapiens

<400> 445

catatatattt ttgctacttt tgctgtttta tttttttaaa ttatgttcta aacctatttt 60

cagtttaggt ccctcaataa aaattgctgc tgcttc 96

<210> 446

<211> 269

<212> DNA

<213> Homo sapiens

<400> 446

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pctgb2013053202-seq1.txt

gtttgaaaga agatttaaag tttcaaagtt ttttgttctg tttttgcttt gcatttggag 120

aaaatattga aagcagggtg tggtgtttca ttcaccttga aaaaacatg agtaaattggg 180

gatatagaat ctctgaatag ctcgctaaaa gattcaagca agggacatga attttgttcc 240

atctatcaat aatatccaga agaacaact 269

<210> 447

<211> 188

<212> DNA

<213> Homo sapiens

<400> 447

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ccatttgctt agtatccgtg cacatgtcgt actagacccc aatcaagttg cttattttaa 120

attctttcag ctgtttccct attatttcct tacttttgctg aacatgtccg ctgttttacc 180

tcactgct 188

<210> 448

<211> 246

<212> DNA

<213> Homo sapiens

<400> 448

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ttcatgatct gtcgggtctc agcagctcag gccacaggag gaggtgggtc tcctgactgg 120

cctgtgcatt ctcccaaaca agatgtttaa gactcttctt tatctcgtca caaacgcaca 180

ggacacacac gcacacacat gcacacacag ttacaaaacg cacggtacac acacgcatga 240

cacatg 246

<210> 449

<211> 217

<212> DNA

<213> Homo sapiens

<400> 449

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ggggagcaca gagaagcgga gggaagggtc ccacgtcgag gggccggggg aggcggtgac 120

tggggggcgg agtggaggct gcacccggac cgcgggcgcc cagctcggtt tgggccgacg 180

gagccctctg ccgtcgcgag cccgggcctc gggaggg 217

<210> 450

<211> 172

<212> DNA

<213> Homo sapiens

<400> 450

tgca tgccta gtcccggcat cctgatggct ccgacaggcc tgctccagag cacggctgac 60

catttttgct ccgggatctc agctcccggt cccaagcac actcctagct gctccagtct 120

cagcctgggc agcttcccc tgccttttgc acgtttgcat cccagcatt tc 172

<210> 451

<211> 188

<212> DNA

<213> Homo sapiens

<400> 451

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pctgb2013053202-seq1.txt

ggacttttggg tgataatgat atgtaggttc gtcagttgtt aacaaatgta tccctctgtt 120

gggggctatt gataatgggg aaggctgtgc atgtgtggga gtaggaggtg tatgggacat 180

ctctgtac 188

<210> 452

<211> 242

<212> DNA

<213> Homo sapiens

<400> 452

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accacctaga agcacatcct ttgttcgcag agggggggaga aaaagtcgga gagaaagaat 120

gaaagagggg aaaaaaggca gttcggcacc cggagaaagg aggcaattcg gggagaggag 180

gaggagaaga agaaaacaca cacgcgcgca cgcacacaca caccgcggag agaaaagaac 240

ag 242

<210> 453

<211> 33

<212> DNA

<213> Homo sapiens

<400> 453

gtgagcccat atcgtactgc tgcagtccag cct

33

<210> 454

<211> 83

<212> DNA

<213> Homo sapiens

<400> 454

taaccttagg aaaccagaat agcgtttggc agacacgacg ttttcagttt acctttgaca

60

cctgccccac tccattttgc ttt

83

<210> 455

<211> 232

<212> DNA

<213> Homo sapiens

<400> 455

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60

pctgb2013053202-seq1.txt

cctgttggaa ttaatttaag cttaagtata tatcaacatt attttattgt gcaattaaaa 120

caatacaaat tcatggtttt ttaaagttaa aaattttaac cactgtaaca acagtttttg 180

tgttattttc tgtattaaac atcttgttgc acgcatttga ggtcatcagg gt 232

<210> 456

<211> 275

<212> DNA

<213> Homo sapiens

<400> 456

acacaatata atcaggagtt ttcaaatttt tgattcagta tttgaatttc ttcttcataa 60

atgtagttgg aatttatcct agtatatttc ttacctgaa ggagggccat ttatttttaa 120

tttactaca tttttcttg catgattatt aaaataaaaa ctgcctctgt tgtgtttctc 180

actggaggct ggaatgaatg atcactagaa cacaaaagag tgaatgatga cacttgaagt 240

caaagcagtt gtactgatca ccagaaccaa taaag 275

<210> 457

<211> 220

<212> DNA

<213> Homo sapiens

<400> 457

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atatcttgac ttctcagcat catagaaggg ggtactgatt tcctaaagtc tttcttgaat 120

ttctattatg caaaattgcc ctgaggccgg gtgtggtggc tcacacctgt aatcccagca 180

ctttgggagg ctgaggtggg aagatccctt actgccagga 220

<210> 458

<211> 187

<212> DNA

<213> Homo sapiens

<400> 458

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aattgtagtg tcttcatcat caattaaaga aaactgtcta aatgaattca tggatgtaaa 120

tattagtggt ccttaatgtc ttgattgct ggacatgaaa caaactgcca attaaatttt 180

gcggaga 187

<210> 459

<211> 176

<212> DNA

<213> Homo sapiens

<400> 459

tcctgcaggc atccgtgggg gaaaaaaat ctctcagaac cctcaactat tctgttccac 60

acccaatgct gctccaccct cccccagaca cagcccaagt ccctccgcgg ctggagcgaa 120

gccttctgca gcaggaactc tggaccctg ggcctcatca cagcaatatt taacaa 176

<210> 460

<211> 266

<212> DNA

<213> Homo sapiens

<400> 460

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gctagtaggc atattatgct aataaaatta ctaaattaaa agtgtgtcaa ggatttgaca 120

aactgccatt tttctccaga agtcaagccc ctaagtgatt gtctagaggc aagaattttt 180

pctgb2013053202-seq1.txt

tgatatgttg tctcaacaat gcttctcact tcgtcttcag gtgccccaac ccgcaagtac 240

acatactatg tactcacttg aaaatg 266

<210> 461

<211> 286

<212> DNA

<213> Homo sapiens

<400> 461

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ctgagtatat atttacaatg ctttttaaaa gggtcgttac cagagattta cccatcgggt 120

aagatgctcc tgggtggctgg gaggcatacag ttgctatata ttaaaaacaa aaaagaaaaa 180

aaaggaaaat gtttttaaaa aggtcatata ttttttgcta cttttgctgt tttatTTTTT 240

taaattatgt tctaaaccta ttttcagttt aggtccctca ataaaa 286

<210> 462

<211> 278

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (214)..(214)

<223> n is a, c, g, or t

<400> 462

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agggaggagc agatggccat gtggctcagc ccctgcctgg gaaagcgagt ccacagttca 120

ctaacaaca caataccatc cacaacaag tagccacaaa gaccacagtt agcaaacaca 180

cacagtcaca cacacacaca cacacacaca catnacggga ggtgggcagg accgcagtct 240

gcagtgggga ggcaagtgtt agttgcatca tcaggtgg 278

<210> 463

<211> 122

<212> DNA

<213> Homo sapiens

<400> 463

aggtaggtgtt ggcagaggct atcgggctgg acaaggacaa acccaaccgt gtgaccaaag 60

tggctgtgaa gatgttgaag tcggacgcaa cagagaaaga cttgtcagac ctgatctcag 120

aa 122

<210> 464

<211> 161

<212> DNA

<213> Homo sapiens

<400> 464

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ggctaaagtg agagggtggc tctagcacag tcatcaaggc tgcaggaggc tatgatggag 120

ccactgcact ccagcctaga tgacaagggtg agacgctgtc t 161

<210> 465

<211> 162

<212> DNA

<213> Homo sapiens

<400> 465

tgtttttgac atcagctgta atcattcctg tgctgtgttt ttattacc ttggtaggta 60

ttagacttgc ctttttttaa aaaaagggtt ttgcatcgtg gaagcatttg acccagagtg 120

gaacgcgtgg cctatgcagg tggattcctt caggtctttc ct 162

<210> 466

<211> 114

<212> DNA

<213> Homo sapiens

<400> 466

tttttttagtt gccaacagtt tatgtttgct gattatttat gacctgaaat tatatatattt 60

tttttttaag aagacatttt gttacataag gatgactttt ttatacaaag gaaa 114

<210> 467

<211> 223

<212> DNA

<213> Homo sapiens

<400> 467

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pctgb2013053202-seq1.txt

ttaataaaat ttaaaattaa aactgtgttg tttttttctc ttctgctaga tacatatata 120

attaaagtac tcaagttagt tgttttgcag agatgttgcc ttcagatgtt aatcagggtct 180

ctcaagtttc atggagtcta tgctgaccc ttaattgaca aat 223

<210> 468

<211> 289

<212> DNA

<213> Homo sapiens

<400> 468

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tcaaaaatga attagatgag tacaaaagtg acgaaatgaa agaattgtcaa gaatggacca 120

caaagacagt gttttatgac ctaaagatta agatttatcc atttgtgtac aattgtggac 180

tatataaaat aaaacaagac ttgaccta gtggataaga agtatttgga tgtactaatc 240

aatatTTTTG gtctgggtca gtgggtgggtt catctgtgtt tgttgtatt 289

<210> 469

<211> 36

<212> DNA

<213> Homo sapiens

<400> 469

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36

<210> 470

<211> 156

<212> DNA

<213> Homo sapiens

<400> 470

aatataacctg atgcgctgta gaatgaaaat gtaaaagata acctgtatgt gttccgagct

60

ttaatttttt gtttaciaat tgaacagtgt tacatgggct gtccagtcct gattatagag

120

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156

<210> 471

<211> 298

<212> DNA

<213> Homo sapiens

<400> 471

pctgb2013053202-seq1.txt

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ccactcacag ggagctggca atgccctacc tgcctgttct ccagatggag aaacaggctc 120

tgagatttca caggtcttgc ccaaagtcac tgattttgat gattaaaaag aataaacaca 180

gtgtttcctg agtagcagtg attgttatgc ctgctatatt taataaagat tctattttcg 240

tataacattg tcaagtggaa acatgctgaa atctattaaa ccatctttgt ttgtggaa 298

<210> 472

<211> 98

<212> DNA

<213> Homo sapiens

<400> 472

aaagagtcaa ctttccggcg gcggggggaga aatgataaaa gagagagagg agggcagatc 60

accacctaga agcacatcct ttgttcgcag agggggga 98

<210> 473

<211> 103

<212> DNA

<213> Homo sapiens

<400> 473

gtttgtcttg cgcagtgcctt actccagctg tggcatgcag gtgtcagcaa gtatgatcag 60

caatgaggcg gtggtcaata tcctgtcgag ctcatcacca cag 103

<210> 474

<211> 191

<212> DNA

<213> Homo sapiens

<400> 474

aatctctttt tttctggagg ctggcacctg attttgtatc cccctgtagc agcattactg 60

aaatacatag gcttatatac aatgcttctt tcctgtatat tctcttgtct ggctgcaccc 120

ctttttcccg cccccagatt gataagtaat gaaagtgcac tgcagtgagg gtcaaaggag 180

agtcaacata t 191

<210> 475

<211> 220

<212> DNA

<213> Homo sapiens

pctgb2013053202-seq1.txt

<400> 475

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ctgtgttttt gctttgcatc cgccatttgt gtgtgttttt ggactgtggg ctgtgtgtac 120

cttggttggt gactcagtga gaagaagcag gaatgccaaa gatactatga atgttttgag 180

ttttgttgct gttgttggtg agaggttgtt tcactggtat 220

<210> 476

<211> 258

<212> DNA

<213> Homo sapiens

<400> 476

gatcgtctgg taactttcta actttaaata atatgtttga gcaataattt cttgacttac 60

tgactttaca acatctttaa taattcccca ttacaaaaga taaggattta acttacacta 120

tcgccacttt ctttgtcca tctctctcca aatgtctgat agttacatca ctttttaata 180

catctattgg tttgatttta tagctttgaa caatacacta atcctctagt tcttgttcca 240

ttaactgaag atcttttc 258

<210> 477

<211> 233

<212> DNA

<213> Homo sapiens

<400> 477

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ttaggtcaga tggaggttct cagagccaag tcctccctct ctactggagt ggaaggtcta 120

ttggccaaca atcctttctg cccacttccc cttccccaat tactattccc ttgacttca 180

gctgcctgaa acagccatgt ccaagttctt cacctctatc caaagaactt gat 233

<210> 478

<211> 96

<212> DNA

<213> Homo sapiens

<400> 478

ggatcgatga tgagtcccc ataaaaacat tccttggaag agctgaacaa aatgagtgag 60

aactcatacc gtcgttctca tcggaactga ggtcca 96

<210> 479

<211> 181

<212> DNA

<213> Homo sapiens

<400> 479

tggtgacaga gtttgggacc gaggtggagc ccgagtttgg gaccaaggtg gagcccgagt 60

ttgagaccca gttggagcct gagtttgaga cccagctgga acccgagttt gaggaagagg 120

aggaggagga gaaagaggag gagatagcca ctggccaggc attccccttc acaacagtag 180

a 181

<210> 480

<211> 135

<212> DNA

<213> Homo sapiens

<400> 480

gatatcagat cagttgagac taacagttga aagcagtaaa catattacgg acatattatt 60

gataaaagac atttatgaag aggataaact gtgaaggtgt acagacacta aaccatagtt 120

gctaaacaca tacaa 135

<210> 481

<211> 80

<212> DNA

<213> Homo sapiens

<400> 481

agagccagga cagtgaggtc aactttgaca attccatcca ccagaagtc ttggagctgc 60

tgcttgacta tgcgtactcc 80

<210> 482

<211> 96

<212> DNA

<213> Homo sapiens

<400> 482

ggatcgatga tgagtcccc ataaaaacat tccttgaaa agctgaacaa aatgagtgag 60

aactcatacc gtcgttctca tcagaactga ggtcca 96

pctgb2013053202-seq1.txt

<210> 483

<211> 290

<212> DNA

<213> Homo sapiens

<400> 483

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gttgatccat tgacttctgg cattcagtgt tgctgatgac aaatctgtta gcagtctatt 120

tctcatccat ttttgtgttg agctaatacgt gatgacctca tttgttttct ccctggccac 180

tttaatatct tccttctatc cttaatattc caaaatttta caatattgtg tctagatgta 240

gattgtattg ggccctctca atctggagac ttagcttgct ctgttcttca 290

<210> 484

<211> 197

<212> DNA

<213> Homo sapiens

<400> 484

atgtcaagaa aatgacggtc acagaccagg tgaactgccc caagctctcg taaccaggtt 60

ctacagggag gctgcaccca ctccatgtta cttctgcttc gctttcccct accccacccc 120

ccccccataa agacaaacca atcaaccacg acaaaggaag ttgacctgaa catgtaacca 180

tgccctaccc tgttacc 197

<210> 485

<211> 113

<212> DNA

<213> Homo sapiens

<400> 485

tgtcactggg gaaagacgac ttgggtgccca atttttaata aacacaatgc tattagcgctc 60

actccaattt agtgtctgat tgttaaattg taatgtactg cactctacag ttt 113

<210> 486

<211> 183

<212> DNA

<213> Homo sapiens

<400> 486

ggattataat atcctcactg gccacaatct gtaaaagtcg atactggcac tttttttgcc 60

ccctcaaagg aaatatgcta atagacagcc cctttgcaaa tataattcct ccttcccaac 120

ccttcaaatt gctaaggccc cactggtcag caccttcctt ttcgagtcca ggactactgt 180

tct 183

<210> 487

<211> 275

<212> DNA

<213> Homo sapiens

<400> 487

agcattaata atttccatgc atgtgtcttt ttccagtagg tatggttgaa tttatgtaaa 60

tttattgcta atcccatccc ttacgattta gagtataagc tgcgcaaggg cagaagtttt 120

tatttggttt gttcatggat gtattttaag agctgagaac agggcctgga cacaataagc 180

attcaataaa tatttactga atgaatgaac tcctacctat attcctattt ataatttggc 240

tccactttat cctacttttag ctcccattca attca 275

<210> 488

<211> 123

<212> DNA

<213> Homo sapiens

<400> 488

catttaaata agaggagatc cacaaagagc aacagagata agagaagaaa ggaaataatc 60

aataaaataa ttcaagaaaa tccaaggaca tgagttttca gattgtaaga gactacttga 120

gtg 123

<210> 489

<211> 99

<212> DNA

<213> Homo sapiens

<400> 489

aattcatatc ccctgttcgt ctcatgcgcg tcctccgtcc ccaatctaaa aagcaattga 60

aaaggtctat gcaataaagg cagtcgcttc attcctctc 99

<210> 490

<211> 97

<212> DNA

<213> Homo sapiens

<400> 490

tggatc gatg atgagtcctc caaaaaaaca ttccttggaa aagctgaaca aaatgagtga 60

gaactc atac cgtcgttctc atcggaactg aggtcca 97

<210> 491

<211> 119

<212> DNA

<213> Homo sapiens

<400> 491

attttctatc tgtggttgga ttcagaccac atgaacactg agggctgact gtagttttga 60

atgtctgtta ctgaggaggc accagcataa agtattttat cacttcagac gctgacaat 119

<210> 492

<211> 121

<212> DNA

<213> Homo sapiens

<400> 492

ttatat tttat gtttagcacc gtcagtgttc ctatccaatt tcaaaaaagg aaaaaaaga 60

gggaaaatta caaaaagaga gaaaaaaagt gaatgacgtt tgttttagcca gtaggagaaa 120

a 121

<210> 493

<211> 168

<212> DNA

<213> Homo sapiens

<400> 493

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gaccccatct ttacaaaaac ttcacagatt agccaggtat ggtggcattt tcctgtagtc 120

ccagctactc agaatgctga ggcaggagag tggcttgtga ccaagagt 168

<210> 494

<211> 47

<212> DNA

<213> Homo sapiens

<400> 494

aggataaact tgtgtggtgt agagaagtta aaatcctcac gttgtac 47

<210> 495

<211> 286

<212> DNA

<213> Homo sapiens

<400> 495

acttcaggga agtttcataa aaggaagaat tttaactcag cgtagaaaga tgggtaaatt 60

ttcctcatgt gaaggtgtac tgcctgggggt gctgcaggct ggagatgagt attaaaatag 120

gaggagagtg agtgaaagca caggaggagg aagggtcagg caagtttggt gaacacagca 180

actggctata gaacaggagc agtggggagaa agtccagaaa ggtctgctga gcttcagttg 240

tacaaagctg tggagtttgg ccttttgtca tggctagatt aggtct 286

<210> 496

<211> 94

<212> DNA

<213> Homo sapiens

<400> 496

tggatcgatg atgacctcaa tacatgcatt ccttggaag ctgaacaaaa tgagtgaaaa 60

ctctataccg tcgtcctcgt caaactgagg tcca 94

<210> 497

<211> 174

<212> DNA

<213> Homo sapiens

<400> 497

gtttgaggta tttaactgac acctaagtgg atctgttgag gaaacagttg gatatacaaa 60

tttagtgttt aaggcagact tccaggcttg aaggaaaaat ttggaagtca tcacgacata 120

tatgtggtat ttaaaattgt gaggttcaag gaccaagccc cataccattt agag 174

<210> 498

<211> 255

<212> DNA

<213> Homo sapiens

<400> 498

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gctttaaaat aaccagctt gctgcaggag gtgggtattg tgtgtgtggg aaggtgggga 120

ggctgcggga ggaagagatg acccaagatt aggcagatgt tgttaactgt ggaagcaggg 180

tggtgagtgg gggctcatga cattatgctc tctactttgt gtacgtgtga acatttcgt 240

aataaaagat gcctt 255

<210> 499

<211> 137

<212> DNA

<213> Homo sapiens

<400> 499

ggattttttc ccctgtagta gtgaggtaac atgcttgaat gtcactgtga tatttatttc 60

ctctttgttc agttgttttt gaattcctgt taagtacatg ttttaatact ttgagcgatt 120

taagatactt ttctttt 137

<210> 500

<211> 33

<212> DNA

<213> Homo sapiens

<400> 500

aaacgatgat aatctttact ggtgaaaagg atg 33

<210> 501

<211> 195

<212> DNA

<213> Homo sapiens

<400> 501

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aaatagcccc atctttcaga gtgataccat ttctacattt gataatgcct gtattcctgt 120

aggatgtata tagtttaggg gatttttttt ttgtttgggt ttgtttttta gaagtcaata 180

tgtctggttt ttttt 195

<210> 502

<211> 255

<212> DNA

<213> Homo sapiens

<400> 502

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agaaagctgt agagattggg tttcattgtt aattggtttg ggagcctcct atgtgtgact 120

pctgb2013053202-seq1.txt

tatgacttct ctgtgttctg tgtatttggt tgaattaatg acctgggata taaagctatg 180

ctagctttca aacaggagat gcctttcaga aatttggtata ttttgagtt gccagaccaa 240

taaaatacct gggtg 255

<210> 503

<211> 217

<212> DNA

<213> Homo sapiens

<400> 503

gtgtgttaaa atgagggctct cactgcttta ggattgaagt ggctggaaag agtgatgcct 60

ggggaaggag atggagttat gaggggtactg tggctggtac tttctgtact aaacatttcc 120

tttttctatt ttaccactaa ttttggttta aactgtgagc cgtccaagtc agaagaagac 180

agcaaaaaaa gcaacttttc caacatacaa tttactt 217

<210> 504

<211> 92

<212> DNA

<213> Homo sapiens

<400> 504

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agccacaaag accacagtta gcaaacacac ac 92

<210> 505

<211> 251

<212> DNA

<213> Homo sapiens

<400> 505

atataattgg acaaacgctg gcaaaaagaa aaaaatggta agcaaaaaac ccaagataaa 60

gtttcgagga catcaggcct ttgaaatac aatgtcaaata gacacattgt acggtttcaa 120

aaaatccgct agacatgtca taagttttta ctgtaatgcc caggaaagga tatcttaaaa 180

tattctaaac ttgtgtaaca aaggaataat taactgtaat agtttttcaa taaatcgagt 240

tgggtgtttc c 251

<210> 506

pctgb2013053202-seq1.txt

<211> 261

<212> DNA

<213> Homo sapiens

<400> 506

gaatggttac tgtttatact gtggtatggt tttgattaca gcagataatg ctttcttttc 60

cagtcgtctt tgagaataaa ggaaaaaaaa tcttcagatg caatggtttt gtgtagcatc 120

ttgtctatca tgttttgtaa atactggaga agctttgacc aatttgactt agagatggaa 180

tgtaactttg cttacaaaaa ttgctattaa actcctgctt aaggtgttct aattttctgt 240

gagcacacta aaagcgaaaa a 261

<210> 507

<211> 175

<212> DNA

<213> Homo sapiens

<400> 507

tatttcttgc tattgtgata tgacaagaga cttacttat cttgctctgt tttcccctgt 60

acacgctgta tataggggtc aatgtgatgc tgctggagac gagaataaac tggactagaa 120

tagtgcatg tatttagtct gtattgatca tggatgccct ctttaatagc catat 175

<210> 508

<211> 251

<212> DNA

<213> Homo sapiens

<400> 508

gaaccgcaga ttatgggttaa tccaattctg tgcacctgag gtccataaat aaaagaataa 60

gtattgaaat gaaagaatga cagaaagaat gaatggacac atgaacgact gaattagaaa 120

tggaaatgcc tggcacagcc aggaaggagc tgcccatggg attgtcattc atttcactct 180

gggcacctga ggtccataag cgtgaaaaga ggcaggaaga gaagtgtcag ggagtcaaag 240

atagagctaa g 251

<210> 509

<211> 237

<212> DNA

<213> Homo sapiens

<400> 509

pctgb2013053202-seq1.txt

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atgacactta caaaaaataa aagaccaaga caccagagt gagatgcatg ttggggacgg 120

gggaggctgg cagcaggggg gccccggcgg ctcacccag ggctcccga gggggctgtt 180

tccatccacc acccaaaaaa acaccacaag ggtcagtcct agcccaccg acagctt 237

<210> 510

<211> 133

<212> DNA

<213> Homo sapiens

<400> 510

gtatggatgg gtatgttgag actcaattac ttttttatta gcttccccgt ttggaagatc 60

ccaaacacca aagatggaag gtgaaaataa agactgcgtg accgggaaga aagtttgaat 120

tactaatagt ggg 133

<210> 511

<211> 263

<212> DNA

<213> Homo sapiens

pctgb2013053202-seq1.txt

<400> 511

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aacacctgaa tgcggaagag ctcggctccc gtttagcatt ttgtacttaa ggaaataaaa 120

aaccaacaaa ggatttcaca tttttttaaa aagtgaagat tgctgtatac tatttattca 180

acttataatt tatgttactc cttgatcttt gtcttttgtc atgacaaagc atttatttaa 240

taaagttatg cattcagcaa ctt 263

<210> 512

<211> 48

<212> DNA

<213> Homo sapiens

<400> 512

taggttgtca acaggtacta tttgtcacat aactaacttt cgaggcac 48

<210> 513

<211> 161

<212> DNA

<213> Homo sapiens

pctgb2013053202-seq1.txt

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attgatcaca ttgtttgacc cagtatgttt tgtagacacg ttagttataa tcaccttgta 120

tctctaaata tgggtgtgata tgaaccagtc cattcacatt g 161

<210> 514

<211> 286

<212> DNA

<213> Homo sapiens

<400> 514

gtcttcacca actaagaaag ctctgttatt ctggcctggg tgcttgctcc agactcagga 60

acatctgggc aacacaagca tcactgggct ggggaattgt gtgtgtgctg catcatctcc 120

gactctcttg tagttccttc cttccctccc tcactcttac atgcagacac agacagacac 180

agtctgggtg ggacatgcag tggcagctcc tgggtgtataa catctttcac acaccttgag 240

tctatctgct tgctgccttt gactgaccc gaaatgggtg gccttt 286

<210> 515

<211> 208

<212> DNA

<213> Homo sapiens

<400> 515

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ttgtgctgtg gcagactggg gctttggaag tgggtgtatgt ttaacttacc tgagagtgag 120

agatgtgtag gaagaatagc tggaagaaag tgaaagatga gtgccagtac ttttggcctg 180

ttatccagta gagagaaagt gacagtga 208

<210> 516

<211> 201

<212> DNA

<213> Homo sapiens

<400> 516

aactctgtaa ggaggacat gtcagactat tgtaagctaa gcattaggac tgatacaaat 60

aatatatgct cctggcatag aaaaataaac cacagagaac gagttcaaag aatagcaaag 120

aaagaaagag gaccagtg gcgaaagatg agagtgtact tttaacaaaa gttatctaag 180

cctgagcact tgaagtctgc a

201

<210> 517

<211> 119

<212> DNA

<213> Homo sapiens

<220>

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<222> (91)..(91)

<223> n is a, c, g, or t

<400> 517

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tagatgcaat tgaggttcat aaataaaaaga ntaaatactt aaacgtgaaa ggtgactaa 119

<210> 518

<211> 36

<212> DNA

<213> Homo sapiens

<400> 518

ataatgaaag ttagtaacgt ccattattta ataaag

36

<210> 519

<211> 91

<212> DNA

<213> Homo sapiens

<400> 519

tgtacagggt catTTtgaca gtaactggta tattcctttg catTTtatgt tgcattgcca

60

atTTtttagtg tatccagttt gaaagtataa t

91

<210> 520

<211> 178

<212> DNA

<213> Homo sapiens

<400> 520

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60

ttccatttcc accatttata gtgagcctct ccataattag tgccaaccat tagtttcggt

120

catatTTtta caccaggagt caacaaactg tggccattgg ccaaatatgg cctcccaa

178

<210> 521
 <211> 242
 <212> DNA
 <213> Homo sapiens

<400> 521
 aggaagtacc cgctccataa gacccttaca tttggacagt caaggtgcac aattgtatgt 60
 gaccacaacc atgcaccttg gacataaatg tgtgtaactg cacatggccc atcccatctg 120
 aataaggtcc tactctcaga ccccttttgc agtacagtag gtgtgctgat aaccaaggcc 180
 cctcttcctg gcctgttaac gtatgtgatt atatttgtct gggttccagt gtataagaca 240
 tg 242

<210> 522
 <211> 199
 <212> DNA
 <213> Homo sapiens

<400> 522
 gggagtcaat gaatagtacc taaaatggaa accaaacaaa acaacttcag gaagtaacaa 60

pctgb2013053202-seq1.txt

gggcttgctt agagacatga cggtaaacc c tgaaccatca gctaaaagag gtagatagca 120

gtggttgccc ctggggagag gtaaattgtga tggagaggga acaactgtgt acaaactgt 180

gactttacgt tttgatcaa 199

<210> 523

<211> 127

<212> DNA

<213> Homo sapiens

<400> 523

aagagttaaa cagtctagag tgaagggaat gttttaaaat ccagaggcga tcaagtgaag 60

ccaacctttg gaggcccgta gaagtcattt ggaggaattt ggacttcgtg cagtaggaaa 120

gagggaa 127

<210> 524

<211> 46

<212> DNA

<213> Homo sapiens

<400> 524

gacaggggtt ctaattactg tctgtgagag ttactacttt gtaact 46

<210> 525

<211> 115

<212> DNA

<213> Homo sapiens

<400> 525

taatattttt tgctgcctag gcaaattggct tttgtgaaaa cacttgatg aaaagcaata 60

caccatttgt ttttacttac caatcactat cattaggttt tgatgcaaata gggaa 115

<210> 526

<211> 138

<212> DNA

<213> Homo sapiens

<400> 526

ttccaagcc catgagtcct tgaaaatatt ttttatatat acagtaactt tatgtgtaaa 60

tacataagcg gcgtaagttt aaaggatggt ggtgttcac gtgttttatt cctgtatggt 120

gtccaattgt tgacagtt 138

<210> 527

<211> 269

<212> DNA

<213> Homo sapiens

<400> 527

cttaggatat gaaatcttca gaggatggta gaagagaaag gttaaagcca taagaaagta 60

gagtacttgt ggtcattgaa accatggaat ttactcaggg atagtgtata tagtgagaaa 120

tcaggtaact aagatttgag cctaaacgta atctgtaaaa ggggagctca aaggaaaagg 180

gaatgggagg accggatttt gtaaggatag tagggcaaat gttaagagag agaagtagag 240

agttgagtat ggcaaagagt gactcaatt 269

<210> 528

<211> 282

<212> DNA

<213> Homo sapiens

<400> 528

tcacctcctg ctggctaccg gggcaggcat gcacccggtg ccagccccgc tctgggcacc 60

pctgb2013053202-seq1.txt

acctgccttc cagcccctcc aggacccggt cccctgctg cccctcactt caggaggggc 120

ctggagcagg gtgaggctgg actttggggg gctgtgaggg aaatatactg ggggtcccag 180

attttgcttt aagggggcca gaccctttgc caggctggat tgtacgggcc ccaccttcgc 240

tgtgttcttg ctgcaaagtc tgggtcaataa atcactgcac tg 282

<210> 529

<211> 131

<212> DNA

<213> Homo sapiens

<400> 529

atacctgtta aatagatcaa ttttgattgc ctactatgtg aactcactgt taaaggcact 60

gaaaatttat catatttcat ttagccacag caaaaataa cgcaatacct atgttagcat 120

tttgtgaact c 131

<210> 530

<211> 183

<212> DNA

<213> Homo sapiens

<400> 530

tcacctgagg cgttcaaaag atataaccaa ataaacaagt catccacaat caaaatacaa 60

cattcaatac ttccagggtg gtcagacttg ggatgggacg ctgatataat agggtagaaa 120

gaagtaacac gaagaagtgg tggaaatgta aaatccaagt catatggcag tgatcaatta 180

tta 183

<210> 531

<211> 263

<212> DNA

<213> Homo sapiens

<400> 531

ttgttggtag agacggtgat tcactatggt gccaggcta gtcacgaact cctgacctcg 60

tgatccgccc acctcggcct cccaaagtgc tgggattaca ggtgtgagcc accgtgccccg 120

gcctcttttt atttattcct aaaatattac cttgaggcca aattctgcgc ttaaggagaa 180

tgtgcaccaa gtgctgggggt gggggctggt tataaacgag gccacaaatc atgcttggtta 240

ataaattgtg tggttcaaat ctg

<210> 532

<211> 140

<212> DNA

<213> Homo sapiens

<220>

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<222> (71)..(71)

<223> n is a, c, g, or t

<220>

<221> misc_feature

<222> (82)..(82)

<223> n is a, c, g, or t

<220>

<221> misc_feature

<222> (94)..(94)

<223> n is a, c, g, or t

<400> 532

cacagccaaa acctctacat ccctacattc acacacttcc tccacacacc atcctgaagt

60

caccccaact nctaccacca anatcaccac caancccacc agtataggaa gcagcacacc 120

catggcccac actacctcag 140

<210> 533

<211> 134

<212> DNA

<213> Homo sapiens

<400> 533

cagaggagct ttattagagg gacagggtga aacatattta caccggccga gcagggacct 60

taagaagcag gcgtgggagc aggggtcccag ctcagacgag ttccaccttg gcattggggt 120

acaccgccac cacg 134

<210> 534

<211> 207

<212> DNA

<213> Homo sapiens

<400> 534

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pctgb2013053202-seq1.txt

gcacgggtgt cagcatgtgt atataagtgt gggcatgtgt atgtgattgt gtgagtgtgg 120

gcaggtgagt gtgttgggga tgtgggtag ggtggggagt ggtgctttct ctagtgtgtc 180

ctccggaaca tcttgcttac ctagcaa 207

<210> 535

<211> 113

<212> DNA

<213> Homo sapiens

<400> 535

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agctgaactt gctcaatcta aggctgattg tcgtgttcct ctttaaattg ttt 113

<210> 536

<211> 66

<212> DNA

<213> Homo sapiens

<400> 536

gtttttatta aaacacaaac gcacacacac aaaaattag ccaggcatgg tggtccatcc 60

ctgtaa 66

<210> 537

<211> 66

<212> DNA

<213> Homo sapiens

<400> 537

gtcacccag agtcattgtc acctcagagt cattgtcact ccagagtcac tgtcacctca 60

gagtca 66

<210> 538

<211> 128

<212> DNA

<213> Homo sapiens

<400> 538

caggctgggc cgtgagcagg tgggccgttg agttacctct gtgctggatc ccgtgcccc 60

acttgcctac cctctgtcct gccttggttat tgtaagtgcc ttcaatactt tgcattttgg 120

gataataa 128

<210> 539

<211> 49

<212> DNA

<213> Homo sapiens

<400> 539

tgattactag tgtaaactgg ttattgagat agattatgac attggtgga 49

<210> 540

<211> 209

<212> DNA

<213> Homo sapiens

<400> 540

cagagtcatt cattgtcacc ccagagtcatt tgtcacccga gtcattgtca gtcagagtc 60

attgtcaccc cagagtcatt gtcacccag agtcattgtc acccattgt caccagag 120

tcattgtcac ctgagagtc ttgtcactcc agagtcattg tcacctcaga gtcaatgtca 180

ccccagagtc atcgtcaccc cagagacat 209

<210> 541

<211> 237

<212> DNA

<213> Homo sapiens

<400> 541

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atataccatt ttgggtcctg aggataagag agatgagggc attagatcac tgacagctga 120

agatagaaga acatctttgg tttgattggt taaataatat ttcaatgcct attctttgca 180

aggtactatg tttcgtaaata taaataggtc tggcccagaa gaccactca attgcct 237

<210> 542

<211> 62

<212> DNA

<213> Homo sapiens

<400> 542

tatgtaatta taagatgaag cgtagtgaat tgtacagctg ttgtaataat gacctatttc 60

ta 62

<210> 543

<211> 277

<212> DNA

<213> Homo sapiens

<400> 543

taccccccttt tatatctaata gtagaaaaag cgaaattgaa tctggaaagc aaactgttgt 60

atatagttgc ggtaacaatc atgaagagag agccgggctg tcccctcagt aattcatttt 120

aaataacaaa ttatttaaaa ataaaattca tgccagagcc agctgaagag gccttccttc 180

atcaccactg aggccacccc caatctgggc cctctgtcca tctggcatgt ctctcccag 240

caagattcat ctgttcaatg ccatttgcgt ttcaata 277

<210> 544

<211> 203

<212> DNA

<213> Homo sapiens

<400> 544

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taagaaaagg caaggctggc tcttcctat ggtccttttag tggagctata tttgcataga 120

tcctagacaa atgatgcaaa acaaattccc tccaatttcc actagcaatc tccctaattc 180

gctcaaccct tacataagca tca 203

<210> 545

<211> 75

<212> DNA

<213> Homo sapiens

<400> 545

agaacctgag tataaattta ctttctcaaa ttcttgccat gagaggttga tgagttaatt 60

aaaggagaag attcc 75

<210> 546

<211> 248

<212> DNA

<213> Homo sapiens

<400> 546

aaaaactcaa cctatctggt gttttatattt aatggataaa aatgtaattt ttttaaggta 60

gcaacttatt tccaaattaa tatagatgaa aaatagatac caattagact aaattgaaag 120

pctgb2013053202-seq1.txt

ctttttgttc tatatttgca tagcctttga aatatttctt agtgcctagg aggtctgggg 180

attcctcttt cgtggtgggc actaacctta cttgatgcag ataaaatcac ttgtcaatgc 240

aaaatgtg 248

<210> 547

<211> 174

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (27)..(27)

<223> n is a, c, g, or t

<220>

<221> misc_feature

<222> (78)..(78)

<223> n is a, c, g, or t

<220>

<221> misc_feature

<222> (96)..(96)

<223> n is a, c, g, or t

<220>

<221> misc_feature

<222> (123)..(123)

<223> n is a, c, g, or t

<400> 547

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agtggagtcg ggggcttngt gctgggcctg ctcttncttg gggccgggct gttcatctac 120

ttnaggaatc agaaaggaca ctctggactt cagccaacag gattcctgaa ctga 174

<210> 548

<211> 251

<212> DNA

<213> Homo sapiens

<400> 548

agagagtgga catttgtcgg gaaactccta acatatgccc ccattctgga gagaacacag 60

agtacgacac aatccctcac actaatagaa caatcctaaa ggaagatcca gcaaatacgg 120

tttactccac tgtggaaata ccgaaaaaga tggaaaatcc ccactcactg ctcacgatgc 180

cagacacacc aaggctatatt gcctatgaga atgttatcta gacagcagtg cactgcccct 240

aagtctctgc t 251

<210> 549

<211> 88

<212> DNA

<213> Homo sapiens

<400> 549

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ataatgatcc tgtgtcctaa attaatat 88

<210> 550

<211> 284

<212> DNA

<213> Homo sapiens

<400> 550

aactgaaatg tcaacctgtg gactgtggca ttcctgaatc cattgagaat ggtaaagttg 60

pctgb2013053202-seq1.txt

aagacccaga gagcactttg tttggttctg tcatccgcta cacttgtgag gagccatatt 120

actacatgga aaatggagga ggtggggagt atcactgtgc tggtaacggg agctgggtga 180

atgaggtgct gggcccggag ctgccgaaat gtgttccagt ctgtggagtc cccagagaac 240

cctttgaaga aaaacagagg ataattggag gatccgatgc agat 284

<210> 551

<211> 214

<212> DNA

<213> Homo sapiens

<400> 551

gacttattcc cgctgactga gtttttgagg ggctaccagg aaagcgctc caaccctagc 60

aaaagtgcaa gatggggagt gagaggctgg gaatggaggg gcagagccag gaagatcccc 120

cagaaaagaa agctacagaa gaaactgggg ctctccagg gtggcagcaa caataaatag 180

acacgcacgg cagccacagc ttgggtgtgt gttc 214

<210> 552

<211> 72

<212> DNA

<213> Homo sapiens

<400> 552

gaatggcagt accagaaggc attggttaag tgtcccagga accacacaag cagtgactcc 60

taaagaagtt ca 72

<210> 553

<211> 180

<212> DNA

<213> Homo sapiens

<400> 553

gcttccttaa aggtcagaac atcaggccaa agtacaacgt ttaatttcag aacttgcctt 60

ccaatttacg cattttcaat ttgctctccc catttggtga gtcagaagaa gcagcattgc 120

ccagaaacag gtattacgta acatgcacat actttaaaaa gtactcatcc cttgttttct 180

<210> 554

<211> 173

<212> DNA

<213> Homo sapiens

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<400> 554

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agtaagctgc tttattgtag ctttcttga tgttgcttag tcacttattt cataaacaac 120

ttaatgtttt gaataatttc ttactaaaca ttttggttatt gggcaagtga ttg 173

<210> 555

<211> 243

<212> DNA

<213> Homo sapiens

<400> 555

aaaacttggc actttttcgt gtggatcttg ccacatttct gatcagaggt gtacactaac 60

atttcccccg agctcttggc ctttgcatth atttatacag tgccttgctc ggcgcccacc 120

acccccctcaa gccccagcag ccctcaacag gccagaggag ggaagtgtga gcgccttggt 180

atgacttaaa attggaaatg tcacttaacc attagtcatt gtgtgaacac ataaggacgt 240

gtg 243

<210> 556

<211> 201

<212> DNA

<213> Homo sapiens

<400> 556

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agtggcaggg gctggagatg ggtgtgtgtg tgtgtgtgtg tgtgtgtgtg tgtgtgcgcg 120

cgcgccagtg caagaccgag attgagggaa agcatgtctg ctgggtgtga ccatgtttcc 180

tctcaataaaa gttcccctgt g 201

<210> 557

<211> 174

<212> DNA

<213> Homo sapiens

<400> 557

tgggcgtccg ggcccccaat attcacgcac tcgcaccacg cactcatatt ccctcacccc 60

accatcacgg ccccaaagaa ggtcttcctt ctgcgaagt ccaccatata ggggtgactg 120

atgttgagc tacaccctct cgcccctccg gagctgcacc aggccgccga accc 174

<210> 558

<211> 259

<212> DNA

<213> Homo sapiens

<400> 558

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tgggtttatt tcaaggcagc agcctgagcc caggagcaga ggaccagtt gttataaggc 180

gctgggagag gatgggcagc tcccactgcc ccagagcgga gctcgaagca cccaggttgc 240

ccacggaaaa tccaataaa 259

<210> 559

<211> 60

<212> DNA

<213> Homo sapiens

<400> 559

tttctggggt ctttgagctc caaaaaataa acatttcctt tgagggagag cccccccca 60

<210> 560

<211> 159

<212> DNA

<213> Homo sapiens

<400> 560

gagcttcctt cttcgttctt ggcaccatct tatgaaaagg gtccagatta agatTTTTga 60

ctgagtcatt ctaaagtaag ttgcaagacc catgatata gaccactaaa tacttcatca 120

cacacctcct aagaataaga accaacatta tcacaccaa 159

<210> 561

<211> 278

<212> DNA

<213> Homo sapiens

<400> 561

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acttataagt agaagctaaa cattgagtac acatggatac aaagaaggga accgcagaca 120

ctggggccta cctgaggtcg gagcatggaa ggagggtgag gatcaaaaaa ctacctatct 180

ggtactatgc tttttatctg gatgatgaaa taatctgtac aacaaaccct ggtgacatgc 240

aatttaccta tatagcaagc ctacacatgt gccctga 278

<210> 562

<211> 241

<212> DNA

<213> Homo sapiens

<400> 562

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aggaacgggg atctttctag cttttggcca cttcctggga cctcacgccc ctgttgacag 120

atggagattg ggcagcaggg ccttgctgca ttgttatctg ctgttccgac ttggtttgtc 180

ttgtccaagg gtgacgaaag agccaggcac cagggtctca tgggatgagg tccaactttt 240

t 241

<210> 563

<211> 283

<212> DNA

<213> Homo sapiens

<400> 563

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gccctggagt gtcaccttta ttagctgtga gagacacccc agagccctgg gcactgtcag 180

tgattgggggt agaacaaaaa caggacctgg tcagagccca cagatgtggc tagaggaact 240

gtggggtggg gagctccctc ataggctcct gaccacaata tcc 283

<210> 564

<211> 186

<212> DNA

<213> Homo sapiens

<400> 564

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gcagagcagg aaacatgact cgtatatgtc tcaggtccct gcagggccaa gcacctagcc 120

tcgctcttgg cagggtactca gcgaatgaat gctgtatatg ttgggtgcaa agttccctac 180

ttcctg

186

<210> 565

<211> 267

<212> DNA

<213> Homo sapiens

<400> 565

gcatttcaaa gtgacttcta tgaagctttt tttttaatgt gaaattttca gaatgttggt 60

tttttcatgt agatactcca ggaagagtta agcactgctt tcagttttta tatccacctt 120

gaggggtcgc tgcttgaggg ctcttatccc aggggacttt ttaattcgga tgttacttaa 180

tgtggcttct ctaatgtagt ttctttgatt accgactaca caattatgta ccatcacagt 240

attagtggaa aagtaccatg tgattta 267

<210> 566

<211> 45

<212> DNA

<213> Homo sapiens

<400> 566

tgcttataca cttacacttt atgcacaaaa tgtagggtta taata 45

<210> 567

<211> 241

<212> DNA

<213> Homo sapiens

<400> 567

aactggaccc tgcgttctc catcttctca gtcagttggt tcaagtgttc ctgataactc 60

ctctccttct gttccatcat ctgctcattc tttctttgca tttcctgcaa cttttttgct 120

gaagcctgtg cagactcagc tttcacaagt tccacttcaa tctccttttc tttttctgtg 180

agagtctggg ctgtctggag aattgcatca gtcatagact ccttggattt caagtatgtc 240

t 241

<210> 568

<211> 159

<212> DNA

<213> Homo sapiens

<400> 568

gagcttcctt cttcgttctt ggcaccatct tatgaaaagg gtccagatta agatTTTTga 60

ctgagtcatt ctaaagtaag ttgcaagacc catgatacta gaccactaaa tacttcatca 120

cacacctcct aagaataaga accaacatta tcacaccaa 159

<210> 569

<211> 107

<212> DNA

<213> Homo sapiens

<400> 569

tactcccgag gctctgtaca ttgctgccac atactcctgc cagcttgggg gagtgttcct 60

tcaccctcac agtatttatt atcctgcacc acctcactgt tcccat 107

<210> 570

<211> 273

<212> DNA

<213> Homo sapiens

<400> 570

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pctgb2013053202-seq1.txt

caaagccatt ttcctgccta ctggatgctt acagtgactg tggatacggg ggttcccttt 120

ccccattcag tgacatgtcc tctttgcttg gtgtaaacca ttcttgggag gacacttttg 180

ccaatgaact ctttccccag ctgattagtg tctaaggaat gatccaatac tgttgccctt 240

ttccttgact attacactgc ctggaggata gca 273

<210> 571

<211> 228

<212> DNA

<213> Homo sapiens

<400> 571

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tcaagcctgc catcaaggac attttttaag acccaactgg catgagttgg ggtaatttcc 120

tattattttc attttggaca acttttttaa cttatattct ttatagagga ttccccaaaa 180

tgtgctcctc atttttggcc tctcatgttc caaacctcat tgaataaa 228

<210> 572

<211> 286

<212> DNA

<213> Homo sapiens

<400> 572

gctgtgttgg ccctcacttg ggattctcag cagttacatg aaagttgtgc tgataatctc 60

ttctcttgta ccaatttttag tcaggcagaa aatggtaaac atgagggtgc tcttgtgact 120

taatttttgt tcaagggtact aaattgctta tgtttattcc ctgtcagcgg agtggagaat 180

gtcattcatc aataaaccaa agccaatagc tggagaattg agatctgggt gaaagtgggt 240

tatggtttac atgctgtact atcctgagga attgcgagat attgct 286

<210> 573

<211> 266

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (214)..(214)

<223> n is a, c, g, or t

<400> 573

ccctgcgctt atcaggtcgt gaggccaggg gtctacaagt cccgggcccc ccagttcacg 60

attctggcgc ggacttcgct cccccaagac aacactcgga agccagggcc cgcggcctac 120

aacgtggatc agcaccggaa gccccgcggc tggagtttcg ggatccggca ctcggactac 180

ctggccccgc tggtgaccga cgcggacaac tganccgcca ggcgggagcg gccccacacg 240

tgtttgctta aagtctgcga gtccgc 266

<210> 574

<211> 270

<212> DNA

<213> Homo sapiens

<400> 574

ccagggtga gagacacgtg aaggaagatg atgggaggaa aagcccagga gaagtccac 60

cagggaccag cccagcctgc atacttgcca cttggccacc aggactcctt gttctgctct 120

ggcaagagac tactctgcct gaacactgct tctcctggac cctggaagca gggactgggt 180

gaggagtggt ggaggtggta agaacacctg acaacttctg aatattggac attttaacaa 240

cttacaaata aatccaagac tgtcatattt

270

<210> 575

<211> 227

<212> DNA

<213> Homo sapiens

<400> 575

gaagatgaag ccccatgctc agtcccctcc catccccac gcagctccac ccagtccca 60

agccaccagc tgtttgctcc tgggtgggagg tggcctcctc agcccctcct ttctgacctt 120

taacctcact ctcaccttgc accgtgcacc aacccttcac ccctcctgga aagcaggcct 180

gatggcttcc cactggcctc caccacctga ccagagtgtt ctcttca 227

<210> 576

<211> 279

<212> DNA

<213> Homo sapiens

<400> 576

gcatttgctg tgtttcgtta gcatctggct ccaggacaga ctttcaactt ccaaattgga 60

pctgb2013053202-seq1.txt

tactgctgcc aagaagttgc tctgaagtca gtttctatca ttttgctctt tgattcaaag 120

cactgtttct ctactgggc ctccaaccat gttccctttt ttttagcacc acaaataatc 180

aaaaccaac atgactgttt gttttccttt aaaaatatgc accaaatcat ctctcatcac 240

ttttctttga gggtttttagt agacagtagg agttaataa 279

<210> 577

<211> 123

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (52)..(52)

<223> n is a, c, g, or t

<400> 577

gcggactcgc agactttaag caaacacgtg tggggccgct cccgcctggg tngcagttgt 60

ccgcgtcggc caccagcggg gccaggtagt ccgagtgccg gatcccgaaa ctccagccgc 120

ggg 123

<210> 578

<211> 82

<212> DNA

<213> Homo sapiens

<400> 578

gtgctcagta gtcagactgg atagtccgtt tttgcttata cgttagccgt ggggatttag 60

caggaagctg tgagagcagt tt 82

<210> 579

<211> 151

<212> DNA

<213> Homo sapiens

<400> 579

acacagaaga gtgacatggt taaaacctc aagccagcct tgctcctggc tggggcctgt 60

tgaagatgct tgtatattac ttttcattg taattgctat cgccatcaca gctgaacttg 120

ttgagatccc cgtgttactg cctatcagca t 151

<210> 580

<211> 82

<212> DNA

<213> Homo sapiens

<400> 580

tttaaaatac tcagaggaca ggatcactgt ggaatcgaat cagaagtggg ggctggaatt 60

ccacgcaccg atcagtactg gg 82

<210> 581

<211> 109

<212> DNA

<213> Homo sapiens

<400> 581

aagagaagac tcacagtatc aggtctactg aaggagatac ggtgattcct gttcttggct 60

ttgtagattc atctgggtata aacagcactc ctgagttatg accttttga 109

<210> 582

<211> 118

<212> DNA

<213> Homo sapiens

<400> 582

tttgaagatt agaaatttag ccgtaggtaa agaatacaaa ggaaaaataa tttttaaattc 60

atcaaccaga tcaacaaaat atatgttaat gccgagactt tgaattagag tgcgaatt 118

<210> 583

<211> 242

<212> DNA

<213> Homo sapiens

<400> 583

catcttctag cagatctttt tcagttaaga ttacttggtc ttccatgtat tcatatttag 60

ccagctcctt gatcagccgc agtatgtcac tgcagtcggc ggagtggtt gggcggatca 120

cgaatttagc cattttcgtc ttttgctttt cttccctttg cggaccaggc ccctgtactt 180

gaacagtagg aggagtggt tcctcattcg tctcccgga gcgtcctctt ctcatcagg 240

ct 242

<210> 584

<211> 34

<212> DNA

<213> Homo sapiens

<400> 584

gaaatcattg tgggattgct agctttccct ctt

34

<210> 585

<211> 272

<212> DNA

<213> Homo sapiens

<400> 585

caacctctta caaccaggc attccttct atcgataatt actctttcaa ccaattgcca

60

atcagaaaat tggtatatct acctataatc tagaagcccc cacatcaagt tgttttgcct

120

ttctggacag gaccaatgta tatcttaa

180

aatgtataaa accacgctgt tccccgacca cctggagcac atgttctcag ggtctcctga

240

gggctgtgtc acaggccatg ttcacttaca tt

272

<210> 586

<211> 189

<212> DNA

<213> Homo sapiens

<400> 586

ccctgcagag aatcacgtcc tggaactgca tgttcttgcg actcttggga cttcatttta 60

acttctcgct gccccagcca tgttttcaac catggcatcc ctcccccaat tagttccctg 120

tcacctcgt caaccttctc tgtaagtgcc tggtaagctt gcccttgctt aagaactcaa 180

aacatagct 189

<210> 587

<211> 163

<212> DNA

<213> Homo sapiens

<400> 587

tgagcagact gcacccaag ctcccgactc caggtcccct gatcttgggg cctgtttccc 60

atgggattca agagggacag cccagcttt gtgtgtgttt aagcttagga atgccttta 120

tggaagggc tatgtgggag agtcagctat cttgtctggt ttt 163

<210> 588

<211> 296

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (75)..(75)

<223> n is a, c, g, or t

<220>

<221> misc_feature

<222> (262)..(262)

<223> n is a, c, g, or t

<400> 588

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aatggaaggg gtggnaaaca gagtacaata acatgagtaa tttgatgggg gctattatga 120

actgagaaat gaactttgaa aagtatcttg gggccaaatc atgtagactc ttgagtgatg 180

tgtaaggaa tgctatgagt gctgagaggg catcagaagt ccttgagagc ctccagagaa 240

aggctcttaa aaatgcagcg cnatctccag tgacagaaga tactgctaga aatctg 296

<210> 589

<211> 246

<212> DNA

<213> Homo sapiens

<400> 589

tgtacagatt caagcaatgg atgcaaggaa catgctgtat gtaatagaag aaagaagtcc 60

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tgataaagag aaagatgttt actcataaac cttcaaaag gtattaacaa atgtttacca 180

aacctattgc tttattttta aaacataatt tgtgttttct atttgtaaga tctgacattt 240

cgaggc 246

<210> 590

<211> 121

<212> DNA

<213> Homo sapiens

<400> 590

ggcagcgacc cggaaacagc gtatcactga gaccgagtcg cttatcagg agctccaggg 60

tcagaggtcg gatgtctaca gcgacctcaa cacacagagg ccgtattaca aatgagcccg 120

a 121

<210> 591

<211> 262

<212> DNA

<213> Homo sapiens

<400> 591

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agctcttgag gctttttccg cagcttctag gagatgtggt aggtcattaa cagtaatgct 120

cctacagttt ttgttcccat ccaaccacca ttgattttca cttttgtaga cttgacctag 180

tgtatctgaa atataggaat ttttaggtgc tttcattttg gcctgacgtg cccagtccag 240

agctgtgtta aagtccttct ct 262

<210> 592

<211> 226

<212> DNA

<213> Homo sapiens

<400> 592

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ggaatgccat cccagaagct cattttcaga tgcacaacag ccagaacagt ctcaagcagc 180

attctagagc ttggaattta agaactacgc attgcctata aagtga 226

<210> 593

<211> 272

<212> DNA

<213> Homo sapiens

<400> 593

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aagagccctc tgctctagga tttgggttga aaaacagaga gagaagtggg gagttgccac 120

aggagctaac acgctgggag gcagttgggg gcgggtgaac tttgtgtagc cgaggccgca 180

ccctccctca ttccaggctc attcattttc atgctccatt gccagactct tgctgggagc 240

ccgtccagaa tgcctccca ataaaactcc at 272

<210> 594

<211> 151

<212> DNA

<213> Homo sapiens

<400> 594

tagggattaa cttcctgtat gctgcaactc atgaacttgg ccattctttg ggtatgggac 60

attcctctga tcctaatagca gtgatgtatc caacctatgg aaatggagat ccccaaaatt 120

ttaaactttc ccaggatgat attaaaggca t 151

<210> 595

<211> 243

<212> DNA

<213> Homo sapiens

<400> 595

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gcaggtgtcc ctgagaaccc aaacttccca gagagtatgt gagaaccaac caatgaaaac 120

agtcccatcg ctcttaccg gtaagtaa acgtcagaaa ttagcatgaa agcagtttag 180

cattgggagg aagctcagat ctctagagct gtcttgctgc cgcccaggat tgacctgtgt 240

gta 243

<210> 596

<211> 82

<212> DNA

<213> Homo sapiens

<400> 596

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atctaggtaa gactggattt aa 82

<210> 597

<211> 236

<212> DNA

<213> Homo sapiens

<400> 597

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aagcctgaga cagctgtctt gtgagggact gagatgcagg atttcttcac gcctcccctt 120

tgtgacttca agagcctctg gcatctcttt ctgcaaaggc acctgaatgt gtctgcgtcc 180

ctgttagcat aatgtgagga ggtggagaga cagcccaccc ttgtgtccac tgtgac 236

<210> 598

<211> 119

<212> DNA

<213> Homo sapiens

<400> 598

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caggccgaag ttactgagaa cttggacaga aaaaatagcc agcaagtgtt caaactact 119

<210> 599

<211> 264

<212> DNA

<213> Homo sapiens

<400> 599

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tgcttcacat ccaccccggc tccccctgcc agcaacgctc actctacccc caacaccacc 120

ccttgcccag ccaatgcaca cagtagggct tggatgaatgc tgctgagtga atgagtaaata 180

aaactttttca aggccaaggg acagtgggtt aattcaactc tgtgtcccag cacctggcac 240

accagaagtg ccatgctcag aaat 264

<210> 600

<211> 273

<212> DNA

<213> Homo sapiens

<400> 600

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gacacctatgg tttctccatc caattctttg aatttcccag tctcccctat gtaaaactta 120

gcaacttggg ggacctcatt cctgggacta tgctgtaacc aaattattgt ccaaggctat 180

atTTTTggga tgaatataat ttgaggaagg gagttaaaga ccctcctggg gctctcagtg 240

tgccatagag gacagcaact ggtgattggt tca 273

<210> 601

<211> 275

<212> DNA

<213> Homo sapiens

<400> 601

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gcccagttctg tcctatgtaa gggacaaagc caggtttaat ggtactgggt agggggcact 120

gccaagacaa taagctaggc tactgggtcc agctactact ttggtgggat tcaggtgagt 180

ctccatgcac ttcacatggt acccagtgtt cttgttactt ccaaggagaa ccaagaatgg 240

ctctgtcaca ctcgaagcca ggtttgatca ataaa 275

<210> 602

<211> 261

<212> DNA

<213> Homo sapiens

<400> 602

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caaacagcaa gtggggccca tggaactgaa tctttactcc ttggtgcacc gcttttgtcg 120

pctgb2013053202-seq1.txt

tgcgttgcct tgctccgttt ttcccaaaaa gcaactggctt catcaaggcc accgacgatt 180

tcctgagtgc actgggaaat ttgggtatag gtcaggcttg gcagccttga tcccaggaga 240

gtactaatgg taacaagtca a 261

<210> 603

<211> 241

<212> DNA

<213> Homo sapiens

<400> 603

ttgttcccga ctagctgcct tgcacattat tttcattttc ctggaatttg atacagagag 60

caatttatag ccaattgata gcttatgctg tttcaatgta aattcgtggt aaataactta 120

ggaactgcct tttctttttc ttgaaaacc tacttataac tgttgctaata aagaatgtgt 180

attgttcagg acaacttgct tccatacagt tgggttgtaa ccctcatgct tggcccaaata 240

a 241

<210> 604

<211> 107

<212> DNA

<213> Homo sapiens

<400> 604

taaataaat atcgacacag tgctttccgt ggcactgcat acaatctgag gcctcctctc 60

tcagttttta tatagatggc gagaacctaa gtttcagttg attttac 107

<210> 605

<211> 252

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (180)..(182)

<223> n is a, c, g, or t

<400> 605

gtggagcagt tggactgctc tctctgctct caggatgata ctgtgagaac aatttaaata 60

tgctaagcac atgtcaggaa acagttttgt ggtctttgga cactcgctgt agccattccg 120

ttccatttca ggtgatttta ttcatttcat ttgtagaata aaataaatcc atttcacacn 180

nncacacaca cacacacaca cacacacaca caccctctat acaccactaa agcctcccat 240

taaaccata ga 252

<210> 606

<211> 96

<212> DNA

<213> Homo sapiens

<400> 606

tcgacacagt gctttccgtg gcactgcata caatctgagg cctcctctct cagtttttat 60

atagatggcg agaacctaag tttcagttga ttttac 96

<210> 607

<211> 181

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (43)..(44)

<223> n is a, c, g, or t

<220>

<221> misc_feature

<222> (78)..(79)

<223> n is a, c, g, or t

<220>

<221> misc_feature

<222> (99)..(99)

<223> n is a, c, g, or t

<220>

<221> misc_feature

<222> (110)..(110)

<223> n is a, c, g, or t

<400> 607

gccagagaag cgattagaaa cccctgaggg ccgattactg acnncataaa tcatgagttt 60

ggggggctttg cctgggtntt gttggtacca ggagacatng ttataaccan caacgtcact 120

gctggttcca gtgcaggaga tggatgatcga ctgtccagga gaccagaca cggaggcagg 180

c 181

<210> 608

<211> 115

<212> DNA

<213> Homo sapiens

<400> 608

aggagctgag gtgctaccg gagccccatt cccccacc tgcccacttg ggaatctgag 60

gcagaggagg gtgaggcctg tgtgccaacc ttgttcacat accaccttcg tcccc 115

<210> 609

<211> 53

<212> DNA

<213> Homo sapiens

<400> 609

aagcaagata tcaatgtagc agaattgcac ttgtgcctca cgaacataca taa 53

<210> 610

<211> 155

<212> DNA

<213> Homo sapiens

<400> 610

gttgttgatc atggatcata ctccccttgt ttctttgggt gagaagggat cgcagtttgg 60

aaactccggc ggctgcgtgc ggggtttcag tcccagctgt aggcttgtaa ataccgccc 120

cgccaaaccg catagagaac gtggcagcaa gctga 155

<210> 611

<211> 190

<212> DNA

<213> Homo sapiens

<400> 611

cacagggaaa tcagggttac aaatcttctt gatccacttc tctcaggatc ccctctcttc 60

ctacccttcc tcaccacttc cctcagtccc aactcctttt ccctatttcc ttctcctcct 120

gtctttaaag cctgcctctt ccaggaagac ccccctattg ctgctggggc tccccatttg 180

cttactttgc 190

<210> 612

<211> 63

<212> DNA

<213> Homo sapiens

<400> 612

attagaacct tagtataaat ttactttctc aaattcttgc catgagaggt tgatgagtta 60

att 63

<210> 613

<211> 281

<212> DNA

<213> Homo sapiens

<400> 613

ggagacagat ggagggtacc ctattttacaa ctgagtcagc caagccactg atgggaatat 60

acagatttag gtgctaaacc atttattttc cacggatgag tcacaatttg aagaatcaaa 120

cttccatcct gaaaatttat atgtttcaaa accacttgcc atcctgttag attgccagtt 180

cctgggacca ggcctcagac tgtgaagtat atatcctcca gcattcagtc cagggggagc 240

cacggaaacc atgtttttgc ttaagccatt aaagtcagag a 281

<210> 614

<211> 239

<212> DNA

<213> Homo sapiens

<400> 614

agatgcgctc gagaccacg ggccttcac ctccctcagc ttctgcatg gaccacctt 60

actggccagt ctgcatcctt gcctagacca ttctcccctc caggagagccc accctgaccc 120

acccccactg cccccctcc ccatgggttc tctccttct ctgaacttct ttaggagtca 180

ctgcttgtgt ggttcctggg acacttaacc aatgccttct ggtactgcca ttctttttt 239

<210> 615

<211> 196

<212> DNA

<213> Homo sapiens

<400> 615

gcctttaaga taccttgatg aagacctgga ctattgaatg gagcagaaat tcacctctct 60

cactgactat tacagttgca tttttatgga gttcttcttc tcctaggatt cctaagactg 120

ctgctgaatt tataaaaatt aagtttgtga atgtgactac ttagtggtgt atatgagact 180

ttcaagggaa ttaaatt 196

<210> 616

<211> 38

<212> DNA

<213> Homo sapiens

<400> 616

agtctgccta tgatctttga atgagctttt taaggaag 38

<210> 617

<211> 110

<212> DNA

<213> Homo sapiens

<400> 617

tttaacttga gggtagtag gtcctccacg cttgtttgcc tgaaagtaat ataattgatgc 60

tgtctgaaca gggtttactg cttgctttcc aagtaaaggt taattatgat 110

<210> 618

<211> 173

<212> DNA

<213> Homo sapiens

<400> 618

tattttccct ctttcgaaca aagacattgg ttgcccgaag gactacaaat aaaccaacgg 60

gaaaaaagaa aggttccagt ttgtctgaa aattctgatt aagcctctgg gccctacagc 120

ctggagaacc tggagaatcc tacaccaca gaaccggct ttgtcccaa aga 173

<210> 619

<211> 82

<212> DNA

<213> Homo sapiens

<400> 619

gttatttaag atggctatcc agataatcct gaacactgtg tttttatttt atttagacta 60

ccagcaaaga ttaaagcatg aa 82

<210> 620

<211> 266

<212> DNA

<213> Homo sapiens

<400> 620

gcttggggaa caatgatggt gcacaaaggc ttagatttgc cttgtctcaa aataaggaat 60

ttttagtggt ttttcaaaaa taattcaaca aagaaacaat acaaaaagtg ggtagaatta 120

cctatcacat ttcccaatct tgactattca gaatgctggt tatttagtga tgaggattag 180

cacttgattg aagattcttt taaaatacta tcagttaaac atttaatatg attatgatta 240

atgtattcat tatgctacag aactga 266

<210> 621

<211> 115

<212> DNA

<213> Homo sapiens

<400> 621

cagaaagcca agtggactca acggagaggc cagcaagttt caggaaatgg tgcatttggt 60

gaacaaggag tcgtcagaaa ctccagacca gtttatgaca gctgatgaga caagg 115

<210> 622

<211> 262

<212> DNA

<213> Homo sapiens

<400> 622

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tccagccatt gctacaaaga acctttatTT gttcagtaac ggtagaaaat ccttcccgat 120

taaaaacttc agacttgctg aatatcctgc aatgtcaaga tgaccgatgt tgagttgggt 180

ggatttgcta acgagtcaga tttgaacatg aggctattgg aaccaatag gcgtcattga 240

tggcggcaag ccatagcttt ca 262

<210> 623

<211> 94

<212> DNA

<213> Homo sapiens

<400> 623

ggggagccag gcttcctca cgcagcctgt ggtggatgtg ggaaggagat caacttctcc 60

tcactctggg acagacgatg tatggaaact aaaa 94

<210> 624

<211> 114

<212> DNA

<213> Homo sapiens

<400> 624

ctgcacagct cagcacaaca ttccaagctc aaaatagaag ctttctcagt gagctccagc 60

acgcccagag gactgttaat aacgatgac catgtgtttt actctaaagt gcta 114

<210> 625

<211> 37

<212> DNA

<213> Homo sapiens

<400> 625

cagggactgg ctatcccaag acctggcaga tgtggct 37

<210> 626

<211> 74

<212> DNA

<213> Homo sapiens

<400> 626

gtgaaaggga agtagaaccg aaacaagatt agtcctgagt taacaatggc tgcaagctgg 60

atacatggaa ttca 74

<210> 627

<211> 201

<212> DNA

<213> Homo sapiens

<400> 627

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ggactgtgga ggagggggct gagaccctg tctacttggc cctcttgctt ccagatgcca 120

ctgagccaca aggccagttg gtccatgaca aagttgtgca aaactggtaa acgtctgctt 180

cggagcttgc tgcttaataa a 201

<210> 628

<211> 217

<212> DNA

<213> Homo sapiens

<400> 628

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ggagcctggg ggtgtcgggg caggaggctg gggatggggg tgggatatga ggggtggcatg 120

cagctgaggg cagggccagg gctgggtgtcc ctaaggttgt acagactctt gtgaatattt 180

gtattttcca gatggaataa aaaggcccgt gtaatta 217

<210> 629

<211> 33

<212> DNA

<213> Homo sapiens

<400> 629

ttctgtgcct cagccgttct tgacatcaag aat 33

<210> 630

<211> 222

<212> DNA

<213> Homo sapiens

<400> 630

gacacagtcg ggttgacca gggctgtctc cctccagagc ctccctccgg acaatgagtc 60

pctgb2013053202-seq1.txt

ccccctcttg tctcccaccc tgagattggg catgggggtgc ggtgtggggg gcatgtgctg 120

cctgttgta tgggtttttt ttgcgggggg ggttgctttt ttctggggtc tttgagctcc 180

aaaaaataaa cacttccttt gagggagagc acaccttccc aa 222

<210> 631

<211> 278

<212> DNA

<213> Homo sapiens

<400> 631

tgagaggcaa gaggttgtcc tgcccttccc tttgtgactt gaagaaccct gactttgttt 60

ctgcaaaggc acctgcatgt gtctgtgttc gtgtaggcat aatgtgagga ggtggggaga 120

gcaccccacc cccatgtcca ccatgaccct cttcccacgc tgacctgtgc tccctctcca 180

atcatctttc ctgttccaga gaggtggggc tgaggtgtct ccatctctgt ctcaacttca 240

tggtgcactg agctgtaact tcttccttcc ctattaa 278

<210> 632

<211> 90

<212> DNA

<213> Homo sapiens

<400> 632

aaattaaagc taaagtatct gtattgcatt aaatataata tcgacacagt gctttccgtg 60

gcactgcata caatctgagg cctcctctct 90

<210> 633

<211> 198

<212> DNA

<213> Homo sapiens

<400> 633

accgcaggat cctttgctct gcacgagtta cctgttaaac tttggaacac ctaccaaaaa 60

ataagtttga taacatttaa aagatgggcg tttcccccaa tgaaatacac aagtaaacad 120

tccaacattg tctttaggag tgatttgcac cttgcaaaaa tggtcctgga gttggtagat 180

tgctgttgat cttttatc 198

<210> 634

<211> 243

<212> DNA

<213> Homo sapiens

<400> 634

ttcatgctgg acctcaggta caaaagggtta agaacttctc agttcattat atgatcatca 60

ttggcgcctc cgagctctct ctctctccct tgatttattt ggtccctttt atctccagtc 120

cttactccca tatctaacct cttacccta cctcataggt aaacatttta atgaatttga 180

tgtttccttt tatttgata gacctctgt aatatgtagt agtgtccagt gtacatgtat 240

ttt 243

<210> 635

<211> 211

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (140)..(140)

<223> n is a, c, g, or t

<400> 635

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atggtgagag tgaagtctgt cccagaccca ctgccactga acctgtctgg gatgccagtg 120

gccctgctgg atgcaccatn gatgaggagc ctgggagcct ggccaggttt ctgctggtac 180

caggctaagt agctgctgct aacactctga c 211

<210> 636

<211> 256

<212> DNA

<213> Homo sapiens

<400> 636

agagagtgga catttgtcgg gaaactccta acatatgccc ccattctgga gagaacacag 60

agtacgacac aatccctcac actaatagaa caatcctaaa ggaagatcca gcaaatacgg 120

tttactccac tgtggaaata ccgaaaaaga tggaaaatcc ccactcactg ctcacgatgc 180

cagacacacc aaggctatth gcctatgaga atgttatcta gacagcagtg cactgcccct 240

aagtctctgc tcaaaa 256

<210> 637
 <211> 239
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (138)..(138)
 <223> n is a, c, g, or t

<400> 637
 gaagggtaaa tgaagctatc gtagcttcac ttgggaaaag ggagagaaca gatgaccagc 60
 accaaggata gaagagggat ttcttacttt aaaaaaatg gtccaaagaa taaacaaact 120
 gaaaacagcc aaaagagnaa ggaagaattt gttagaatag ggcaagacta aaggacagag 180
 taagggtgct ggccgccacc tgactcaagt tcaagtcgag ctgccactgt tgaaatttc 239

<210> 638
 <211> 204
 <212> DNA
 <213> Homo sapiens

<220>

<221> misc_feature

<222> (63)..(63)

<223> n is a, c, g, or t

<400> 638

attttatgac atttcgaagt ttctgtgtct taactctttt taattaattt tctgcacgtt 60

gcnttttttc tctttgtttt taattccata cagagtattc aattcttgaa acacattaaa 120

ataatttgct tgctagggtta tggtttattt tataattaca ttcttagtct tgtgtggtta 180

ttgtaatgat gtctggtcct aatt 204

<210> 639

<211> 231

<212> DNA

<213> Homo sapiens

<400> 639

tgtctcccg cctgatacca gatacaggtt gttgatttca tcgtgggtag caagctagta 60

ataaatttca aagtgctttc tcttttcattg ctttttgcca ataactgtta ccgccgttct 120

tattctctcc cttaactcat tgtctttggg ggagttagac accaggaggt gccttgtcgg 180

tcataatttt cagcacgtca tcaatcctat catcttcaat aacaaccgc t 231

<210> 640

<211> 237

<212> DNA

<213> Homo sapiens

<400> 640

gcatggcatc aaaaggtagg tcaacatatt aaataattcc atgtattgaa atatccagaa 60

aatatataga cagatctata gagatagaaa ctggtctgcc caggactagg ggttgcttaa 120

ggataaggag cttctttttt ggatggtgaa ataacctaaa atatattgtg ccattgtttg 180

cacaactttg tgaatatatt aaaaacctgt taattgtact cactaaatgt cctcctt 237

<210> 641

<211> 228

<212> DNA

<213> Homo sapiens

<400> 641

attgatagtg cttcttacca ggtgaaggga agggctactt tttcctaaag gagaaaaaag 60

ctttcagaca aagctcgtac caaccctga actgcaaatt tgctcaagt accgtgcata 120

cttatattcc taatttaa at gattatttat gtcaaacgct cattgtgaaa cttgaaaatg 180

ttgtattaca ttacatcaaa taaagtttac ttgtagcaga cagaaaga 228

<210> 642

<211> 188

<212> DNA

<213> Homo sapiens

<400> 642

gaagcagcca acaaaaacgt aattagtaac taggacttcc tcatgggata gaccaaataa 60

ggcaactgta taactgtgta actgtataac tgtaaccaat gaaatattat ctttgctttt 120

atctattttgt ctaaaaaagc ctccctcctca tgttctctct ggggagctcc ctagccactt 180

ctggcttg 188

<210> 643

pctgb2013053202-seq1.txt

<211> 259

<212> DNA

<213> Homo sapien

<400> 643

gactggacca aagagcatgt gaaaaaatgg gttaatgaag accttaagat taatgagcaa 60

tacgggcaaa ttctgctcag tgaagaagta acaggattag tcctgcagga attaactgag 120

aaggaccttg tagaaatggg gctaccatgg ggtccagcac ttttgataaa acgttcatac 180

aacaaattga atagtaagtc ccctgaaagt gacaatcatg atccgggaca attagataat 240

tcaaaaccgt ccaaaacag 259

<210> 644

<211> 242

<212> DNA

<213> Homo sapiens

<400> 644

tgttctagag agctcatgta caccatggtg accatagtta ataatactgg attgtatgct 60

taaaatttgc taagagagta gatcttaagt catcaccaaa aaaagtaact gtaagatgat 120

pctgb2013053202-seq1.txt

ggagatgtgt taattagctt gacggtggta atcacaatat atgtgtatat caaaacatca 180

cattatacac cttaaagtga tataatattt gtcaattata cctcagtaaa gccaaaaaga 240

aa 242

<210> 645

<211> 205

<212> DNA

<213> Homo sapiens

<400> 645

ataggcagga accaatttgc atttaagtag tatgggaagc ctcgagtatg ttttcttgtc 60

cagagtgaag caaccaagaa agtaagatgc tggagatatc ttagactcaa gagatagaaa 120

gcaagaccct aggggagata agtaggagca ggatttcaag gacggaatta gtattgcaca 180

gagattaggg acacttcttc cttgg 205

<210> 646

<211> 217

<212> DNA

<213> Homo sapiens

<400> 646

aaaggcaaaa cactccagga cctctcccgg atctgtctcc tcctctagcc agcagtatgg 60

acagctggac ccctgaactt cctctcctct tacctgggca gagtgttgtc tctcccaaaa 120

tttataaaaa ctaaaatgca ttccattcct ctgaaagcaa aacaaattca taattgagtg 180

atattaaata gagaggtttt cggaagcaga tctgtga 217

<210> 647

<211> 253

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (208)..(208)

<223> n is a, c, g, or t

<400> 647

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gagcggacaa cagaagacat tataagatct gtgaaagtgg aaagagaaga aagagcagaa 120

pctgb2013053202-seq1.txt

gagtcaattg aggacatcta tgctaatatc cctgaccttc caaagtccta cataccttct 180

aggttaagga aggagataaa tgaagaanaa gaagatgatg aacaaaatag gaaagcttta 240

tatgccatgg aaa 253

<210> 648

<211> 249

<212> DNA

<213> Homo sapiens

<400> 648

aggaggtaga ccctttagct cccttccaat taaaggagtc cccaattctg gcacctgaga 60

gtccccctggg tctaacagct atgatattta tgtagtgtgt tgcttaccta aatgaataca 120

atttccttcc agacacgtga cactgatatt aaagtgctaa tgagagggat ctatttcttc 180

ttgtacgcta aaagagaaac agcagttcag atttcccatc agaagtccga ggactttgtt 240

cttgataac 249

<210> 649

<211> 185

<212> DNA

<213> Homo sapiens

<400> 649

ttgatattct cttttggttt tattgttgtg gttcattgaa aaaaaaagat aatTTTTTTTT 60

tctgatccgg ggagctgtat cccagtaga aaaaacattt taatcactct aatataactc 120

tggaatgaaac acacTTTTTT ttttaataag aaaagagaat taactgcttc agaaatgact 180

aataa 185

<210> 650

<211> 234

<212> DNA

<213> Homo sapiens

<400> 650

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ccccagggcg tgcggggctg tgcagactgg ggtgccaggc atctcctccc caccgggggt 120

gtccccacat gcagtactgt ataccccca tccctcctc ggtccactga acttcagagc 180

agttccatt cctgccccgc ccattctttt gtgtctcgct gtgatagatc aata 234

<210> 651

<211> 270

<212> DNA

<213> Homo sapiens

<400> 651

ggattttgat ccaagctggt ccactcagtc catagcagag aatgaaaggg cccagagagg 60

gtggtgacct ctgcctgaag tcacacagtg agtcgaggac agggaggtga cccaggttt 120

ctatgtgtag ggcgggagga tgttctggga cacagttcaa ttctcatttg tcacacactt 180

tggctattag agatcaacc cttcgctcct gtgtcttgca atggcagcct tggcaaacgc 240

taaatgaaaa tcgtgacaac acttgtgtta 270

<210> 652

<211> 37

<212> DNA

<213> Homo sapiens

<400> 652

cccaaattat cccaattat cccacacat aaaaaa

37

<210> 653

<211> 173

<212> DNA

<213> Homo sapiens

<400> 653

gttggtgttt catgacatgt ggacttcttt tgaaatagca agtcaaagt agtgaccaa 60

ttgtggaaga gatttctgtc aaataggaaa tgtgtaagtt cgtctaaaag ctgatggtta 120

tgtaagttgc tcagcactca gatgacagca gattctgggt tctgggagtg ttc 173

<210> 654

<211> 236

<212> DNA

<213> Homo sapiens

<400> 654

gaaaccatgg gcaggagtag gaattgagtg ataaacaatt gggctaata agaaaacttc 60

tcttattgtt cagttcatcc agattataac ttcaatggga cacttttagac cattagacaa 120

ttgacactgg gattaaacaa attcacataa tgccaaatac acaatgtatt tatagcaacg 180

tataatttgc aaagatggac tttaaaagga tgctgtgtaa ctaaactgaa ataatt 236

<210> 655

<211> 187

<212> DNA

<213> Homo sapiens

<400> 655

taatccacta aactggtctt cttcaagaga gctaagtata cactatctgg tgaaacttgg 60

attctttcct ataaaagtgg gaccaagcaa tgatgatctt ctgtggtgct taaggaaact 120

tactagagct ccactaacag ttcataagg aggcagccat cataaccatt gaatagcatg 180

caagggt 187

<210> 656

<211> 79

<212> DNA

<213> Homo sapiens

<400> 656

ctcagttctg gtccttcaag cctgtatggg ttggattttc agtaggggac agttgatgtg 60

gagtcaatct ctttgggtac 79

<210> 657

<211> 94

<212> DNA

<213> Homo sapiens

<400> 657

taacaaatca tcaacttcca ctggtcaata tatagatttt ggggtgtctga ggccccaaga 60

ttagatgccca ctaatctcca aagattccct ccaa 94

<210> 658

<211> 246

<212> DNA

<213> Homo sapiens

<400> 658

gaggcttggc cttctttgtg aggcagtgtg agcagaagct gatgccagca tgtcactggg 60

tttgaaggga tgagcccaga cttgatgttt tgggattgtc cttattttta cctcaaggtc 120

pctgb2013053202-seq1.txt

tcgcatgggtg gggcccctga ccaacctaca caagttccct cccacaagtg gacatcagtg 180

tcttctctgt gaggcatctg ggccattcgc actccctggt gtggtcagcc tctctcacac 240

aaggag 246

<210> 659

<211> 270

<212> DNA

<213> Homo sapiens

<400> 659

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agaaaagggtt cattttacac ttgccaatag gaatgaaact atttcgctgc cacaatagct 120

aactgttttt ctaaattggcc tatttcgtca acaacaatca ggaaagtgtg ggaaggtaca 180

atctctaattg attgtagccc gtgcttaagg tgaggaaaaa agtcaaaaaa ttacacatga 240

gaaacctgaa tccaggcaga tcttacccaa 270

<210> 660

<211> 195

<212> DNA

<213> Homo sapiens

<400> 660

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aaaaatcagg atgagtctta gatatacaaa agataaatgg atatttataa tagttatata 120

tgctttttta gcaaaatatt cacgtgttaa gtatttctgg atcttaaaat acaaaatcca 180

cttattttat tagtt 195

<210> 661

<211> 147

<212> DNA

<213> Homo sapiens

<400> 661

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cggttcattt tcttgagttt cattctgcga ttttgaaacc agattttgac ttgtctgtct 120

gtaagggttaa tggctctgct tatctcc 147

<210> 662

<211> 106

<212> DNA

<213> Homo sapiens

<400> 662

gaaagatcca gtaagttcag tttctctatg aactaatcat tcaagtcaaa ggcacactga 60

tgcaaaatca gtatatggac cccggtgtct gattagcaag gttttc 106

<210> 663

<211> 268

<212> DNA

<213> Homo sapiens

<400> 663

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cccaaagac aatgagttaa gggagagaat aagaacggcg gtaacagtta ttggcaaaaa 120

gcatgaaaag agaaagcact ttgaaattta ttactagctt gctaccacg atgaaatcaa 180

caacctgtat ctggtatcag gccgggagac agatgaggcg agaggaggag gaggaggagg 240

agaaggctct gggctcctct gcaaaaaa 268

<210> 664

<211> 160

<212> DNA

<213> Homo sapiens

<400> 664

accagcaaag caatgcactc ctgaccaagt agattctttt aaaaattaga gtgcattact 60

ttgaatcaaa aatttattta tatttcaaga ataaagtact aagattgtgc tcaatacaca 120

gaaaagtttc aaacctacta atccagcgac aatttgaatc 160

<210> 665

<211> 239

<212> DNA

<213> Homo sapiens

<400> 665

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cctatgggga tggaaaaggg actcctgggt gtctttgtga ctgtttagtg tgttctgtga 120

atgtgcgggc aggtatTTTT gcccacatct gtatatTTTgt ctattaatgt gatgtatttg 180

agtattgttg tgggggcggg tatgtctgta tataaatctg tgcagccact agtcaacaa 239

<210> 666

<211> 259

<212> DNA

<213> Homo sapiens

<400> 666

gaagaaagct ataccattac cataatacat ttttcatctc atggctacaa tggaattctt 60

gaaaaggaaa aaaaatccta tctacatata aaacctgca tgaatgaatc actacatatg 120

cttataatga ggaagagtta tgggtcctga gtgtaatttt ttatcctttc ttaaaaagtt 180

tctgtattat gcattttgat aacactactg atgacccctc cacttatatt tgaaatgtta 240

tgtaccacat ttgcacaat 259

<210> 667

<211> 234

<212> DNA

<213> Homo sapiens

<400> 667

ggctactctg aaatgttgca gtgtggaaca atggaaagag cctgggtgtt tgggtcagat 60

aaatgaagat caaactccag ctccagcctc atttgcttga gactttgtgt gtatggggga 120

cttgatatga tgggagtgag gagtttcagg gccattgcaa acatagctgt gcccttgaag 180

agaatagtaa tgatgggaat ttagaggttt atgactgaat tccctttgac atta 234

<210> 668

<211> 294

<212> DNA

<213> Homo sapiens

<400> 668

ctcgattatt ccctgtacaa tattttaaatt ttattgcttg atacttttga caacaaatta 60

ggttttgtac aattgaactt aaataaatgt cattaaaata aataaatgca atatgtatta 120

atattcattg tataaaaaata gaagaataca aacatatttg tttaatattt acatatgaaa 180

tttaatatag ctatTTTTAT ggaatttttc attgatatga aaaatatgat attgcatatg 240

catagttccc atgttaaadc ccattcataa ctttcattaa agcatttact ttga 294

pctgb2013053202-seq1.txt

<210> 669

<211> 265

<212> DNA

<213> Homo sapiens

<400> 669

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ttgctttctt ttctattgag tctgggcttg tttgtgttac tgcatactgt gattagcata 120

ataattgttt ctttgaggtc atctaaatat ttttttccta aaggaataaa gggtgaggaa 180

agaaaaatat taaaaaagct aatatttgat actgtgcttg ctgtcagtat gcattacatt 240

taaattattc tctattcaag tggga 265

<210> 670

<211> 190

<212> DNA

<213> Homo sapiens

<400> 670

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pctgb2013053202-seq1.txt

tgaccctcag ctgttccaat ctagtatttt ttttcttttt taaaattact gtatttatta 120

tgacgatggt gactccccag tgcaaagggg ggccagattc tgtgtgtttc tctaacctct 180

ttgtaaataa 190

<210> 671

<211> 138

<212> DNA

<213> Homo sapiens

<400> 671

aagaattaca gggatgtttt taatcccact atggactcag tctcctggaa ataggtctgt 60

ccactcctgg tcattggtgg atgttaaacc catattcctt tcaactgctg cctgctaggg 120

aaaactgctc ctcattat 138

<210> 672

<211> 257

<212> DNA

<213> Homo sapiens

<400> 672

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tattagctgt aaatacatgt gtggatgtgt aaatggagct tgtacatatt ggaaagggtca 120

ttgtggctat ctgcatttat aaatgtgtgg tgctaactgt atgtgtcttt atcagtgatg 180

gtctcacaga gccaaactcac tcttatgaaa tgggctttta caaaacaaga aagaaacgta 240

cttaactgtg tgaagaa 257

<210> 673

<211> 231

<212> DNA

<213> Homo sapiens

<400> 673

accatgtaca gagaaatttt aggccaaact taaaatatgt aaggaggcag ctttaggcta 60

aacttgattt aacagcacca ataccctta ctttagtga gcacatctgc acattccaat 120

tttaatgaca gtccttaga atttcttatc aacgaagaca ctaacaaaga atggcgcat 180

cctccttctc ctttctgagg atgccctacc ctgtaacaaa gtcgtttcta a 231

<210> 674

<211> 132

<212> DNA

<213> Homo sapiens

<400> 674

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gcatagcata ggacgtctga acctttgtac aaatgtgtag atgacatctt gctacagctt 120

ttatattgtga at 132

<210> 675

<211> 283

<212> DNA

<213> Homo sapiens

<400> 675

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agaaaccaga agctctgata tttaactgcc gtgataatga attcaatgtg caactatggg 120

caaattgtat ttaatagtaa ttgcatattg tacatatattt tcattcttat taacactgat 180

aaacttttca acttatactg actttaataa aattgtatta ctaggctatt aacatgatat 240

tttgtttccc attaaatgtg acatgcaaag acgtttatta aat 283

<210> 676

<211> 229

<212> DNA

<213> Homo sapiens

<400> 676

actgtacaaa gtataagtct tagatgtata tatttcctat attgttttca gtgtacatgg 60

aataacatgt aattaagtac tatgtatcaa tgagtaacag gaaaatttta aaaatacaga 120

tagatatatg ctctgcatgt tacataagat aaatgtgctg aatggttttc aaataaaaat 180

gagggtactct cctggaaata ttaagaaaga ctatctaaat gttgaaaga 229

<210> 677

<211> 39

<212> DNA

<213> Homo sapiens

<400> 677

gttgctgacc tgctgtgctc gcagtagatt ccaaaaaaa 39

<210> 678

<211> 259

<212> DNA

<213> Homo sapiens

<400> 678

gacatcccca ctcacgaata ttatgccag tttctgcctc tgagggaag cccagaaaag 60

gacagaaacg aagtagaaag gggcccagtc ctggcctggc ttctccttg gaagtgaggc 120

attgcacggg gagacgtacg tatcagcggc cccttgactc tggggactcc gggtttgaga 180

tggacacact ggtgtggatt aacctgccag ggagacagag ctcacaataa aaatggctca 240

gatgccactt caaagaaaa 259

<210> 679

<211> 236

<212> DNA

<213> Homo sapiens

<400> 679

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pctgb2013053202-seq1.txt

tttctaggta ggaaatgtgg tagcctcact tttaatgaac aaatggcctt tattaataaac 120

tgagtgactc tatatagctg atcagttttt tcacctggaa gcatttgttt ctactttgat 180

atgactgttt ttcggacagt ttatttgttg agagtgtgac caaaagttac atgttt 236

<210> 680

<211> 280

<212> DNA

<213> Homo sapiens

<400> 680

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agttggaatg ttgtagttac ctactgagta ggcggcgatt tttgtatggt atgaacatgc 120

agttcattat tttgtggttc tattttactt tgtacttgtg tttgcttaaa caaagtgact 180

gtttggctta taaacacatt gaatgcgctt tattgcccatt gggatatgtg gtgtatatcc 240

ttccaaaaaa ttaaaacgaa aataaagtag ctgcgattgg 280

<210> 681

<211> 215

<212> DNA

<213> Homo sapiens

<400> 681

caaacttgga gcaggtgtcc atcccagccc tgtgtagtta gagcaggaat caagatctca 60

acacaaatgt ggctgccaag cactcagccc cggggcgagg ggtcaagttc ttctcagaga 120

aagaggaata agttggttct cagaagacat cacaagatac gtgtgtaccc aacaatctct 180

gatctctgct gatcttttgc ttagacgtta acttg 215

<210> 682

<211> 258

<212> DNA

<213> Homo sapiens

<400> 682

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ggccacccta gaaagaagtc cgctggcacc cataggaagg ggcctcagga gcaggaaggg 180

ccaggaccag aaccttgccc acggcaactg ctttcctgcc tctccccttc ctcctctgct 240

cttgatctgt gtttcaat 258

<210> 683

<211> 248

<212> DNA

<213> Homo sapiens

<400> 683

gaaactccct agttccttca tgtaacttcc ctgaaaaatc taagtgtttc ataaatttga 60

gagtctgtga cccacttacc ttgcatctca caggtagaca gtatataact aacaaccaaa 120

gactacatat tgtcactgac acacacgtta taatcattta tcatatatat acatacatgc 180

atacactctc aaagcaaata atttttcact tcaaaacagt attgacttgt ataccttgta 240

atttgaaa 248

<210> 684

<211> 39

<212> DNA

<213> Homo sapiens

<400> 684

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<210> 685

<211> 72

<212> DNA

<213> Homo sapiens

<400> 685

tctattttatt tattgaggac ccatggtaaa atgcaaatag atccggtgtc taaatgcatt 60

catattttta tg 72

<210> 686

<211> 241

<212> DNA

<213> Homo sapiens

<400> 686

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tttttaaaaa cactcttatt agcctgggca acacagttag actccatctc ttaaaaaaaaa 120

aattagctgg gtatagtgg atgtgcctgt agtcccaggt actcaggagg ctgaggcagg 180

aggattgcct gagcccagga ggtggaaact gcagagagtc atgatcatgt cttacactc 240

c 241

<210> 687

<211> 278

<212> DNA

<213> Homo sapiens

<400> 687

gtaataaact ctctagggcc aaaacctggt atggtcattg ggaaatgagt gctcaggagg 60

atggagctta ggggaggtgg gtgcttcct cctagatgtc agcatacact ctttcttctt 120

ttgtcccagg tctaaaacat ctttcctaga gaaaacaaaa gggactaaac tagaaatata 180

aagagcccta tacatgacag gtgatcacgt actgaatgat tttgaagtag tacaacaat 240

aaaaattctc attccgcatc atcatgcggt ccatgatg 278

<210> 688

<211> 244

<212> DNA

<213> Homo sapiens

<400> 688

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tctctagggt ctgagctctg gctttgcctt ggctttgcca gggctctgtg accaggaagg 120

aagtcagcat gcctctagag gcaaggaggg gaggaacact gcactcttaa gcttccgccg 180

tctcaacccc tcacaggagc ttactggcaa acatgaaaaa tcggcttacc attaaagttc 240

tcaa 244

<210> 689

<211> 118

<212> DNA

<213> Homo sapiens

<400> 689

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cataactgaa ggcatatgct ggcccataaa caccctgtag gttcttgata ttataaat 118

<210> 690

<211> 264

<212> DNA

<213> Homo sapiens

<400> 690

aataccatt atattcctgt aagtaaata ctatttttcc cttaactcag tgattagaca 60

ggaaggaaga cattagtgt tagacaggag ggaagatatt agtgattaga cagcaggga 120

gatattagt gtaaagagt aatgatagta gtgaatata atggggctga ggaaacttta 180

agcataaaag attcctgaga tgactttaca agtctgtacg aatctgcctt gactgtatat 240

ttcactatgc ccaacaaaac aata 264

<210> 691

<211> 270

<212> DNA

<213> Homo sapiens

<400> 691

gttcctattc ttccattgta cgataatgtc tttaatatga aatgctacat tatttataat 60

tggtagagtt attgtatctt tttatagttg taagtacaca gaggtggtat atttaaactt 120

pctgb2013053202-seq1.txt

ctgtaatata ctgtatttag aaatggaaat atatatagtg ttaggtttca cttcttttaa 180

ggtttacccc tgtggtgtgg tttaaaaatc tataggcctg ggaattccga tcctagctgc 240

agatcgcatc ccacaatgcg agaatgataa 270

<210> 692

<211> 187

<212> DNA

<213> Homo sapiens

<400> 692

aattcatagt aatttcactc tctgcattga cttatgagat aattaatgat taaactatta 60

atgataaaaa taatgcattt gtattgttca taatatcatg tgcacttcaa gaaaatggaa 120

tgctactctt ttgtggttta cgtgtattat tttcaatatc ttaataccct aataaagagt 180

ccataaa 187

<210> 693

<211> 249

<212> DNA

<213> Homo sapiens

<400> 693

tcaccacaac agaacatgca gtactaaagc aatatatttg tgattcccca tgtaattctt 60

caatgttaaa cagtgcagtc ctctttcgaa agctaagatg accatgcgcc ctttcctctg 120

tacatatacc cttagaacg cccctccac aactgcccc ccagtatatg ccgcattgta 180

ctgctgtgtt atatgctatg tacatgtcag aaaccattag cattgcatgc aggtttcata 240

ttctttcta 249

<210> 694

<211> 199

<212> DNA

<213> Homo sapiens

<400> 694

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gccctagact aactgtattg tcctagtcac agctccttgc ttgatttca tccttgataa 120

aatgaagatg aaacttacac tacttctcca agccttttgc tgtcttaaga ataagacctg 180

agattaacac taaccctag

199

<210> 695

<211> 190

<212> DNA

<213> Homo sapiens

<400> 695

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caaattaata ttggtgttca agactatatc taattcctct gatcactttg agaaacaaac 120

ttttattaaa tgtaaggcac ttttctatga attttaata taaaaataaa tattgttctg 180

attattactg 190

<210> 696

<211> 235

<212> DNA

<213> Homo sapiens

<400> 696

gttttgctgg agaaacatca ggtttgtagg agactgagtt gtttagcaggt gtgcttagct 60

cttgatagtg aacgtgtacc ttgggaactg gctcaccac ctgctaatag caccatcgtc 120

actattaagc agacatttca gttggtagaa tccatgtaga agtcatggac ttttctggga 180

aatgactttt ctgggaaatg acagtttctt tgacatattt tctttgccca cttta 235

<210> 697

<211> 243

<212> DNA

<213> Homo sapiens

<400> 697

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gagtgtgagc agggcttgct cctgccaacc acaattcaat gaatccccga cccccctacc 120

ccatgctgta cttgtgggtc tctttttgta ttttgcattt gaccccgagg ggctgggaca 180

gattggcaat gggccgtccc ctctcccctt ggttctgcac tgttgccaat aaaaagctct 240

taa 243

<210> 698

<211> 192

<212> DNA

<213> Homo sapiens

<400> 698

gctgtttgtt ctcctggggc gctccctcca acttttgcag attcttgcaa cctcctcctg 60

agccgggatt gtccaattac taaaatgtaa ataatcacgt attgtgggga ggggagttcc 120

aagtgtgccc tcctctcttc tcctgcctgg attatttaaa aagccatgtg tggaaaccca 180

ctatttaata aa 192

<210> 699

<211> 114

<212> DNA

<213> Homo sapiens

<400> 699

agcaagtgtg gacaccttcg agggcagaga tcgggagatt taagatgtta cagcatattt 60

ttttttcttg ttttacagta ttcaattttg tgttgattca gctaaattat gaaa 114

<210> 700

<211> 123

<212> DNA

<213> Homo sapiens

<400> 700

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tcctcactct gggacagacg atgtatggaa actaaaaaga acatgcggca ctttaaaaaa 120

aaa 123

<210> 701

<211> 158

<212> DNA

<213> Homo sapiens

<400> 701

cagccccacc cctgtaaatg gaatttacca gatgaaggga atgaagtccc tcaactgagcc 60

tcagatttcc tcacctgtga aatgggctga ggcaggaaat gggaaaaagt gttagtgctt 120

ccaggcggca ctgacagcct cagtaacaat aaaaacaa 158

<210> 702

<211> 206

<212> DNA

<213> Homo sapiens

<400> 702

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atttttcact ttgagaacca acattaattc catatgaatc aagtgttttg taactgctat 120

tcatttattc agcaaattt tattgatcat ctcttctcca taagatagtg tgataaacac 180

agtcatgaat aaagttattt tccaca 206

<210> 703

<211> 252

<212> DNA

<213> Homo sapiens

<400> 703

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tcattgacaa taaatgtaag aaattggaat aaaaaagaga gacctgctgt tattcgcttt 120

tgttctccag tgatttgatt aactcagggc aaggctgaat atcagagtgt atcgactga 180

agaataataa tccattcagt aatgttatag ttatcctcaa tctaaatatg tcaactgtca 240

ttttgctgct tt 252

<210> 704

<211> 227

<212> DNA

<213> Homo sapiens

<400> 704

ctaaggtagc aacttatttc caaattaata tagatgaaaa atagatacca attagactaa 60

attgaaagct ttttgttcta tatttgcata gcctttgaaa tatttcttag tgcctaggag 120

gtctggggat tcctctttcg tgggtggcac taaccttact tgatgcagat aaaatcactt 180

gtcaatgcaa aatgtgttag aacttgataa agctttgagt ttgagaa 227

<210> 705

<211> 262

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (77)..(117)

<223> n is a, c, g, or t

<400> 705

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ctgagctgtg acaaggnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnaag 120

ggcaagtgc tttttcctgt tttcttcctt atcttagttg taatgaatca cttttataac 180

ttgtacctgc tacactaagt attgtctcag caaagtcatt cattttactg gtaacaaaag 240

ccaggaataa cgtgctatgg aa 262

<210> 706

<211> 275

<212> DNA

<213> Homo sapiens

<400> 706

gcctggatag aggtatatga tcgtgtgcc aagaatttatc ccagactccc ctgtgtgaca 60

gcttcataat aaagttactt aactgtgcct cttcctcctt cctctcccca cacaggatgg 120

atgggcatct ttctccttga ccaccctact ctcccttcct cccctgatca cctccccctcc 180

ctgctcttcc ctggatgatgg acttctaaca tgagatTTTT ttaaaaaatt tctatttctt 240

ttataatttt gctgagtttt cagggtttct tctgt 275

<210> 707

<211> 81

<212> DNA

<213> Homo sapiens

<400> 707

agctatctga gccttgacgc tgagcaagtg gaagtccac agaagctaca agttgccagg 60

tcaacgcatg aaggagcca c 81

<210> 708

<211> 147

<212> DNA

<213> Homo sapiens

<400> 708

cagtatgtca tgtttgctgt agtgctcata tttattgttg tttttgtttt agtactcact 60

tgtttcataa tatcaagatt actaaaaatg ggggaaagga cttctaattct ttttttcata 120

atatctttga cacatattac agaagaa 147

<210> 709

<211> 47

<212> DNA

<213> Homo sapiens

<400> 709

acacagtgct ttccgtggca ctgcatacaa tctgaggcct cctctct 47

<210> 710

<211> 52

<212> DNA

<213> Homo sapiens

<400> 710

taaatatcca cagtactcac tttttccaaa tgatcctagt aattgcctag aa 52

<210> 711

<211> 222

<212> DNA

<213> Homo sapiens

<400> 711

ggtgttggca ctaacgctgc ttgtttggca aatcatcatc actgaggtat tccaccaga 60

gactttttca aaaaagtcaa ctaaagtgc aagtcataag aggagagcca ttataccgt 120

tgtctttctg ggctccttga gtttatctgg attccaacag cacttgaaa gtaccgcct 180

ccactacctc aaatgcaaac acaatctctg ccagtagaca tt 222

<210> 712

<211> 284

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (33)..(33)

<223> n is a, c, g, or t

<400> 712

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pctgb2013053202-seq1.txt

agcaatcaag gcatgtcttt aaattctata catagatata gccaaaaata gtgcatttag 120

taacattctt ttccaaaact atattcttgg gaatgaatat ctgtttcttc taacagtttg 180

agtgataatc tatacctgta gatataagtt attttgcata taaaattaat cttaatcttt 240

tatggaatgt tctctgtctg tggcattaata tgaaccttaa gaac 284

<210> 713

<211> 224

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (144)..(144)

<223> n is a, c, g, or t

<400> 713

tgtgcccagc tgacatattc tcacttaata gaattataga gaaatttttc atgtttttct 60

ttttctctcc cactttttca tattcctctt tttcattttt gcctttccgt ttctgtctat 120

gatgtaggct tctgaggaga accnagaagc ttggcttttag tggtagaatg acagaactta 180

gggatccctt gcaggctaga acaaagttct gacccttaga ccaa 224

<210> 714

<211> 224

<212> DNA

<213> Homo sapiens

<400> 714

gaaattgcat caagcgtccg aacatgctgc ttacaacttt agaaacgcaa aatgcgttgt 60

tgtgggagtt gtgtaatttt tagtaggtgc tcaaatactt gctgaacttg gtgtctattt 120

ttaagtcttg cccattgatg taaactgtcc ctaggtcacg tgtatcttga ggtctaaaag 180

attatttatg caataaattg aaattcccat agccaattaa agat 224

<210> 715

<211> 194

<212> DNA

<213> Homo sapiens

<400> 715

tggtgggctg aggatgtctt cttcctgtcc aggatgcaat atggtcaagg atgaaaggaa 60

pctgb2013053202-seq1.txt

agagatgctg ggagcaagtc tgcattgaag atgtatttct gttgctttac taccaaccct 120

ggttataaat gatgaaacta taatgggtct gtaatagcta ctttcccata tagctcttgt 180

ctgtacatac ataa 194

<210> 716

<211> 227

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (71)..(72)

<223> n is a, c, g, or t

<220>

<221> misc_feature

<222> (185)..(187)

<223> n is a, c, g, or t

<220>

<221> misc_feature

<222> (189)..(191)

<223> n is a, c, g, or t

<220>

<221> misc_feature

<222> (193)..(195)

<223> n is a, c, g, or t

<220>

<221> misc_feature

<222> (199)..(199)

<223> n is a, c, g, or t

<220>

<221> misc_feature

<222> (201)..(202)

<223> n is a, c, g, or t

<400> 716

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gcaccatgtg nntttttttt tttatctagt tcttgatac tacagataat atttgaactt 120

tgtcatctca ctgtaaaact tttgttcatt tctcattatg gtaataaata gctattataa 180

ccaannnann nannnaaana nnttatttcc ctaagtgtta ttttgac 227

<210> 717
<211> 183
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (126)..(127)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (135)..(135)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (138)..(138)
<223> n is a, c, g, or t

<400> 717
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60

ttatctatatt atagttatga gattaagact ggagtgccat caccgcgggt gatgatttag 120

cttttnntgt gtgtntgngt gtgtgccttc caaatcatgc cataattgta atgttgaatc 180

gga 183

<210> 718

<211> 288

<212> DNA

<213> Homo sapiens

<400> 718

tgtgcccaac cattgtaata tgcgtattga cgtatatgat aggagaaaac actagcattt 60

tgagttaata agtaggtcag tttggattaa tggaaagttt gaagcttaga gtgttttaat 120

aatgatttta ttcttttcaa tacacaagtg gaaatgtttc tccagtctaa attcccccta 180

gtattctcct gaaacaaaat ttttatatgc agatatttgc ttcttttgca agtttgagaa 240

tttcacagta acttctgggt accctggggt gtgtcttgca gttaccaa 288

<210> 719

<211> 183

<212> DNA

<213> Homo sapiens

<400> 719

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ccttgctcct ggctggggcc tgttgaagat gcttgtatatt tactttttcca ttgtaattgc 120

tatcgccatc acagctgaac ttgttgagat ccccggtgta ctgcctatca gcattttact 180

act 183

<210> 720

<211> 205

<212> DNA

<213> Homo sapiens

<400> 720

gctgcttcct cctggaaatt gacgaggggt gtcttgggca gagctggctc tgagcgcctc 60

catccaaggc caggttctcc gttagctcct gtggccccac cctggggcct gggctggaat 120

caggaatatt ttccaaagag tgatagtctt ttgcttttgg caaaactcta cttaatccaa 180

tgggtttttc cctgtacagt agatt 205

<210> 721

<211> 189

<212> DNA

<213> Homo sapiens

<400> 721

gcccacctga agcagcaagt gagcgggctg gaggggtgtgc aggacgacct gttctggctg 60

accttcgagg ggaagcccct ggaggaccag ctcccgtgg gggagtacgg cctcaagccc 120

ctgagcaccg tgttcatgaa tctgcgctg cggggaggcg gcacagagcc tggcgggcgg 180

agctaaggg 189

<210> 722

<211> 191

<212> DNA

<213> Homo sapiens

<400> 722

caaacagagt gaactttctg ccaagatgcg ggagtggttt tcagagacat ttcagaaagt 60

gaaggagaaa ctcaagattg actcatgagg acctgaaggg tgacatccca ggaggggcct 120

ctgaaatttc ccacacccca ggcctgtgc tgaggactcc ctccatgtgg cccaggtgc 180

caccaataaa a 191

<210> 723

<211> 217

<212> DNA

<213> Homo sapiens

<400> 723

aggttagatt ctcattcacg ggactagtta gctttaagca ccctagagga ctagggtaat 60

ctgacttctc acttcctaag ttcccttcta taccctcaag gtagaaatgt ctatgttttc 120

tactccaatt cataaatcta ttcataagtc tttggtacaa gtttacatga taaaaagaaa 180

tgtgatttgc cttcccttct ttgcactttt gaaataa 217

<210> 724

<211> 233

<212> DNA

<213> Homo sapiens

<400> 724

ggagagtaga acatttttcc tcattttatc aaatcctctc ttgccctccc tcaattcccc 60

tgtaacattc ctgaagctgt tcccactccc agatggtttt atcaatagcc tagaggtaaa 120

gaactgtctt tttctctgat tctttaataa attatcttta tagaatatgc acaagttttt 180

ctacactcag tgttaaagta tttattaatg ggaagtcaac ttaatgtttt gaa 233

<210> 725

<211> 250

<212> DNA

<213> Homo sapiens

<400> 725

ttgcatttca tgtttaacct ccggctggaa atagaaagca ttcccttaga gatgaggata 60

aaagaaagtt tcagattcaa cagggggaag aaaatggaga tttaatccta aaactgtgac 120

ttggggagggt cagtcattta cagttagtcc tgtgtctttc gacttctgtg attattaacc 180

ccactcacta ccctgtttca gatgcatttg gaataccaaa gattaaatcc ttgacataag 240

atctcatttg 250

pctgb2013053202-seq1.txt

<210> 726

<211> 183

<212> DNA

<213> Homo sapiens

<400> 726

ggagtgggtgg cctctctgag atttcctaaa gttgctcaac agcccctgat caactaagtt 60

ttgtggtact tcaccctctt ctgccctcat ttcattgtgac agccattgtg agactgatgc 120

acaaactgtc acttggttaa tttaagcact tctgttttcg tgaatttact tgattgtttc 180

ttc 183

<210> 727

<211> 77

<212> DNA

<213> Homo sapiens

<400> 727

accaccacca gaatgcagtt ccagcttagg aagccacaaa caagccaccc aggaggaaca 60

aaacaccgcc agcgtgg 77

pctgb2013053202-seq1.txt

<210> 728

<211> 231

<212> DNA

<213> Homo sapiens

<400> 728

aataattcct ttctactgca tacaaaggga cctgaagctt aaattcagtt agttttggag 60

aaatccaaaa tgagaaaaac agaaagcatg tagcattcca tgaagcaaga acagcgtgca 120

tatgctattc ctggaaatac tgaagtgtcc gaatttcag cctaaaaagt ctggaaatca 180

cactgaatca gttgctgggt tctgatgtct ctgggatgtg ctattacaaa c 231

<210> 729

<211> 77

<212> DNA

<213> Homo sapiens

<400> 729

attcagcaaa aactcagcca gctctttcta tggggcagtt gctaatttag ttctaggcaa 60

acgtggacac attaaat 77

pctgb2013053202-seq1.txt

<210> 730

<211> 269

<212> DNA

<213> Homo sapiens

<400> 730

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ttttttttga gatgggttct cactatattg tccaggctag agtgcagtgg ctattcacag 120

atgcgaacat agtacactgc agcctccaac tcctagcctc aagtgatcct cctgtctcaa 180

cctcccaagt aggattacaa gcatgcgccg acgatgccca gaatccagaa ctttgtctat 240

cactctcccc aacaacctag atgtgaaaa 269

<210> 731

<211> 229

<212> DNA

<213> Homo sapiens

<400> 731

aaatatgttt acagaccaaa gtgtgatttc acactgtttt taaatctagc attattcatt 60

pctgb2013053202-seq1.txt

ttgcttcaat caaaagtggg ttcaatattt ttttttagttg gttagaatac tttcttcata 120

gtcacattct ctcaacctat aatttggaat attgttgtgg tcttttgttt tttctcttag 180

tatagcattt ttaaaaaaat ataaaagcta ccaatctttg tacaatttg 229

<210> 732

<211> 216

<212> DNA

<213> Homo sapiens

<400> 732

gtgatctggc aatgctatcc agcatctttg gagaccaatg gtcagtcttt tcctggccag 60

aggaaagatt gatggccctc ccacttgaac tgacagcctg tgagcccctt gggggcatag 120

actgccttcc ttggaccctt ccaaagtgtg tggtaggggg ctcagtgcac agagtattca 180

cccagcatca tgaatcaact tgggaggagt caacca 216

<210> 733

<211> 165

<212> DNA

<213> Homo sapiens

pctgb2013053202-seq1.txt

<400> 733

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tgggaaggcg cgagaccgcg caggcgcagt accgcgggtg ccgcccaggt gatgcgcatg 120

cgcacccgggt agcagagcta gcgctactca gtaaaaatcc aatat 165

<210> 734

<211> 124

<212> DNA

<213> Homo sapiens

<400> 734

gacctggggc tgacggggcc ttctcagccc gttttgagga cagacagtcc cccgaggtag 60

gctacatccc cccaccccag ctggtctgct tggatttcct acagcccccg tgggcatgga 120

ccac 124

<210> 735

<211> 156

<212> DNA

<213> Homo sapiens

<400> 735

gttataattt acactgaggg tttcaaaatt cgactagaag tggagatata ttattttattt 60

atgcactgta ctgtattttt atattgctgt ttaaaacttt taagctgtgc ctcacttatt 120

aaagcacaaa atgttttacc tactccttat ttacga 156

<210> 736

<211> 276

<212> DNA

<213> Homo sapiens

<400> 736

gagtaagctc tagtccctct gtcctgtaga aagagccctg aagaatcagc aattttgttg 60

ctttattgtg gcatctgttc gaggtttgct tcctctttaa gtctgtttct tcattagcaa 120

tcatatcagt tttaatgcta ctactaacia tgaacagtaa caataatata cccctcaatt 180

aatagagtgc tttctatgtg caaggcactt ttcacgtgtc acctatttta acctttccaa 240

ccacataaat aaaaaaggcc attattagtt gaatct 276

pctgb2013053202-seq1.txt

<210> 737

<211> 257

<212> DNA

<213> Homo sapiens

<400> 737

gcctctggct tctcaggcct ctgctctccg acctctctcc tctgaaaccc tcctccacag 60

ctgcagccca tcctcccggc tccctcctag tctgtcctgc gtcctctgtc cccgggtttc 120

agagacaact tcccaaagca caaagcagtt tttcccccta ggggtgggag gaagcaaaag 180

actctgtacc tatTTTgtat gtgtataata atttgagatg tttttaatta ttttgattgc 240

tggaataaaag catgtgg 257

<210> 738

<211> 283

<212> DNA

<213> Homo sapiens

<400> 738

cgcatgttat ggtgctaata tactttcact tttaaactct agatcagaat tgttgacttg 60

cattcagaac ataaatgcac aaaatctgta catgtctccc atcagaaaga ttcattggca 120

pctgb2013053202-seq1.txt

tgccacaggg gattctcctc cttcatcctg taaaggtcaa caataaaaac caaattatgg 180

ggctgctttt gtcacactag catagagaat gtgttgaaat ttaactttgt aagcttgtat 240

gtggttggtg atcttttttt tccttacaga caccataat aaa 283

<210> 739

<211> 254

<212> DNA

<213> Homo sapiens

<400> 739

aattcagtgg tgtgagtata ttcataagat ttatacttgg tgtctattca taagacttat 60

atccagcata ttcataacta gagccatatac acagatgcat tcatcataat aattccagac 120

attttcatca ccctaaaagg aaaccctgaa acccattagc agtcattccc cattcctcca 180

acccattctc tccctaatacc ctagaaccca ccaatctgct gtgtatttca tctattgcca 240

acatttcata taaa 254

<210> 740

<211> 217

<212> DNA

<213> Homo sapiens

<400> 740

tattttttgag atatcccttt ggaagacctt gcttggaaga gcctggacac taacaattct 60

acaccaaatt gtctcttcaa atacgtatgg actggataac tctgagaaac acatctagta 120

taactgaata agcagagcat caaattaaac agacagaaac cgaaagctct atataaatgc 180

tcagagttct ttatgtattt cttattggca ttcaaca 217

<210> 741

<211> 171

<212> DNA

<213> Homo sapiens

<400> 741

atcgctggtc accatgggtga tcaaggtgct cctggctccg tgggtcctgc tggtcctagg 60

ggccctgctg gtccttctgg ccctgctgga aaagatggtc gcactggaca tcctggtaca 120

gttggacctg ctggcattcg aggccctcag ggtcaccaag gccctgctgg c 171

<210> 742

<211> 289

<212> DNA

<213> Homo sapiens

<400> 742

aaaccctcag gaaactccca gggatgatgct tggagaagct gtgagttgag ctgaagctgg 60

agaacttcct ccagagcaaa gggcttaaga aagaaagaag aactctaagc tgggtctgct 120

aacatcactc cagtttagat ggatcttggc agagagacat gcttggttcct ctggattgga 180

aagatgattt actctcggga atcttctctg tcagcctgta catctaaagg catgaagcac 240

tcaattgggc aattaacatt agtgtttgtt ctctgatggt atctctgag 289

<210> 743

<211> 271

<212> DNA

<213> Homo sapiens

<400> 743

gtggtcatgc ggaacactct gttatttaag atggctatcc agataatcct gaacactgtg 60

pctgb2013053202-seq1.txt

tattttatttt atttagacta ccagcaaaga ttaaagcatg aaatgtaaaa catctgataa 120

aacttacagc cccctacacc aagagtgtat ctgtgaaaga gtcctacac tttgaaaact 180

taagaatccc ttatcatgaa gtttgcctgt tctagaattg taagattggt aatttccttc 240

aatctctagt gacaacactt aatttccttt c 271

<210> 744

<211> 193

<212> DNA

<213> Homo sapiens

<400> 744

cacctggctt catgttcccg gtattagtagt aatgccaaaa tattttaaata tcttaaaggt 60

taactcaaat atcttaagtt ttacttcact tacaatttca ataatgctga aattttgatt 120

gaatattgtg tttgtagtgc tacctctttt tcgttcataa gaacaaaagc ctatcattct 180

cttagtttct aaa 193

<210> 745

<211> 206

<212> DNA

<213> Homo sapiens

<400> 745

cctgtaactc tttaaaactt ggctataggc tgtttagcac agtacagatt aaagatacag 60

ttacgtaaac agcaaagtaa ttttatagtg cttcatccat ttatcatgct ttggtttgct 120

aatTTTTtca catacTTTT tctatcacag tctgttgctt ttgtacacat ttctcatatt 180

ggggttcgac aggtaaacac aaactg 206

<210> 746

<211> 242

<212> DNA

<213> Homo sapiens

<400> 746

gtgctataat ccctatttag ttcaaaatta accagaattc ttccatgtga aatggaccaa 60

actcatatta ttgttatgta aatacagagt tttaatgcag tatgacatcc cacaggggaa 120

aagaatgtct gtagtgggtg actgttatca aatattttat agaatacaat gaacggtgaa 180

cagactggta acttgtttga gttcccatga cagatttgag acttgtcaat agcaaatacat 240

tt 242

<210> 747

<211> 266

<212> DNA

<213> Homo sapiens

<400> 747

ttatcaactg tgcacaagga aaaaaataga tatgtgaaag gttcacgtaa atttcctcac 60

atcacagaag attaaaattc agaaaggaga aaacacagac caaagagaag tatctaagac 120

caaagggatg tgttttatta atgtctagga tgaagaaatg catagaacat tgtagtactt 180

gtaaataact agaaataaca tgatttagtc ataattgtga aaaataataa taatttttct 240

tggatttatg ttctgtatct gtgaaa 266

<210> 748

<211> 202

<212> DNA

<213> Homo sapiens

<400> 748

gtggaggata ttgcaactgg agttcagaca ctgtactcga agtggaagga ctttcatttt 60

gagaagatac catttgatcc agcagaaatg tccaaatgat atcaggtcct caatcttcag 120

ctacagggaa tgagtaactt tgagtggaga agaaacaaac atagtgggta taatcatgga 180

tcgcttgtag ccctgtgaaa at 202

<210> 749

<211> 208

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (124)..(124)

<223> n is a, c, g, or t

<400> 749

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ggtttattgt tgggactatt ctttaaaata tccattgttc actacagtga agatctctga 120

tttnaccgtg tactatccac atgcattaca aacatttcgc agagctgctt agtatataag 180

cgtacaatgt atgtaataac catctcat 208

<210> 750

<211> 150

<212> DNA

<213> Homo sapiens

<400> 750

gctgataaat agcattaggg ttctttgcaa tgtggtatct agctgtatta ttggttttat 60

ttactttaaa cattttgaaa agcttatact ggcagcctag aaaaacaaac aattaatgta 120

tctttatgtc cctggcacat gaataaactt 150

<210> 751

<211> 97

<212> DNA

<213> Homo sapiens

<400> 751

caaattcaag tcactagact tcagagttca acacctggac atgagaagat attatattat 60

gtaccataaa tatttcctgt atctgactgc ctgaaca

97

<210> 752

<211> 237

<212> DNA

<213> Homo sapiens

<400> 752

agcaagactt gctgcctaaa ggagcccacc attttacttt tcacatttaa tctgccacgt 60

tgaatcaatt ggaataaaac ctgactcgca ggtgactgga caggaaatcc caaagttcca 120

ccatttctat gcttaatttt aacgtccccc cgcttttttt tttgtagaaa ataaaaacaa 180

gaaaatcggt ccaatgtaag atgtttgtta tagaaacttt aggcaataca ggtgtgt 237

<210> 753

<211> 292

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (54)..(55)

<223> n is a, c, g, or t

<400> 753

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tttttgtgtg aatatttaaat ggtgctccat gactgttgag ttttaaaaac ctcgttaaat 120

tttgccaaat cagttgcccc caaaagggaat tatgcttttc cttatTTTTT tttctaaaat 180

gctatttatc tctaaggaaa aaaaaaaaaag actattactc atttaacatt gtttaagcag 240

gttgagctag ctgtgaaaat agcttttgtg agccttctaa ttcctaaacg tc 292

<210> 754

<211> 243

<212> DNA

<213> Homo sapiens

<400> 754

gttaacactg tggatcacct tcggccaagg gacacgactg gagattaaac gtaagtaatt 60

tttcactatt gtcttctgaa atttgggtct gatggccagt attgactttt agaggcttaa 120

ataggagttt ggtaaagatt ggtaaatgag ggcatttaag atttgccatg ggttgcaaaa 180

gttaaactca gcttcaaaaa tggatttgga gaaaaaaga ttaaattgct cttaaactgaa 240

tga 243

<210> 755

<211> 120

<212> DNA

<213> Homo sapiens

<400> 755

tcattctcat ccattccagga tgtactaaaa cagtgtgttt aataaattgt aattattttg 60

tgtacagttc tatactgtta tctgtgtcca tttccaaaac ttgcacgtgt ccctgaattc 120

<210> 756

<211> 185

<212> DNA

<213> Homo sapiens

<400> 756

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gaattagagg acagtggcct accctaaata aagacatgag tgatgtataa agtctagtgt 120

caatttattc agaaaatatac aaaattattc tgggagctat gggtaaagt tgataggcac 180

aaaca 185

<210> 757

<211> 130

<212> DNA

<213> Homo sapiens

<400> 757

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taaccaggg ggaccttagc atgcctaagt gactaaacca ataaaaatgt tctggtctgg 120

cctgaaaaaa 130

<210> 758

<211> 86

<212> DNA

<213> Homo sapiens

<400> 758

aagcagacta cgagaaacac aaagtctacg cctgcgaagt caccatcag ggcctgagct 60

cgccccgtcac aaagagcttc aacagg 86

<210> 759

<211> 264

<212> DNA

<213> Homo sapiens

<400> 759

ggtacacaaa tctggttctc aatggtgagg tgggatcaga gatattctcc ctgttggttca 60

gaggaacaat aattcggatg tttctctcca caatgtcctc attaggatct tcggaagaac 120

ggatgaccta ggaagtaatc cgggcacact tacatttggt gtcaacaaga acaatccttt 180

catcttcttg ggctttcaca tgaacagcct taataaaaac cgccaggact cccagaaaa 240

gcaaataggt cttcatcttg accc 264

<210> 760

<211> 101

<212> DNA

<213> Homo sapiens

<400> 760

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gtcttagtgct caaaacttgc agctagaatt gagggaagag a 101

<210> 761

<211> 233

<212> DNA

<213> Homo sapiens

<400> 761

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atgaagacag agccccaccc tcagatgcac atgagctggc gggattgaaa gatgctgtct 120

tcgtactggg aaagggattt tcagccctca gaatcgctcc accttcgagc tctccccttc 180

tctgtattcc tagaaactga cacatgctga acatcacagc ttatttcctc att 233

<210> 762

<211> 256

<212> DNA

<213> Homo sapiens

<400> 762

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cccatcttcc aagggtataa ggaatctttc tgctttgggg ttatcagaa ttctcagaat 120

ctcaaataac taaaagggtat gcaatcaaat ctgcttttta aagaatgctc ttactttcat 180

ggacttccac tgccatcctc ccaaggggcc caaattcttt cagtggctac ctacatacaa 240

ttccaaacac atacag 256

<210> 763

<211> 259

<212> DNA

<213> Homo sapiens

<400> 763

acagaagcca ttgcctccct tgtttacctt ggttccacct ccacaaaac ccaacagacc 60

accaaagtgt gacctgacga aattccacaa aacctcttct ggaaacagta ctagcaaagg 120

ccagacgtct tactcaacaa cttccctgcc accacctcca ccatcccatc cggccagcca 180

accaccattg ccagcatctc acccatcaca accaccagtc ccaagcctac ctcccagaaa 240

cattaaacct ccgtttgac

259

<210> 764

<211> 114

<212> DNA

<213> Homo sapiens

<400> 764

ggacctgtac accacgagca gccagctgac cctgccggcc acacagtgcc tagccggcaa 60

gtccgtgaca tgccacgtga agcactacac gaatcccagc caggatgtga ctgt 114

<210> 765

<211> 265

<212> DNA

<213> Homo sapiens

<400> 765

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attattaaaa acaccaccaa agaaaataaa tatatcctac ttgaaattta ctctatggac 120

ttaccactg ctagaataaa tgtatcaaat cttatttgta aattctcaat tttgatatat 180

atatgtatat atgcatatac atatccacac ttgtctgcaa gaatattgat taaaattgct 240

aaatttgtac ttgttcacca gaaaa 265

<210> 766

<211> 198

<212> DNA

<213> Homo sapiens

<400> 766

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gcccagagga ctgttaataa cgatgatcca tgtgttttac tctaaagtgc taaatatggg 120

agtttccttt ttttactctt tgtcactgat gacacaacag aaaagaaact gtagaccttg 180

ggacaatcaa catttaaa 198

<210> 767

<211> 162

<212> DNA

<213> Homo sapiens

<400> 767

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tctcttagga atacagtttc tagcattaaa caaataaaca aggggagaaa ataaaactca 120

aggagtgaaa atcaggaggt gtaataaaat gttcctcgca tt 162

<210> 768

<211> 256

<212> DNA

<213> Homo sapiens

<400> 768

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cgccctgttt ctctcaggaa gccttgctct tttccatcat gcctctaatac acagcttata 120

atcggatatt tatttctgtg tctacagtct tgccctgccca gactgtatgc cccatgtggg 180

caggcgctca tgattgtttc tgattgtttc acgcatgctg ctaaccaga gcctgggccc 240

aaagctagtt agtact 256

<210> 769

<211> 294

<212> DNA

<213> Homo sapiens

<400> 769

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tttgttttgc tctattgttt agtttttact tgggtgcaat gtgtacgtca aaagttttta 120

ttttgatatt tgaaagagac caaatcaggc ccagaccgcc tctctggaag gtgtttagg 180

ccattcaaaa cgcctccgga gtgtcgcaaa ccaagtgcgg aggggccctg aggttgtact 240

gtaaacatca tagtgacttg tcttttcaaa tatattccca ctattttcgc agaa 294

<210> 770

<211> 221

<212> DNA

<213> Homo sapiens

<400> 770

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ggcagcaggg gaacatcttc tcatgctccg tgatgcatga ggctctgcac aaccgcttca 120

cgcagaagag cctctccctg tctccgggta aatgagtgcg acggccggca agcccccgct 180

ccccgggctc tcgggggtcgc gcgaggatgc ttggcacgta c 221

<210> 771

<211> 239

<212> DNA

<213> Homo sapiens

<400> 771

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tcagtttcct catctgcaga ataatgactg acttgtctaa ttcgtaggga tgtgaggttc 180

tgctgaggaa atgggtatga atgtgccttg aacacaaagc tctgtcaata agtgataca 239

<210> 772

<211> 181

<212> DNA

<213> Homo sapiens

<400> 772

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gataaatcaa gtgattgggtg tgcctgggtc tcactacaag cagcctatct gcttaagaga 120

ctctggagtt tcttatgtgc cctgggtggac acttgcccac catcctgtga gtaaaagtga 180

a 181

<210> 773

<211> 228

<212> DNA

<213> Homo sapiens

<400> 773

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tcaggggagg ggaggggtgac agtggccgcc caaggccac gagcttggtc tttgttcttt 120

gtcacaggga ctgaaaacct ctcctcatgt tctgctttcg attcgtaaag agagcaacat 180

tttaccacac cacagataaa gttttccctt gaggaacaa cagcttta 228

<210> 774

<211> 136

<212> DNA

<213> Homo sapiens

<400> 774

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acgtctgcta acttggagcc ccagtgccaa gcacagtgcc tgcattgtatt tatccaataa 120

atgtgaaatt ctgtcc 136

<210> 775

<211> 193

<212> DNA

<213> Homo sapiens

<400> 775

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aaaaaaatcc cccagcactt cccacagtgc ctattgatac ttggggaggg tgcttggcac 120

ttattgaata tatgatcggc catcaaggga agaactattg tgctcagaga cactgttgat 180

aaaaactcag gca 193

<210> 776

<211> 175

<212> DNA

<213> Homo sapiens

<400> 776

aaattttaatt ttctacgcct ctggggatat ctgctcagcc aatggaaaat ctgggttcaa 60

ccagcccctg ccatttctta agactttctg ctgcactcac aggatcctga gctgcactta 120

cctgtgagag tcttcaaact tttaaactt gccagtcagg acttttgcta ttgca 175

<210> 777

<211> 183

<212> DNA

<213> Homo sapiens

<400> 777

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gtttccaaaa aatggtactc cacatacttc agtgagggta agtatTTTcc tgttgtcaag 120

aatagcattg taaaagcatt ttgtaataat aaagaatagc tttaatgata tgcttgtaac 180

taa 183

pctgb2013053202-seq1.txt

<210> 778

<211> 235

<212> DNA

<213> Homo sapiens

<400> 778

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gcccatcaaa tcctgagtgt cagtttggtg tccctattgt agatgaaata gtgatgtagc 120

aaaaacctag taaattctga atgcttttcc acgtagactt atctggaatg tgaacacaac 180

tctttgggta atagtaaag cttaactgta gtcctgagta ggtgcatttc tgtct 235

<210> 779

<211> 154

<212> DNA

<213> Homo sapiens

<400> 779

agtatatttt ctatcttctg gtgacttgag cttgagctct gacagggcatg ggcctctccg 60

accttcatca ctattcttag gataatgctg gcgggcagag atgatcaatc atcatattaa 120

atcataatga gcttataatc ctcccactgg aaaa

154

<210> 780

<211> 280

<212> DNA

<213> Homo sapiens

<400> 780

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gcatgggggtg ttggcagggg tcaaaaagct tatttctttt aatctcttac tcaacgaaca 120

catcttctga tgatttccca aaattaatga gaatgagatg agtagagtaa gatttggggtg 180

ggatgggtag gatgaagtat attgcccaac tctatgtttc ttgattcta acacaattaa 240

ttaagtgaca tgatttttac taatgtatta ctgagactag 280

<210> 781

<211> 206

<212> DNA

<213> Homo sapiens

<400> 781

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ataaaattat tgtatagaca tctgcttctt aaacagattg tgagttcttt gagaaacagc 120

gtggatttta cttatctgtg tattcacaga gcttagcaca gtgcctggta atgagcaagc 180

atacttgcca ttacttttcc ttccca 206

<210> 782

<211> 247

<212> DNA

<213> Homo sapiens

<400> 782

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tagactgtgt gcgtgtgcgt tgatgggcac tcaagagtcc cgtgagtcac ccagccctgc 120

ctttcccctg cgccccatc ctctcacgtc ccgccctgcc tccacttggg gaccctgcct 180

cgtgtcgtct ttatctgcct attactcagc ctaaggaaac aagtacactc cacacatgca 240

taaagga 247

<210> 783

<211> 190

<212> DNA

<213> Homo sapiens

<400> 783

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cttgagtgtg ttacctcctt tccaagctcc tcgtgataat gcagacttcc tggagtacaa 120

acacaggatt tgtaattcct tactgtaacg gagtttagag ccagggctga tgctttggtg 180

tggccagcac 190

<210> 784

<211> 165

<212> DNA

<213> Homo sapiens

<400> 784

cccatgaaa agaccgagcc ttgtatgtat gttatggata cataaaatgc acgcaagcca 60

ttatctctcc atgggaagct aagttataaa aataggtgct tgggtgtacaa aactttttat 120

atcaaaaggc tttgccattt ctatatgagt gggtttactg gtaaa 165

<210> 785

<211> 260

<212> DNA

<213> Homo sapiens

<400> 785

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ctggaggggg aagagctctc aaccagagg gatctgacca ggaaggttca cccccctcc 120

accaggaag cccctgcaga cagtatgtgt ttaggcttt gctggccaaa tggctctctgc 180

cgtgactact cagctctgcc attgtggctg cagagtgacc atagaccttc tgaaagtgaa 240

tgagtatgac tgtgttccaa 260

<210> 786

<211> 197

<212> DNA

<213> Homo sapiens

<400> 786

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pctgb2013053202-seq1.txt

atgtttattc cctgtcagcg gaggaggagaa tgctattcat caataaacca aagccaatag 120

ctggagaatt gagatctggg tgaaagggt ttatggttta catgctgtac taccctgagg 180

aattgagaga tattgct 197

<210> 787

<211> 187

<212> DNA

<213> Homo sapiens

<400> 787

aaaacatctg gttcaattac gctgaactct gactacatgt gggccagtaa taatatgaat 60

tggacttaag aataaacctt gtgtttaatc tctttttttc cttaaaattt taatgtgagt 120

tttctgttac gcaaattatc catgttagca catttgaac aaatgtataa atgtactttc 180

tgaataa 187

<210> 788

<211> 228

<212> DNA

<213> Homo sapiens

<400> 788

gggatgacat gcactcagct cttggctcca ctgggatggg aggagaggac aagggaatg 60

tcaggggagg ggaggggtgac agtggccgcc caaggccac gagcttggtt tttgttcttt 120

gtcacaggga ctgaaaacct ctcctcatgt tctgctttcg attcgtaag agagcaacat 180

tttaccacac cacagataaa gttttccctt gaggaacaa cagcttta 228

<210> 789

<211> 213

<212> DNA

<213> Homo sapiens

<400> 789

actctccgga ttgaccaagt tcctcctggg ctccattggg tctgccattg cggctgtcat 60

tgcgagggtt tactagctcc ctgcccctcg ccctgcagag aagagaacca tgccagggga 120

gaaggcacc agccatcctg acccagcgag gagccaacta tcccaaatat acctgggggtg 180

aaatatacca aattctgcat ctccagagga aaa 213

pctgb2013053202-seq1.txt

<210> 790

<211> 104

<212> DNA

<213> Homo sapiens

<400> 790

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cgtgtcttcc actttgcata tgagccgtga actgtgcata gtgc 104

<210> 791

<211> 132

<212> DNA

<213> Homo sapiens

<400> 791

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gctctattca atacttctcc tctcagatga tagtaaagat caaaagaatt cgaaggaggt 120

tggtaaacgc tg 132

<210> 792

<211> 281

<212> DNA

<213> Homo sapiens

<400> 792

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gaatgttgctg ctgagctgtg cagcctgttc ctgcatctgt tgttcctgca ttttctgttg 120

ctctgccagc caatcttggt tggctatctc catttaactc acttggtcct gatggagtct 180

ctccctctcc tgcattcatt gctcgttctg ctttgaatc gccgccaacc tttagcgttc 240

agccttttca gcttctgctt tcacttgtgc ctctgaggag a 281

<210> 793

<211> 239

<212> DNA

<213> Homo sapiens

<400> 793

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cccaggctcc cctcacccca gcgggtaatg agcccttaat cgctgcctct aggggagctg 180

attgtagcag cctcgttagt gtcaccccct cctccctgat ctgtcagggc cacttagtg 239

<210> 794

<211> 174

<212> DNA

<213> Homo sapiens

<400> 794

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cacctcacc cactgtggct gatttggaat tttgtgcccc catgtaagca ccccttcatt 120

tggcattccc cacttgagaa ttaccctttt gccccgaaca tgtttttctt ctcc 174

<210> 795

<211> 270

<212> DNA

<213> Homo sapiens

<400> 795

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pctgb2013053202-seq1.txt

gaaacagact gcctgaattg agaattttga tttcttaaag tgtgtttctt tctaaattgc 120

tgttccttaa tttgattaat ttaattcatg tattatgatt aaatctgagg cagatgagct 180

tacaagtatt gaaataatta ctaattaatc acaaattgga agttatgcat gatgtaaaaa 240

atacaaacat tctaattaaa ggctttgcaa 270

<210> 796

<211> 276

<212> DNA

<213> Homo sapiens

<400> 796

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ctttattgtg gcatctgttc gaggtttgct tcctctttaa gtctgtttct tcattagcaa 120

tcatatcagt tttaatgcta ctactaaca tgaacagtaa caataatatc cccctcaatt 180

aatagagtgc tttctatgtg caaggcactt ttcacgtgtc acctatttta acctttccaa 240

ccacataaat aaaaaaggcc attattagtt gaatct 276

<210> 797

<211> 264

<212> DNA

<213> Homo sapiens

<400> 797

taactttttc tcaaagtcac tgatgtttgt tcctgttaaa tgtatagcat tgtaatgaga 60

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aaaaacctag taaattctga atgcttttcc acgtagactt atctggaatg tgaacacaac 180

tctttggtta atagttaaag cttaactgta gtcctgagta ggtgcatttc tgtctgtctc 240

aataaatttt actttgtctg caaa 264

<210> 798

<211> 275

<212> DNA

<213> Homo sapiens

<400> 798

tattccatct acttttctat cgccgtcccc ttttgcagcc ctctctgggg atggactggg 60

taaatgttga cagaggccct gccccgttca cagatcctgg ccctgagcca gccctgtgct 120

pctgb2013053202-seq1.txt

cctccctccc ccaacactcc ctaccaaccc cctaatacccc tactccctcc accccccctc 180

cactgtaggc cactggatgg tcatttgcat ctccgtaaata gtgctctgct cctcagctga 240

gagagaaaaa aataaaactgt atttggctgc aagaa 275

<210> 799

<211> 210

<212> DNA

<213> Homo sapiens

<400> 799

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cgttcccctg ctgccacctg ctcttgtcca cggtgagctt gctatagagg aagaaggagc 120

cgtcggagtc cagcacggga ggcgtggtct tgtagttggt ctccggctgc ccattgctct 180

cccactccac ggcgatgtcg ctgggataga 210

<210> 800

<211> 235

<212> DNA

<213> Homo sapiens

<400> 800

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aaattttaatt ttctacgcct ctggggatat ctgctcagcc aatggaaaat ctgggttcaa 120

ccagcccctg ccatttctta agactttctg ctccactcac aggatcctga gctgcactta 180

cctgtgagag tcttcaaact tttaaaccct gccagtcagg acttttgcta ttgca 235

<210> 801

<211> 162

<212> DNA

<213> Homo sapiens

<400> 801

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taagaaattg ccatttgaaa caatccattt tgtaactgaa ctttatgaaa tatatgtatt 120

tcatggtacg tattctctag cacagtctga gcaattaaat ag 162

<210> 802

pctgb2013053202-seq1.txt

<211> 249

<212> DNA

<213> Homo sapiens

<400> 802

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gtttgttttc catgtcatta cccccagggg ataccgaatg tgtgggtaga aatttctctg 120

tagattaa atcagatatt tacatggatt caacaaagga gcgtcacttg gatTTTTgtt 180

ttcatccatg aatgtagctg cttctgtgta aaatgccatt ttgctattaa aaatcaattc 240

acgctggaa 249

<210> 803

<211> 200

<212> DNA

<213> Homo sapiens

<400> 803

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ttgttgggag atgacactgt cagtcagccc atgatgtctg ttcacacgag atgctTTTT 120

aatagaattg accaatgttt tgctgccact gattaaagta ttatttatac taattgttgc 180

ttgtagtttt gatgtaattc 200

<210> 804

<211> 150

<212> DNA

<213> Homo sapiens

<400> 804

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gcttctagag cttagcatat ctgattgttg tcaggccata ttatcaatgt ttactttttt 120

ggtactataa aagctttctg ccaccctaa 150

<210> 805

<211> 142

<212> DNA

<213> Homo sapiens

<400> 805

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agtgtagaaa gacctgagaa aacgagcctg tttcagagga acatcgtcac aacgaatact 120

tctggaagct taacaaaact aa 142

<210> 806

<211> 224

<212> DNA

<213> Homo sapiens

<400> 806

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tatagtatatt tttttttgtc attttctcca tcagcaacca gggagactgc acctgatgga 180

aaagatatat gactgcttca tgacattcct aaactatctt tttt 224

<210> 807

<211> 176

<212> DNA

<213> Homo sapiens

<400> 807

pctgb2013053202-seq1.txt

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gttggatttg taaggcactt tatccctttt gtctcatggt tcatcgtaaa tggcataggc 120

agagatgata cctaattctg catttgattg tcactttttg tacctgcatt aattta 176

<210> 808

<211> 250

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (221)..(221)

<223> n is a, c, g, or t

<400> 808

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tagtgagggt agtgtggcta agaggaaatg gatccagatg ggcttgatgg ggagcagatg 120

ggcaggcacg atggcagggg tgcacggct cactggggct gcatctgagg taaatggaaa 180

taaaggaggt gaggaaatga ggaagagaag gaagtggcgg nactggctgt ggagttttgt 240

gggagccttc 250

<210> 809

<211> 178

<212> DNA

<213> Homo sapiens

<400> 809

taccagaata ggagttttcc tctgtggacc tgaagccttg gctgaaaccc tgagtaaaca 60

aagcatctcc aactctgagt ctggccctcg gggagtgcatt ttcattttca acaaggaaaa 120

cttctaactt gtctcttcca tgaggaaata aatgtggggtt gtgctgccaa atgctcaa 178

<210> 810

<211> 229

<212> DNA

<213> Homo sapiens

<220>

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<222> (48)..(48)

<223> n is a, c, g, or t

<400> 810

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ggaaatgata atgtaggcca cacgtattac tggagaaaaa tgtgctcccg agactttcca 120

gagcagcaga gctgggacta ggcaggtgag gcagctacgt gcaagtgtag ccctgagaat 180

gagcacctct ttaaagaatg taccttgcgt tagttctgtg cctgttttaa 229

<210> 811

<211> 278

<212> DNA

<213> Homo sapiens

<220>

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<222> (204)..(204)

<223> n is a, c, g, or t

<220>

<221> misc_feature

<222> (230)..(230)

<223> n is a, c, g, or t

<220>

<221> misc_feature

<222> (234)..(234)

<223> n is a, c, g, or t

<400> 811

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tggcgtgggc ctagtttatg cctgtttcag catgattggt gagtaccctg tttcatcctt 120

agcattttct tgattttggt gttaaataat gtataccctt atttccattg aatctgtgct 180

tccaccccc caactgaagt tgtnttcct ttgcttggcc acccttacan cctnttgat 240

ggtgtatcct acagtgtgaag cactaaactg aagaggca 278

<210> 812

<211> 243

<212> DNA

<213> Homo sapiens

<400> 812

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pctgb2013053202-seq1.txt

ggtagacttg actctgcttt atccgggaaa gcttttaaaa ctctgagcca gttaactttg 120

agtaagcata aaacatactg tattggtggtt tgtattttttc atgccacaat attaaaatgg 180

aatttttaa at gtagattatt ataatctata aaagataagt atgcatgtat taggatactg 240

gaa 243

<210> 813

<211> 151

<212> DNA

<213> Homo sapiens

<400> 813

aaatttgtaa atgggattga gtccctaaaa cctggaaaaa ctgacatggg ctagctatatt 60

attcactcat cgagttactt attccttcgt aaaaaaaaaa aaaaaaaaaat catttgagat 120

gataaaaaatg gtaggggtata gtttaagatg a 151

<210> 814

<211> 84

<212> DNA

<213> Homo sapiens

<400> 814

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taaaccacac tatcacctcg gccg 84

<210> 815

<211> 252

<212> DNA

<213> Homo sapiens

<400> 815

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cttgcaaatt tagcacttgg aacatttaaa gaaaggtcta tgctgtcata tggggtttat 120

tgggaactat cctcctggcc ccaccctgcc ctttcttttt ggttttgaca tcattcattt 180

ccacctggga atttctgggtg ccatgccaga aagaatgagg aacctgtatt cctcttcttc 240

gtgataatat aa 252

<210> 816

pctgb2013053202-seq1.txt

<211> 272

<212> DNA

<213> Homo sapiens

<400> 816

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tcagctgccc ttctggcgag tacatgcaca ggattgtaaa tgagaaatgc agtcatatatt 120

ccagtctgcc tctatgatga tgttaaatta ttgctgttta gctgtgaaca agggatgtac 180

cactggagga atagagtatc cttttgtaca ctttttgaaa tgcttcttct gtagtgatag 240

aacaaataaa tgcaacgaat actctgtcaa aa 272

<210> 817

<211> 185

<212> DNA

<213> Homo sapiens

<400> 817

gccacaagct gtccagtcta atcgacagga ttccgattcc tgaacagtgt cattcgaatc 60

agaatgtcag agctgagtct gctgttctga ctttaaggaa aacttgactc agtctcttga 120

tggctggaga atgcacatcc tagctgtcac tggggctaca ggcaggtcag tgagcacgct 180

aaaat 185

<210> 818

<211> 256

<212> DNA

<213> Homo sapiens

<400> 818

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cctacgggga catcgtgatg acccagtctc cagactccct ggctgtgtct ctgggcgaga 120

gggccaccat caagtgaag tccagccaga gtattttata taggtccaac aacaagaact 180

acttagcttg gtaccagcag aaagcaggac agcctcctaa attgttcatt tactgggcat 240

ctacccggga atccgg 256

<210> 819

<211> 146

<212> DNA

<213> Homo sapiens

<400> 819

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cacgtgcaat aaagtcctcg tgcctgctgc tcacagcccc cgagagcccc tcctcctgga 120

gaataaaacc tttggcagct gccctt 146

<210> 820

<211> 122

<212> DNA

<213> Homo sapiens

<400> 820

ccagacgtca accaggaaca tgtaacttgg agagggacga agaaagggtc tgataaacac 60

agaggtttta aacagtcctt accattggcc tgcattcatga caaagttaca aattcaagga 120

ga 122

<210> 821

<211> 225

<212> DNA

<213> Homo sapiens

<400> 821

gaagagtctg ttgccgagct ggactggaaa gcccctaaat cccaggattt cttcttcttt 60

tcttcttcca gtccttctc tctgacctc tgcaatgcac ccctgtatac ctggctctgg 120

cagtagacaa tctgttccat ctggaagtgg aggcggatca gcttctcacc ttctctctct 180

tgctctgctc taatgtcttc aattttggac ttggcggttc tgtgg 225

<210> 822

<211> 274

<212> DNA

<213> Homo sapiens

<400> 822

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gcacctggag gaggtgcctc ttgacctcat cacctgactc cacaagaaac aagggcagct 120

cctcatcact gggcttcacc actttcaggg taaggtggat ggtcttctct ttgtcaatgc 180

cataagatga gaggttctc cgtggcttta agatcttgga gccagcaaa agaacctggt 240

cctgcacagg aaccttggtg gtagaccgga ccca 274

<210> 823
<211> 256
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (201)..(201)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (206)..(206)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (221)..(221)
<223> n is a, c, g, or t

<400> 823
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60

pctgb2013053202-seq1.txt

ttttacaatt taataatgca tacttttaaaa ttcatagataa atcatggaac cccactatac 120

tcactaattc aactattgat ttctttttga gcaactgact ttatgattta tcctttaaag 180

taaggaagta taccagaagg ncaaanggat aaatccaccc ntaaatacta gagtctaagt 240

tattttcctg aaaagg 256

<210> 824

<211> 143

<212> DNA

<213> Homo sapiens

<400> 824

gttgtcccca cagtagacac atatgatggc cgaggtgata gtgtggttta tggactgagg 60

tcaaaatcta agaagtttcg cagacctgac atccagtacc ctgatgctac agacgaggac 120

atcacctcac acatggaaag cga 143

<210> 825

<211> 199

<212> DNA

<213> Homo sapiens

pctgb2013053202-seq1.txt

<400> 825

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gcccagagga ctgttaataa cgatgatcca tgtgttttac tctaaagtgc taaatatggg 120

agtttccttt tttttactct ttgtcactga tgacacaaca gaaaagaaac tgtagacctt 180

gggacaatca acatttaaa 199

<210> 826

<211> 224

<212> DNA

<213> Homo sapiens

<400> 826

ccttgacccc agtacgaagt ctatgccctg aatccccaga gtagcccttc ctggtgccca 60

actggcctgg ggacaaacag cgtccactac atctaggact gccggctaag tggacacact 120

tcttgacctc ctaccaggaa ctttggtaaa agctagcttt ggggaagggg ttgggtgtaa 180

atatgagagg gtggaggagg accagctggt agcaataaac atgg 224

<210> 827

<211> 263

<212> DNA

<213> Homo sapiens

<400> 827

gagatcactt ggtaactggt ttcattgtgta tccaaaaatc agcatttgga ttttaagcttt 60

ctgaatttgg tagtttaaga aacagattta gtttttcaat ggttttaact catgtgaaat 120

aatgattttc caccagctct gatgcaaaga gatataattt taatgaacga tttatccagc 180

agtgtgttcc aggggttgcc tctccttatt tacggggatt actttgtaca tgcagataag 240

ttttcgcaaa cctatttcca ttt 263

<210> 828

<211> 252

<212> DNA

<213> Homo sapiens

<400> 828

cactgtgtat gactgaaatt tctggaataa ctgtaaatgg ttatgttaat ggaataaaac 60

acaaatgttg aaaaatgtaa aatatatata catagattca aatccttata tatgtatgct 120

pctgb2013053202-seq1.txt

tgttttgtgt acaggatfff gttttttctt ttttaagtaca ggttcctagt gttttactat 180

aactgtcact atgtatgtaa ctgacatata taaatagtca tttataaatg accgtattat 240

aacatttgaa aa 252

<210> 829

<211> 226

<212> DNA

<213> Homo sapiens

<400> 829

agatccactg aacatctgtg tctttatfff gctgcttgta tttattgtag tcaaattgctt 60

tacatcagaa tgatgaaaat aggcttgcca ctttctctta ttttaattcc atggtagtca 120

atgaactggc tgccacttta atataactga aaattcattt tgagaccaag caggatcaag 180

tttgtagaat aaacactggg ttcctagcca tcctctgaaa acagta 226

<210> 830

<211> 100

<212> DNA

<213> Homo sapiens

<400> 830

tagaattacc tatcacattt cccaatcttg actattcaga atgctgttta tttagtgatg 60

aggattagca cttgattgaa gattctttta aaatactatc 100

<210> 831

<211> 239

<212> DNA

<213> Homo sapiens

<400> 831

ttctttgagg gctcgcatcc aaaagaatat aacactccaa gcatgaaaga gtggcagcaa 60

atttcatcac tgtatacttt caatccgaag ggccagtact acagcatgtt gcacaaatat 120

gtcaacagaa aagagaagac tcacagtatc aggtctactg aaggagatac ggtgattcct 180

gttcttggct ttgtagattc atctggtata aacagcactc ctgagttatg accttttga 239

<210> 832

<211> 292

<212> DNA

<213> Homo sapiens

<400> 832

catcttagtg cctttatctg tctttatgtc ttggggttgg ggtaggtaga taccaaatga 60

aacactttca ggaccttcct tcctcttgca gttgttcttt aatctccttt actagaggag 120

ataaatatatt tgcatataat gaagaaattt ttctagtata taacgcaggc cttttatttt 180

ctaaaatgat gatagtataa aaatgttagg ataacagaat gatttttagat tttccagaga 240

atattataaa gtgctttagg tatgaaaata aatcatcttt gtctgattaa aa 292

<210> 833

<211> 207

<212> DNA

<213> Homo sapiens

<400> 833

atatttccgg tcatctctgg tggtagagagg ctggtgttct gttttgagga tatcccttta 60

aatctcccaa atgactgtct ctatcttcac gagtgtgact tgaggtgttg ggatgggtga 120

gggagcttct ctaaagagga aagtgagtgg attaaccctt gcttctcttc ttgttccttg 180

ttatcattcc tccccaacat aataata

207

<210> 834

<211> 183

<212> DNA

<213> Homo sapiens

<400> 834

aaaatctgat tttgcagcga tcacttttaa accctgtagt gatgtaagac taaaatataa 60

ttgctaagat tttgttggtt aatgtaaaga tatgactttt ctgcactgta ctctcttcat 120

aggattgtaa aggtgttcta atccaattgc atgatgtagt aagcctctta aatatgtgtg 180

tta 183

<210> 835

<211> 151

<212> DNA

<213> Homo sapiens

<400> 835

gtcttttgcg aaagggattg caggttcaga aggcatctta ccatggctgg ggaattgtct 60

ggtggtgggg ggcaggggac agaggccatg aaggagcaag ttttgtatTT gtgacctcag 120

ctttgggaat aaaggatctt ttgaaggcca a 151

<210> 836

<211> 233

<212> DNA

<213> Homo sapiens

<400> 836

ttggcttcct tcctggcaag gaccaggcag tggggaagga ggaggtcctc cgtggtacat 60

actgggtcag gcactagcat ggaggagggt cacagagtgg ggcacgtgag gacccatgga 120

accgtcctgg tgcccaggcc ctcaacaagta ccaaagccag caccaaagga gtcagggaag 180

gggttggctg agtcaaggga cccagaggg caccaggaat aaaatcttct tga 233

<210> 837

<211> 211

<212> DNA

<213> Homo sapiens

<400> 837

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agagttctag taggctgcta tggaatttct ggcatgaaaa ttcttgaccc ctcacacttt 120

acccctgta cagcacaggc ataccatgga gatattacag gatcagttcc agaccacat 180

aataaagtgg atatcgcaat aaagtgagtc a 211

<210> 838

<211> 270

<212> DNA

<213> Homo sapiens

<400> 838

ctttaaaggt gggtttttgc tgtgataaat gaatacggta ctctgaagga gaaaaaagtt 60

tctcaaatga gcttaaaactg caagtgattt aaaaattaga gaatataatt cttaaagcta 120

ttgaaagttt caaccagaaa acctcaagtg aattttgtat gtaaataaaa tcttgaatgt 180

aagttctgtg attctttaag caaacaatta gctgaaaact tggtattggt gtagtttatg 240

tagtaagtga cttggcaccc atcagaaaat 270

<210> 839

<211> 253

<212> DNA

<213> Homo sapiens

<400> 839

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caaaagaaag ggcttatagt gttagtattg gagcactttg aagatagata ttttcagaaa 120

agatgtagga tttaaaagtt aaattttaaa ttttagaaaa agatatgatg gcaattggaa 180

atagtcacaa tgaagttctt catccagtag gtgtttaaca gtgttatttt gccactggta 240

atgtgtaaac tgt 253

<210> 840

<211> 194

<212> DNA

<213> Homo sapiens

<400> 840

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tccagggcca gatgagcaga agctctcgat ggacaatgaa cggccttgct gggggccgcc 120

ctgtaccctc tttcaccttt ccctaaagac cctaaatctg aggaatcaac agggcagcag 180

atctgtatat tttt 194

<210> 841

<211> 217

<212> DNA

<213> Homo sapiens

<400> 841

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taagccaagg gacgttgacc tggactgaag ttcgcattga actctacaac attctgtggg 120

atatattgtt caaaaagata ttgttgTTTT ccctgattta gcaagcaagt aattttctcc 180

caagctgatt ttattcaata tggttacgtt ggttaaa 217

<210> 842

<211> 180

<212> DNA

<213> Homo sapiens

<400> 842

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ccaagctctc gtaaccaggt tctacagga ggctgcaccc actccatgtt acttctgctt 120

cgctttcccc taccacccc ccccccata aagacaaacc aatcaaccac gacaaaggaa 180

<210> 843

<211> 262

<212> DNA

<213> Homo sapiens

<400> 843

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ttgtcaggac aattaggatt gtaatgctaa tgcaaaggca gcaattcaaa gatcttctag 120

tgcctcatga ataaagttga gatttaaaat ttgtaacatt gatggaacag ctgggaggtt 180

agaccaatca ttaaggaatg tatgccatag ctttctttgc taccataaac attttgagg 240

tgcattctgct atgtgacatg gt 262

<210> 844

<211> 274

<212> DNA

<213> Homo sapiens

<400> 844

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tctcagcctt agccctgtgc cccctgaaac agctgccacc atcactcgca agagaatccc 120

ctccatcttt gggagggggtt gatgccagac atcaccaggt tgtagaagtt gacaggcagt 180

gccatggggg caacagccaa aatagggggg taatgatgta ggggccaagc agtgcccagc 240

tgggggtcaa taaagttacc cttgtacttg caaa 274

<210> 845

<211> 289

<212> DNA

<213> Homo sapiens

<400> 845

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tcatagaaag ggccttgaca tcagttcctt tgtgtgtact cactgaagcc tgcgttggtc 120

pctgb2013053202-seq1.txt

cagagcggag gctgtgtgcc tgggggagtt ttcctctata catctctccc caaccctagg 180

ttccctgttc ttcctccagc tgcaccagag caacctctca ctcccatgc cacgttccac 240

agttgccacc acctctgtgg cattgaaatg agcacctcca ttaaagtct 289

<210> 846

<211> 255

<212> DNA

<213> Homo sapiens

<400> 846

aaccagccgt attttacatg aagctgtata attaattgtc attatTTTTg ttagcaaaga 60

ttaaatgtgt cattggaagc catccctttt ttacatttc atacaacaga aaccagaaaa 120

gcaatactgt ttccatttta aggatatgat taatattatt aatataataa tgatgatgat 180

gatgatgaaa actaaggatt tttcaagaga tctttctttc caaacattt ctggacagta 240

cctgattgta ttttt 255

<210> 847

<211> 166

<212> DNA

<213> Homo sapiens

<400> 847

attcctgtca ttaccattg taacagagcc acaaactaat actatgcaat gttttaccaa 60

taatgcaata caaaagacct caaaatacct gtgcatttct tgtaggaaaa caacaaaagg 120

taattatgtg taattatact agaagttttg taatctgtat cttatc 166

<210> 848

<211> 198

<212> DNA

<213> Homo sapiens

<400> 848

gcactggcga ggagagggcg ctctctctg cacacctact agtcaccaga gactttaggg 60

ggtagggattc cactcgtgtg tttctatttt ttgaaaagca gacattttta aaaatgggtca 120

cgtttggtgc ttctcagatt tctgaggaaa ttgctttgta ttgtatatta caatgatcac 180

cgactgaaaa tattgttt 198

<210> 849

<211> 187

<212> DNA

<213> Homo sapiens

<400> 849

atccggagaa ttgcctctac ctggaccttt tgtctcacac agcagtaccc tgacctgctg 60

tgcaccttac attcctagag agcagaaata aaaagcatga ctatttccac catcaaatgc 120

tgtagaatgc ttggcactcc ctaaccaaata gctgtctcca taatgccact ggtgttaaga 180

tatatttt 187

<210> 850

<211> 93

<212> DNA

<213> Homo sapiens

<400> 850

atatcttggt ttctgccaat agatttttta aaatgtagtc agcaaaatgg gggtaggggaa 60

gcagagcatg tcctagttca atgttgactt ttt 93

pctgb2013053202-seq1.txt

<210> 851

<211> 257

<212> DNA

<213> Homo sapiens

<400> 851

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tctctagggt ctgagctctg gctttgcctt ggctttgccca gggctctgtg accaggaagg 120

aagtcagcat gcctctagag gcaaggaggg gaggaacact gcactcttaa gcttccgccg 180

tctcaacccc tcacaggagc ttactggcaa acatgaaaaa tcggcttacc attaaagttc 240

tcaatgcaac cataaaa 257

<210> 852

<211> 197

<212> DNA

<213> Homo sapiens

<400> 852

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aggcagcagg actgtcccct tgaaggagaa tcatcaggac cctggacctg atacggctcc 120

ccagtacacc ccacctcttc cttgtaaata tgatttatac ctaactgaat aaaaagctgt 180

tctgtcttcc cacccaa 197

<210> 853

<211> 151

<212> DNA

<213> Homo sapiens

<400> 853

ataaaaaacc aacaaaggat ctcacatttt cttaaaaagt gaagattgct gtatactatt 60

tattcaactt ataatttatg ttactccttg atctttgtct tttgtcatga caaagcattt 120

atttaataaa gttatgcatt cagttaaaaa a 151

<210> 854

<211> 273

<212> DNA

<213> Homo sapiens

<400> 854

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pctgb2013053202-seq1.txt

tcttcagtgg ggggccccct cttgggtccc ctcctctgcc atcacctgaa gacccccacg 120

ccaaacactg aatgtcacct gtgcctgccg cctcgggtcca ccttgcggcc cgtgtttgac 180

tcaactcaac tcctttaacg ctaatatattc cggcaaaatc ccatgcttgg gttttgtctt 240

taaccttgta acgcttgcaa tcccaataaa gca 273

<210> 855

<211> 284

<212> DNA

<213> Homo sapiens

<400> 855

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gaaatgctct cctttcccct gccccagac cttttatcca cttacctaga ttctacatat 120

tcttttaaatt tcatctcagg cctccctcaa ccccaccact tcttttataa ctagtccttt 180

actaatccaa cccatgatga gctcctcttc ctggcttctt actgaaaggt taccctgtaa 240

catgcaattt tgcatttgaa taaagcctgc tttttaagtg ttaa 284

pctgb2013053202-seq1.txt

<210> 856

<211> 245

<212> DNA

<213> Homo sapiens

<400> 856

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atagttaatg aaaacagcat ttttaaaaac cgaaatattg aaatgggtgta atgttgtacc 120

atttgactg tgagcaaagc ctaatacagt aaatatattg tgtttgctga caatcagccg 180

gcctataaat ctccttattt ttttcttgt ttttatagca taaagcttta gtttggcctg 240

aaaaaa 245

<210> 857

<211> 268

<212> DNA

<213> Homo sapiens

<400> 857

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cgagatcgag atgatgctca gtacagccac cttggaggaa actgggctcg gaacaagtga 180

acctgagact ggtggcttct agaagcagcc attaccaact gtaccttccc ttcttgctca 240

gccataaat atatcctctt tcactcag 268

<210> 858

<211> 251

<212> DNA

<213> Homo sapiens

<400> 858

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tgctatgatt tgtacttgct tgagtcccat gactgtttct cttcctctct ttcttccttt 120

tggaatagta atatccatcc tatgtttgtc ccactattgt attttggaag cacataactt 180

gtttggtttc acaggttcac agttaagaag gaattttgcc tctgaataaa tagaatcttg 240

agtctcatgc a 251

<210> 859

<211> 32

<212> DNA

<213> Homo sapiens

<400> 859

ctcagcccaa cttcttacc gaaagcatca ct

32

<210> 860

<211> 268

<212> DNA

<213> Homo sapiens

<400> 860

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60

gcacctcttc tggaaattga gtaaattttg cttttttttt tttactcagt tgcaacttac

120

gcttggcatc ttcagaatgc ttttctagca ttaagagatg taaatgataa aggaattatt

180

gtatgaaata ttacaaagcg tagactatgc attggtattc attataatat tttttgctgt

240

cataatcgcc tcataaagac aggtttca

268

<210> 861

<211> 259

<212> DNA

<213> Homo sapiens

<400> 861

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ttgctttaaa ataaccagc ttgctgcagg aggtgggtat tgtgtgtgtg ggaaggtggg 120

gaggctgcgg gaggaagaga tgaccaaga ttaggcagat gttgttaact gtggaagcag 180

ggtggtgagt gggggctcat gacattatgc tctctacttt gtgtacgtgt gaacatttcc 240

gtaataaaaag atgccttca 259

<210> 862

<211> 166

<212> DNA

<213> Homo sapiens

<400> 862

gatttttcaa ttgtggtaaa tagcaaataa caatcttgta ttctaacata atctgcagtt 60

gtctgtatgt gttttaacta ttacagtgcg tgtagggag aaattccctg aatttcttta 120

gttttgtatt caaacaatta tgccactcga tgcaacaaac ataata 166

<210> 863

<211> 158

<212> DNA

<213> Homo sapiens

<400> 863

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gggaatcctt gctgcactgt tgcagtcatt ctgaaaggac ctttcctgt acttaccttt 120

caacatgctt caatcttatc aacgctacat tttgtatt 158

<210> 864

<211> 88

<212> DNA

<213> Homo sapiens

<400> 864

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tctgaaagac tcagcctaata taaaggat 88

<210> 865

<211> 168

<212> DNA

<213> Homo sapiens

<400> 865

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aatttgatga atacccagtt ctcttctttt ctagagaaag atagttgcaa cctcacctcc 120

ctcactcaac actttgaata cttattgttt ggcaggtcat ccacacac 168

<210> 866

<211> 237

<212> DNA

<213> Homo sapiens

<400> 866

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ggtgtaattg gtttacggga attaaactgt tataaaaaca taaggtaaca ttcagaaatc 120

agagagcctc tgtttaaccc ttaaagacac aattaatgct tctaatactg taactactga 180

tctccctctt tctcctcagc tactctttcc ccaaacagta gcacctcctc tttactt 237

<210> 867

<211> 277

<212> DNA

<213> Homo sapiens

<400> 867

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atcttcattt ttcattttcc gggagatgta atatgtccta aaaatcacag tcgctagatt 120

gaaatcaacc ttaaaaatca tctagtccaa tgtctactcc cagtccacta cttgaatccc 180

ctgtgtcccc tcccagtagt cgtcttgaca acctccactg aaaggcaatt tctacactcc 240

atccacccca ccaccaaccc atggttcatg atctctt 277

<210> 868

<211> 280

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (55)..(63)

<223> n is a, c, g, or t

<400> 868

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nnngtgaaaa aaatgaagat aggcattttg tagacaatct ggaagttctg gaccggaatc 120

catgatgtag tcagggaaga aatgaccctg gtccagtaac ccaggcctc gagtgtgtgg 180

tgtatttttc tacataattg taatcattct atacatacaa attcatgtct tgaccatcat 240

attaatatatt ggtaagtttc tctctcttta gagactccac 280

<210> 869

<211> 89

<212> DNA

<213> Homo sapiens

<400> 869

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accatctgtg tatgtgtgat tgaggtgtt

89

<210> 870

<211> 274

<212> DNA

<213> Homo sapiens

<400> 870

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gagaagccca gtctgtccta tgtaaggac aaagccaggt ctaatggtac tgggtagggg 120

gcactgccaa gacaataagc taggctactg ggtccagcta ctactttggt gggattcagg 180

tgagtctcca tgcacttcac atgttaccca gtgttcttgt tacttccaag gagaaccaag 240

aatggctctg tcacactcga agccaggttt gatc 274

<210> 871

<211> 135

<212> DNA

<213> Homo sapiens

<400> 871

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gattttgaga actgacttcc cgccctgggt gaggattcag ctttcttact gtgccttcct 120

catgcacatg tgcct 135

<210> 872

<211> 221

<212> DNA

<213> Homo sapiens

<400> 872

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tataattcag aggttcaaaa tggaaatgac cttgctctaa tgaaactctg ttcccatcac 120

ataattgata ggcaatgttt ctcaccattt atatgatacg gactaaaaca aggaatggaa 180

ttgatattga acccttggca aaaataacat tcatccatag g 221

<210> 873

<211> 245

<212> DNA

<213> Homo sapiens

<400> 873

gctggtacca agctaagtag ttcttattgt tggagctgta taaaacactc tggctggact 60

tgcaattgat ggtggccctc tcgcccagag acacagccag ggagtctgga gactgggtca 120

tcacgatgtc cccgtaggca ccagagatcc agagcaacag agaaatgaag acctgggtct 180

gcaacaccat cttgctgccc ctgcctgcct gttgtagctc agttcacaat gcaaacggcc 240

cgttt 245

<210> 874

<211> 292

<212> DNA

<213> Homo sapiens

<400> 874

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ccatctgctc cccatcaagc ccatctggat ccatttcctc ttagccacac taccctcact 120

acacccatgt ttacagttta agacttcttc ttacacaggt cttgccctcc atcctgttct 180

acctttcctc ctctcttgct ctctaccttg cgtctttcaa acatgaagcc ctcatcccag 240

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cacccgacac cctgaccctc tccaaactct gggcatactc tctcccactg gg 292

<210> 875

<211> 292

<212> DNA

<213> Homo sapiens

<400> 875

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ctcttcttag tggaacttta ggtctctttt caagtctcct cagtcacaa tagttcctgg 180

ggaaaaacag agctggtaga cttgaagagg agcattgatg ttgggtggct tttgttcttt 240

cactgagaaa ttcggaatac atttgtctca ccctgatat tggttcctga tg 292

<210> 876

<211> 90

<212> DNA

<213> Homo sapiens

<400> 876

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tttccaaatg atcctagtaa ttgcctagaa 90

<210> 877

<211> 75

<212> DNA

<213> Homo sapiens

<400> 877

ctttatgaga attctcaggc tgaactatag gccattgttc ccaggcaaat caatacatca 60

atgcatcctc aaaaa 75

<210> 878

<211> 208

<212> DNA

<213> Homo sapiens

<400> 878

tttcccatg tgcttttagtg ggcttttggtt ttctttttgt gcgagtgtgt gtgagaatgg 60

ctgtgtggtg agtgtgaact ttgttctgtg atcatagaaa gggtatttta ggctgcaggg 120

gagggcaggg ctggggaccg aaggggacaa gttccccttt catcctttgg tgctgagttt 180

tctgtaaccc ttggttgcca gagataaa 208

<210> 879

<211> 148

<212> DNA

<213> Homo sapiens

<400> 879

accagaattt atggatgaac tgattgctta tatttttagtc agggtttata aatgtagatg 60

gtcaaattta cattgcctag tgatggaaaa ttcaactttt ttgattttt tttccaata 120

ttaaaaaagg ctctgtatgc atggtggg 148

<210> 880

<211> 207

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (182)..(182)

<223> n is a, c, g, or t

<400> 880

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tgtcatcaat ggcaatctct ccggaacgtc ctttcctat cactccctcg aacacaatct 120

ggtactccat gtcgtagctg ggcaggatga tccgccctg cttccactcg ccgccctggt 180

cntcacggat gaccacagc aacttgc 207

<210> 881

<211> 233

<212> DNA

<213> Homo sapiens

<400> 881

ggtggtttgg cctctaattt aattctgatt cagactctcc tgtcaggact caagaaaatt 60

taattaatta ccaaggatta agtcttctgg ttaaggtttc tgggaaaaaa aaatagcaaa 120

gatgttgatt tcttggaatc cttttacagg ttcataacag aaaaatcttc attccctgta 180

ggcatttaat taaacctagt tgagaagtgt gtgggattcc tcaattatga aca 233

<210> 882

<211> 254

<212> DNA

<213> Homo sapiens

<400> 882

gaagcaatgt gccaaaggtc atgattctta tcacggatgg gaaatcatca gatgctttca 60

gagatcctgc gataaaactg aggaattcag atgttgaaat ctttgcagtt ggtgtgaagg 120

atgccgttcg ctcagaattg gaagctattg cctctcctcc tgcagagacc catgtgttca 180

cagtggaaga ttttgatgct tttcagagga tatcttttga actcacacag tctatctgcc 240

ttagaattga gcaa 254

<210> 883

<211> 244

<212> DNA

<213> Homo sapiens

<400> 883

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atacaccaag tggtaatgaa atttcgtgac tggcccacac gtgcatagag gtctggggagg 120

accaggaaac agcctcagtg gccagaggat caccagtgc tcttcatca cagcatgtgc 180

aatatgccaa gattaccctc ggtcattcct gtcaacaagg ggtcaatgtc ataaatgtca 240

caat 244

<210> 884

<211> 291

<212> DNA

<213> Homo sapiens

<400> 884

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ctagagatga ggtagctcat gctaagaaat gttgggtcat ttttcctatg aaagttcaaa 120

ggccaaatgg tctaattcca atcatcacat ttgattagag tcagctccac aactcagttt 180

ctagatcttt ttcttcatta taggcttcag gatgatgaga ttgtacatgt ggaagagtct 240

caatttagag tccttgaca tatgtttgta aagttctata tgtcacctcg t 291

<210> 885
 <211> 191
 <212> DNA
 <213> Homo sapiens

<400> 885
 caaacagagt gaactttctg ccaagatgcg ggagtggttt tcagagacat ttcagaaagt 60
 gaaggagaaa ctcaagattg actcatgagg acctgaaggg tgacatccca ggaggggcct 120
 ctgaaatttc ccacacccca ggcctgtgc tgaggactcc ctccatgtgg cccaggtgc 180
 caccaataaa a 191

<210> 886
 <211> 238
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (194)..(206)

<223> n is a, c, g, or t

<400> 886

aagatggcta gaatgggtgcc tttctgagtg tctaaaactt gacaccctg gtaaattctt 60

caacacactt ccactgcctg cgtaatgaag ttttgattca tttttaacca ctggaatttt 120

tcaatgccgt cattttcagt tagatgattt tgcactttga gattaaaatg ccatgtctat 180

ttgattagtc ttannnnnnn nnnnnnacag gcttatcatt ctcactgttg gctgtcat 238

<210> 887

<211> 188

<212> DNA

<213> Homo sapiens

<400> 887

gcacaccaga ttcagggaga ctgaccacca agggatagtg taaaaggaca ttttctcagt 60

tgggtccatc agcagttttt cttcctgcat ttattgttga aaactattgt ttcatttctt 120

cttttatagg ccttattact gcttaatcca aatgtgtacc attggtgaga cacatacaat 180

gctctgaa 188

<210> 888
 <211> 191
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (38)..(51)
 <223> n is a, c, g, or t

<400> 888
 gaggtgtcaa acagcagagt gtactttcca aagaacannn nnnnnnnnnn nacacagcaa 60
 atcccaagcc ttcccagtct cacacctttc cacccattca taaaaaaaca cacgaatttc 120
 tcgcaagttc caatatcact gtctctttat catctaaata gggccagttg gacacctcat 180
 tgaaacaaaa a 191

<210> 889
 <211> 288
 <212> DNA
 <213> Homo sapiens

<220>

<221> misc_feature

<222> (114)..(145)

<223> n is a, c, g, or t

<220>

<221> misc_feature

<222> (219)..(232)

<223> n is a, c, g, or t

<400> 889

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ttaataagac agaaagtatt tctccttcta gtctcatcgt ctgatttgaa aggnnnnnnn 120

nnnnnnnnnn nnnnnnnnnn nnnnngtgag ttccaggaag aaatgttttt cttttttcat 180

ataaaatggg agctgtatgt atgtaactct gaattaaann nnnnnnnnn nncagtcact 240

ctggttctaa atccttattg ggcaagctgg agttttgaag tgacccaa 288

<210> 890

<211> 189

<212> DNA

<213> Homo sapiens

<400> 890

accacacaag cagtgactcc taaagaagtt cagaggaagg agagaacca tggggagggg 60

gtgcagtggg ggtgggtcag ggtgggctcc ctggagggga aattggtcta ggcaaggatg 120

cagactggcc agtaaggtgg gtccatgcag gaagctgagg gaggtggaag gcccgtgggt 180

ctcgagcgc 189

<210> 891

<211> 269

<212> DNA

<213> Homo sapiens

<400> 891

ttccttcttg gcctaactct tccagttagg atctagaact ttgccttttt tttttttttt 60

ttttttttga gatgggttct cactatattg tccaggctag agtgcagtgg ctattcacag 120

atgcgaacat agtacactgc agcctccaac tcctagcctc aagtgacct cctgtctcaa 180

cctcccaagt aggattacaa gcatgcgccg acgatgccca gaatccagaa ctttgtctat 240

cactctcccc aacaacctag atgtgaaaa 269

<210> 892

<211> 183

<212> DNA

<213> Homo sapiens

<400> 892

gagagttaa ctaagaaagg tcacatatgt gaaagcccaa ggacactgtt tgatatacag 60

caggtattca atcagtgtta ttgaaacca aatctgaatt tgaagtttga atcttctgag 120

ttggaatgaa tttttttcta gctgaggga actgtatttt tctttccca aagaggaatg 180

taa 183

<210> 893

<211> 187

<212> DNA

<213> Homo sapiens

<400> 893

ccttcatgct gccttcaaag ctagatcatg ttgccttgc ttagagaatt actgcaaadc 60

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agccccagtg cttggcgatg catttacaga tttctaggcc ctcagggttt tgtagagtgt 120

gagccctggg gggcagggtt ggggggtctg tcttctgctg gatgctgctt gtaatccatt 180

tggtgta 187

<210> 894

<211> 183

<212> DNA

<213> Homo sapiens

<400> 894

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ccttgctcct ggctggggcc tggtgaagat gcttgtatct tacttttcca ttgtaattgc 120

tatcgccatc acagctgaac ttgttgagat ccccggtgta ctgcctatca gcattttact 180

act 183

<210> 895

<211> 272

<212> DNA

<213> Homo sapiens

<400> 895

tcctcacccc ggtatgaatg tgtttcctcc acattgtata tccttcacc ctctggctgc 60

ctagatcagt aaataaaatt gatgtaatat aatttataag taacactggt gaaaccctga 120

tcccagtgga ggctgtaacc cacctgcccc cgcaccaccc ccctgacccc tgttaccgca 180

tttgtgtgta ttaatgctga agaattaaat gtttaaagag tttaaatttt gaaggcgttt 240

gctatatata gttgtcctgc attattataa ag 272

<210> 896

<211> 224

<212> DNA

<213> Homo sapiens

<400> 896

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tttaagatac cttgatgaag acctggacta ttgaatggag cagaaattca cctctctcac 120

tgactattac agttgcattt ttatggagtt cttcttctcc taggattcct aagactgctg 180

ctgaatttat aaaaattaag tttgtgaatg tgactactta gtgg 224

<210> 897

<211> 191

<212> DNA

<213> Homo sapiens

<400> 897

caaacagagt gaactttctg ccaagatgcg ggagtggttt tcagagacat ttcagaaagt 60

gaaggagaaa ctcaagattg actcatgagg acctgaaggg tgacatccca ggaggggcct 120

ctgaaatttc ccacacccca gcgcctgtgc tgaggactcc ctccatgtgg cccaggtgc 180

caccaataaa a 191

<210> 898

<211> 217

<212> DNA

<213> Homo sapiens

<400> 898

aggttagatt ctcatcacg ggactagtta gctttaagca ccctagagga ctagggtaat 60

pctgb2013053202-seq1.txt

ctgacttctc acttcctaag ttcccttcta taccctcaag gtagaaatgt ctatgttttc 120

tactccaatt cataaatcta ttcataagtc ttggtacaa gtttacatga taaaagaaa 180

tgtgatttgt cttcccttct ttgcactttt gaaataa 217

<210> 899

<211> 174

<212> DNA

<213> Homo sapiens

<400> 899

tccccagagt tcttgacccc tcattccctc gggaccctcc cagtgagaag ggcctgctct 60

gcttttcctg tctgtatata acttatttgc cctaagaact ttgagaatcc caattattta 120

ttttaatgta ttttttagac cctctattta cctgcgaact tgtgtttata ataa 174

<210> 900

<211> 269

<212> DNA

<213> Homo sapiens

<400> 900

pctgb2013053202-seq1.txt

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ttttttttga gatgggttct cactatattg tccaggctag agtgcagtgg ctattcacag 120

atgcgaacat agtacactgc agcctccaac tcctagcctc aagtgatcct cctgtctcaa 180

cctcccaagt aggattacaa gcatgcgccg acgatgccca gaatccagaa ctttgtctat 240

cactctcccc aacaacctag atgtgaaaa 269

<210> 901

<211> 231

<212> DNA

<213> Homo sapiens

<400> 901

aaaacttggc actttttcgt gtggatcttg ccacatttct gatcagaggt gtacactaac 60

atttcccccg agctcttggc ctttgcattt atttatacag tgccttgctc ggggccacc 120

acccctcaa gcccagcag ccctcaacag gccagggag ggaagtgtga gcgccttgg 180

atgacttaaa attggaaatg tcatctaacc attaagtcac gtgtgaacac a 231

pctgb2013053202-seq1.txt

<210> 902

<211> 186

<212> DNA

<213> Homo sapiens

<400> 902

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gaagtatttt tagaataaga atttgcatac ttacctagtg aaacttttct agaattattt 120

ttcactctaa gtcatgtatg tttctctttg attatttgca tgttatgttt aataagctac 180

tagcaa 186

<210> 903

<211> 159

<212> DNA

<213> Homo sapiens

<400> 903

caccctcaga tgcacatgag ctggcgggat tgaaggatgc tgtcttcgta ctgggaaagg 60

gattttcagc cctcagaatc gctccacctt gcagctctcc ctttctctgt attcctagaa 120

actgacacat gctgaacatc acagcttatt tcctcattt 159

<210> 904

<211> 295

<212> DNA

<213> Homo sapiens

<400> 904

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aattctaaaa gaaacttcta gagatcatct ggcaatcgct tttaaagact cggctcaccg 120

tgagaaagag tcactcacat ccattcttcc cttgatggtc cctattcctc cttcccttgc 180

ttcttggact tcttgaaatc aatcaagact gcaaaccctt tcataaagtc ttgccttgct 240

gaactccctc tctgcaggca gcctgccttt aaaaatagtt gctgtcatcc acttt 295

<210> 905

<211> 175

<212> DNA

<213> Homo sapiens

<400> 905

ccccacgtga cagtgccctgg gaatgtatta ttctgcagca tgacctgtga ccagcactgt 60

ctcagtttca ctttcacata gatgtccctt tcttggccag ttatcccttc cttttagcct 120

agttcatcca atcctcactg ggtgggggtga ggaccactcc tgtacactga atatt 175

<210> 906

<211> 228

<212> DNA

<213> Homo sapiens

<400> 906

gttgtgggggt caaccgtaca atggtgtggg agtgacgatg atgtgaatat ttagaatgta 60

ccatattttt tgtaaattat ttatgttttt ctaaacaat ttatcgata ggttgatgaa 120

acgtcatgtg ttttgccaaa gactgtaaat atttatttat gtgttcacat ggtcaaaatt 180

tcaccactga aaccctgcac ttagctagaa cctcattttt aaagatta 228

<210> 907

<211> 293

<212> DNA

<213> Homo sapiens

<400> 907

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ttgctctttg actgtcagca agactgaaga tggcttttcc tggacagcta gaaaacacaa 120

aatctttag gtcattgcac ctatctcagc cataggtgca gtttgcttct acatgatgct 180

aaaggctgcg aatgggatcc tgatggaact aaggactcca atgtcgaact cttctttgct 240

gcattccttt ttcttcactt acaagaaagg cctgaatgga ggacttttct gta 293

<210> 908

<211> 137

<212> DNA

<213> Homo sapiens

<400> 908

gtcagacaga tgtggttgca tcctaactcc atgtctctga gcattagatt tctcatttgc 60

caataataat acctccctta gaagtttggt gtgaggatta aataatgtaa ataaagaact 120

agcataacac tcaaaaa 137

<210> 909

pctgb2013053202-seq1.txt

<211> 267

<212> DNA

<213> Homo sapiens

<400> 909

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tcaaatgggg aggggtattc ttcatgcagg agaccccagg ccctggaggc tgcaacatac 120

ctcaatcctg tcccaggccg gatcctcctg aagccctttt cgcagcactg ctatcctcca 180

aagccattgt aaatgtgtgt acagtgtgta taaaccttct tcttcttttt ttttttttaa 240

actgaggatt gtcattaaac acagttg 267

<210> 910

<211> 254

<212> DNA

<213> Homo sapiens

<400> 910

aattcagtgg tgtgagtata ttcataagat ttatacttgg tgtctattca taagacttat 60

atccagcata ttcataacta gagccatata acagatgcat tcatacataat aattccagac 120

pctgb2013053202-seq1.txt

attttcatca ccctaaaagg aaaccctgaa acccattagc agtcattccc cattcctcca 180

acccattctc tccctaattcc ctagaaacca ccaatctgct gtgtatttca tctattgcca 240

acatttcata taaa 254

<210> 911

<211> 162

<212> DNA

<213> Homo sapiens

<400> 911

tacgttatgt atttgacaag tgggtggtgaa acaaaatcaa aacagatttg atttgtgttt 60

ttgaaatgtc agtacatttt gtgccactaa cactgtgatg tataaaagag ctgtttgaat 120

gccttttaat gttgtgtttt gtactctgga atcatatgga aa 162

<210> 912

<211> 254

<212> DNA

<213> Homo sapiens

<400> 912

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ttgaaatttg tggtttttta atttatttaa aattgggggg agggcatggg aaggatttaa 120

caccgatata ttgttaccgc tgaaaatgaa ctttatgaac cttttccaag ttgatctatc 180

cagtgcgtg gcctgggtgg cgtttcttct tgtacttatg tggttttttg gcttttaata 240

cagacatttt cctc 254

<210> 913

<211> 83

<212> DNA

<213> Homo sapiens

<400> 913

tctgctgaac atgagcttca gttgctactc ggagcattga gagggaggcc taagaataat 60

aacaatccag tgcttaagag tca 83

<210> 914

<211> 296

<212> DNA

<213> Homo sapiens

pctgb2013053202-seq1.txt

<400> 914

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ctctgacggg ctccactccc gtctgcaggc agccaggagg gcaggaagcc cttgctctgt 120

gctgccatcc tgcctccctc ctccagcctc agggcactcg ggcttgggtg ggagtcaacg 180

ccttcccctc tggactcaaa taaaaccag tgacctcact tcttttctct gcaaaagggtg 240

cttgtggggc tgggagtga gacattggtg tttctgctga tgtcccttgt gaaaaa 296

<210> 915

<211> 244

<212> DNA

<213> Homo sapiens

<400> 915

atttacctat atagcaagcc tacacatgtg cccctgaacc taaaaaaaaa gttaaaagaa 60

aaacgtttgg attattttcc ctctttcgaa caaagacatt ggtttgccca aggactacaa 120

ataaaccaac gggaaaaaag aaaggttcca gttttgtctg aaaattctga ttaagcctct 180

gggccctaca gcctggagaa cctggagaat cctacacca cagaaccgg ctttgtcccc 240

aaag 244

<210> 916

<211> 253

<212> DNA

<213> Homo sapiens

<400> 916

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cttttctccc tcttactgat tatgcttttg aaattttctc ttgtaaaaca tttagaaaac 120

aaaaacaaaa aaaatgtgat ttgtttctgt cttcaaaatc tcattagaat tttttcactg 180

gaggaagatt ttcccttgct tctgcataaa attttaactc cataacttat aagctcactc 240

tttattgtta ctt 253

<210> 917

<211> 74

<212> DNA

<213> Homo sapiens

<400> 917

aaaaatttaa ctcccatatg tgttcctctt gttcctaatac ttgtcaaccc agtgcaagtg 60

accgacaaaa ttcc 74

<210> 918

<211> 294

<212> DNA

<213> Homo sapiens

<400> 918

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cagctcttta attttgtaac atctaatagat atcaccgcct tgaagtgatt aaagtagatt 120

gcttaaagaa ttaaagcttt aaagatgaaa gatgttattg cttttgctgg acatgaggaa 180

cagttgtaaa gtttccaggt ctacaataac tttctggaac cctctcagtg aactgtttct 240

tgtaaaagtt ttccctaaga taaaagctca atcccattgt ttccacactc aaaa 294

<210> 919

<211> 153

<212> DNA

<213> Homo sapiens

<400> 919

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acgtgcagtt tcatttcttt tgagagtggg attgctggag cctatgttaa gggtacgttc 120

aactcatcag ctcaactgtc ttccaaatgg cag 153

<210> 920

<211> 266

<212> DNA

<213> Homo sapiens

<400> 920

ttatcaactg tgcacaagga aaaaaataga tatgtgaaag gttcacgtaa atttcctcac 60

atcacagaag attaaaaattc agaaaggaga aaacacagac caaagagaag tatctaagac 120

caaagggatg tgttttatta atgtctagga tgaagaaatg catagaacat tgtagtactt 180

gtaaataact agaaataaca tgatttagtc ataattgtga aaaataataa taatttttct 240

tggatttatg ttctgtatct gtgaaa 266

<210> 921

<211> 202

<212> DNA

<213> Homo sapiens

<400> 921

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gagaagatac catttgatcc agcagaaatg tccaaatgat atcaggtcct caatcttcag 120

ctacagggaa tgagtaactt tgagtggaga agaaacaaac atagtgggta taatcatgga 180

tcgcttgtag ccctgtgaaa at 202

<210> 922

<211> 208

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (124)..(124)

<223> n is a, c, g, or t

<400> 922

gaatatgtgg cagagctcct ggaaatgatg cagattaggt ggcatttttg tcagctctgt 60

ggtttattgt tgggactatt ctttaaaata tccattgttc actacagtga agatctctga 120

tttnaccgtg tactatccac atgcattaca aacatttcgc agagctgctt agtatataag 180

cgtacaatgt atgtaataac catctcat 208

<210> 923

<211> 150

<212> DNA

<213> Homo sapiens

<400> 923

gctgataaat agcattaggg ttctttgcaa tgtggtatct agctgtatta ttggttttat 60

ttactttaaa cattttgaaa agcttatact ggcagcctag aaaaacaaac aattaatgta 120

tccttatgtc cctggcacat gaataaactt 150

<210> 924

<211> 97

<212> DNA

<213> Homo sapiens

<400> 924

caaattcaag tcactagact tcagagttca acacctggac atgagaagat attatattat 60

gtaccataaa tatttcctgt atctgactgc ctgaaca 97

<210> 925

<211> 237

<212> DNA

<213> Homo sapiens

<400> 925

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tgaatcaatt ggaataaaac ctgactcgca ggtgactgga caggaaatcc caaagttcca 120

ccatttctat gcttaatttt aacgtccccc cgcttttttt tttgtagaaa ataaaaacaa 180

gaaaatcggt ccaatgtaag atgtttgtta tagaaacttt aggcaataca ggtgtgt 237

<210> 926

<211> 292

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (54)..(55)

<223> n is a, c, g, or t

<400> 926

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tttttgtgtg aatatttaat ggtgctccat gactgttgag ttttaaaaac ctcgttaaatt 120

tttgccaaat cagttgcccc caaaagggaat tatgcttttc cttatTTTTT tttctaaaat 180

gctatttatc tctaaggaaa aaaaaaaaaag actattactc atttaacatt gtttaagcag 240

gttgagctag ctgtgaaaat agcttttgtg agccttctaa ttcctaaacg tc 292

<210> 927

<211> 243

<212> DNA

<213> Homo sapiens

<400> 927

gttaacactg tggatcacct tcggccaagg gacacgactg gagattaaac gtaagtaatt 60

tttcactatt gtcttctgaa atttgggtct gatggccagt attgactttt agaggcttaa 120

ataggagttt ggtaaagatt ggtaaataag ggcatttaag atttgccatg ggttgcaaaa 180

gttaaaactca gcttcaaaaa tggatttgga gaaaaaaaga ttaaattgct ctaaactgaa 240

tga 243

<210> 928

<211> 120

<212> DNA

<213> Homo sapiens

<400> 928

tcattctcat ccatccagga tgtactaaaa cagtgtgttt aataaattgt aattattttg 60

tgtacagttc tatactgtta tctgtgtcca tttccaaaac ttgcacgtgt ccctgaattc 120

<210> 929

<211> 185

<212> DNA

<213> Homo sapiens

<400> 929

aaggtttggc agaaattggt ttttgagtgg ctcaccagag taccagaag aatcagtatg 60

gaattagagg acagtggcct accctaaata aagacatgag tgatgtataa agtctagtgt 120

caatttattc agaaaatattc aaaattattc tgggagctat ggggtcaaagt tgataggcac 180

aaaca 185

<210> 930

<211> 130

<212> DNA

<213> Homo sapiens

<400> 930

atcccaatag atatccccct atgtgcatgc acacctgcac actcacggct gaaatctccc 60

taaccaggg ggaccttagc atgcctaagt gactaaacca ataaaaatgt tctggtctgg 120

cctgaaaaaa 130

<210> 931

<211> 86

<212> DNA

<213> Homo sapiens

<400> 931

aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag ggcctgagct 60

cgcccgtcac aaagagcttc aacagg 86

<210> 932

<211> 264

<212> DNA

<213> Homo sapiens

<400> 932

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gaggaacaat aattcggatg tttctctcca caatgtcctc attaggatct tcggaagaac 120

ggatgatcct ggaagtaatc cgggcacact tacatttggt gtcaacaaga acaatccttt 180

catcttcttg ggctttcaca tgaacagcct taataaaaac cgccaggact cccagaaaa 240

gcaaattggtt cttcatcttg accc 264

<210> 933

<211> 101

<212> DNA

<213> Homo sapiens

<400> 933

ttgataggga tagcattgaa ctatttgctc aactcaacat tttaggaatt tatttctgct 60

gtcttagtgct caaaacttgc agctagaatt gagggaagag a 101

<210> 934

<211> 233

<212> DNA

<213> Homo sapiens

<400> 934

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atgaagacag agccccaccc tcagatgcac atgagctggc gggattgaaa gatgctgtct 120

tcgtactggg aaagggattt tcagccctca gaatcgtcc accttcagc tctccccttc 180

tctgtattcc tagaaactga cacatgctga acatcacagc ttatttcctc att 233

pctgb2013053202-seq1.txt

<210> 935
<211> 256
<212> DNA
<213> Homo sapiens

<400> 935
ctgaggtgct atgttccttag tggatgttct gaccctgctt caaatatttc cctcaccttt 60

cccatcttcc aagggtataa ggaatctttc tgctttgggg ttatcagaa ttctcagaat 120

ctcaaataac taaaaggat gcaatcaaat ctgcttttta aagaatgctc ttacttcat 180

ggacttccac tgccatcctc ccaaggggcc caattcttt cagtggctac ctacatacaa 240

ttccaaacac atacag 256

<210> 936
<211> 259
<212> DNA
<213> Homo sapiens

<400> 936
acagaagcca ttgcctcctt tgtttacctt gggtccacct ccacaaaac ccaacagacc 60

pctgb2013053202-seq1.txt

accaaagtgtt gacctgacga aattccacaa aacctcttct ggaaacagta ctagcaaagg 120

ccagacgtct tactcaacaa cttccctgcc accacctcca ccatcccatc cggccagcca 180

accaccattg ccagcatctc acccatcaca accaccagtc ccaagcctac ctcccagaaa 240

cattaaacct ccgtttgac 259

<210> 937

<211> 114

<212> DNA

<213> Homo sapiens

<400> 937

ggacctgtac accacgagca gccagctgac cctgccggcc acacagtgcc tagccggcaa 60

gtccgtgaca tgccacgtga agcactacac gaatcccagc caggatgtga ctgt 114

<210> 938

<211> 265

<212> DNA

<213> Homo sapiens

<400> 938

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attattaaaa acaccaccaa agaaaataaa tatatcctac ttgaaattta ctctatggac 120

ttaccactg ctagaataaa tgtatcaaat cttatttgta aattctcaat ttgatatat 180

atatgtatat atgcatatac atatccacac ttgtctgcaa gaatattgat taaaattgct 240

aaatttgtac ttgttcacca gaaaa 265

<210> 939

<211> 198

<212> DNA

<213> Homo sapiens

<400> 939

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gcccagagga ctgttaataa cgatgatcca tgtgttttac tctaaagtgc taaatatggg 120

agtttccttt ttttactctt tgtcactgat gacacaacag aaaagaaact gtagaccttg 180

ggacaatcaa catttaaa 198

pctgb2013053202-seq1.txt

<210> 940

<211> 162

<212> DNA

<213> Homo sapiens

<400> 940

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tctcttagga atacagtttc tagcattaa caaataaaca aggggagaaa ataaaactca 120

aggagtgaaa atcaggaggt gtaataaaat gttcctcgca tt 162

<210> 941

<211> 256

<212> DNA

<213> Homo sapiens

<400> 941

tcctgtttac cttcaagtt tcaagttcat gtcactgtct cagagagggtt ttctgtgct 60

cgccctgttt ctctcaggaa gccttgctct tttccatcat gcctctaatac acagcttata 120

atcggatatt tatttctgtg tctacagtct tgccctgcc a gactgtatgc cccatgtggg 180

caggcgctca tgattgtttc tgattgtttc acgcatgctg ctaaccaga gcctgggccc 240

aaagctagtt agtact 256

<210> 942

<211> 294

<212> DNA

<213> Homo sapiens

<400> 942

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tttgttttgc tctattgttt agtttttact tgggtgcaat gtgtacgtca aaagttttta 120

ttttgatatt tgaaagagac caaatcaggc ccagaccgcc tctctggaag gtgtttagg 180

ccattcaaaa cgcctccgga gtgtcgcaaa ccaagtgcgg aggggccctg aggttgtact 240

gtaaacaatca tagtgacttg tcttttcaaa tatattccca ctattttcgc agaa 294

<210> 943

<211> 221

<212> DNA

<213> Homo sapiens

<400> 943

tgctggactc cgacggctcc ttcttcctct acagcaagct caccgtggac aagagcaggt 60

ggcagcaggg gaacatcttc tcatgctccg tgatgcatga ggctctgcac aaccgcttca 120

cgcagaagag cctctccctg tctccgggta aatgagtgcg acggccggca agcccccgct 180

ccccgggctc tcggggctgc gcgaggatgc ttggcacgta c 221

<210> 944

<211> 239

<212> DNA

<213> Homo sapiens

<400> 944

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ctctgacttt gctgtttcca gtggtatgac cttggagaag tcacttatcc tcttgagacc 120

tcagtttcct catctgcaga ataatgactg acttgtctaa ttcgtaggga tgtgaggttc 180

tgctgaggaa atgggtatga atgtgccttg aacacaaagc tctgtcaata agtgataca 239

<210> 945

<211> 181

<212> DNA

<213> Homo sapiens

<400> 945

gaggaccgag cacagaaatc ttagagattt cttgtcccct ctcaggatcat gtgtagatgc 60

gataaatcaa gtgattgggtg tgcctgggtc tcactacaag cagcctatct gcttaagaga 120

ctctggagtt tcttatgtgc cctgggtggac acttgcccac catcctgtga gtaaaagtga 180

a 181

<210> 946

<211> 228

<212> DNA

<213> Homo sapiens

<400> 946

gggatgacat gcactcagct cttggctcca ctgggatggg aggagaggac aagggaatg 60

tcaggggcgg ggagggtgac agtggccgcc caaggcccac gagcttgttc tttgttcttt 120

gtcacaggga ctgaaaacct ctcctcatgt tctgctttcg attcgtaag agagcaacat 180

tttaccacaca cacagataaa gttttccctt gaggaacaa cagcttta 228

<210> 947

<211> 136

<212> DNA

<213> Homo sapiens

<400> 947

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acgtctgcta acttggagcc ccagtgccaa gcacagtgcc tgcattgtatt tatccaataa 120

atgtgaaatt ctgtcc 136

<210> 948

<211> 193

<212> DNA

<213> Homo sapiens

<400> 948

gcagtctact agattgtgat cccttgagat atggaaggat gccttttttt ctctgcattt 60

aaaaaaatcc cccagcactt cccacagtgc ctattgatac ttggggaggg tgcttggcac 120

ttattgaata tatgatcggc catcaaggga agaactattg tgctcagaga cactgttgat 180

aaaaactcag gca 193

<210> 949

<211> 175

<212> DNA

<213> Homo sapiens

<400> 949

aaatttaatt ttctacgcct ctggggatat ctgctcagcc aatggaaaat ctgggttcaa 60

ccagcccctg ccatttctta agactttctg ctgcactcac aggatcctga gctgcactta 120

cctgtgagag tcttcaaact tttaaactt gccagtcagg acttttgcta ttgca 175

<210> 950

<211> 183

<212> DNA

<213> Homo sapiens

<400> 950

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pctgb2013053202-seq1.txt

gtttccaaaa aatggtactc cacatacttc agtgagggta agtatatttcc tgttgtcaag 120

aatagcattg taaaagcatt ttgtaataat aaagaatagc tttaatgata tgcttgtaac 180

taa 183

<210> 951

<211> 235

<212> DNA

<213> Homo sapiens

<400> 951

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gccccatcaa tcctgagtgt cagtttggtg tccctattgt agatgaaata gtgatgtagc 120

aaaaacctag taaattctga atgcttttcc acgtagactt atctggaatg tgaacacaac 180

tctttggtta atagtaaag cttaactgta gtcctgagta ggtgcatttc tgtct 235

<210> 952

<211> 154

<212> DNA

<213> Homo sapiens

<400> 952

agtatatattt ctatcttctg gtgacttgag cttgagctct gacaggcatg ggcctctccg 60

accttcatca ctattcttag gataatgctg gcgggcagag atgatcaatc atcatattaa 120

atcataatga gcttataatc ctcccactgg aaaa 154

<210> 953

<211> 280

<212> DNA

<213> Homo sapiens

<400> 953

atcagaaagg gcaacttact cttcctggca tcttattgta ttggagggtg accaccctgg 60

gcatgggggtg ttggcagggg tcaaaaagct tatttctttt aatctcttac tcaacgaaca 120

catcttctga tgatttccca aaattaatga gaatgagatg agtagagtaa gatttgggtg 180

ggatgggtag gatgaagtat attgcccaac tctatgtttc ttgattcta acacaattaa 240

ttaagtgaca tgatttttac taatgtatta ctgagactag 280

<210> 954

<211> 206

<212> DNA

<213> Homo sapiens

<400> 954

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ataaaattat tgtatagaca tctgcttctt aaacagattg tgagttcttt gagaaacagc 120

gtggatttta cttatctgtg tattcacaga gcttagcaca gtgcctggta atgagcaagc 180

atacttgcca ttacttttcc ttccca 206

<210> 955

<211> 247

<212> DNA

<213> Homo sapiens

<400> 955

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tagactgtgt gcgtgtgcgt tgatgggcac tcaagagtcc cgtgagtcac ccagccctgc 120

ctttcccctg cgccccatc ctctcacgtc ccgccctgcc tccacttggg gaccctgcct 180

cgtgtcgtct ttatctgcct attactcagc ctaaggaaac aagtacactc cacacatgca 240

taaagga 247

<210> 956

<211> 190

<212> DNA

<213> Homo sapiens

<400> 956

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cttgagtgtg ttacctcctt tccaagctcc tcgtgataat gcagacttcc tggagtacaa 120

acacaggatt tgtaattcct tactgtaacg gagtttagag ccagggctga tgctttggtg 180

tggccagcac 190

<210> 957

<211> 165

<212> DNA

<213> Homo sapiens

<400> 957

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ttatctctcc atgggaagct aagttataaa aataggtgct tggtgtacaa aactttttat 120

atcaaaaggc tttgccattt ctatatgagt gggtttactg gtaaa 165

<210> 958

<211> 260

<212> DNA

<213> Homo sapiens

<400> 958

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ctggaggggg aagagctctc aaccagagg gatctgacca ggaaggttca cccccctcc 120

accaggaag cccctgcaga cagtatgtgt tttaggcttt gctggccaaa tggtctctgc 180

cgtgactact cagctctgcc attgtggctg cagagtgacc atagaccttc tgaaagtga 240

tgagtatgac tgtgttccaa 260

<210> 959

<211> 197

<212> DNA

<213> Homo sapiens

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atgtttattc cctgtcagcg gaggggagaa tgcattcat caataaacca aagccaatag 120

ctggagaatt gagatctggt tgaaagtggg ttatggTTTA catgctgtac ttcctgagg 180

aattgcgaga tattgct 197

<210> 960

<211> 187

<212> DNA

<213> Homo sapiens

<400> 960

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tggaacttaag aataaacctt gtgtttaatc tctTTTTTt cttaaaattt taatgtgagt 120

tttctgttac gcaaattatc catgttagca ctttggaaac aaatgtataa atgtactttc 180

tgaataa

187

<210> 961

<211> 228

<212> DNA

<213> Homo sapiens

<400> 961

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tcaggggcgg ggagggtgac agtggccgcc caaggccac gagcttgttc tttgttcttt 120

gtcacaggga ctgaaaacct ctcctcatgt tctgctttcg attcgттаag agagcaacat 180

tttaccacaca cacagataaa gttttccctt gaggaacaa cagcttta 228

<210> 962

<211> 213

<212> DNA

<213> Homo sapiens

<400> 962

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tgcgaggttc tactagctcc ctgcccctcg ccctgcagag aagagaacca tgccagggga 120

gaaggcacc agccatcctg acccagcgag gagccaacta tcccaaatat acctgggggtg 180

aaatatacca aattctgcat ctccagagga aaa 213

<210> 963

<211> 104

<212> DNA

<213> Homo sapiens

<400> 963

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<210> 964

<211> 132

<212> DNA

<213> Homo sapiens

<400> 964

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gctctattca atacttctcc tctcagatga tagtaaagat caaaagaatt cgaagggagt 120

tggtaaacgc tg 132

<210> 965

<211> 281

<212> DNA

<213> Homo sapiens

<400> 965

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ctctgccagc caatthttgtt tggctatctc catttaactc acttgttcct gatggagtct 180

ctccctctcc tgcattcattt gctcgttctg cttttgaatc gccgccaacc tttgcgcttc 240

agccttttca gcttctgctt tcacttgtgc ctctgaggag a 281

<210> 966

<211> 239

<212> DNA

<213> Homo sapiens

<400> 966

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cccaggctcc cctcacccca gcgggtaatg agcccttaata cgctgcctct aggggagctg 180

attgtagcag cctcgttagt gtcaccccct cctccctgat ctgtcagggc cacttagtg 239

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<211> 174

<212> DNA

<213> Homo sapiens

<400> 967

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cacctacccc cactgtggct gatttggaat tttgtgcccc catgtaagca ccccttcatt 120

tggcattccc cacttgagaa ttaccctttt gccccgaaca tgtttttctt ctcc 174

<210> 968

<211> 270

<212> DNA

<213> Homo sapiens

<400> 968

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gaaacagact gcctgaattg agaattttga tttcttaaag tgtgtttctt tctaaattgc 120

tggttccttaa ttgattaat ttaattcatg tattatgatt aaatctgagg cagatgagct 180

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atacaaacat tctaattaaa ggctttgcaa 270

<210> 969

<211> 276

<212> DNA

<213> Homo sapiens

<400> 969

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ctttattgtg gcatctgttc gaggtttgct tcctctttaa gtctgtttct tcattagcaa 120

tcatatcagt tttaatgcta ctactaaca tgaacagtaa caataatatc cccctcaatt 180

aatagagtgc tttctatgtg caaggcactt ttcacgtgtc acctatttta acctttccaa 240

ccacataaat aaaaaaggcc attattagtt gaatct 276

<210> 970

<211> 264

<212> DNA

<213> Homo sapiens

<400> 970

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aaaaacctag taaattctga atgcttttcc acgtagactt atctggaatg tgaacacaac 180

tctttgggta atagtaaag cttaactgta gtcctgagta ggtgcatttc tgtctgtctc 240

aataaatttt actttgtctg caaa 264

<210> 971

<211> 275

<212> DNA

<213> Homo sapiens

<400> 971

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taaatgttga cagaggccct gccccgttca cagatcctgg ccctgagcca gccctgtgct 120

cctccctccc ccaacactcc ctaccaaccc cctaataccc tactccctcc accccccctc 180

cactgtaggc cactggatgg tcatttgcat ctccgtaaat gtgctctgct cctcagctga 240

gagagaaaaa aataaaactgt atttggtgc aagaa 275

<210> 972

<211> 210

<212> DNA

<213> Homo sapiens

<400> 972

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cgttcccctg ctgccacctg ctcttgtcca cggtgagctt gctatagagg aagaaggagc 120

cgtcggagtc cagcacggga ggcgtggtct tgtagttgtt ctccggctgc ccattgctct 180

cccactccac ggcgatgtcg ctgggataga

210

<210> 973

<211> 235

<212> DNA

<213> Homo sapiens

<400> 973

gagtgtctca gaagtgtgct cctctggcct cagttctcct cttttggaac aacataaaac 60

aaatttaatt ttctacgcct ctggggatat ctgctcagcc aatggaaaat ctgggttcaa 120

ccagcccctg ccatttctta agactttctg ctccactcac aggatcctga gctgcactta 180

cctgtgagag tcttcaaact tttaaactt gccagtcagg acttttgcta ttgca 235

<210> 974

<211> 162

<212> DNA

<213> Homo sapiens

<400> 974

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taagaaattg ccatttgaaa caatccattt tgtaactgaa ctttatgaaa tatatgtatt 120

tcatggtacg tattctctag cacagtctga gcaattaaat ag 162

<210> 975

<211> 249

<212> DNA

<213> Homo sapiens

<400> 975

aggccctctt gagagtctat ccagggaccc attgtttttac ttttaacagac cagaaaagat 60

gtttgttttc catgtcatta cccccagggg ataccgaatg tgtgggtaga aatttctctg 120

tagattaaaa atcagatttt tacatggatt caacaaagga gcgtcacttg gatttttgtt 180

ttcatccatg aatgtagctg cttctgtgta aaatgccatt ttgctattaa aaatcaattc 240

acgctggaa 249

摘要

本发明提供了方法和组合物，以用于识别癌症的分子诊断测试。所述测试可识别对血管生成和血管发育相关的生物标志物的表达具有上调或下调作用的癌症亚型。本发明可以用于确定癌症患者在任何抗血管生成剂的给药之前对治疗方案是临床响应或非临床响应。所述测试可用于不同的癌症类型和直接或间接影响血管生成或血管生成信号的不同药物。此外，本发明可用作某些癌症类型的预后指标。特别地，本发明涉及使用某些组合的预测性标志物，其中所述预测性标志物的表达与对治疗方案的响应性或非响应性相关。