DETECTION AND TREATMENT OF CONDITIONS CHARACTERIZED BY PERFUSION SHORTAGE

CROSS-REFERENCE

[0001] This application claims the benefit of U.S. Provisional Patent Application No. 63/027,289, filed May 19, 2020, which is entirely incorporated herein by reference in its entirety.

FIELD

[0002] The present disclosure is related to detection, prevention, and treatment of conditions comprising perfusion shortage, such as conditions comprising neoangiogenesis, or ischemia, or both.

BACKGROUND

[0003] Diseases comprising perfusion shortage can include neoangiogenesis, ischemia, or both. Ischemic diseases are diseases in which a lack of tissue perfusion (usually due to vascular disease) results in oxygen deprivation and pathology (for example, infarct, lack of function, or chest pain). Example ischemic disease include, but are not limited to, cardiovascular disease (e.g., angina pectoris, coronary artery disease. myocardial infarction, microvascular disease), cerebrovascular disease (e.g., TIA, stroke, microvascular disease) and peripheral artery disease (e.g., claudication). The prognosis and therapy responsiveness of other diseases are also dependent on tissue perfusion, ischemia, or both (including, but not limited to, oncological disease, diabetes mellitus, kidney disease, pulmonological disease, ophthalmological disease, gynecological disease, but also determines outcome and therapy response in for instance, but not limited to sepsis, inflammation, oncological disease and mechanical ventilation of patients).

SUMMARY

[0004] In an aspect, the present disclosure describes methods for analyzing a biological sample, comprising (a) obtaining said biological sample from a subject; (b) wherein when said subject is a female subject, assaying expression levels of two or more genes from a female targeted set of genes to generate an output comprising said expression levels from (b) indicative of said female subject's having or risk of having a condition comprising perfusion shortage or neoangiogensis; and (c) wherein when said subject is a male subject, assaying

expression levels of two or more genes from a male targeted set of genes to generate an output comprising said expression levels from (c) indicative of said male subject's having or risk of having a condition comprising perfusion shortage or neoangiogensis.

[0005] In some embodiments, the subject has or is at risk of having a condition comprising perfusion shortage. In some embodiments, the female targeted set of genes comprises a plurality of genes listed in Tables 1, 3, and 5. In some embodiments, the male targeted set of genes comprises a plurality of genes listed in Tables 2, 4, and 6. In some embodiments, the methods further comprise obtaining a range of control expression levels of said female targeted set of genes.

[0006] In some embodiments, the assaying comprises comparing said expression levels of (b) with said range of control expression levels of said female targeted set of genes. In some embodiments, the methods further comprise obtaining a range of control expression levels of said male targeted set of genes. In some embodiments, the assaying comprises comparing said expression levels of (c) with said range of control expression levels of said male targeted set of genes. In some embodiments, wherein when said expression levels from either (b) or (c) are outside said range of control expression levels, the subject has said condition comprising perfusion shortage or neoangiogenesis is at risk for having said condition.

[0007] In some embodiments, the biological sample comprises isolated hematopoietic endothelial precursor cells (EPCs), fractions thereof, or secretions thereof. In some embodiments, the hematopoietic endothelial precursor cells (EPCs) is Flk-1+. In some embodiments, the hematopoietic endothelial precursor cells do not express a cell surface marker, Flk-1. In some embodiments, the hematopoietic endothelial precursor cells are positive for makers selected from Flt1, Flt4, VEGFR1, CXCR4, CD31, CD34, CD105, CD133, Sca-1, and c-Kit. In some embodiments, the output from (b) and said output from (c) both have an accuracy greater than about 84%.

[0008] In another aspect, the present disclosure provides the methods for analyzing a biological sample obtained from a subject, comprising: (i) subjecting a plurality of hematopoietic endothelial precursor cells (EPCs), fractions of said plurality of hematopoietic EPCs, secretions of said plurality of hematopoietic EPCs, or any combination thereof isolated from said biological sample, to a gene expression analysis, wherein said gene expression

analysis comprises assaying expression levels of two or more genes from a plurality of identified genes; and (ii) generating an output comprising said gene expression levels, wherein said gene expression levels are indicative of said subject's having or risk of having a condition comprising perfusion shortage at least in part based on said expression levels.

[0009] In some embodiments, the plurality of hematopoietic EPCs comprises a cell surface marker of Flk-1/KDR. In some embodiments, the plurality of hematopoietic EPCs does not comprise a cell surface marker of Flk-1/KDR. In some embodiments, the plurality of hematopoietic EPCs are positive for makers selected from Flt1, Flt4, VEGFR1, CXCR4, CD31, CD34, CD105, CD133, Sca-1, and c-Kit.

[0010] In another aspect, the present disclosure provides methods of analyzing a biological sample obtained from a subject, comprising: (i) subjecting a biological sample obtained from said subject to a gene expression analysis, wherein said gene expression analysis comprises assaying expression levels of two or more genes from a plurality of identified genes; and (ii) generating an output comprising said gene expression levels indicative that said subject has or is at risk of having a condition comprising perfusion shortage with an accuracy that is greater than 91%, wherein when said assaying comprises a method selected from the group consisting of cDNA chip array analysis, quantitative (RT) PCR, microarray analysis, multiplexing, Luminex analysis, nucleic acid sequencing, northern blot analysis, genomic high throughput sequencing, nanostring, massive parallel signature sequencing (MPSS),serial analysis of gene expression (SAGE), enzyme-linked immunosorbent assay (ELISA), protein sequencing, mass spectrometry (such as MALDI TOF, QTOF, or SELDI TOF), quantitative western blot analysis, and peptide barcoding.

[0011] In some embodiments, the biological sample comprises isolated hematopoietic endothelial precursor cells (EPCs), fractions, or secretions thereof. In some embodiments, the plurality of identified genes comprises a female targeted set of genes and a male targeted set of genes. In some embodiments, the female targeted set of genes comprises a plurality of genes listed in Tables 1, 3, and 5. In some embodiments, the male targeted set of genes comprises a plurality of genes listed in Tables 2, 4, and 6.

[0012] In some embodiments, the methods comprise obtaining a range of control expression levels of said female targeted set of genes or of said male targeted set of genes and comparing said gene expression levels from (i) of either claim 12 or claim 13 to said range of

control expression levels. In some embodiments, the said expression levels from (i) of either claim 12 or claim 13 are outside said range of control expression levels, said subject has perfusion shortage or is at risk for having said condition comprising perfusion shortage.

[0013] In another aspect, the present disclosure provides methods of analyzing a biological sample, comprising: obtaining said biological sample from a subject that has or is at risk for having a condition comprising perfusion shortage, wherein said perfusion shortage is at an early stage and has not caused any detectable tissue damage; assaying expression levels of two or more genes from a plurality of identified genes to generate an output comprising said expression levels indicative of said subject's having or is at risk of having said condition comprising perfusion shortage.

[0014] In some embodiments, the perfusion shortage is neoangiogenesis. In some embodiments, the perfusion shortage is ischemic heart disease. In some embodiments, the subject is a female subject, further comprising assaying less than 60, 40, or 14 genes from said plurality of genes listed in Tables 1, 3, and 5. In some embodiments, the methods omprise assaying less than 14 genes from said plurality of genes listed in Tables 1, 3, and 5. In some embodiments, the subject is a male subject, further comprising assaying less than 40, 25, 15 genes from said plurality of genes listed in Tables 2, 4, and 6.

[0015] In some embodiments, the methods comprise assaying less than 15 genes from said plurality of genes listed in Tables 2, 4, and 6. In some embodiments, the output has an accuracy greater than about 99%. In some embodiments, the output has an accuracy greater than about 98%. In some embodiments, the output further comprises providing an assessment of a severity of said subject's perfusion shortage. In some embodiments, the output further comprises providing a prognosis report of said subject's perfusion shortage. In some embodiments, the output further comprises providing a response report of said subject upon, during, and/or after a medical intervention. In some embodiments, the output further comprises providing a monitoring report of said subject before or after receiving said medical intervention.

[0016] In some embodiments, the methods further comprise providing a treatment to said subject, wherein said subject has or is at risk of having a condition comprising perfusion shortage, at least in part based on said output. In some embodiments, the treatment comprises administering an anti- or pro-ischemic medical intervention, anti- or pro- neoangiogenesis

medical intervention to the subject, invasive monitoring, advanced imaging, or any combinations thereof. In some embodiments, the medical intervention comprises a pharmacotherapy, or surgical or percutaneous procedure.

[0017] In some embodiments, the surgical or percutaneous procedure comprises a bypass surgery or a percutaneous coronary procedure. In some embodiments, the medical intervention comprises administering a pharmaceutical composition selected from the group consisting of beta-blockers, calcium channels antagonists, nitrates, aspirin, cholesterol-lowering compounds, angiotensin-converting enzyme (ACE) inhibitors, and ranolazine. In some embodiments, the medical intervention targets one or more genes listed in Tables 1-6. In some embodiments, the medical intervention further comprises modulating expression levels of one or more genes listed in Tables 1-6.

[0018] In some embodiments, at least based in part on response report, prognosis report, or both, the methods further comprise ceasing said medical intervention. In some embodiments, at least based in part on monitoring report, the methods further comprise employing advanced imaging comprising invasive angiography, advanced imaging, nuclear imaging, MSCT, MRI analysis, tissue biopsy, monitoring of mechanical ventilation, or a combination thereof. In some embodiments, the subject does not have any symptom. In some embodiments, the subject is at least diagnosed with one of ischemic cardiovascular disease, ischemic heart disease, coronary artery disease, cardiovascular congenital disease, stroke, transient ischemic attacks, microvascular disease, microvascular dementia, claudication intermittents, Burgers disease, Thromboangiitis obliterans, Buerger disease, lymphangiogenic disease, hypertrophic or dilating cardiomyopathy, heart failure, pulmonary and peripheral emboli, oncological disease (including solid tumors, and hematological and lymphogenic metastatic oncological disease), macro angiopathy, micro angiopathy, neo angiogenesis, diabetes mellitus, ophthalmic disease, nephrological disease, orthopedic disease, gynecological disease, Parkinson's disease, multiple sclerosis, inflammatory or auto-immune disease, erectile dysfunction, sports injury, Crohn's disease, colitis ulcerosa, pulmonary fibrosis, COPD, emphysema, and cystic fibrosis. In some embodiments, the subject has at least one symptom of chest pain, chest discomfort, shortness of breath, limited exercise tolerance, ventricular or atrial arrhythmia, profuse sweating, aphasia, loss of motor or sensory function, and vision disturbance. In some embodiments, the subject has at least one risk factor for having

a condition comprising perfusion shortage, wherein said risk factor is selected from the group consisting of high blood pressure; glucose intolerance; family history of cardiovascular disease, hypercholesterolaemia, or dyslipidemia ; aging; smoking; physical inactivity; obesity; previous cardiovascular disease; diagnosis of diabetes mellitus, kidney disease, peripheral artery disease, or metabolic syndrome; gender; high low density lipoprotein (LDL) level; high cholesterol level; and specific DNA polymorphism associated with higher cardiovascular risk.

[0019] In some embodiments, the hematopoietic EPCs are positive for makers selected from VEGFR2, CD309, Flt1, Flt4, KDR1, VEGFR1, CXCR4, CD31, CD34, CD105, CD133, Sca-1, and c-Kit. In some embodiments, the methods further comprise isolating said Flk1+ cells, fractions thereof, or secretions thereof from a biological sample of said subject. In some embodiments, the biological sample is selected from the group consisting of blood or blood fractions, saliva, urine, stool, cerebrospinal fluid, semen, vaginal secretions, sputum, sweat, breast milk, synovial fluid, mucus, tears, bile, gastric fluid, interstitial fluid, transudate, exudate, and tissue biopsy.

[0020] In some embodiments, the assaying further comprises detecting nucleic acid expression levels, splice variant expression levels, peptide expression levels, or any combination thereof corresponding to said plurality of genes listed in Tables 1-6.

[0021] In some embodiments, the methods further comprise detecting said nucleic acid expression levels or splice variant expression levels or both expression levels comprising employing cDNA chip array analysis, quantitative (RT) PCR, microarray analysis, multiplexing, Luminex analysis, nucleic acid sequencing, northern blot analysis, genomic high throughput sequencing, nanostring, massive parallel signature sequencing (MPSS),and serial analysis of gene expression (SAGE), or any combination thereof. In some embodiments, the methods comprise detecting peptide expression levels comprises employing enzyme-linked immunosorbent assay (ELISA), protein sequencing, mass spectrometry (such as MALDI TOF, QTOF, or SELDI TOF), quantitative western blot analysis, and peptide barcoding, or any combination thereof. In some embodiments, the methods further comprise transmitting said output onto an intranet or internet.

[0022] In some embodiments, the methods further comprise at least one of: identifying a previous episode of the condition in the subject when the expression levels of at least two genes from Tables 1-6 are outside of a range of control expression levels of said at

least two genes from Tables 1-6; diagnosing the subject as having the condition when the expression levels of at least two genes from Tables 1-6 are outside of a range of control expression levels of said at least two genes from Tables 1-6; determining the subject to be at risk of the condition when the expression levels of at least two genes from Tables 1-6 are outside of a range of control expression levels of said at least two genes from Tables 1-6; prognosticating an outcome in the subject based on a presence of, or degree to which the expression levels of at least two genes from Tables 1-6 are outside of a range of control expression levels of said at least two genes from Tables 1-6; predicting a response of the subject to a medical intervention based on a presence of, or degree to which the expression levels of at least two genes from Tables 1-6 are outside of a range of control expression levels of said at least two genes from Tables 1-6; selecting a medical intervention for the subject, (for example such as, by way of a surrogate marker) based on a presence of, or degree to which the expression levels of at least two genes from Tables 1-6 are outside of a range of control expression levels of said at least two genes from Tables 1-6; selecting a dose and/or frequency of a medical intervention based on a presence of, or degree to which the expression levels of at least two genes from Tables 1-6 are outside of a range of control expression levels of said at least two genes from Tables 1-6; validating a candidate medical intervention based on an effect of the candidate medical intervention on a presence of, or degree to which the expression levels of at least two genes from Tables 1-6 are outside of a range of control expression levels of said at least two genes from Tables 1-6; measuring a response to a candidate medical intervention, wherein the measuring comprises the expression levels of at least two genes from Tables 1-6 are outside of a range of control expression levels of said at least two genes from Tables 1-6; monitoring a subject's response to a medical intervention based on the expression levels of at least two genes from Tables 1-6; or treating a subject with a nucleotide sequence listed in Tables 3 and 4 or a peptide sequence listed in Tables 3 and 4.

[0023] In another aspect, the present disclosure provides a kit comprising a plurality of probes that is configured to detect expression levels of two or more genes listed in Tables 1-6. In some embodiments, the plurality of probes is a nucleic acid probe configured to bind to a sequence of a gene listed in Tables 1-6. In some embodiments, the plurality of probes is an antibody configured to bind to a protein encoded by a gene listed in Tables 1-6.

[0024] In another aspect, the present disclosure provides methods of profiling gene expression for determining one or more genes as signature for a perfusion shortage risk, comprising: (a) assaying gene expression in a cell from a subject with a perfusion shortage risk, and a control set; (b) detecting a subset of genes expressed at an altered state in the cell of the subject compared to the control set; (c) using a machine learning algorithm for analysis of a combination of genes expressed at an altered state to determine the sufficient number of such genes to identify a gene expression signature for a perfusion shortage risk; (d) rectifying a possible accuracy score based on a follow-up monitoring period with the subject; (e) generating an output of one or more genes that is a signature for a perfusion shortage risk, such that the signature has a predictive accuracy of a perfusion shortage risk that exceeds 66%.

BRIEF DESCRIPTION OF THE DRAWINGS

[0025] FIG. 1 shows a plot exemplifying percent accuracy (Accuracy %) scores to diagnose ischemic heart disease using various combinations of RNA probes in female subjects, with the indicated number of selected probes using different statistical methods as indicated. As used herein, "accuracy" has its ordinary and customary meaning as would be understood by one of ordinary skill in the art in view of this disclosure. It refers to the percentage of results that are neither false positives nor false negatives. Accuracy may be represented mathematically as 100% - ((type 1 error) + (type 2 error)). Type 1 error may also be referred to as "alpha error." Type 2 error may also be referred to as "beta error." A combination of 8 to 14 RNA probes is able to predict ischemic heart disease in female patients with near 100% accuracy (or >99.95% accuracy). The X-axis depict the number of nucleotide RNA probe biomarkers in the diagnostic classifier. The Y-axis depict the accuracy of diagnosis for ischemic heart disease in a cohort of subjects with symptomatic chest pain (n=244). These subjects were referred by the general practitioner for further analysis of complaints suspect for ischemic heart disease (i.e. coronary artery disease; CAD disease) in the cardiology outpatient clinic. The correct diagnoses of these patients were prospectively and retrospectively verified at baseline using standard-of-care/best-of-care diagnostic analysis, and by clinical follow-up at 6 month follow-u The different prediction curves in the graph depict the different biostatistical analysis algorithms used in the analysis of female subjects: grey closed circles depict Diagonal Discriminant Analysis; black closed squares depict Fisher's Discriminant

Analysis; black open squares depicts partial Least Squares w subsequent logistic regression analysis; black closed circles depict Partial Least Squares analysis w subsequent Random Forest analysis; black open circles depict Quadratic Discriminant Analysis.

[0026] FIG. 2 shows a plot exemplifying percent accuracy (Accuracy %) scores to diagnose ischemic heart disease using various combinations of exon biomarkers in female subjects with fitted curves for exons expression levels using different statistical methods according to some embodiments. A particular exon expression level is indicative of a gene expression level associated, which the gene comprises the particular exon region. The X-axis depict the number of nucleotide RNA Exon biomarkers in the diagnostic classifier. The Y-axis depict the accuracy of diagnosis for ischemic heart disease in a cohort of subjects with symptomatic chest pain (n=244). These subjects were referred by the general practitioner for further analysis of complaints suspect for ischemic heart disease (i.e. coronary artery disease; CAD disease) in the cardiology outpatient clinic. The correct diagnoses of these patients were prospectively and retrospectively verified at baseline using standard-of-care/best-of-care diagnostic analysis, and by clinical follow-up at 6-month follow-up. The different prediction curves in the graph depict the different biostatistical analysis algorithms used in the analysis of female subjects: grey closed circles depict Diagonal Discriminant Analysis; black closed squares depict Fisher's Discriminant Analysis; grey open circles depict Linear Discriminant Analysis; and black open squares depicts partial Least Squares w subsequent logistic regression analysis. A combination of 9 to 14 exon biomarkers is able to predict ischemic heart disease in female patients with about 98% accuracy.

[0027] FIG. 3 shows a plot exemplifying percent accuracy (Accuracy %) scores to diagnose ischemic heart disease using the expression levels of various combinations of genes (for instance as detected by nucleotide biomarkers) in female subjects. The X-axis depict the number of gene biomarkers in the diagnostic classifier. The Y-axis depict the accuracy of diagnosis for ischemic heart disease in a cohort of subjects with symptomatic chest pain (n=244). These subjects were referred by the general practitioner for further analysis of complaints suspect for ischemic heart disease (i.e. coronary artery disease; CAD disease) in the cardiology outpatient clinic. The correct diagnoses of these patients were prospectively and retrospectively verified at baseline using standard-of-care/best-of-care diagnostic analysis, and by clinical follow-up at 6-month follow-up. The different prediction curves in the graph depict

the different biostatistical analysis algorithms used in the analysis of female subjects: grey closed circles depict Diagonal Discriminant Analysis; black closed squares depict Fisher's Discriminant Analysis; grey open circles depict Linear Discriminant Analysis; and black open squares depicts partial Least Squares w subsequent logistic regression analysis

[0028] FIG. 4 shows a plot exemplifying percent accuracy (Accuracy %) scores to diagnose ischemic heart disease using various combinations of RNA probes as nucleotide biomarkers in female subjects using Diagonal Discriminant Analysis versus Linear Discriminant Analysis. The X-axis depict the number of nucleotide RNA probe biomarkers in the diagnostic classifier. The Y-axis depict the accuracy of diagnosis for ischemic heart disease in a cohort of subjects with symptomatic chest pain (n=244). These subjects were referred by the general practitioner for further analysis of complaints suspect for ischemic heart disease (i.e. coronary artery disease; CAD disease) in the cardiology outpatient clinic. The correct diagnoses of these patients were prospectively and retrospectively verified at baseline using standard-of-care/best-of-care diagnostic analysis, and by clinical follow-up at 6-month follow-up. The different prediction curves in the graph depict the different biostatistical analysis algorithms used in the analysis of female subjects: black closed circles depict Diagonal Discriminant Analysis; and grey closed circles depict Linear Discriminant Analysis. A combination of 8 to 27 RNA probes as nucleotide biomarkers is able to predict ischemic heart disease in female patients with near 100% accuracy.

[0029] FIG. 5 shows a plot exemplifying percent accuracy (Accuracy %) scores to diagnose ischemic heart disease using various combinations of exon biomarkers in female subjects using Linear Discriminant Analysis. The X-axis depict the number of nucleotide RNA Exon biomarkers in the diagnostic classifier. The Y-axis depict the accuracy of diagnosis for ischemic heart disease in a cohort of subjects with symptomatic chest pain (n=244). These subjects were referred by the general practitioner for further analysis of complaints suspect for ischemic heart disease (i.e. coronary artery disease; CAD disease) in the cardiology outpatient clinic. The correct diagnoses of these patients were prospectively and retrospectively verified at baseline using standard-of-care/best-of-care diagnostic analysis, and by clinical follow-up at 6-month follow-up. The prediction curve in the graph depict the use of Linear Discriminant Analysis in the prediction of the disease allocation of the female subjects. A combination of 9

to 58 exon biomarkers as nucleotide biomarkers is able to predict ischemic heart disease in female patients with about 96-99% accuracy.

[0030] FIG. 6 shows a plot exemplifying percent accuracy (Accuracy %) to diagnose ischemic heart disease using various combinations of RNA probes as nucleotide biomarkers in male subjects. The X-axis depict the number of nucleotide RNA probe biomarkers in the diagnostic classifier. The Y-axis depict the accuracy of diagnosis for ischemic heart disease in a cohort of subjects with symptomatic chest pain (n=244). These subjects were referred by the general practitioner for further analysis of complaints suspect for ischemic heart disease (i.e. coronary artery disease; CAD disease) in the cardiology outpatient clinic. The correct diagnoses of these patients were prospectively and retrospectively verified at baseline using standard-of-care/best-of-care diagnostic analysis, and by clinical follow-up at 6-month follow-up. The different prediction curves in the graph depict the different biostatistical analysis algorithms used in the analysis in male subjects: grey closed circles depict Diagonal Discriminant Analysis; black closed squares depict Fisher's Discriminant Analysis; and black open circles depict Quadratic Discriminant Analysis. A combination of 14 to 40 RNA probes is able to predict ischemic heart disease in male patients with about 98% accuracy.

[0031] FIG. 7 shows a plot exemplifying percent accuracy (Accuracy %) to diagnose ischemic heart disease using the expression of various combinations of genes (for instance as detected by nucleotide biomarkers) in male subjects. The X-axis depict the number of genetic biomarkers in the diagnostic classifier. The Y-axis depict the accuracy of diagnosis for ischemic heart disease in a cohort of subjects with symptomatic chest pain (n=244). These subjects were referred by the general practitioner for further analysis of complaints suspect for ischemic heart disease (i.e. coronary artery disease; CAD disease) in the cardiology outpatient clinic. The correct diagnoses of these patients were prospectively and retrospectively verified at baseline using standard-of-care/best-of-care diagnostic analysis, and by clinical follow-up at 6-month follow-up. The different prediction curves in the graph depict the different biostatistical analysis algorithms used in the analysis of male subjects: grey closed circles depict Diagonal Discriminant Analysis; black closed squares depict Fisher's Discriminant Analysis; grey open circles depict Linear Discriminant Analysis; black open squares depicts partial Least Squares w subsequent logistic regression analysis; black closed circles depict

Partial Least Squares analysis w subsequent Random Forest analysis; black open circles depict Quadratic Discriminant Analysis; and black diamonds depict Random Forrest Analysis. A combination of 14 to 22 nucleotide biomarkers (to indicate corresponding specific genes expression levels) is able to predict ischemic heart disease in male patients with about 93-96% accuracy.

[0032] FIG. 8 provides an illustrative framework for a clinical study for ischemic biomarker diagnostic methods.

[0033] FIG. 9 provides a thorough summary of sensitivity and specificity results of invasive tests currently used to diagnosis coronary artery disease.

[0034] FIG. 10 provides a study assessment schedule for the clinical study outlined in FIG. 8.

DETAILED DESCRIPTION

[0035] Ischemia in cardiovascular patients is typically caused by a coronary artery stenosis and/or occlusion (due to progressive coronary atherosclerosis), leading to a local low oxygen (ischemic) condition in the heart, and may eventually result in myocardial damage and irreversible loss of cardiac contractile function. The narrowing of blood vessels is usually caused by atherosclerosis (fat deposition/ inflammation in the vessel wall). However, the presence of atherosclerosis per se does not mean there is oxygen deprivation. Although ischemia accounts for the onset of heart disease, early ischemic conditions can be quiescent or transient, and therefore may escape detection by conventional diagnostic methods. Further, some available biomarkers are correlated with a greater chance to develop atherosclerosis, which may or may not lead to ischemia.

[0036] Described herein are methods, compositions, kits, and uses for detecting a condition or a likelihood of developing such condition comprising perfusion shortage, such as a condition comprising neoangiogenesis or ischemia, or a risk of such a condition. Without being limited by theory, it is contemplated that ischemia or neoangiogenesis can form the basis of the pathogenesis of some diseases (like ischemic heart or cerebrovascular disease) or determine the prognosis, therapy responsiveness or risk for other diseases). The present disclosure also describes a gender-specific or sex-based approach in detecting the condition or a likelihood of developing such condition comprising perfusion shortage or a risk thereof. In

addition, the present disclosure presents methods for detecting conditions comprising ischemia or a risk thereof in a subject when the subject may not have developed any detectable tissue damages due to ischemic conditions.

[0037] Further, the present disclosure describes methods for identifying and measuring blood markers that are activated due to an oxygen stress response, which may be independent of atherosclerosis. In some aspects, hematopoietic endothelial precursor cells (EPCs) positive for Flk1+ (or its human orthologue, VEGFR2 or KDR) (for convenience, the cells may be referred to herein as "Flk1+ cells," or "Flk1-positive cells"), and optionally at least one of Flt1, Flt4, KDR1, VEGFR1, VEGFR2, CD309, CXCR4, CD31, CD34, CD105, CD133, Sca-1, and c-Kit can exhibit different expression profiles of genes in subjects that are at risk for conditions comprising perfusion shortage (for example conditions comprising neoangiogenesis and/or ischemia). In some cases, the expression profiles of genes can be generated by measuring or detecting the genes' corresponding transcripts, splice variants, exon regions, or peptides. In some embodiments, the genes of interest are listed in Tables 1-6 attached as appendix herein.

[0038] Moreover, the method, composition, use, or kit (e.g., protocol, biomarkers, reference values, and/or algorithm) can be used for the identification of current and past ischemic events (irrespective of its location), or can be used for the selection of patients for more advanced diagnostic workup or initiation/ cessation or modulation of specific therapy, for example to measure a response to the therapy (such as a "gate keeper" or "companion diagnostic" use, rather than a stand-alone diagnostic). The methods, compositions, uses, or kits of some embodiments are therefore able to (with sufficient accuracy) to exclude diseases comprising perfusion shortage (such as neoangiogenesis and/or ischemia) in subjects, as well as identify such diseases.

Gender-specific approach in detecting a condition comprising perfusion shortage or a risk thereof

[0039] Researches have shown that there are sex-related differences between women and men. These sex-related differences may include varying risk factor profiles, accuracy of diagnostic testing, clinical presentations, treatment practices, and outcomes. For example, women have been shown to present cardiovascular symptoms late, and some of these

symptoms may not recognized by health care professionals. In oncology, sex-related differences also include incidence, outcome, and response to therapies after adjusting of known epidemic risk factors. Specifically, large differences in mutation density and frequency of mutation of specific oncogenes have been shown, such as β-catenin and *BAP1*.

[0040] The present disclosure discloses a gender specific approach in detecting a condition comprising perfusion shortage or a risk thereof. In some cases, the methods for analyzing a biological sample comprises obtain the biological sample from the subject. When the subject is a female, a female targeted set of genes is identified and utilized. Further, a set of nucleotide sequences and peptide sequences encoded therefrom as disclosed in Table 3 in female subjects is also identified and utilized. Expression levels of at least two genes (or nucleotide or protein biomarkers) from the female targeted set of genes are measured or detected. Based on the signals detected or measured from the at least two genes (or nucleotide or protein biomarkers) from the female targeted set of genes, an output indicative of the female subject's having or at risk of having the condition comprising perfusion shortage may be generated and reported to a health care professional. In some cases, the methods further comprise obtaining a range of control expression levels of said female targeted set of genes (or nucleotide or protein biomarkers). Tables 1, 3, and 5 attached herein as appendix comprise the female targeted set of genes (including nucleotide sequences that can be used to detect gene expression levels or protein biomarkers that can be used to detect protein expression levels). Table 3 also lists a first plurality of nucleotide sequences that are identified to detect the expression levels of corresponding genes. The listed first plurality of nucleotide sequences are not meant to be limiting as other regions of genes can also be used to detect expression levels of genes. Further, Table 3 lists a send plurality of nucleotide sequences that can hybridize to the first plurality of nucleotide sequences. Additionally, Table 3 lists a third plurality of peptide sequences that are encoded by the first plurality of nucleotide sequences. Peptide sequences (e.g., antibodies (or protein ligands)) that may hybridize to the third plurality of peptide sequences may be used to detect expression levels of the corresponding genes (or protein expression levels). In some cases, the female targeted set of genes does not overlap with the male targeted set of genes. Moreover, Table 5 comprises a set of exon regions of genes in female subjects.

[0041] Further, when the subject is a male, a male targeted set of genes is identified and utilized. Further, a set of nucleotide sequences and peptide sequences encoded therefrom as disclosed in Table 4 in female subjects is also identified and utilized. Expression levels of at least two genes (or nucleotide or protein biomarkers) from the male targeted set of genes (or nucleotide or protein biomarkers) are measured or detected. Based on the signals detected or measured from the at least two genes (or nucleotide or protein biomarkers) from the male targeted set of genes, an output indicative of the male subject's having or at risk of having the condition comprising perfusion shortage may be generated and reported to a health care professional. In some cases, the methods further comprise obtaining a range of control expression levels of said male targeted set of genes (or nucleotide or protein biomarkers). Tables 2, 4, and 6 attached herein as appendix comprise the male targeted set of genes (including nucleotide sequences that can be used to identify genes and peptide sequences encoded therefrom). Table 4 also lists a first plurality of nucleotide sequences that are identified to detect the expression levels of corresponding genes. The listed first plurality of nucleotide sequences are not meant to be limiting as other regions of genes can also be used to detect expression levels of genes. Further, Table 4 lists a send plurality of nucleotide sequences that can hybridize to the first plurality of nucleotide sequences. Additionally, Table 4 lists a third plurality of peptide sequences that are encoded by the first plurality of nucleotide sequences. Peptide sequences (e.g., antibodies (or protein ligands)) that may hybridize to the third plurality of peptide sequences may be used to detect expression levels of the corresponding genes or proteins. Moreover, Table 6 comprises a set of exon regions of genes in male subjects.

[0042] In some cases, pilot data in murine and swine models of ischemia had shown that certain genes were indeed upregulated upon an ischemic myocardial event. Moreover, upregulated expression levels of other specific marker genes as disclosed herein has also been detected in circulating mononuclear cells in the blood of patients with myocardial ischemic events by use of qPCR analysis or any other suitable methods. The differentially expression levels of genes described herein (which have been observed to be differentially expressed in Flk1+ cells or fractions or secretions thereof in subjects suffering from hypoxemia), can comprise any nucleotide sequence, transcript, splice variant, and/or peptide identified by any of SEQ ID NOs: 1-5103, Genes Number 1-9280 (from **Tables 1, 2, 5 & 6**), or a peptide

sequence encoded therefrom. Differential expression levels of these gene(s) as described herein can be indicative of a presence, risk, or severity of a condition comprising perfusion shortage (such as a condition comprising neoangiogenesis or ischemia). Without being limited by theory, the differentially expressed genes identified during hypoxemia as described herein (e.g., any nucleotide sequence, transcript, splice variant, and/or peptide identified by any of SEQ ID NOs: 1-5103, Genes Number 1-9280, or a peptide sequence encoded therefrom) may, in some embodiments, also represent a therapeutic target or lead to promote or regulate (the reactive hypoxemic) neoangiogenesis response and vascular modelling in disease. By enhancing, stabilizing, inhibiting, or ameliorating the gene expression levels of potential therapeutic target(s) or lead(s) or interfering with protein deliveries of potential therapeutic target(s) or lead(s), neoangiogenesis may be inhibited to treat diseases involving neoagiogenesis, for instance, not meant to be limiting, ophthalmic / retinal neoangiogenesis conditions. Also, tumor angiogenesis may be inhibited to slow down the growth a solid tumor and deteriorate tumor growth environment.

[0043] Further, in some case, a female targeted set of genes is listed in Tables 1, 3, and 5. In some cases, a male targeted set of genes is listed in Tables 2, 4, and 6. A control range of the expression levels of genes listed in Tables 1, 3, and 5 and listed in Tables 2, 4, and 6 are obtained from healthy subjects that do not have oxygen stress response due to ischemic conditions. In certain embodiments, when expression levels of the two or more genes from the female targeted genes are measure or detected outside of the control ranges in a female subject, an output or a report may be generated to indicate that the female subject might have or at risk of having a condition comprising perfusion shortage. Moreover, in certain embodiments, when expression levels of the two or more genes from the male targeted genes are measure or detected outside of the control ranges in a male subject, an output or a report may be generated to indicate that the male subject might have or at risk of having a condition comprising perfusion shortage.

[0044] In some embodiments, a method for detecting a condition comprising perfusion shortage (such as a condition comprising neoangiogenesis or ischemia), or risk thereof in a subject is described. The method can comprise detecting, in a biological sample of the subject, expression levels of at least two specified different genes (or nucleotide sequences or peptide biomarkers) listed in Tables 1, 3, and 5 for female subjects and Tables 2, 4, and 6

for male subjects. The method may further comprise detecting expression levels of exon regions as disclosed in Table 5 for female subjects and in Table 6 for male subjects. As disclosed herein, nucleotide and peptide sequences encoded therefrom listed in Tables 3 and 4 maybe used to measure expression levels of corresponding genes. The method can comprise receiving a set of control ranges of expression levels of the specified different gene products (as described herein, the control ranges can be determined experimentally, or received as a set of stored values, for example electronically or optically stored values). The method can comprise detecting the condition comprising neoangiogenesis or ischemia or a risk thereof when the expression levels of the specified different genes are outside of the control ranges. By way of example, the expression level of a DNA, RNA, splice variant, peptide, or a combination thereof of a gene from either a female or male targeted set of genes can be measured or detected. The method may comprise determining the copy number, level of expression, or level of activity of the at least two specified different genes (or nucleotide sequences or peptide biomarkers) in a biological sample from the subject. In some embodiments, the method comprises comparing the copy number, level of expression, or level of activity of the at least two specified different gene products with control ranges of copy number, level of expression, or level of activity, in which a significantly modulated copy number, level of expression, or level of activity of the target, relative to the control ranges, is an indication of neoangiogenesis or ischemia, or risk thereof in the subject. By way of example, expression levels of the genes can be determined to be outside of the control range using a statistical method selected from the group consisting of Fisher Discriminant analysis (FDA), Diagonal linear discriminant analysis (DLDA), Linear discriminant analysis (LDA), linear discriminant analysis based on partial least-squares (PLSLDA), partial least squares random Forest (PLSRF), orthogonal discriminant analysis (QDA), and Random Forest (RF), or a combination of any two of the listed methods. In some embodiments, the method is an *in vitro* method.

[0045] In some cases, the at least two specified different gene products correspond to two different genes selected from Tables 1-6. In some cases, the at least two specified different gene products comprise at least two different sequences in SEQ ID NOs: 1-5103, Genes Number 1-9280, or a peptide sequence encoded therefrom. The at least two different sequences may be any combination of different sequences or gene products among SEQ ID

NOs: 1-5103, Genes Number 1-9280, or a peptide sequence encoded therefrom. For example, the method, composition, kit, or use of some embodiments can comprise measuring or detecting the expression levels of at least 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, 50, or 60 genes from Tables 1-6, including ranges between any two of the listed values, for example, 2-14, 2-15, 2-16, 2-17, 2-18, 2-19, 2-20, 2-40, 20-50, 20-60, 4-14, 4-15, 4-20, 4-25, 4-30, 4-35, 4-40, 4-50, 4-60, 5-10, 5-14, 5-15, 5-16, 5-17, 5-18, 5-19, 5-20, 5-40, 5-50, 5-60, 6-14, 6-15, 6-20, 6-25, 6-30, 6-35, 6-40, 6-50, 6-60, 8-14, 8-15, 8-20, 8-25, 8-30, 8-35, 8-40, 8-50, 8-60, 9-10, 9-14, 9-15, 9-16, 9-20, 9-40, 9-50, 9-60, 10-14, 10-15, 10-20, 10-25, 10-30, 10-35, 10-40, 10-50, or 10-60 genes from Tables 1-6. In some embodiments, for example, if the subject is male, the methods disclosed herein comprise assaying no more than 40 different genes, for example no more than 40, 39, 38, 37, 36, 35, 34, 33, 32, 31, 30, 29, 28, 27, 26, 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 6, 5, 4, 3 or 2 different genes (or nucleotide or protein biomarkers) from Tables 2, 4, and 6, for example 2-14, 2-15, 2-16, 2-17, 2-18, 2-19, 2-20, 2-40, 20-50, 20-60, 4-14, 4-15, 4-20, 4-25, 4-30, 4-35, 4-40, 5-10, 5-14, 5-15, 5-16, 5-17, 5-18, 5-19, 5-20, 5-40, 5-50, 5-60, 6-14, 6-15, 6-20, 6-25, 6-30, 6-35, 6-40, 8-14, 8-15, 8-20, 8-25, 8-30, 8-35, 8-40, 8-50, 8-60, 9-10, 9-14, 9-15, 9-16, 9-20, 9-40, 10-14, 10-15, 10-20, 10-25, 10-30, 10-35, or 10-40 different genes (or nucleotide or protein biomarkers). In some embodiments, for example, if the subject is female, the methods disclosed herein comprise assaying no more than 40 different genes, for example no more than 60, 59, 58, 57, 56, 55, 54,53, 52, 51, 50, 49, 48, 47, 46, 45, 44, 43, 42, 41, 40, 39, 38, 37, 36, 35, 34, 33, 32, 31, 30, 29, 28, 27, 26, 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 6, 5, 4, 3 or 2 different genes (or nucleotide or protein biomarkers) from Tables 1, 3, and 5, for example, 2-14, 2-15, 2-16, 2-17, 2-18, 2-19, 2-20, 2-40, 20-50, 20-60, 4-14, 4-15, 4-20, 4-25, 4-30, 4-35, 4-40, 4-50, 4-60, 5-10, 5-14, 5-15, 5-16, 5-17, 5-18, 5-19, 5-20, 5-40, 5-50, 5-60, 6-14, 6-15, 6-20, 6-25, 6-30, 6-35, 6-40, 6-50, 6-60, 8-14, 8-15, 8-20, 8-25, 8-30, 8-35, 8-40, 8-50, 8-60, 9-10, 9-14, 9-15, 9-16, 9-20, 9-40, 9-50, 9-60, 10-14, 10-15, 10-20, 10-25, 10-30, 10-35, 10-40, 10-50, or 10-60 different genes (or nucleotide or protein biomarkers).

[0046] In some embodiments, when the expression levels of the at least two different gene products are outside of the control ranges, the condition comprising perfusion shortage, or a risk thereof is detected. For example, if the expression levels of the at least two different

genes (or nucleotide or protein biomarkers) exceed the control range, the condition or risk thereof may be detected. In some embodiments, the expression levels of the at least two different genes (or nucleotide or protein biomarkers) are outside of the control ranges, and the condition or a risk thereof is detected.

[0047] In the method of some embodiments, when the expression levels of about 4 to about 40, about 4 to about 60, about 6 to about 40, about 6 to about 60, about 8 to about 40, about 8 to about 60, about 10 to about 40, or about 10 to about 60 specified different genes are outside of the control ranges, and the condition comprising perfusion shortage or a risk thereof is detected. In the method of some embodiments, when the expression levels of about 4 to about 30 specified different genes are outside of the control ranges, and the condition or a risk thereof is detected. In the method of some embodiments, when the expression levels of about 4 to about 20 specified different gene products are outside of the control ranges, and the condition or a risk thereof is detected. In the method of some embodiments, when the expression levels of about 6 to about 40 specified different gene products are outside of the control ranges, and the condition or a risk thereof is detected. In the method of some embodiments, when the expression levels of about 6 to about 30 specified different gene products are outside of the control ranges, and the condition or a risk thereof is detected. In the method of some embodiments, when the expression levels of about 6 to about 20 specified different gene products are outside of the control ranges, and the condition or a risk thereof is detected. In the method of some embodiments, when the expression levels of about 2 to about 30 specified different gene products are outside of the control ranges, and the condition or a risk thereof is detected. In the method of some embodiments, when the expression levels of about 5 to about 10 specified different gene products are outside of the control ranges, and the condition or a risk thereof is detected. In the method of some embodiments, when the expression levels of about 8 to about 14 specified different gene products are outside of the control ranges, and the condition or a risk thereof is detected. In the method of some embodiments, when the expression levels of about 10 to about 15 specified different gene products are outside of the control ranges, and the condition or a risk thereof is detected. In the method of some embodiments, the expression levels of fewer than 15 specified different genes are outside of the control ranges, and the condition or a risk thereof is detected. In the method

of some embodiments, when the expression levels of about 15 to about 20 specified different gene products are outside of the control ranges, and the condition or a risk thereof is detected.

[0048] In some embodiments, when the subject is female, the method comprises detecting the condition comprising perfusion shortage or a risk thereof in the subject when the expression levels of at least two specified different genes (or nucleotide or protein biomarkers) that each comprise a sequence from SEQ ID NOs: 1-5103, Genes Number 1-9280, or a peptide sequence encoded therefrom are outside of the control ranges, for example 2-60 or 2-40 specified different genes, including subranges within the listed range, for example, about 2-14, 2-15, 2-16, 2-17, 2-18, 2-19, 2-20, 2-40, 20-50, 20-60, 4-14, 4-15, 4-20, 4-25, 4-30, 4-35, 4-40, 4-50, 4-60, 5-10, 5-14, 5-15, 5-16, 5-17, 5-18, 5-19, 5-20, 5-40, 5-50, 5-60, 6-14, 6-15, 6-20, 6-25, 6-30, 6-35, 6-40, 6-50, 6-60, 8-14, 8-15, 8-20, 8-25, 8-30, 8-35, 8-40, 8-50, 8-60, 9-10, 9-14, 9-15, 9-16, 9-20, 9-40, 9-50, 9-60, 10-14, 10-15, 10-20, 10-25, 10-30, 10-35, 10-40, 10-50, or 10-60 specified different genes that each comprise a sequence from Tables 1, 3, and 5 (or peptide sequence encoded therefrom). Other suitable nucleotide sequences or probes that can detect and measure the expression levels of genes listed in Tables 1, 3, and 5 may also be used to detect the condition or the likelihood of developing such condition comprising perfusion shortage in female subjects. Moreover, other suitable peptide sequences that can detect and measure the expression levels of genes listed in Tables 1, 3, and 5 may also be used to detect the condition or the likelihood of developing such condition comprising perfusion shortage in female subjects. When the subject is male, the method comprises detecting the condition comprising perfusion shortage or a risk thereof in the subject when the expression levels of at least two specified different genes that each comprise a sequence from SEQ ID NOs: 1-5103, Genes Number 1-9280, or a peptide sequence encoded therefrom are outside of the control ranges, for example 2-60 or 2-40 specified different genes, including subranges within the listed range, for example, about 2-14, 2-15, 2-16, 2-17, 2-18, 2-19, 2-20, 2-40, 4-14, 4-15, 4-20, 4-25, 4-30, 4-35, 4-40, 5-10, 5-14, 5-15, 5-16, 5-17, 5-18, 5-19, 5-20, 5-40, 6-14, 6-15, 6-20, 6-25, 6-30, 6-35, 6-40, 8-14, 8-15, 8-20, 8-25, 8-30, 8-35, 8-40, 9-10, 9-14, 9-15, 9-16, 9-20, 9-40, 10-14, 10-15, 10-20, 10-25, 10-30, 10-35, or 10-40 specified different genes that each comprise a sequence from Tables 2, 4, and 6 (or peptide sequence encoded therefrom). Other suitable nucleotide sequences or probes that can detect and measure the expression levels of genes listed in Tables 2, 4, and 6 may also be used to detect the condition

or the likelihood of developing such condition comprising perfusion shortage in male subjects. Moreover, other suitable peptide sequences that can detect and measure the expression levels of genes listed in Tables 2, 4, and 6 may also be used to detect the condition or the likelihood of developing such condition comprising perfusion shortage in male subjects. In some embodiments, the same numerical of genes is detected for male and female subjects.

[0049] In some embodiments, when the subject is female, the method comprises detecting the condition comprising perfusion shortage or a risk thereof in the subject when the expression levels of at least two specified different genes (or nucleotide or protein biomarkers) from Tales 1, 3, and 5 are outside of the control ranges, for example 2-60 specified different genes, including subranges within the listed range, , for example, 2-14, 2-15, 2-16, 2-17, 2-18, 2-19, 2-20, 2-40, 20-50, 20-60, 4-14, 4-15, 4-20, 4-25, 4-30, 4-35, 4-40, 4-50, 4-60, 5-10, 5-14, 5-15, 5-16, 5-17, 5-18, 5-19, 5-20, 5-40, 5-50, 5-60, 6-14, 6-15, 6-20, 6-25, 6-30, 6-35, 6-40, 6-50, 6-60, 8-14, 8-15, 8-20, 8-25, 8-30, 8-35, 8-40, 8-50, 8-60, 9-10, 9-14, 9-15, 9-16, 9-20, 9-40, 9-50, 9-60, 10-14, 10-15, 10-20, 10-25, 10-30, 10-35, 10-40, 10-50, or 10-60 specified different genes (or nucleotide or protein biomarkers).

[0050] In some embodiments, when the subject is male, the method comprises detecting the condition or a risk thereof in the subject when the expression levels of at least two specified different genes (or nucleotide or protein biomarkers) from Tables 2, 4, and 6 are outside of the control ranges, for example at least 2 and less than 15, 14, 13, 12, 11, or 10 specified different genes (or nucleotide or protein biomarkers).

[0051] In some embodiments, when the subject is female, the method comprises detecting, from the biological sample, expression levels of only 2-40 specified different genes from Tables 1, 3, and 5, including subranges within the listed range, for example, about 2-14, 2-15, 2-16, 2-17, 2-18, 2-19, 2-20, 2-40, 4-14, 4-15, 4-20, 4-25, 4-30, 4-35, 4-40, 5-10, 5-14, 5-15, 5-16, 5-17, 5-18, 5-19, 5-20, 5-40, 6-14, 6-15, 6-20, 6-25, 6-30, 6-35, 6-40, 8-14, 8-15, 8-20, 8-25, 8-30, 8-35, 8-40, 9-10, 9-14, 9-15, 9-16, 9-20, 9-40, 10-14, 10-15, 10-20, 10-25, 10-30, 10-35, or 10-40 specified different genes. When the subject is male, the method comprises detecting, from the biological sample, expression levels of only 2-40 specified different genes (or nucleotide or protein biomarkers) from Tables 2, 4, and 6, for example, only 2-14, 2-15, 2-16, 2-17, 2-18, 2-19, 2-20, 2-40, 4-14, 4-15, 4-20, 4-25, 4-30, 4-35, 4-40, 5-10, 5-14, 5-15, 5-16, 5-17, 5-18, 5-19, 5-20, 5-40, 6-14, 6-15, 6-20, 6-25, 6-30, 6-35, 6-40, 8-14,

8-15, 8-20, 8-25, 8-30, 8-35, 8-40, 9-10, 9-14, 9-15, 9-16, 9-20, 9-40, 10-14, 10-15, 10-20, 10-25, 10-30, 10-35, or 10-40 specified different genes (or nucleotide or protein biomarkers). In some embodiments, the same numerical of gene products is detected for male and female subjects.

[0052] In some embodiments, when the subject is female, the method comprises detecting, from the sample, expression levels of only 2-14, 2-15, 2-16, 2-17, 2-18, 2-19, 2-20, 2-40, 4-14, 4-15, 4-20, 4-25, 4-30, 4-35, 4-40, 5-10, 5-14, 5-15, 5-16, 5-17, 5-18, 5-19, 5-20, 5-40, 6-14, 6-15, 6-20, 6-25, 6-30, 6-35, 6-40, 8-14, 8-15, 8-20, 8-25, 8-30, 8-35, 8-40, 9-10, 9-14, 9-15, 9-16, 9-20, 9-40, 10-14, 10-15, 10-20, 10-25, 10-30, 10-35, or 10-40 specified different genes (or nucleotide or protein biomarkers) from Tables 1, 3, and 5. In some embodiments, the same numerical of gene products is detected for male and female subjects. In some embodiments, when the subject is male, the method comprises detecting, from the sample, expression levels of only 2-14, 2-15, 2-16, 2-17, 2-18, 2-19, 2-20, 2-40, 4-14, 4-15, 4-20, 4-25, 4-30, 4-35, 4-40, 5-10, 5-14, 5-15, 5-16, 5-17, 5-18, 5-19, 5-20, 5-40, 6-14, 6-15, 6-20, 6-25, 6-30, 6-35, 6-40, 8-14, 8-15, 8-20, 8-25, 8-30, 8-35, 8-40, 9-10, 9-14, 9-15, 9-16, 9-20, 9-40, 10-14, 10-15, 10-20, 10-25, 10-30, 10-35, or 10-40 specified different genes (or nucleotide or protein biomarkers) from Tables 2, 4, and 6.

[0053] In some embodiments, receiving a set of control ranges of expression levels of the specified different gene products comprises receiving a set of electronically or optically stored values. For example, control ranges may be obtained from a reference, such as an electronic database in which control ranges are stored.

[0054] In some embodiments, receiving a set of control ranges of expression levels of the specified different gene products comprises detecting expression levels of the specified different gene products of isolated hematopoietic endothelial precursor cells (EPCs), which includes EPCs expressing surface marker Flk1, or EPCs expression other surface markers, such as Flt1, Flt4, CD31, CD34 and more, of a control individual who does not have the condition and does not have a risk thereof.

Methods for detecting a condition comprising perfusion shortage using hematopoietic endothelial precursor cells (EPCs) cells, fractions or secretions thereof

[0055] Blood-based diagnostics are challenged by a high abundances of non-biomarker species, such as albumin, globulins, and blood group glycans, and relatively low abundances of biomolecules useful for disease and risk assessment. Many blood biomarkers correlate with the current health status of a patient, and provide minimal insight into the patient's propensity for developing a disease or condition. Furthermore, as blood biomolecules are derived from disparate cell and tissue types, direct blood analysis can be blind to risk factors for localized conditions.

[0056] The present disclosure provides a range of strategies which circumvent these challenges and enable biological state and disease predisposition diagnoses patient blood samples. While many blood biomarkers correlate weakly with perfusion shortage and related factors (e.g., neoangiogenesis or ischemia), the expression patterns of hematopoietic lineage endothelial precursor cells (EPCs), and in particular cases Flk1+ EPCs, can be highly responsive to perfusion shortage risk and development. In some aspects, the present disclosure presents methods for analyzing a biological sample obtained from a subject. The methods comprise subjecting a plurality of hematopoietic lineage endothelial precursor cells (EPCs), fractions of said plurality of hematopoietic lineage EPCs, secretions of said plurality of hematopoietic lineage EPCs, or any combination thereof isolated from said biological sample, to a gene (nucleotide or protein) expression analysis, wherein said gene (nucleotide or protein) expression analysis comprises assaying expression levels of two or more genes (nucleotides or proteins) from a plurality of identified genes (nucleotides or proteins); and generating an output comprising said gene (nucleotide or protein) expression levels, wherein said gene (nucleotide or protein) expression levels are indicative of said subject's having or risk of having a condition comprising perfusion shortage at least in part based on said expression levels. Hematopoietic lineage EPCs or other vascular precursor cells that have the same characteristics are involved in the neoangiogenesis response. For example, hematopoietic lineage EPCs respond and react to low oxygen conditions such as low perfusion, hypoxemia, or ischemia, and play a role in new blood vessel formation at the site of low oxygen condition in order to correct such condition.

[0057] In some cases, hematopoietic EPCs may be Flk1+, meaning, the EPCs express FlK1 receptors on cell surface (maybe referred as Flk1+ cells). Flk1 may be referred to as "VEGFR2,", "CD309", "Kdr" and "Kdr1," and these terms may be used interchangeably

herein. In a biological sample of a certain organism, the relevant Flk1 orthologue for that organism is detected. For example, in a human biological sample (or for a human subject), "Flk1" or "Kdr1" or "VEGFR2" is understood to refer to the *Homo sapiens* orthologue of this gene. As used herein, "Flk1+ cell" or fractions or secretions thereof" (including variations of these root terms) has its ordinary and customary meaning as would be understood by one of ordinary skill in the art in view of this disclosure. The Flk1+ phenotype may identify endothelial precursor cells, and the shorthand "Flk1+ cell" refers to cells that are positive for Flk1. The Flk1+ cells may be further positive for markers selected from Flt1 (also referred to as VEGFR1), Flt4 (also referred to as VEGFR3), VEGFR1, CXCR4, CD31, CD34, CD105, CD133, Sca-1, and c-Kit. For example, the Flk1+ cell may be Flk1+, Flk1+ Flt1+, Flk1+ Flt4+, Flk1+ Flt1+ Flt4+, Flk1+ Flt1+ VEGFR1+, or Flk1+ Flt1+ VEGFR1+ CXCR4+, or any combinations comprising the additional markers listed above.

[0058] In some cases, hematopoietic EPCs may express cell surface markers selected from Flt1, Flt4, KDR1, VEGFR1, VEGFR2, CD309, CXCR4, CD31, CD34, CD105, CD133, Sca-1, and c-Kit. The hematopoietic EPCs may not express Flk1. The hematopoietic EPCs may express cell surface markers, such as CD34, Flt4, CD105, and CD133. As disclosed herein, hematopoietic EPCs could be endothelial precursor cells that express any combinations of the cell surface markers disclosed herein.

[0059] As used herein, a "biological sample" refers to bodily fluids and/or tissues including blood, plasma, serum, stool, lymph, cerebrospinal fluid, saliva, sputum, tears, sweat, semen, transudate, urine, exudate, tissue biopsy, and synovial fluid. In some embodiments, the sample comprises, consists essentially of, or consists of Flk1+ cells, or gene products produced from Flk1+ cells (for example fractions of Flk1+ cells, and/or proteins secreted by Flk1+ cells). In some embodiments, the sample comprises, consists essentially of, or consists of hematopoietic EPCs that does not express Flk1 but express cell surface markers selected from Flt1, Flt4, KDR1, VEGFR1, CXCR4, CD31, CD34, CD105, CD133, Sca-1, and c-Kit, or gene products produced from these cells (for example fractions of these cells, and/or proteins secreted by these cells). In some embodiments, the sample comprises, consists essentially of, or consists of whole Flk1+ cells as described herein. In some embodiments, the sample comprises, consists essentially of, or consists of whole hematopoietic EPCs that does not express Flk1, but express cell surface markers selected from Flt1, Flt4, KDR1, VEGFR1,

CXCR4, CD31, CD34, CD105, CD133, Sca-1, and c-Kit, as described herein. In some embodiments, the sample comprises, consists essentially of, or consists of isolated Flk1+ cells. For example, at least 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95%, 97%, or 99% of the cells in the biological sample can be Flk1+ cells, including ranges between any two of the listed values, for example, 5%-80%, 5%-99%, 20%-80%, 20%-99%, 50%-80%, or 50%-99%. In some embodiments, the sample comprises, consists essentially of, or consists of isolated hematopoietic EPCs that does not express Flk1, but express cell surface markers selected from Flt1, Flt4, KDR1, VEGFR1, CXCR4, CD31, CD34, CD105, CD133, Sca-1, and c-Kit. In some embodiments, single cells of the biological sample are analyzed. In some embodiments, the sample comprises, consists essentially of, or consists of a sample of isolated Flk1+ cells, or a fraction or cellular secretion of these cells. In some embodiments, the sample comprises, consists essentially of, or consists of a sample of isolated hematopoietic EPCs that does not express Flk1 but express cell surface markers selected from Flt1, Flt4, KDR1, VEGFR1, CXCR4, CD31, CD34, CD105, CD133, Sca-1, and c-Kit, or a fraction or cellular secretion of these cells. For example, the expression level of a nucleic acid sequence or a peptide sequence encoded therefrom of one or more of SEQ ID NOs: 1-5103, Genes Number 1-9280, or a peptide sequence encoded therefrom in the cellular secretions or fractions may be measured or detected.

[0060] To avoid or minimize contamination with gene products of other cells, the hematopoietic EPCs disclosed herein may be obtained as whole cells. However, once these whole cells have been isolated, cellular secretions or fractions may be used. Accordingly, in some embodiments, a sample comprises a cellular secretion or fraction of, or isolated hematopoietic EPCs disclosed herein. In some embodiments, the sample comprises one or more Flk1+ cells. In some embodiments, the sample can comprise at least 10^4, 10^5, 10^6, 10^7, 10^8, 10^9, or more (including ranges between any two of the listed values, for example 10^4-10^6, 10^4-10^9, or 10^6-10^9) hematopoietic EPCs or fractions or secretions thereof. Samples comprising hematopoietic EPCs (or fractions or secretions thereof) may also comprise body fluids and/or tissues (including but not limited to blood, plasma, serum, stool, lymph, cerebrospinal fluid, saliva, sputum, tears, sweat, semen, transudate, exudate, tissue biopsies and synovial fluid). The body fluid and/or tissue may comprise one or more hematopoietic EPCs, or fractions or sections of one more hematopoietic EPCs.

[0061] As used herein "isolated" hematopoietic EPC has its ordinary and customary meaning as would be understood by one of ordinary skill in the art in view of this disclosure. It refers to hematopoietic EPCs in a composition that is enriched for this cell type. The hematopoietic EPCs may be present in concentrations relative to other cell types sufficient for detection of expression profiles of gene products described herein associated with conditions comprising ischemia or neoangiogenesis. In methods, compositions, kits, and uses of some embodiments, the biological samples comprise at least 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, or 99% isolated hematopoietic EPCs, fractions, or secretions thereof compared to other cell types, including ranges between any two of the listed values such as 20-99%, 20-90%, 20-80%, 40-99%, 40-90%, 40-80%, 50%-99%, 50%-90%, 50%-80%, 70%-99%, 70%-90%, 70%-80%, 90%-99%, 90%-95% or 95%-99%. In some embodiments, the biological samples consist essentially of or consist of hematopoietic EPCs, fractions, or secretions thereof. In some embodiments, the biological samples comprise isolated whole mononuclear peripheral blood cells that consists essentially of the hematopoietic EPCs. In some embodiments, the isolated hematopoietic EPCs are in a biological sample that is free of other cell types. Hematopoietic EPCs may be isolated using any suitable technique, for example, flow cytometry for cells positive for Flk1, Flt1, Flt4, CD31, CD34, or any other cell surface markers disclosed herein and/or separation of cells using antibodies for Flk1, Flt1, Flt4, CD31, CD34, or any other cell surface markers disclosed herein, affixed to a solid phase (so that cells comprising Flk1, Flt1, Flt4, CD31, CD34, or any other cell surface markers disclosed herein can be bound to the solid phase, while other cells are washed away or discarded). By way of example, the solid phase may comprise beads such as magnetic beads. By way of example, isolation of cells such as hematopoietic EPCs with Flk1 marker is described in US 6,852,533 B1, which is hereby incorporated by reference in its entirety. Flk1+ cells may be isolated from biological samples such as blood samples. Flk1+ cells may be isolated from tissue biopsy samples. Cells can be isolated using methods such as (but not limited to) flow cytometry/FACS, Dynabeads magnetic beads, based on surface markers that are specifically expressed in the cells of interest.

Detecting a condition comprising perfusion shortage or a risk thereof with a high accuracy

[0062] In some aspects, the present disclosure presents methods for detecting conditions comprising perfusion shortage or a risk thereof with an accuracy level of above at least 91%. As used herein, "accuracy" refers to the percentage of results that are neither false positives nor false negatives. Accuracy may be represented mathematically as 100% - ((type 1 error) + (type 2 error)). Type 1 error may also be referred to as "alpha error." Type 2 error may also be referred to as "beta error."

[0063] Conventionally, patients analyzed for chest pain reminiscent of angina pectoris are analyzed using a combination of ECG, standard blood work, exercise testing, myocardial contrast echocardiography (MCE), CT analysis (including calcium imaging, CT angiography and MSCT), or more advanced perfusion imaging (including scintigraphy or nuclear imaging (PET, PET/CT, MIBI, SPECT, or CZT-SPECT)) or CMR perfusion imaging which has yielded an adequate diagnosis in 74% of the cases. Even with advanced perfusion imaging, the adequate/accurate diagnosis of ischemic heart disease does not exceed 84% using these conventional approaches. In addition, setting up a multi-disciplinary analysis of these patients remains a logistical challenge (involving functional testing and imaging, involvement of the departments of cardiology, nuclear medicine, and radiology) and represents a laborious and costly diagnostic track (with disappointing accuracy). In addition, with these conventional approaches, the extent of ischemia, or the biological response to ischemia cannot be readily quantified (or expressed in AU) for use in monitoring of these patients for disease progression or therapy responsiveness.

[0064] The present disclosure shows measuring or detecting signals from multiple genes (protein or nucleotide biomarkers) in accordance with some embodiments can yield superior accuracy for detecting conditions comprising perfusion shortage or a risk thereof. Based on the organism studied, biological samples containing cells expressing relevant markers (as such, it will be appreciated that for a human subject, a "Flk1+" cell refers to a "VEGFR2+" or "CD309" cell, and that in a mouse, a "Flk1+ cell refers to a "Flk1+" cell) are obtained for further analysis. These expression profiles can offer accurate identification, prediction, and monitoring of conditions comprising perfusion shortage, having substantially lower misclassification scores than conventional approaches. However, not all cell types exhibit gene product expression profiles indicative of such conditions or risks thereof, and the presence of expression data from other cell types can cause noise that interferes with

identification, prediction, and monitoring of conditions comprising perfusion shortage. Thus, in accordance with methods, compositions, kits, and uses of some embodiments, gene expression profiles can be detected in isolated hematopoietic EPCs disclosed herein or fractions or secretions thereof, so as to avoid noise that may be caused by detection of expression profiles in other cell populations. Furthermore, it is observed that superior classification of conditions comprising perfusion shortage (or risk of the same) can be obtained when the number of different gene products utilized is within a certain range. Accordingly, in some embodiments, a condition comprising perfusion shortage, or a risk of such a condition is detected by detecting the expression level of a specified number (for example, at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12, or 4-40, 4-60, 6-40, 6-60, 8-40, 8-60, 10-40, or 10-60) different gene products selected from Tables 1-6. The expression levels can be detected in isolated subject hematopoietic EPCs disclosed herein or fractions or secretions thereof of the subject.

In some embodiments, when the subject is female, the expression levels of less than 60, 55, 50, 45, 40, 35, 30, 25, 20, 15, 14, 13, 12, 10, 8, 6, 4 or 2 genes (nucleotide or protein biomarkers) from the plurality of genes listed in Tables 1, 3, and 5 are measured and detected. In some cases, when the subject is female, the expression levels of less than 60, 55, 50, 45, 40, 35, 30, 25, 20, 15, 14, 13, 12, 10, 8, 6, 4 or 2 genes (nucleotide or protein biomarkers) from the plurality of genes listed in Table 1 are measured and detected. In some cases, when the subject is female, the expression levels of less than 60, 55, 50, 45, 40, 35, 30, 25, 20, 15, 14, 13, 12, 10, 8, 6, 4 or 2 genes (nucleotide or protein biomarkers) from the plurality of genes are selected from the group consisting of ZNF807, LOC100130331, LOC100130872, LINC01502, FAM66A, SRGAP3-AS3, MIR1185-1, MIR1266, MIR1261, MIR4262, MTRNR2L10, MIR3928, LOC100507065, LOC100507642, MIR1273F, MIR4519, MIR4799, MIR4747, PTPRU, LOC100996660, DNAL4, XXYLT1-AS2, LOC101927230, LOC101927377, LOC101927479, LOC101927503, LINC01186, LOC101927735, LOC101927880, LINC01486, LOC101928775, RHOXF1P1, LOC101929108, LOC101929330, LOC101929696, CEACAM5, LAMTOR5, CELP, SLC27A4, RCC1, STMN2, CAPN11, FDX1L, MIR155HG, CSMD2, PNMA5, HSPA12B, CLN5, LRRC38, COL3A1, ARHGEF19, PROKR2, COX6C, PTRH1, KRTAP13-1, ASB9, CRYGC, VTI1A, BEST3, SLC22A31, ADIG, LINC01104, PYDC2, PRSS3P2, OTUD7A, DCC, RBM46, TCEANC, ADAMTS17, EFNA5, CELSR2, U2AF1L4, PIKFYVE, KCTD6, PTPLB, EMX1,

OR9I1, JAZF1, LAMB4, FOXC2, NCOA6, MESDC2, FBXO28, DNMBP, U2SURP, ABCA6, CBX5, CBLC, KIF4A, C20orf166-AS1, NUDT8, NUP210P1, SMCO1, MAP7D2, ALX3, FAM133B, SUN2, HECTD1, WIPI2, SNORD53, GJA8, DHDH, GPR4, MRGPRG-AS1, LOC283731, LINC00304, ZNF763, IGHV1-58, LOC284933, RBMY1A3P, GPX5, MED4, C6orf15, GUCY1A2, GUCA2A, HUNK, TFAP2E, POTEA, LEUTX, OR2T3, IGFALS, C19orf45, FAM99A, IGFL3, OR2M1P, FAM90A25P, C8orf86, TMEM8C, PABPN1L, LIG4, FLJ26245, KRT16P2, PRSS57, LTBP3, MIR215, ARSF, MEF2C, IQSEC3, LOC441179, ZNRF2P1, MT1M, MTIF2, MYO7A, NDUFB9, ATP2B1, MIR422A, CEND1, LARS, UFM1, PDHA2, CES1P1, PLTP, LURAP1, MRPS21, MED1, PPP1R3C, RBM41, ASIC4, ZNF821, PPP1R9A, TRMU, UTP6, CCDC177, TBC1D24, GPR158, NYNRIN, BAI2, GBA3, PTPRO, RAC3, CDH26, RPLP0, BGN, FAM204A, PJA1, MT1IP, SHBG, LOC646513, SLA, SKOR2, SLC34A1, SNRPD1, SOX9, SP1, MIR532, TDG, TNNI3, DNLZ, LOC729739, C8A, VIPR2, USP7, DDX39B, ICE2, DCSTAMP, HIST1H4J, ZNF484, REG4, LRRIQ1, FAM126A, DOCK7, RNMT, ST3GAL5, GAL3ST3, SLC25A21, FATE1, UNC5A, TBX18, FIBP, DLGAP1, MGME1, SYCE1, HAND1, TNFRSF8, MAP4K4, GOSR1, SETDB1, SLC23A2, DOPEY2, TBX5-AS1, MIR216B, LOC100128364, LOC100130093, LINC01387, PSORS1C3, LOC100131372, UBE2DNL, LOC100133331, SNAR-I, NCAM1-AS1, WI2-2373I1.2, LOC100288866, MIR1289-2, MIR1976, MIR1250, MIR3115, MIR3907, MIR3944, CCDC179, CEBPZOS, LOC100505940, LOC100506125, LOC100506713, NA, MIR378D1, MIR4489, NA, PQBP1, USP12-AS2, ARHGEF38-IT1, LINC01314, LOC100996637, LOC101060400, LRPPRC, LOC101926941, LOC101927029, LOC101927419, LOC101927542, LOC101927585, LOC101927722, MRGPRF-AS1, LOC101928765, LOC101928850, LOC101929074, LOC101929239, LAMP5-AS1, LOC101929374, NA, ENOX2, ARFGEF2, PROKR1, AFG3L2, GLIPR1, TLK2, INSL6, KLK8, VPS45, ATG4A, MRGPRE, C10orf71, C10orf32, ZFP3, CHMP4B, FAM83C, AP1S3, TRIM71, ADORA1, C9orf85, MAGEC3, SAMD10, C11orf40, SERPINA12, TMED6, MGAT5B, ZNRF4, C1orf64, FAM71A, LINC00896, CYP2A7, CYP2E1, C9orf163, RIBC1, ANKFN1, ZNF579, GPR125, MIER3, DEFB4A, C10orf91, COX7B2, DLX5, DNASE1L2, B3GNT6, LCE4A, LINC00870, OR8J1, OPN5, SCUBE3, FGF6, FGF11, ATG14, FOXD4, MYO16, DDN, FLNB, EHBP1, SLC16A8, FUT3, MYADML2, HIST1H2BA, GABRB3, NATD1, FSCN2, DFNB31, MTHFD1L, ANKRD2, RGS17,

CACNG4, ARHGEF16, GOLGA1, GPR6, HECTD4, LINC00523, OR4N4, FADS6, LINC00482, SLC9C2, IGHV1-2, GPR25, RPL34-AS1, TRBV30, LCN12, IGLV6-57, ALG6, LMCD1, TLX3, RAX, HCRT, HMMR, HOXA7, APOA1, LOC338667, C2orf70, LOC339807, ZSCAN22, GPR149, MPC1L, SLC6A18, LINC00265, IL13, AQP5, KCNC3, ARF6, KRT81, LCN15, CES1P2, KRT39, OR7A10, LINC01121, LOC401127, CD180, MAT1A, LOC440300, FLJ31662, NDUFS1, Sep-02, NEUROD1, NOTCH4, COL5A3, BOLA1, DESI2, GAL, CDC40, EIF3L, COMMD10, PGF, PKP1, CPXCR1, PRKAG3, FXYD7, POU3F3, NUTM2F, PCSK4, VPS13C, EPS8L1, PPL, CCDC40, RBM23, TMEM38B, RIC8B, ETNK2, DDX19A, ZNF280C, WDR11, C1orf106, EAPP, USE1, ECHDC1, PCDHA6, TEX13B, PROC, KLK6, TBX20, CD177, PSMD13, TTYH1, CLK4, LRTM1, ZNF512B, PTK6, ADGRB2, PTN, VAT1L, IGDCC4, PBOV1, NYX, RPL15, RPS6, RPS21, SCT, CCL19, NECAB3, WIPF3, TMEM168, FLJ38668, LOC644961, EBF2, ANHX, ST3GAL4, BRD9, ELOVL4, MIR591, TF, TP73, C5, UBE2V2, UMOD, MIR802, ZNF226, SLC30A3, HSD17B8, TUBAL3, TRAPPC13, TMEM62, ACAD10, THUMPD2, WBSCR16, PVRL4, TKTL1, INHBE, ATAD3B, CASP7, GFM2, KRTAP4-4, TTBK1, RNASE7, CCDC54, MYO18B, ZSCAN10, FIBCD1, ATG4C, RERG, TCAP, DENR, AKR7A2, CADPS, CBFB, MBTPS1, MYH13, PER2, GYG2, CDK5R2, HIST1H3F, PAPLN, BAZ1B, CTU1, BTAF1, PIAS2, CERS5, INA, SYNGR3, ACBD5, SLFN11, BMP15, LGI1, MEX3A, DMKN, TCEAL1, LHX2, PPT2, NCR2, MED7, CABP1, ADAMTS1, NUP155, ADAMTSL2, FAM115A, ZBTB39, HNRNPDL, and DMTF1. In some cases, when the subject is female, the expression levels of two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, twenty or more, thirty or more, forty or more, fifty or more, sixty or more, seventy or more, eighty or more, ninety or more, one hundred or more, two hundred or more genes, three hundred or more, four hundred or more, or five hundred or more (nucleotide or protein biomarkers) for the plurality of genes listed above are measured and detected.

[0065] In some cases, when the subject is female, the expression levels of less than 60, 55, 50, 45, 40, 35, 30, 25, 20, 15, 14, 13, 12, 10, 8, 6, 4 or 2 genes (nucleotide or protein biomarkers) from the plurality of genes listed in Table 1 are measured and detected. In some cases, when the subject is female, the expression levels of less than 60, 55, 50, 45, 40, 35, 30, 25, 20, 15, 14, 13, 12, 10, 8, 6, 4 or 2 genes (nucleotide or protein biomarkers) from the plurality

of genes are selected from the group consisting of ZNF807, LOC100130331, LOC100130872, LINC01502, FAM66A, SRGAP3-AS3, MIR1185-1, MIR1266, MIR1261, MIR4262, MTRNR2L10, MIR3928, LOC100507065, LOC100507642, MIR1273F, MIR4519, MIR4799, MIR4747, PTPRU, LOC100996660, DNAL4, XXYLT1-AS2, LOC101927230, LOC101927377, LOC101927479, LOC101927503, LINC01186, LOC101927735, LOC101927880, LINC01486, LOC101928775, RHOXF1P1, LOC101929108, LOC101929330, LOC101929696, CEACAM5, LAMTOR5, CELP, SLC27A4, RCC1, STMN2, CAPN11, FDX1L, MIR155HG, CSMD2, PNMA5, HSPA12B, CLN5, LRRC38, COL3A1, ARHGEF19, PROKR2, COX6C, PTRH1, KRTAP13-1, ASB9, CRYGC, VTI1A, BEST3, SLC22A31, ADIG, LINC01104, PYDC2, PRSS3P2, OTUD7A, DCC, RBM46, TCEANC, ADAMTS17, EFNA5, CELSR2, U2AF1L4, PIKFYVE, KCTD6, PTPLB, EMX1, OR9I1, JAZF1, LAMB4, FOXC2, NCOA6, MESDC2, FBXO28, DNMBP, U2SURP, ABCA6, CBX5, CBLC, KIF4A, C20orf166-AS1, NUDT8, NUP210P1, SMCO1, MAP7D2, ALX3, FAM133B, SUN2, HECTD1, WIPI2, SNORD53, GJA8, DHDH, GPR4, MRGPRG-AS1, LOC283731, LINC00304, ZNF763, IGHV1-58, LOC284933, RBMY1A3P, GPX5, MED4, C6orf15, GUCY1A2, GUCA2A, HUNK, TFAP2E, POTEA, LEUTX, OR2T3, IGFALS, C19orf45, FAM99A, IGFL3, OR2M1P, FAM90A25P, C8orf86, TMEM8C, PABPN1L, LIG4, FLJ26245, KRT16P2, PRSS57, LTBP3, MIR215, ARSF, MEF2C, IQSEC3, LOC441179, ZNRF2P1, MT1M, MTIF2, MYO7A, NDUFB9, ATP2B1, MIR422A, CEND1, LARS, UFM1, PDHA2, CES1P1, PLTP, LURAP1, MRPS21, MED1, PPP1R3C, RBM41, ASIC4, ZNF821, PPP1R9A, TRMU, UTP6, CCDC177, TBC1D24, GPR158, NYNRIN, BAI2, GBA3, PTPRO, RAC3, CDH26, RPLP0, BGN, FAM204A, PJA1, MT1IP, SHBG, LOC646513, SLA, SKOR2, SLC34A1, SNRPD1, SOX9, SP1, MIR532, TDG, TNNI3, DNLZ, LOC729739, C8A, VIPR2, USP7, DDX39B, ICE2, DCSTAMP, HIST1H4J, ZNF484, REG4, LRRIQ1, FAM126A, DOCK7, RNMT, ST3GAL5, GAL3ST3, SLC25A21, FATE1, UNC5A, TBX18, FIBP, DLGAP1, MGME1, SYCE1, HAND1, TNFRSF8, MAP4K4, GOSR1, SETDB1, SLC23A2, DOPEY2, and TBX5-AS1. In some cases, when the subject is female, the expression levels of two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, twenty or more, thirty or more, forty or more, fifty or more, sixty or more, seventy or more, eighty or more,

ninety or more, one hundred or more, or two hundred or more genes (nucleotide or protein biomarkers) for the plurality of genes listed above are measured and detected.

[0066] In some cases, when the subject is female, the expression levels of less than 60, 55, 50, 45, 40, 35, 30, 25, 20, 15, 14, 13, 12, 10, 8, 6, 4 or 2 genes (nucleotide or protein biomarkers) detected using the plurality of probes and/or mRNA targets listed in **Table 3** are measured and detected. The probes and/or mRNA target sequences are designed to measure and/or detect certain genes. In some cases, the plurality of exon regions of genes selected from **Table 5** are selected from the group of genes in **Table 19**. In some cases, when the subject is female, the expression levels of less than 60, 55, 50, 45, 40, 35, 30, 25, 20, 15, 14, 13, 12, 10, 8, 6, 4 or 2 exon regions (nucleotide or protein biomarkers) from the plurality of exon regions of genes listed in **Table 5** are measured and detected. In some cases, the plurality of exon regions of genes selected from **Table 5** are selected from the group of genes in **Table 20**. In some cases, the plurality of exon regions of genes selected from **Table 5** comprise at least one of the genes selected from the group consisting of Gene Number 1554, Gene Number 1558 (ARHGEF16), Gene Number 1606 (SAMD13), Gene Number 1782 (ELK4), Gene Number 1785 (ESRRG), Gene Number 1788, Gene Number 1790 (HHIPL2), Gene Number 1792 (TRIM17), Gene Number 1822 (GHITM), and Gene Number 1837 (BTRC). In some cases, the plurality of exon regions of genes selected from **Table 5** comprise at least two of the genes selected from the group consisting of Gene Number 1554, Gene Number 1558 (ARHGEF16), Gene Number 1606 (SAMD13), Gene Number 1782 (ELK4), Gene Number 1785 (ESRRG), Gene Number 1788, Gene Number 1790 (HHIPL2), Gene Number 1792 (TRIM17), Gene Number 1822 (GHITM), and Gene Number 1837 (BTRC). In some cases, the plurality of exon regions of genes selected from **Table 5** comprise at least three of the genes selected from the group consisting of Gene Number 1554, Gene Number 1558 (ARHGEF16), Gene Number 1606 (SAMD13), Gene Number 1782 (ELK4), Gene Number 1785 (ESRRG), Gene Number 1788, Gene Number 1790 (HHIPL2), Gene Number 1792 (TRIM17), Gene Number 1822 (GHITM), and Gene Number 1837 (BTRC). In some cases, the plurality of exon regions of genes selected from **Table 5** comprise at least four of the genes selected from the group consisting of Gene Number 1554, Gene Number 1558 (ARHGEF16), Gene Number 1606 (SAMD13), Gene Number 1782 (ELK4), Gene Number 1785 (ESRRG), Gene Number 1788, Gene Number 1790 (HHIPL2), Gene Number 1792 (TRIM17), Gene Number 1822 (GHITM),

and Gene Number 1837 (BTRC). In some cases, the plurality of exon regions of genes selected from **Table 5** comprise at least five of the genes selected from the group consisting of Gene Number 1554, Gene Number 1558 (ARHGEF16), Gene Number 1606 (SAMD13), Gene Number 1782 (ELK4), Gene Number 1785 (ESRRG), Gene Number 1788, Gene Number 1790 (HHIPL2), Gene Number 1792 (TRIM17), Gene Number 1822 (GHITM), and Gene Number 1837 (BTRC). In some cases, the plurality of exon regions of genes selected from **Table 5** comprise at least six of the genes selected from the group consisting of Gene Number 1554, Gene Number 1558 (ARHGEF16), Gene Number 1606 (SAMD13), Gene Number 1782 (ELK4), Gene Number 1785 (ESRRG), Gene Number 1788, Gene Number 1790 (HHIPL2), Gene Number 1792 (TRIM17), Gene Number 1822 (GHITM), and Gene Number 1837 (BTRC). In some cases, the plurality of exon regions of genes selected from **Table 5** comprise Gene Number 1554, Gene Number 1558 (ARHGEF16), Gene Number 1606 (SAMD13), Gene Number 1782 (ELK4), Gene Number 1785 (ESRRG), Gene Number 1788, Gene Number 1790 (HHIPL2), Gene Number 1792 (TRIM17), Gene Number 1822 (GHITM), and Gene Number 1837 (BTRC). In some cases, the plurality of exon regions of genes selected from **Table 5** consists of Gene Number 1554, Gene Number 1558 (ARHGEF16), Gene Number 1606 (SAMD13), Gene Number 1782 (ELK4), Gene Number 1785 (ESRRG), Gene Number 1788, Gene Number 1790 (HHIPL2), Gene Number 1792 (TRIM17), Gene Number 1822 (GHITM), and Gene Number 1837 (BTRC).

[0067] In some cases, the plurality of exon regions of genes selected from **Table 5** comprise at least one of the genes selected from the group consisting of Gene Number 1562 (CLCN6), Gene Number 1576 (EXTL1), Gene Number 1577 (ATPIF1), Gene Number 1580 (GJB3), Gene Number 1591, Gene Number 1606 (SAMD13), Gene Number 1626 (VPS45), Gene Number 1658 (KCTD3), Gene Number 1693 and (AIM1L). In some cases, the plurality of exon regions of genes selected from **Table 5** comprise at least two of the genes selected from the group consisting of Gene Number 1562 (CLCN6), Gene Number 1576 (EXTL1), Gene Number 1577 (ATPIF1), Gene Number 1580 (GJB3), Gene Number 1591, Gene Number 1606 (SAMD13), Gene Number 1626 (VPS45), Gene Number 1658 (KCTD3), Gene Number and 1693 (AIM1L). In some cases, the plurality of exon regions of genes selected from **Table 5** comprise at least three of the genes selected from the group consisting of Gene Number 1562 (CLCN6), Gene Number 1576 (EXTL1), Gene Number 1577 (ATPIF1), Gene Number 1580

(GJB3), Gene Number 1591, Gene Number 1606 (SAMD13), Gene Number 1626 (VPS45), Gene Number 1658 (KCTD3), and Gene Number 1693 (AIM1L). In some cases, the plurality of exon regions of genes selected from **Table 5** comprise at least four of the genes selected from the group consisting of Gene Number 1562 (CLCN6), Gene Number 1576 (EXTL1), Gene Number 1577 (ATPIF1), Gene Number 1580 (GJB3), Gene Number 1591, Gene Number 1606 (SAMD13), Gene Number 1626 (VPS45), Gene Number 1658 (KCTD3), and Gene Number 1693 (AIM1L). In some cases, the plurality of exon regions of genes selected from **Table 5** comprise at least five of the genes selected from the group consisting of Gene Number 1562 (CLCN6), Gene Number 1576 (EXTL1), Gene Number 1577 (ATPIF1), Gene Number 1580 (GJB3), Gene Number 1591, Gene Number 1606 (SAMD13), Gene Number 1626 (VPS45), Gene Number 1658 (KCTD3), and Gene Number 1693 (AIM1L). In some cases, the plurality of exon regions of genes selected from **Table 5** comprise at least six of the genes selected from the group consisting of Gene Number 1562 (CLCN6), Gene Number 1576 (EXTL1), Gene Number 1577 (ATPIF1), Gene Number 1580 (GJB3), Gene Number 1591, Gene Number 1606 (SAMD13), Gene Number 1626 (VPS45), Gene Number 1658 (KCTD3), and Gene Number 1693 (AIM1L). In some cases, the plurality of exon regions of genes selected from **Table 5** comprise Gene Number 1562 (CLCN6), Gene Number 1576 (EXTL1), Gene Number 1577 (ATPIF1), Gene Number 1580 (GJB3), Gene Number 1591, Gene Number 1606 (SAMD13), Gene Number 1626 (VPS45), Gene Number 1658 (KCTD3), and Gene Number 1693 (AIM1L). In some cases, the plurality of exon regions of genes selected from **Table 5** consist of Gene Number 1562 (CLCN6), Gene Number 1576 (EXTL1), Gene Number 1577 (ATPIF1), Gene Number 1580 (GJB3), Gene Number 1591, Gene Number 1606 (SAMD13), Gene Number 1626 (VPS45), Gene Number 1658 (KCTD3), and Gene Number 1693 (AIM1L).

[0068] In some cases, the plurality of exon regions of genes selected from **Table 5** comprise at least one gene selected from the group consisting of Gene Number 1553 (AGRN), Gene Number 1555, Gene Number 1565 (PDPN), Gene Number 1573 (C1orf213), Gene Number 1576 (EXTL1), Gene Number 1588 (KIF2C), Gene Number 1620 (MAN1A2), Gene Number 1636 (USP21), and Gene Number 1770. In some cases, the plurality of exon regions of genes selected from **Table 5** comprise at least two genes selected from the group consisting of Gene Number 1553 (AGRN), Gene Number 1555, Gene Number 1565 (PDPN), Gene

Number 1573 (C1orf213), Gene Number 1576 (EXTL1), Gene Number 1588 (KIF2C), Gene Number 1620 (MAN1A2), Gene Number 1636 (USP21), and Gene Number 1770. In some cases, the plurality of exon regions of genes selected from **Table 5** comprise at least three genes selected from the group consisting of Gene Number 1553 (AGRN), Gene Number 1555, Gene Number 1565 (PDPN), Gene Number 1573 (C1orf213), Gene Number 1576 (EXTL1), Gene Number 1588 (KIF2C), Gene Number 1620 (MAN1A2), Gene Number 1636 (USP21), and Gene Number 1770. In some cases, the plurality of exon regions of genes selected from **Table 5** comprise at least four genes selected from the group consisting of Gene Number 1553 (AGRN), Gene Number 1555, Gene Number 1565 (PDPN), Gene Number 1573 (C1orf213), Gene Number 1576 (EXTL1), Gene Number 1588 (KIF2C), Gene Number 1620 (MAN1A2), Gene Number 1636 (USP21), and Gene Number 1770. In some cases, the plurality of exon regions of genes selected from **Table 5** comprise at least five genes selected from the group consisting of Gene Number 1553 (AGRN), Gene Number 1555, Gene Number 1565 (PDPN), Gene Number 1573 (C1orf213), Gene Number 1576 (EXTL1), Gene Number 1588 (KIF2C), Gene Number 1620 (MAN1A2), Gene Number 1636 (USP21), and Gene Number 1770. In some cases, the plurality of exon regions of genes selected from **Table 5** comprise at least six genes selected from the group consisting of Gene Number 1553 (AGRN), Gene Number 1555, Gene Number 1565 (PDPN), Gene Number 1573 (C1orf213), Gene Number 1576 (EXTL1), Gene Number 1588 (KIF2C), Gene Number 1620 (MAN1A2), Gene Number 1636 (USP21), and Gene Number 1770. In some cases, the plurality of exon regions of genes selected from **Table 5** comprise Gene Number 1553 (AGRN), Gene Number 1555, Gene Number 1565 (PDPN), Gene Number 1573 (C1orf213), Gene Number 1576 (EXTL1), Gene Number 1588 (KIF2C), Gene Number 1620 (MAN1A2), Gene Number 1636 (USP21), and Gene Number 1770. In some cases, the plurality of exon regions of genes selected from **Table 5** consist of Gene Number 1553 (AGRN), Gene Number 1555, Gene Number 1565 (PDPN), Gene Number 1573 (C1orf213), Gene Number 1576 (EXTL1), Gene Number 1588 (KIF2C), Gene Number 1620 (MAN1A2), Gene Number 1636 (USP21), and Gene Number 1770.

[0069] In some cases, the plurality of exon regions of genes selected from **Table 5** comprise at least one gene selected from the group consisting of Gene Number 1555, Gene Number 1562 (CLCN6), Gene Number 1566 (PRDM2), Gene Number 1616, Gene Number 1627 (SETDB1), Gene Number 1648 (CAMSAP2), Gene Number 2729 (ZNF765), Gene

Number 2739 (GPR108), Gene Number 2764, Gene Number 2824 (C2orf15), Gene Number 2879 (SPEG), Gene Number 2890 (SEPT2), and Gene Number 2892. In some cases, the plurality of exon regions of genes selected from **Table 5** comprise at least two genes selected from the group consisting of Gene Number 1555, Gene Number 1562 (CLCN6), Gene Number 1566 (PRDM2), Gene Number 1616, Gene Number 1627 (SETDB1), Gene Number 1648 (CAMSAP2), Gene Number 2729 (ZNF765), Gene Number 2739 (GPR108), Gene Number 2764, Gene Number 2824 (C2orf15), Gene Number 2879 (SPEG), Gene Number 2890 (SEPT2), and Gene Number 2892. In some cases, the plurality of exon regions of genes selected from **Table 5** comprise at least three genes selected from the group consisting of Gene Number 1555, Gene Number 1562 (CLCN6), Gene Number 1566 (PRDM2), Gene Number 1616, Gene Number 1627 (SETDB1), Gene Number 1648 (CAMSAP2), Gene Number 2729 (ZNF765), Gene Number 2739 (GPR108), Gene Number 2764, Gene Number 2824 (C2orf15), Gene Number 2879 (SPEG), Gene Number 2890 (SEPT2), and Gene Number 2892. In some cases, the plurality of exon regions of genes selected from **Table 5** comprise at least four genes selected from the group consisting of Gene Number 1555, Gene Number 1562 (CLCN6), Gene Number 1566 (PRDM2), Gene Number 1616, Gene Number 1627 (SETDB1), Gene Number 1648 (CAMSAP2), Gene Number 2729 (ZNF765), Gene Number 2739 (GPR108), Gene Number 2764, Gene Number 2824 (C2orf15), Gene Number 2879 (SPEG), Gene Number 2890 (SEPT2), and Gene Number 2892. In some cases, the plurality of exon regions of genes selected from **Table 5** comprise at least five genes selected from the group consisting of Gene Number 1555, Gene Number 1562 (CLCN6), Gene Number 1566 (PRDM2), Gene Number 1616, Gene Number 1627 (SETDB1), Gene Number 1648 (CAMSAP2), Gene Number 2729 (ZNF765), Gene Number 2739 (GPR108), Gene Number 2764, Gene Number 2824 (C2orf15), Gene Number 2879 (SPEG), Gene Number 2890 (SEPT2), and Gene Number 2892. In some cases, the plurality of exon regions of genes selected from **Table 5** comprise at least six genes selected from the group consisting of Gene Number 1555, Gene Number 1562 (CLCN6), Gene Number 1566 (PRDM2), Gene Number 1616, Gene Number 1627 (SETDB1), Gene Number 1648 (CAMSAP2), Gene Number 2729 (ZNF765), Gene Number 2739 (GPR108), Gene Number 2764, Gene Number 2824 (C2orf15), Gene Number 2879 (SPEG), Gene Number 2890 (SEPT2), and Gene Number 2892. In some cases, the plurality of exon regions of genes selected from **Table 5** comprise Gene Number 1555, Gene Number 1562 (CLCN6), Gene

Number 1566 (PRDM2), Gene Number 1616, Gene Number 1627 (SETDB1), Gene Number 1648 (CAMSAP2), Gene Number 2729 (ZNF765), Gene Number 2739 (GPR108), Gene Number 2764, Gene Number 2824 (C2orf15), Gene Number 2879 (SPEG), Gene Number 2890 (SEPT2), and Gene Number 2892. In some cases, the plurality of exon regions of genes selected from **Table 5** consist of Gene Number 1555, Gene Number 1562 (CLCN6), Gene Number 1566 (PRDM2), Gene Number 1616, Gene Number 1627 (SETDB1), Gene Number 1648 (CAMSAP2), Gene Number 2729 (ZNF765), Gene Number 2739 (GPR108), Gene Number 2764, Gene Number 2824 (C2orf15), Gene Number 2879 (SPEG), Gene Number 2890 (SEPT2), and Gene Number 2892.

[0070] In some cases, the plurality of exon regions of genes selected from **Table 5** comprise at least one gene selected from the group consisting of Gene Number 1573 (C1orf213), Gene Number 1636 (USP21), Gene Number 1639 (DDR2), Gene Number 1778 (LOC730227), Gene Number 2869 (NRP2), Gene Number 3666 (HLA-A), Gene Number 3689 (SYNGAP1), Gene Number 3694, Gene Number 3710 (HOXA-AS2), and Gene Number 3781 (NPC1L1). In some cases, the plurality of exon regions of genes selected from **Table 5** comprise at least two genes selected from the group consisting of Gene Number 1573 (C1orf213), Gene Number 1636 (USP21), Gene Number 1639 (DDR2), Gene Number 1778 (LOC730227), Gene Number 2869 (NRP2), Gene Number 3666 (HLA-A), Gene Number 3689 (SYNGAP1), Gene Number 3694, Gene Number 3710 (HOXA-AS2), and Gene Number 3781 (NPC1L1). In some cases, the plurality of exon regions of genes selected from **Table 5** comprise at least three genes selected from the group consisting of Gene Number 1573 (C1orf213), Gene Number 1636 (USP21), Gene Number 1639 (DDR2), Gene Number 1778 (LOC730227), Gene Number 2869 (NRP2), Gene Number 3666 (HLA-A), Gene Number 3689 (SYNGAP1), Gene Number 3694, Gene Number 3710 (HOXA-AS2), and Gene Number 3781 (NPC1L1). In some cases, the plurality of exon regions of genes selected from **Table 5** comprise at least four genes selected from the group consisting of Gene Number 1573 (C1orf213), Gene Number 1636 (USP21), Gene Number 1639 (DDR2), Gene Number 1778 (LOC730227), Gene Number 2869 (NRP2), Gene Number 3666 (HLA-A), Gene Number 3689 (SYNGAP1), Gene Number 3694, Gene Number 3710 (HOXA-AS2), and Gene Number 3781 (NPC1L1). In some cases, the plurality of exon regions of genes selected from **Table 5** comprise at least five genes selected from the group consisting of Gene Number 1573

(C1orf213), Gene Number 1636 (USP21), Gene Number 1639 (DDR2), Gene Number 1778 (LOC730227), Gene Number 2869 (NRP2), Gene Number 3666 (HLA-A), Gene Number 3689 (SYNGAP1), Gene Number 3694, Gene Number 3710 (HOXA-AS2), and Gene Number 3781 (NPC1L1). In some cases, the plurality of exon regions of genes selected from **Table 5** comprise at least six genes selected from the group consisting of Gene Number 1573 (C1orf213), Gene Number 1636 (USP21), Gene Number 1639 (DDR2), Gene Number 1778 (LOC730227), Gene Number 2869 (NRP2), Gene Number 3666 (HLA-A), Gene Number 3689 (SYNGAP1), Gene Number 3694, Gene Number 3710 (HOXA-AS2), and Gene Number 3781 (NPC1L1). In some cases, the plurality of exon regions of genes selected from **Table 5** comprise Gene Number 1573 (C1orf213), Gene Number 1636 (USP21), Gene Number 1639 (DDR2), Gene Number 1778 (LOC730227), Gene Number 2869 (NRP2), Gene Number 3666 (HLA-A), Gene Number 3689 (SYNGAP1), Gene Number 3694, Gene Number 3710 (HOXA-AS2), and Gene Number 3781 (NPC1L1). In some cases, the plurality of exon regions of genes selected from **Table 5** consist of Gene Number 1573 (C1orf213), Gene Number 1636 (USP21), Gene Number 1639 (DDR2), Gene Number 1778 (LOC730227), Gene Number 2869 (NRP2), Gene Number 3666 (HLA-A), Gene Number 3689 (SYNGAP1), Gene Number 3694, Gene Number 3710 (HOXA-AS2), and Gene Number 3781 (NPC1L1).

[0071] Further, the expression levels may be compared to control ranges disclosed here to generate an output/report indicative of the subject's having or risk of having a condition comprising perfusion shortage with an accuracy greater than about 99%. In some embodiments, the accuracy is about 99.9%, 99.8%, 99.7%, 99.6%, 99.5%, 99.4%, 99.3%, 99.2%, 99.1%, 98.9%, 98.5%, 98%, 97.5%, 97%, 96.5%, 96%, 95.5%, 95%, 94.5%, 94%, 93.5%, 93%, 92.5%, 92%, or 91.5%.

Table 19

Code PSC	***biomarker nucleotide seq probe***	***biomarker nucleotide seq target mRNA***
2102	ATCAGAGGCAGTTAAGATCCAATGT	TAGTCTCCGTCAATTCTAGGTTACA
8673	AAGTATAGACGCCCCGTCTCTGCCT	TTCATATCTGCGGGGCAGAGACGGA
11464	CTTTATCCCATTTTCGACGTGCCCG	GAAATAGGGTAAAAGCTGCACGGGC
16663	CTGAGACTCCCAGTACGCGGATCGT	GACTCTGAGGGTCATGCGCCTAGCA
21817	ACTCTCTTGCCAGTCGAACCTCGTG	TGAGAGAACGGTCAGCTTGGAGCAC

24286	NA	NA
25439	CGTGTAAATCCCACCGTACCGGAGA	GCACATTTAGGGTGGCATGGCCTCT
29371	AGGCACACTCCCAAGTTCCGGTTCG	TCCGTGTGAGGGTTCAAGGCCAAGC
30491	AGGCCTGTCCCAACTCCATCGAGAG	TCCGGACAGGGTTGAGGTAGCTCTC
31618	AGTGCCTGTCCCTATCTCCAAACGG	TCACGGACAGGGATAGAGGTTTGCC
32943	CTGTTCTCGTCCCTCGGTGTAGGAC	GACAAGAGCAGGGAGCCACATCCTG
33806	TCCGGAATCCAGAAGATAACAGTCT	AGGCCTTAGGTCTTCTATTGTCAGA
36050	GTTACGGTTTCCAGTCAGATCCAGG	CAATGCCAAAGGTCAGTCTAGGTCC
40648	ACCATACTTCCACGACCGGTGTCGG	TGGTATGAAGGTGCTGGCCACAGCC
44512	CCGCCGTCGTCCAATTCCTGTGAAA	GGCGGCAGCAGGTTAAGGACACTTT
48445	GTATAATGACCCTTATTTACTCCAG	CATATTACTGGGAATAAATGAGGTC
52624	AGTCTACGGTCCCTCCTATTTCGTC	TCAGATGCCAGGGAGGATAAAGCAG
53091	CTACAACTCCCTCGTGTAAACACAA	GATGTTGAGGGAGCACATTTGTGTT
53355	ACGACTGTTCCCTCTTAGTGGTGTC	TGCTGACAAGGGAGAATCACCACAG
59716	ACGTCGGTGACCCTAAGTCGAAGGG	TGCAGCCACTGGGATTCAGCTTCCC
62038	ACAAGAGATCCTGACCCTCTTCGAC	TGTTCTCTAGGACTGGGAGAAGCTG
65216	AAAGACGTCTCCTTTGCCCTACCAA	TTTCTGCAGAGGAAACGGGATGGTT
65253	CTCAGGATCCTGGTAGACCCGAGAC	GAGTCCTAGGACCATCTGGGCTCTG
66201	GGGCTCTCTCCTTCACCAGTCGATT	CCCGAGAGAGGAAGTGGTCAGCTAA
71233	ATTCCGGTCCTGTCTCTCAAATTAC	TAAGGCCAGGACAGAGAGTTTAATG
88970	AGGTGCCACCAGTCCATGTACTACG	TCCACGGTGGTCAGGTACATGATGC
89503	GGAATAAACCACTAAACTCGGAGAC	CCTTATTTGGTGATTTGAGCCTCTG
98630	GAGGTGACAGTACCACCCGAGGACA	CTCCACTGTCATGGTGGGCTCCTGT
112599	GTTCTTTCTACCTACCCTTTTGAGG	CAAGAAAGATGGATGGGAAAACTCC
121129	CCGAGTTTCCGATATCTTTATGGTG	GGCTCAAAGGCTATAGAAATACCAC
143577	AACGGTGCACCGTGTCGGAAGGTTT	TTGCCACGTGGCACAGCCTTCCAAA
149915	AGGTCTTGGGAGTTCTTATTAGGGA	TCCAGAACCCTCAAGAATAATCCCT
151536	TTAGGACCGGGGTATCGGACTCCCT	AATCCTGGCCCCATAGCCTGAGGGA
156137	ATAAATAGGGCTAGAAACTTGTGGT	TATTTATCCCGATCTTTGAACACCA
175079	AAAACAGTGGCAGGTCTTAGTGACC	TTTTGTCACCGTCCAGAATCACTGG
179722	ATCCGACATGGACCGCGTCTCCGGA	TAGGCTGTACCTGGCGCAGAGGCCT
196695	ATTTTTGGTGGATGACCGATGGTAC	TAAAAACCACCTACTGGCTACCATG
200539	ACGTCAATTGGTCATAAACTCCAGA	TGCAGTTAACCAGTATTTGAGGTCT
202647	AAATTGTGGTTGAGTCGTTCTCTAG	TTTAACACCAACTCAGCAAGAGATC
232609	AGAGTCCCTAGGATCACAGACCATC	TCTCAGGGATCCTAGTGTCTGGTAG
235679	GACTTAGTAGAAGGTTTTCTAAAGA	CTGAATCATCTTCCAAAAGATTTCT
239356	AGCTCCAGAGGTTCACCCTGTTTGG	TCGAGGTCTCCAAGTGGGACAAACC
239483	ACAGGTGAAGGTCTTTTCTCGGCGG	TGTCCACTTCCAGAAAAGAGCCGCC
241691	CATGTATACGAGGTGGAATTGGAAC	GTACATATGCTCCACCTTAACCTTG

243938	TTGGTACTGAGGTAAACAGTCAGAC	AACCATGACTCCATTTGTCAGTCTG
279663	ATATAAAACGGTAGCGAGTGGGCTT	TATATTTTGCCATCGCTCACCCGAA
433854	TTACCGGAGAAGAGCTAAGACGTTG	AATGGCCTCTTCTCGATTCTGCAAC
449476	CTCCAAGAAGTTTGAGGCCCGTATT	GAGGTTCTTCAAACTCCGGGCATAA
508151	GTCAGGTATTACAACATCAATGCCT	CAGTCCATAATGTTGTAGTTACGGA
617278	ATAACGCCCACTACTACTGTCCGAG	TATTGCGGGTGATGATGACAGGCTC
680209	ATACTGACTAAGAACGGCAACTCTG	TATGACTGATTCTTGCCGTTGAGAC
854711	CTGGTTTTTACTGTCCCGTTTCGCT	GACCAAAAATGACAGGGCAAAGCGA
1279720	GTTATTATTTATTCCCACTGCCCGA	CAATAATAAATAAGGGTGACGGGCT
1326871	TTGTGTACCCTAGATCCCTGACAGT	AACACATGGGATCTAGGGACTGTCA

Table 20

Affymetrix Exon ID B	Transcript Cluster ID	SEQ Name	Strand	Strand Start	Strand Stop
16650141	16650141	---	---	---	---
16650467	16650467	---	---	---	---
16650951	16650951	---	---	---	---
16650957	16650957	---	---	---	---
16651195	16651195	---	---	---	---
16651411	16651411	---	---	---	---
16651571	16651571	---	---	---	---
16651811	16651811	---	---	---	---
16651885	16651885	---	---	---	---
16652173	16652173	---	---	---	---
16653133	16653133	---	---	---	---
16653857	16653857	---	---	---	---
16654419	16654419	---	---	---	---
16654495	16654495	---	---	---	---
16655639	16655639	---	---	---	---
16656867	16656867	---	---	---	---
16656939	16656939	---	---	---	---
16657644	16657598	chr1	+	990376.00	990400.00

16657765	16657764	chr1	+	1363700.00	1364109.00
16657951	16657948	chr1	+	1982386.00	1982410.00
16658183	16658159	chr1	+	3397184.00	3397501.00
16659119	16659102	chr1	+	11893647.00	11893671.00
16659462	16659459	chr1	+	13910596.00	13910623.00
16659488	16659478	chr1	+	14095565.00	14095589.00
16660661	16660654	chr1	+	23697718.00	23697938.00
16661046	16661031	chr1	+	26361797.00	26361821.00
16661535	16661533	chr1	+	28562744.00	28562770.00
16662326	16662322	chr1	+	35250766.00	35250799.00
16663974	16663958	chr1	+	45223239.00	45223263.00
16664693	16664690	chr1	+	52518107.00	52518332.00
16666650	16666640	chr1	+	84791390.00	84791414.00
16667753	16667752	chr1	+	101616117.00	101616433.00
16669265	16669255	chr1	+	118008956.00	118009010.00
16670417	16670404	chr1	+	150049779.00	150049803.00
16670661	16670632	chr1	+	150933479.00	150933503.00
16672757	16672754	chr1	+	161130244.00	161130268.00
16673093	16673075	chr1	+	162740364.00	162740388.00
16675168	16675158	chr1	+	186280181.00	186280231.00
16675682	16675673	chr1	+	200811130.00	200811197.00
16677481	16677473	chr1	+	215752419.00	215752443.00
16683833	16683817	chr1	-	26663713.00	26663737.00
16697485	16697484	chr1	-	195727752.00	195728362.00
16698228	16698226	chr1	-	203270218.00	203270406.00
16698507	16698504	chr1	-	205569009.00	205569033.00
16699306	16699290	chr1	-	216896744.00	216896768.00
16699434	16699433	chr1	-	220160865.00	220160943.00
16699580	16699574	chr1	-	222700336.00	222700389.00
16700232	16700218	chr1	-	228604260.00	228604398.00

16706718	16706712	chr10	+	85902423.00	85902496.00
16708482	16708468	chr10	+	103295201.00	103295225.00
16864956	16864946	chr19	+	53928352.00	53928381.00
16867866	16867837	chr19	-	6737283.00	6737307.00
16871804	16871800	chr19	-	37996874.00	37996940.00
16883383	16883380	chr2	+	99758755.00	99758852.00
16889881	16889879	chr2	+	206546738.00	206546762.00
16891318	16891273	chr2	+	220341679.00	220341703.00
16893475	16893449	chr2	+	242283265.00	242283289.00
16894005	16894001	chr2	-	3581378.00	3581429.00
17037682	17037670	chr6_qbl_hap6	+	1205278.00	1205318.00
17041405	17041393	chr6_ssto_hap7	+	4886478.00	4886502.00
17042074	17042060	chr6_ssto_hap7	-	3080352.00	3080376.00
17044504	17044491	chr7	+	27163662.00	27163824.00
17057318	17057305	chr7	-	44571379.00	44571428.00

[0072] In some embodiments, when the subject is male, the expression levels of less than 40, 35, 30, 25, 20, or 15 genes (nucleotide or protein biomarker) from said plurality of genes (nucleotide or protein sequences) listed in **Tables 2, 4, and 6** are measured and detected. Further, the expression levels are compared to control ranges disclosed here to generate an output/report indicative of the subject's having or risk of having a condition comprising perfusion shortage with an accuracy greater than about 98%. In some embodiments, when the subject is male, the expression levels of less than 40, 35, 30, 25, 20, or 15 genes (nucleotide or protein biomarker) from said plurality of genes (nucleotide or protein sequences) listed in **Table 2** are measured and detected. In some cases, when the subject is male, the expression levels of less than 40, 35, 30, 25, 20, or 15 genes (nucleotide or protein biomarkers) selected from the group of genes consisting of SNORD115-37, SNORD115-24, SNORA11B, MIR876, COL4A2-AS2, LOC100130373, LOC100130548, LOC100131496, LINC00240, BCL2L11, MED16, ERVV-2, KRTAP21-3, LOC100289230, LOC100289283, MIR1275, MIR1912, MIR1302-7, MIR1231, MIR1238, MIR1179, MIR1908, MIR1237, MIR2116, CSN1S2BP, MIR3148, MIR4280, MIR3116-1, MIR3129, MIR4275, MIR4326, MIR4254, LINC00673,

MIR3926-2, MIR3678, MIR548Z, MIR3657, MIR3935, LOC100505478, LINC01364, C16orf95, LINC00837, MIR3529, MIR4475, MIR4492, MIR4784, MIR4732, MIR4684, MIR4773-2, MIR4429, MIR4442, LINC00507, LOC100996345, CYYR1-AS1, LOC100996635, CDK4, LOC101927053, PDZRN3-AS1, MEOX2-AS1, LINC01186, NA, GBAT2, LINC01214, LOC101928101, LOC101928118, NA, LOC101928195, LOC101928385, TCONS_00029157, LOC101928668, LINC01450, NA, LOC101928823, LOC101928919, LINC01262, LOC101929031, LOC101929159, LOC101929468, LOC101929497, ZNF267, CHERP, IFI44, FUT9, RFPL2, IFI44L, MAPRE2, SLC27A5, CHD1, RABL2B, FSTL1, MRPL3, GLB1L3, GPR182, CHRM5, SMIM12, LRRC37B, SMYD4, TBCB, KLHDC3, RPL39L, CLTB, PRSS30P, PCP2, FITM2, SNTN, TMEM68, OTUD6A, CRP, DYNLL2, CRYGD, NA, TMC8, CSTB, SLC35F3, CCDC140, WDSUB1, SH3D19, TEX28, FEZF1-AS1, ESCO2, ZNF645, CYP51A1, DAB1, ZCCHC12, DNMT3A, DRP2, EGR2, ABCA2, CDY2B, SENP5, EVI2B, ALCAM, ABCD1, F12, FAH, OR5A2, CCDC89, FABP5P3, FGF4, FGF14, DIP2A, ATP11B, NUP210, EXOC6B, ARC, SASH1, GRIP1, SEC61G, SCRIB, POLA2, GABARAPL1, DEFB108B, DEFB113, FTH1P3, CDRT15L2, HEATR9, ALS2CL, ASPM, OR2F1, GATA2, PLA2G2D, GCNT1, AGO1, OR7A5, OR1J2, SNORA70, GNAI3, BCL9L, OTOGL, SLC46A3, EWSAT1, LINC00927, C16orf54, MAMSTR, MCHR1, LOC284825, IGHD2-21, IGHD2-15, EOGT, C8orf31, IGLV10-54, IGLV3-12, SNX24, ARHGAP35, SCG3, PYCR2, SLC39A3, H3F3B, ANXA5, CXXC1, CDR2L, HNF4A, HNRNPK, SNORD56B, KRTAP20-1, KRTAP20-2, LOC339166, ZFP69, LOC340074, KIAA1875, OR2T8, PAQR9, IFNGR1, IGFBP1, KRTAP10-10, IL13RA1, KCNA3, KCNA5, TPTE2P6, LHFPL3, KCNJ10, LINC00162, KCNS3, KRTAP5-1, CC2D2B, RPRML, LRRC14B, OR52N2, LAMA4, LIPE, LINC00200, LINC00668, ZNF880, LOC400756, ASB18, LRRD1, LDLRAD2, LYN, MIR127, MIR210, MIR181A1, MIR9-1, MIR98, MIR99B, MIR17HG, MAFG, MAS1, MAX, MLF1, SUGT1P1, RPS26P11, MYO10, NDUFB9, NKX3-1, NOS1, NRGN, MIR375, DUOX2, RRP15, NMD3, KLHL5, RPL26L1, EGFL7, PCYT1A, CDC40, UFC1, ERGIC3, SF3B6, PFDN4, PIK3C2G, DDIT4, EGLN1, FAM20A, HEATR3, CEP72, THSD1, PSME2, MIR362, MIR494, MIR520C, MIR516B2, MIR502, MIR508, ERMN, RANBP10, SH3RF1, FBRSL1, RET, EXOC4, TGIF2, RPL3L, BCORL1, CCL5, SDCBP, RRAGC, XYLT2, ACOT6, POPDC3, LINC00535, CCT6P1, TSG1, NA, BLVRA, NARFL, CSMD1, SGSH, NDST4, NA,

EFTUD1P1, SIPA1, SLC5A4, PCP4L1, SLC9A2, LYNX1, MIR539, CAPN15, SPAG1, SPRR3, SQLE, SRI, SCARNA2, SCARNA16, TACR1, SNORD66, SNORD84, SNORD91A, SNORD97, MIR552, MIR563, MIR591, TCF19, TNP1, MIR660, SDHAP3, LOC729224, FAHD2CP, SEC14L6, MEIS1-AS3, WNT9A, SNORD113-3, SNORD114-3, SNORD114-9, SNORD114-18, SNORD114-27, SNORD114-30, MIR758, MIR668, ZNF134, PPDPF, OR5H2, CERS4, OGFOD2, LIN28A, NEK11, DCAKD, GPR157, EFHC2, CXXC4, PBX4, CPTP, NPRL3, OR2B2, AKAP17A, PCDH11Y, FAM103A1, TRAPPC9, HYAL3, CASP5, TTTY11, RAB34, NACAP1, SPOP, ZMYND12, LLPH, C22orf23, GTPBP3, SUV420H2, HAT1, SHANK3, KIAA1755, DENR, NPFF, MARCO, JRKL, PAGE1, PABPC4, SYNGAP1, SGPL1, BUD31, HIST1H3F, SYT8, MAP7, ZFAND2A, RGN, VAPB, RCSD1, SLIT2, NCR2, PAGE4, RNF7, MTFR1, CD59, and ATP2C2. In some cases, when the subject is male, the expression levels of two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, twenty or more, thirty or more, forty or more, fifty or more, sixty or more, seventy or more, eighty or more, ninety or more, one hundred or more, two hundred or more, or three hundred or more genes (nucleotide or protein biomarkers) for the plurality of genes listed above are measured and detected.

[0073] In some cases, when the subject is male, the expression levels of less than 40, 35, 30, 25, 20, or 15 genes (nucleotide or protein biomarkers) selected from the group of genes consisting of SNORD115-37, SNORD115-24, SNORA11B, MIR876, COL4A2-AS2, LOC100130373, LOC100130548, LOC100131496, LINC00240, BCL2L11, MED16, ERVV-2, KRTAP21-3, LOC100289230, LOC100289283, MIR1275, MIR1912, MIR1302-7, MIR1231, MIR1238, MIR1179, MIR1908, MIR1237, MIR2116, CSN1S2BP, MIR3148, MIR4280, MIR3116-1, MIR3129, MIR4275, MIR4326, MIR4254, LINC00673, MIR3926-2, MIR3678, MIR548Z, MIR3657, MIR3935, LOC100505478, LINC01364, C16orf95, LINC00837, MIR3529, MIR4475, MIR4492, MIR4784, MIR4732, MIR4684, MIR4773-2, MIR4429, MIR4442, LINC00507, LOC100996345, CYYR1-AS1, LOC100996635, CDK4, LOC101927053, PDZRN3-AS1, MEOX2-AS1, LINC01186, NA, GBAT2, LINC01214, LOC101928101, LOC101928118, NA, LOC101928195, LOC101928385, TCONS_00029157, LOC101928668, LINC01450, NA, LOC101928823, LOC101928919, LINC01262, LOC101929031, LOC101929159, LOC101929468, LOC101929497, ZNF267, CHERP, IFI44, FUT9, RFPL2, IFI44L, MAPRE2, SLC27A5, CHD1, RABL2B, FSTL1,

MRPL3, GLB1L3, GPR182, CHRM5, SMIM12, LRRC37B, SMYD4, TBCB, KLHDC3, RPL39L, CLTB, PRSS30P, PCP2, FITM2, SNTN, TMEM68, OTUD6A, CRP, DYNLL2, CRYGD, NA, TMC8, CSTB, SLC35F3, CCDC140, WDSUB1, SH3D19, TEX28, FEZF1-AS1, ESCO2, ZNF645, CYP51A1, DAB1, ZCCHC12, DNMT3A, DRP2, EGR2, ABCA2, CDY2B, SENP5, EVI2B, ALCAM, ABCD1, F12, FAH, OR5A2, CCDC89, FABP5P3, FGF4, FGF14, DIP2A, ATP11B, NUP210, EXOC6B, ARC, SASH1, GRIP1, SEC61G, SCRIB, POLA2, GABARAPL1, DEFB108B, DEFB113, FTH1P3, CDRT15L2, HEATR9, ALS2CL, ASPM, OR2F1, GATA2, PLA2G2D, GCNT1, AGO1, OR7A5, OR1J2, SNORA70, GNAI3, BCL9L, OTOGL, SLC46A3, EWSAT1, LINC00927, C16orf54, MAMSTR, MCHR1, LOC284825, IGHD2-21, IGHD2-15, EOGT, C8orf31, IGLV10-54, IGLV3-12, SNX24, ARHGAP35, SCG3, PYCR2, SLC39A3, H3F3B, ANXA5, CXXC1, CDR2L, HNF4A, HNRNPK, SNORD56B, KRTAP20-1, KRTAP20-2, LOC339166, ZFP69, LOC340074, KIAA1875, OR2T8, PAQR9, IFNGR1, IGFBP1, KRTAP10-10, IL13RA1, KCNA3, KCNA5, TPTE2P6, LHFPL3, KCNJ10, LINC00162, KCNS3, KRTAP5-1, CC2D2B, RPRML, LRRC14B, OR52N2, LAMA4, LIPE, LINC00200, LINC00668, ZNF880, LOC400756, ASB18, LRRD1, LDLRAD2, LYN, MIR127, MIR210, MIR181A1, MIR9-1, MIR98, MIR99B, MIR17HG, MAFG, MAS1, MAX, MLF1, SUGT1P1, RPS26P11, MYO10, NDUFB9, NKX3-1, NOS1, NRGN, MIR375, DUOX2, RRP15, NMD3, KLHL5, RPL26L1, EGFL7, PCYT1A, CDC40, UFC1, ERGIC3, SF3B6, PFDN4, PIK3C2G, DDIT4, EGLN1, FAM20A, HEATR3, CEP72, THSD1, PSME2, MIR362, MIR494, MIR520C, MIR516B2, MIR502, MIR508, ERMN, RANBP10, SH3RF1, FBRSL1, RET, EXOC4, TGIF2, RPL3L, BCORL1, CCL5, SDCBP, RRAGC, XYLT2, ACOT6, POPDC3, LINC00535, CCT6P1, TSG1, NA, BLVRA, NARFL, CSMD1, SGSH, NDST4, NA, EFTUD1P1, SIPA1, SLC5A4, PCP4L1, SLC9A2, LYNX1, MIR539, CAPN15, SPAG1, SPRR3, SQLE, SRI, SCARNA2, SCARNA16, TACR1, SNORD66, SNORD84, SNORD91A, SNORD97, MIR552, MIR563, MIR591, TCF19, TNP1, MIR660, SDHAP3, LOC729224, FAHD2CP, SEC14L6, MEIS1-AS3, WNT9A, SNORD113-3, SNORD114-3, SNORD114-9, SNORD114-18, SNORD114-27, SNORD114-30, MIR758, MIR668, ZNF134, PPDPF, OR5H2, CERS4, OGFOD2, LIN28A, NEK11, DCAKD, GPR157, EFHC2, CXXC4, PBX4, CPTP, NPRL3, OR2B2, AKAP17A, PCDH11Y, FAM103A1, TRAPPC9, HYAL3, CASP5, TTTY11, RAB34, NACAP1, SPOP, ZMYND12, LLPH, C22orf23, GTPBP3, SUV420H2, HAT1, SHANK3,

KIAA1755, DENR, NPFF, MARCO, JRKL, PAGE1, PABPC4, SYNGAP1, SGPL1, BUD31, HIST1H3F, SYT8, MAP7, ZFAND2A, RGN, VAPB, RCSD1, SLIT2, NCR2, PAGE4, RNF7, MTFR1, CD59, ATP2C2, ZBTB11-AS1, SNORD115-2, MIR942, MIR708, NFYC-AS1, MIR181A1HG, LOC100133669, FAR2P2, MIR513C, MIR1468, MIR1538, MIR1301, MIR1197, MIR3125, FAM212B-AS1, LOC100506371, LOC100506730, LOC100507419, LOC100507507, MIR4686, MIR378D1, MIR3689F, MIR4756, MIR4499, MIR550A3, MIR4425, MIR4691, HTT-AS,CERS6-AS1, RNU6-81P, FGF14-AS1, SLC9A9-AS1, DHRS9, LOC101927314, LOC101927483, LINC01280, LINC01488, LOC101928399, LOC101928509, LOC101928579, LOC101928668, LOC101928880, LOC101929236, LOC101929284, LOC101929432, LOC101929636, PSMD14, GPA33, CDO1, RGS14, GMEB1, MAPRE2, C9orf9, RABL2A, BIRC8, KLHL2, GPN1, CKM, RAB3C, OR52M1, CLK3, JDP2, SNX20, SHE, DMBX1, EDARADD, C20orf144, COMP, GLYCTK, UBLCP1, APOOL, RNF113B, CST1, CREB3L4, CTSL, NCBP2-AS2, MGC32805, CRYGN, TMEM30B, HBEGF, DUSP5, DVL2, E4F1, FLJ23867, ZNF385C, EPS8, EVPL, EXTL1, EZH2, FOXK1, DKFZP586I1420, DIP2C, ATG2A, WDR43, SCFD1, SIN3B, FMR1, USP22, SZT2, CRTC1, MED13L, DEFB110, PROSER2, C19orf26, GEMIN5, SYF2, RWDD3, GARS, INTS1, GBP2, MYEOV, SNORD14A, B3GAT1, ZNF330, PCDH11XGP9, LOC284009, C17orf89, EMC10, WDR62, OR2V2, HOOK2, RPA4, GYPE, HBA2, HBB, HELLS, FOXA2, HNRNPF, HPN, HPRT1, ERAS, HSD17B1, NRBP2, IDI1, FIGLA, RTN4RL2, AQP1, NANOGNB, PDX1, C9orf50, SLC27A1, TRIM74, KIR2DL3, KRTAP12-3, C10orf99, MFSD2B, DKFZp667F0711, SOHLH1, MIR188, MIR26B, MIR296, MAN2A2, MGST3, MLH1, LOC440910, SMIM4, MYBPH, NASP, NDUFA1, NDUFS1, NFIL3, RNASE12, MIR380, OXTR, TXNDC11, RPS27L, SBDS, POMP, UBE2J1, CWC15, ATP6V1H, RBMX2, SERPINB8, TLR9, FAM193B, NUTM2F, DNAJC25, EPN3, KANSL3, VIMP, ZC3H15, EIF2AK2, PSMA2, PSMA4, MIR412, PRR12, ZNF492, SQRDL, RPL28, MIR487A, RPS6KA3, SCN4B, FAM204A, IRF2BPL, ZNF862, GZF1, ATG3, GGT8P, EBF2, SI, SKI, FOXD4L6, SPAG11A, SLN, MIR376A2, FOXL2, TCF3, MIR550A2, DNAJC7, LOC727710, MRS2P2, LOC729739, TMEM258, NELFA, ZNF41, SNORD113-5, SNORD113-8, MIR769, MIR766, CLMP, GGNBP2, BRD3, SSPN, TUBB1, COIL, SF3A2, NRIP1, PARP9, HSDL2, EIF1AD, BRMS1L, SYVN1, TUBB6, USMG5, POMGNT2, MASTL, MIR22HG, IFITM1, KIAA1656, LRRCC1, KRT38, SUCLA2, DPM1, CDC123,

DDX18, CHRNA6, KLHL6, BRSK2, ZNF622, PAGE5, PDLIM1, BTF3L4, DYRK1B, RAB11B, GRAP2, MUC16, CGB8, MED21, EPSTI1, CYTIP, NCOR2, and TMEM63A.

[0074] In some embodiments, when the subject is male, the expression levels of less than 40, 35, 30, 25, 20, or 15 genes (nucleotide or protein biomarker) detected using the plurality of probes and/or mRNA targets listed in **Table 4** are measured and detected. In some cases, the plurality of genes detected using probes and/or mRNA targets selected from **Table 4** are selected from the group of genes in **Table 21**. In some embodiments, when the subject is male, the expression levels of less than 40, 35, 30, 25, 20, or 15 genes (nucleotide or protein biomarker) from said plurality of exon regions of genes (nucleotide or protein sequences) listed in **Table 6** are measured and detected. In some cases, the plurality of exon regions of genes selected from **Table 6** are selected from the group of genes in **Table 22**.

[0075] In some cases, the plurality of exon regions of genes selected from **Table 6** comprise at least one gene selected from the group consisting of Gene Number 4155 (PLCH2), Gene Number 4166 (VPS13D), Gene Number 4167 (PDPN), Gene Number 4169 (DNAJC16), Gene Number 4181 (LDLRAP1), Gene Number 4184 (RPS6KA1), Gene Number 4203 (MFSD2A), Gene Number 4241, Gene Number 4462 (ZMYND12), Gene Number 4562 (TNFSF18), Gene Number 5518, Gene Number 5726 (LMBR1L). In some cases, the plurality of exon regions of genes selected from **Table 6** comprise at least two genes selected from the group consisting of Gene Number 4155 (PLCH2), Gene Number 4166 (VPS13D), Gene Number 4167 (PDPN), Gene Number 4169 (DNAJC16), Gene Number 4181 (LDLRAP1), Gene Number 4184 (RPS6KA1), Gene Number 4203 (MFSD2A), Gene Number 4241, Gene Number 4462 (ZMYND12), Gene Number 4562 (TNFSF18), Gene Number 5518, Gene Number 5726 (LMBR1L). In some cases, the plurality of exon regions of genes selected from **Table 6** comprise at least three genes selected from the group consisting of Gene Number 4155 (PLCH2), Gene Number 4166 (VPS13D), Gene Number 4167 (PDPN), Gene Number 4169 (DNAJC16), Gene Number 4181 (LDLRAP1), Gene Number 4184 (RPS6KA1), Gene Number 4203 (MFSD2A), Gene Number 4241, Gene Number 4462 (ZMYND12), Gene Number 4562 (TNFSF18), Gene Number 5518, Gene Number 5726 (LMBR1L). In some cases, the plurality of exon regions of genes selected from **Table 6** comprise at least four genes selected from the group consisting of Gene Number 4155 (PLCH2), Gene Number 4166 (VPS13D), Gene Number 4167 (PDPN), Gene Number 4169 (DNAJC16), Gene Number 4181

(LDLRAP1), Gene Number 4184 (RPS6KA1), Gene Number 4203 (MFSD2A), Gene Number 4241, Gene Number 4462 (ZMYND12), Gene Number 4562 (TNFSF18), Gene Number 5518, Gene Number 5726 (LMBR1L). In some cases, the plurality of exon regions of genes selected from **Table 6** comprise at least five genes selected from the group consisting of Gene Number 4155 (PLCH2), Gene Number 4166 (VPS13D), Gene Number 4167 (PDPN), Gene Number 4169 (DNAJC16), Gene Number 4181 (LDLRAP1), Gene Number 4184 (RPS6KA1), Gene Number 4203 (MFSD2A), Gene Number 4241, Gene Number 4462 (ZMYND12), Gene Number 4562 (TNFSF18), Gene Number 5518, Gene Number 5726 (LMBR1L). In some cases, the plurality of exon regions of genes selected from **Table 6** comprise at least six genes selected from the group consisting of Gene Number 4155 (PLCH2), Gene Number 4166 (VPS13D), Gene Number 4167 (PDPN), Gene Number 4169 (DNAJC16), Gene Number 4181 (LDLRAP1), Gene Number 4184 (RPS6KA1), Gene Number 4203 (MFSD2A), Gene Number 4241, Gene Number 4462 (ZMYND12), Gene Number 4562 (TNFSF18), Gene Number 5518, Gene Number 5726 (LMBR1L). In some cases, the plurality of exon regions of genes selected from **Table 6** comprise Gene Number 4155 (PLCH2), Gene Number 4166 (VPS13D), Gene Number 4167 (PDPN), Gene Number 4169 (DNAJC16), Gene Number 4181 (LDLRAP1), Gene Number 4184 (RPS6KA1), Gene Number 4203 (MFSD2A), Gene Number 4241, Gene Number 4462 (ZMYND12), Gene Number 4562 (TNFSF18), Gene Number 5518, Gene Number 5726 (LMBR1L). In some cases, the plurality of exon regions of genes selected from **Table 6** consist of Gene Number 4155 (PLCH2), Gene Number 4166 (VPS13D), Gene Number 4167 (PDPN), Gene Number 4169 (DNAJC16), Gene Number 4181 (LDLRAP1), Gene Number 4184 (RPS6KA1), Gene Number 4203 (MFSD2A), Gene Number 4241, Gene Number 4462 (ZMYND12), Gene Number 4562 (TNFSF18), Gene Number 5518, Gene Number 5726 (LMBR1L).

[0076] In some cases, the plurality of exon regions of genes selected from **Table 6** comprise at least one gene selected from the group consisting of Gene Number 4151 (LOC284628), Gene Number 4216 (DMAP1), Gene Number 4258 (LOC100996635), Gene Number 4444, Gene Number 5586, Gene Number 5590 (TRMT5), Gene Number 5879 (IRX6), Gene Number 6181 (FBXL20), Gene Number 6214 (MEP1B), Gene Number 6810, Gene Number 7536 (FGFR3), and Gene Number 8887 (DNAJC25). In some cases, the plurality of genes of exon regions selected from **Table 6** comprise at least two genes selected

from the group consisting of Gene Number 4151 (LOC284628), Gene Number 4216 (DMAP1), Gene Number 4258 (LOC100996635), Gene Number 4444, Gene Number 5586, Gene Number 5590 (TRMT5), Gene Number 5879 (IRX6), Gene Number 6181 (FBXL20), Gene Number 6214 (MEP1B), Gene Number 6810, Gene Number 7536 (FGFR3), and Gene Number 8887 (DNAJC25). In some cases, the plurality of exon regions of genes selected from **Table 6** comprise at least three genes selected from the group consisting of Gene Number 4151 (LOC284628), Gene Number 4216 (DMAP1), Gene Number 4258 (LOC100996635), Gene Number 4444, Gene Number 5586, Gene Number 5590 (TRMT5), Gene Number 5879 (IRX6), Gene Number 6181 (FBXL20), Gene Number 6214 (MEP1B), Gene Number 6810, Gene Number 7536 (FGFR3), and Gene Number 8887 (DNAJC25). In some cases, the plurality of exon regions of genes selected from **Table 6** comprise at least four genes selected from the group consisting of Gene Number 4151 (LOC284628), Gene Number 4216 (DMAP1), Gene Number 4258 (LOC100996635), Gene Number 4444, Gene Number 5586, Gene Number 5590 (TRMT5), Gene Number 5879 (IRX6), Gene Number 6181 (FBXL20), Gene Number 6214 (MEP1B), Gene Number 6810, Gene Number 7536 (FGFR3), and Gene Number 8887 (DNAJC25). In some cases, the plurality of exon regions of genes selected from **Table 6** comprise at least five genes selected from the group consisting of Gene Number 4151 (LOC284628), Gene Number 4216 (DMAP1), Gene Number 4258 (LOC100996635), Gene Number 4444, Gene Number 5586, Gene Number 5590 (TRMT5), Gene Number 5879 (IRX6), Gene Number 6181 (FBXL20), Gene Number 6214 (MEP1B), Gene Number 6810, Gene Number 7536 (FGFR3), and Gene Number 8887 (DNAJC25). In some cases, the plurality of exon regions of genes selected from **Table 6** comprise at least six genes selected from the group consisting of Gene Number 4151 (LOC284628), Gene Number 4216 (DMAP1), Gene Number 4258 (LOC100996635), Gene Number 4444, Gene Number 5586, Gene Number 5590 (TRMT5), Gene Number 5879 (IRX6), Gene Number 6181 (FBXL20), Gene Number 6214 (MEP1B), Gene Number 6810, Gene Number 7536 (FGFR3), and Gene Number 8887 (DNAJC25). In some cases, the plurality of exon regions of genes selected from **Table 6** comprise Gene Number 4151 (LOC284628), Gene Number 4216 (DMAP1), Gene Number 4258 (LOC100996635), Gene Number 4444, Gene Number 5586, Gene Number 5590 (TRMT5), Gene Number 5879 (IRX6), Gene Number 6181 (FBXL20), Gene Number 6214 (MEP1B), Gene Number 6810, Gene Number 7536 (FGFR3), and Gene Number 8887

(DNAJC25). In some cases, the plurality of exon regions of genes selected from **Table 6** consist of Gene Number 4151 (LOC284628), Gene Number 4216 (DMAP1), Gene Number 4258 (LOC100996635), Gene Number 4444, Gene Number 5586, Gene Number 5590 (TRMT5), Gene Number 5879 (IRX6), Gene Number 6181 (FBXL20), Gene Number 6214 (MEP1B), Gene Number 6810, Gene Number 7536 (FGFR3), and Gene Number 8887 (DNAJC25).

[0077] In some cases, the plurality of exon regions of genes selected from **Table 6** comprise at least one gene selected from the group consisting of Gene Number 4164 (TMEM201), Gene Number 4166 (VPS13D), Gene Number 4337 (IPO9), Gene Number 4344 (LAX1), Gene Number 4350 (MFSD4), Gene Number 4356 (DTL), Gene Number 4578 (MIR181A1HG), Gene Number 4709 (GBF1), Gene Number 5478 (PNN), Gene Number 5518, and Gene Number 7345 (OTTHUMG00000162679). In some cases, the plurality of exon regions of genes selected from **Table 6** comprise at least two genes selected from the group consisting of Gene Number 4164 (TMEM201), Gene Number 4166 (VPS13D), Gene Number 4337 (IPO9), Gene Number 4344 (LAX1), Gene Number 4350 (MFSD4), Gene Number 4356 (DTL), Gene Number 4578 (MIR181A1HG), Gene Number 4709 (GBF1), Gene Number 5478 (PNN), Gene Number 5518, and Gene Number 7345 (OTTHUMG00000162679). In some cases, the plurality of exon regions of genes selected from **Table 6** comprise at least three genes selected from the group consisting of Gene Number 4164 (TMEM201), Gene Number 4166 (VPS13D), Gene Number 4337 (IPO9), Gene Number 4344 (LAX1), Gene Number 4350 (MFSD4), Gene Number 4356 (DTL), Gene Number 4578 (MIR181A1HG), Gene Number 4709 (GBF1), Gene Number 5478 (PNN), Gene Number 5518, and Gene Number 7345 (OTTHUMG00000162679). In some cases, the plurality of exon regions of genes selected from **Table 6** comprise at least four genes selected from the group consisting of Gene Number 4164 (TMEM201), Gene Number 4166 (VPS13D), Gene Number 4337 (IPO9), Gene Number 4344 (LAX1), Gene Number 4350 (MFSD4), Gene Number 4356 (DTL), Gene Number 4578 (MIR181A1HG), Gene Number 4709 (GBF1), Gene Number 5478 (PNN), Gene Number 5518, and Gene Number 7345 (OTTHUMG00000162679). In some cases, the plurality of exon regions of genes selected from **Table 6** comprise at least five genes selected from the group consisting of Gene Number 4164 (TMEM201), Gene Number 4166 (VPS13D), Gene Number 4337 (IPO9), Gene Number 4344 (LAX1), Gene Number 4350 (MFSD4), Gene Number 4356

(DTL), Gene Number 4578 (MIR181A1HG), Gene Number 4709 (GBF1), Gene Number 5478 (PNN), Gene Number 5518, and Gene Number 7345 (OTTHUMG00000162679). In some cases, the plurality of exon regions of genes selected from **Table 6** comprise at least six genes selected from the group consisting of Gene Number 4164 (TMEM201), Gene Number 4166 (VPS13D), Gene Number 4337 (IPO9), Gene Number 4344 (LAX1), Gene Number 4350 (MFSD4), Gene Number 4356 (DTL), Gene Number 4578 (MIR181A1HG), Gene Number 4709 (GBF1), Gene Number 5478 (PNN), Gene Number 5518, and Gene Number 7345 (OTTHUMG00000162679). In some cases, the plurality of exon regions of genes selected from **Table 6** comprise Gene Number 4164 (TMEM201), Gene Number 4166 (VPS13D), Gene Number 4337 (IPO9), Gene Number 4344 (LAX1), Gene Number 4350 (MFSD4), Gene Number 4356 (DTL), Gene Number 4578 (MIR181A1HG), Gene Number 4709 (GBF1), Gene Number 5478 (PNN), Gene Number 5518, and Gene Number 7345 (OTTHUMG00000162679). In some cases, the plurality of exon regions of genes selected from **Table 6** consist of Gene Number 4164 (TMEM201), Gene Number 4166 (VPS13D), Gene Number 4337 (IPO9), Gene Number 4344 (LAX1), Gene Number 4350 (MFSD4), Gene Number 4356 (DTL), Gene Number 4578 (MIR181A1HG), Gene Number 4709 (GBF1), Gene Number 5478 (PNN), Gene Number 5518, and Gene Number 7345 (OTTHUMG00000162679).

[0078] In some cases, the plurality of exon regions of genes selected from **Table 6** comprise at least one gene selected from the group consisting of Gene Number 4257 (RWDD3), Gene Number 4628 (ATP5C1), Gene Number 5514 (TDP1), Gene Number 5681 (FAM81A), Gene Number 5696 (NR2E3), Gene Number 5713 (SEMA4B), Gene Number 5764 (MGC15885), Gene Number 6810, Gene Number 6876, Gene Number 7053 (IL10RB), and Gene Number 7155 (POLR2F). In some cases, the plurality of exon regions of genes selected from **Table 6** comprise at least two genes selected from the group consisting of Gene Number 4257 (RWDD3), Gene Number 4628 (ATP5C1), Gene Number 5514 (TDP1), Gene Number 5681 (FAM81A), Gene Number 5696 (NR2E3), Gene Number 5713 (SEMA4B), Gene Number 5764 (MGC15885), Gene Number 6810, Gene Number 6876, Gene Number 7053 (IL10RB), and Gene Number 7155 (POLR2F). In some cases, the plurality of exon regions of genes selected from **Table 6** comprise at least three genes selected from the group consisting of Gene Number 4257 (RWDD3), Gene Number 4628 (ATP5C1), Gene Number

5514 (TDP1), Gene Number 5681 (FAM81A), Gene Number 5696 (NR2E3), Gene Number 5713 (SEMA4B), Gene Number 5764 (MGC15885), Gene Number 6810, Gene Number 6876, Gene Number 7053 (IL10RB), and Gene Number 7155 (POLR2F). In some cases, the plurality of exon regions of genes selected from **Table 6** comprise at least four genes selected from the group consisting of Gene Number 4257 (RWDD3), Gene Number 4628 (ATP5C1), Gene Number 5514 (TDP1), Gene Number 5681 (FAM81A), Gene Number 5696 (NR2E3), Gene Number 5713 (SEMA4B), Gene Number 5764 (MGC15885), Gene Number 6810, Gene Number 6876, Gene Number 7053 (IL10RB), and Gene Number 7155 (POLR2F). In some cases, the plurality of exon regions of genes selected from **Table 6** comprise at least five genes selected from the group consisting of Gene Number 4257 (RWDD3), Gene Number 4628 (ATP5C1), Gene Number 5514 (TDP1), Gene Number 5681 (FAM81A), Gene Number 5696 (NR2E3), Gene Number 5713 (SEMA4B), Gene Number 5764 (MGC15885), Gene Number 6810, Gene Number 6876, Gene Number 7053 (IL10RB), and Gene Number 7155 (POLR2F). In some cases, the plurality of exon regions of genes selected from **Table 6** comprise at least six genes selected from the group consisting of Gene Number 4257 (RWDD3), Gene Number 4628 (ATP5C1), Gene Number 5514 (TDP1), Gene Number 5681 (FAM81A), Gene Number 5696 (NR2E3), Gene Number 5713 (SEMA4B), Gene Number 5764 (MGC15885), Gene Number 6810, Gene Number 6876, Gene Number 7053 (IL10RB), and Gene Number 7155 (POLR2F). In some cases, the plurality of exon regions of genes selected from **Table 6** comprise Gene Number 4257 (RWDD3), Gene Number 4628 (ATP5C1), Gene Number 5514 (TDP1), Gene Number 5681 (FAM81A), Gene Number 5696 (NR2E3), Gene Number 5713 (SEMA4B), Gene Number 5764 (MGC15885), Gene Number 6810, Gene Number 6876, Gene Number 7053 (IL10RB), and Gene Number 7155 (POLR2F). In some cases, the plurality of exon regions of genes selected from **Table 6** consist of Gene Number 4257 (RWDD3), Gene Number 4628 (ATP5C1), Gene Number 5514 (TDP1), Gene Number 5681 (FAM81A), Gene Number 5696 (NR2E3), Gene Number 5713 (SEMA4B), Gene Number 5764 (MGC15885), Gene Number 6810, Gene Number 6876, Gene Number 7053 (IL10RB), and Gene Number 7155 (POLR2F).

[0079] In some cases, the plurality of exon regions of genes selected from **Table 6** comprise at least one gene selected from the group consisting of Gene Number 4151 (PLEKHN1), Gene Number 4337 (IPO9), Gene Number 4350 (MFSD4), Gene Number 4381

(OR2L13), Gene Number 4402 (FLJ42875), Gene Number 4460 (LOC100130557), Gene Number 4511 (CASQ2), Gene Number 4915 (HEPHL1), and Gene Number 7275 (SLC22A14). In some cases, the plurality of exon regions of genes selected from **Table 6** comprise at least two genes selected from the group consisting of Gene Number 4151 (PLEKHN1), Gene Number 4337 (IPO9), Gene Number 4350 (MFSD4), Gene Number 4381 (OR2L13), Gene Number 4402 (FLJ42875), Gene Number 4460 (LOC100130557), Gene Number 4511 (CASQ2), Gene Number 4915 (HEPHL1), and Gene Number 7275 (SLC22A14). In some cases, the plurality of exon regions of genes selected from **Table 6** comprise at least three genes selected from the group consisting of Gene Number 4151 (PLEKHN1), Gene Number 4337 (IPO9), Gene Number 4350 (MFSD4), Gene Number 4381 (OR2L13), Gene Number 4402 (FLJ42875), Gene Number 4460 (LOC100130557), Gene Number 4511 (CASQ2), Gene Number 4915 (HEPHL1), and Gene Number 7275 (SLC22A14). In some cases, the plurality of exon regions of genes selected from **Table 6** comprise at least four genes selected from the group consisting of Gene Number 4151 (PLEKHN1), Gene Number 4337 (IPO9), Gene Number 4350 (MFSD4), Gene Number 4381 (OR2L13), Gene Number 4402 (FLJ42875), Gene Number 4460 (LOC100130557), Gene Number 4511 (CASQ2), Gene Number 4915 (HEPHL1), and Gene Number 7275 (SLC22A14). In some cases, the plurality of genes selected from **Table 6** comprise at least five genes selected from the group consisting of exon regions of Gene Number 4151 (PLEKHN1), Gene Number 4337 (IPO9), Gene Number 4350 (MFSD4), Gene Number 4381 (OR2L13), Gene Number 4402 (FLJ42875), Gene Number 4460 (LOC100130557), Gene Number 4511 (CASQ2), Gene Number 4915 (HEPHL1), and Gene Number 7275 (SLC22A14). In some cases, the plurality of exon regions of genes selected from **Table 6** comprise at least six genes selected from the group consisting of Gene Number 4151 (PLEKHN1), Gene Number 4337 (IPO9), Gene Number 4350 (MFSD4), Gene Number 4381 (OR2L13), Gene Number 4402 (FLJ42875), Gene Number 4460 (LOC100130557), Gene Number 4511 (CASQ2), Gene Number 4915 (HEPHL1), and Gene Number 7275 (SLC22A14). In some cases, the plurality of exon regions of genes selected from **Table 6** comprise Gene Number 4151 (PLEKHN1), Gene Number 4337 (IPO9), Gene Number 4350 (MFSD4), Gene Number 4381 (OR2L13), Gene Number 4402 (FLJ42875), Gene Number 4460 (LOC100130557), Gene Number 4511 (CASQ2), Gene Number 4915 (HEPHL1), and Gene Number 7275 (SLC22A14). In some

cases, the plurality of exon regions of genes selected from **Table 6** consist of Gene Number 4151 (PLEKHN1), Gene Number 4337 (IPO9), Gene Number 4350 (MFSD4), Gene Number 4381 (OR2L13), Gene Number 4402 (FLJ42875), Gene Number 4460 (LOC100130557), Gene Number 4511 (CASQ2), Gene Number 4915 (HEPHL1), and Gene Number 7275 (SLC22A14).

[0080] In some cases, the plurality of exon regions of genes selected from **Table 6** comprise at least one gene selected from the group consisting of Gene Number 4167 (PDPN), Gene Number 4173 (PLA2G5), Gene Number 4196, Gene Number 4176 (EPHA8), Gene Number 4352 (PFKFB2), Gene Number 4837, Gene Number 5491 (PPM1A), Gene Number 6266 (DTNA), Gene Number 6813 (FAM178B), and Gene Number 7393. In some cases, the plurality of exon regions of genes selected from **Table 6** comprise at least two genes selected from the group consisting of Gene Number 4167 (PDPN), Gene Number 4173 (PLA2G5), Gene Number 4196, Gene Number 4176 (EPHA8), Gene Number 4352 (PFKFB2), Gene Number 4837, Gene Number 5491 (PPM1A), Gene Number 6266 (DTNA), Gene Number 6813 (FAM178B), and Gene Number 7393. In some cases, the plurality of exon regions of genes selected from **Table 6** comprise at least three genes selected from the group consisting of Gene Number 4167 (PDPN), Gene Number 4173 (PLA2G5), Gene Number 4196, Gene Number 4176 (EPHA8), Gene Number 4352 (PFKFB2), Gene Number 4837, Gene Number 5491 (PPM1A), Gene Number 6266 (DTNA), Gene Number 6813 (FAM178B), and Gene Number 7393. In some cases, the plurality of exon regions of genes selected from **Table 6** comprise at least four genes selected from the group consisting of Gene Number 4167 (PDPN), Gene Number 4173 (PLA2G5), Gene Number 4196, Gene Number 4176 (EPHA8), Gene Number 4352 (PFKFB2), Gene Number 4837, Gene Number 5491 (PPM1A), Gene Number 6266 (DTNA), Gene Number 6813 (FAM178B), and Gene Number 7393. In some cases, the plurality of exon regions of genes selected from **Table 6** comprise at least five genes selected from the group consisting of Gene Number 4167 (PDPN), Gene Number 4173 (PLA2G5), Gene Number 4196, Gene Number 4176 (EPHA8), Gene Number 4352 (PFKFB2), Gene Number 4837, Gene Number 5491 (PPM1A), Gene Number 6266 (DTNA), Gene Number 6813 (FAM178B), and Gene Number 7393. In some cases, the plurality of exon regions of genes selected from **Table 6** comprise at least six genes selected from the group consisting of Gene Number 4167 (PDPN), Gene Number 4173 (PLA2G5), Gene Number 4196, Gene

Number 4176 (EPHA8), Gene Number 4352 (PFKFB2), Gene Number 4837, Gene Number 5491 (PPM1A), Gene Number 6266 (DTNA), Gene Number 6813 (FAM178B), and Gene Number 7393. In some cases, the plurality of exon regions of genes selected from **Table 6** comprise Gene Number 4167 (PDPN), Gene Number 4173 (PLA2G5), Gene Number 4196, Gene Number 4176 (EPHA8), Gene Number 4352 (PFKFB2), Gene Number 4837, Gene Number 5491 (PPM1A), Gene Number 6266 (DTNA), Gene Number 6813 (FAM178B), and Gene Number 7393. In some cases, the plurality of exon regions of genes selected from **Table 6** consist of Gene Number 4167 (PDPN), Gene Number 4173 (PLA2G5), Gene Number 4196, Gene Number 4176 (EPHA8), Gene Number 4352 (PFKFB2), Gene Number 4837, Gene Number 5491 (PPM1A), Gene Number 6266 (DTNA), Gene Number 6813 (FAM178B), and Gene Number 7393.

[0081] In some cases, the plurality of exon regions of genes selected from **Table 6** comprise at least one gene selected from the group consisting of Gene Number 4145 (PLEKHN1), Gene Number 4166 (VPS13D), Gene Number 4590 (PLXNA2), Gene Number 4952 (ST14), Gene Number 5042 (LTBP3), Gene Number 5181 (ACSS3), Gene Number 5209 (ATP2A2), Gene Number 6714 (BCS1L), Gene Number 6809, Gene Number 7007 (CPNE1), Gene Number 7354 (COL6A6), Gene Number 7458 (LINC00971), and Gene Number 7474 (HGD). In some cases, the plurality of genes of exon regions selected from **Table 6** comprise at least two genes selected from the group consisting of Gene Number 4145 (PLEKHN1), Gene Number 4166 (VPS13D), Gene Number 4590 (PLXNA2), Gene Number 4952 (ST14), Gene Number 5042 (LTBP3), Gene Number 5181 (ACSS3), Gene Number 5209 (ATP2A2), Gene Number 6714 (BCS1L), Gene Number 6809, Gene Number 7007 (CPNE1), Gene Number 7354 (COL6A6), Gene Number 7458 (LINC00971), and Gene Number 7474 (HGD). In some cases, the plurality of exon regions of genes selected from **Table 6** comprise at least three genes selected from the group consisting of Gene Number 4145 (PLEKHN1), Gene Number 4166 (VPS13D), Gene Number 4590 (PLXNA2), Gene Number 4952 (ST14), Gene Number 5042 (LTBP3), Gene Number 5181 (ACSS3), Gene Number 5209 (ATP2A2), Gene Number 6714 (BCS1L), Gene Number 6809, Gene Number 7007 (CPNE1), Gene Number 7354 (COL6A6), Gene Number 7458 (LINC00971), and Gene Number 7474 (HGD). In some cases, the plurality of exon regions of genes selected from **Table 6** comprise at least four genes selected from the group consisting of Gene Number 4145 (PLEKHN1), Gene Number 4166

(VPS13D), Gene Number 4590 (PLXNA2), Gene Number 4952 (ST14), Gene Number 5042 (LTBP3), Gene Number 5181 (ACSS3), Gene Number 5209 (ATP2A2), Gene Number 6714 (BCS1L), Gene Number 6809, Gene Number 7007 (CPNE1), Gene Number 7354 (COL6A6), Gene Number 7458 (LINC00971), and Gene Number 7474 (HGD). In some cases, the plurality of exon regions of genes selected from **Table 6** comprise at least five genes selected from the group consisting of Gene Number 4145 (PLEKHN1), Gene Number 4166 (VPS13D), Gene Number 4590 (PLXNA2), Gene Number 4952 (ST14), Gene Number 5042 (LTBP3), Gene Number 5181 (ACSS3), Gene Number 5209 (ATP2A2), Gene Number 6714 (BCS1L), Gene Number 6809, Gene Number 7007 (CPNE1), Gene Number 7354 (COL6A6), Gene Number 7458 (LINC00971), and Gene Number 7474 (HGD). In some cases, the plurality of exon regions of genes selected from **Table 6** comprise at least six genes selected from the group consisting of Gene Number 4145 (PLEKHN1), Gene Number 4166 (VPS13D), Gene Number 4590 (PLXNA2), Gene Number 4952 (ST14), Gene Number 5042 (LTBP3), Gene Number 5181 (ACSS3), Gene Number 5209 (ATP2A2), Gene Number 6714 (BCS1L), Gene Number 6809, Gene Number 7007 (CPNE1), Gene Number 7354 (COL6A6), Gene Number 7458 (LINC00971), and Gene Number 7474 (HGD). In some cases, the plurality of exon regions of genes selected from **Table 6** comprise Gene Number 4145 (PLEKHN1), Gene Number 4166 (VPS13D), Gene Number 4590 (PLXNA2), Gene Number 4952 (ST14), Gene Number 5042 (LTBP3), Gene Number 5181 (ACSS3), Gene Number 5209 (ATP2A2), Gene Number 6714 (BCS1L), Gene Number 6809, Gene Number 7007 (CPNE1), Gene Number 7354 (COL6A6), Gene Number 7458 (LINC00971), and Gene Number 7474 (HGD). In some cases, the plurality of genes selected from **Table 6** consist of Gene Number 4145 (PLEKHN1), Gene Number 4166 (VPS13D), Gene Number 4590 (PLXNA2), Gene Number 4952 (ST14), Gene Number 5042 (LTBP3), Gene Number 5181 (ACSS3), Gene Number 5209 (ATP2A2), Gene Number 6714 (BCS1L), Gene Number 6809, Gene Number 7007 (CPNE1), Gene Number 7354 (COL6A6), Gene Number 7458 (LINC00971), and Gene Number 7474 (HGD).

[0082] Further, the expression levels may be compared to control ranges disclosed here to generate an output/report indicative of the subject's having or risk of having a condition comprising perfusion shortage with an accuracy greater than about 99%. In some embodiments, the accuracy is about 98.5%, 98%, 97.5%, 97%, 96.5%, 96%, 95.5%, 95%, 94.5%, 94%, 93.5%, 93%, 92.5%, 92%, or 91.5%.

TABLE 21

Code PSC	*biomarker nucleotide seq Probe*	*biomarker nucleotide seq target mRNA*
1673	GACCGGGTGTTGGTGCGGCTATTAC	CTGGCCCACAACCACGCCGATAATG
6351	AGAAGGAGCCCGACCAGGTTCTACC	TCTTCCTCGGGCTGGTCCAAGATGG
6767	GTGGTGGTGCCCACTGTGGTCCTAC	CACCACCACGGGTGACACCAGGATG
6774	CTGTGTGTGCCCTTCACAAGAGGTT	GACACACACGGGAAGTGTTCTCCAA
9512	CTCGGCGCCCAGCTGCGTGCGTGCA	GAGCCGCGGGTCGACGCACGCACGT
11081	GGAGACTCTCCCAAAGGAACCATAG	CCTCTGAGAGGGTTTCCTTGGTATC
15750	CTCGAGTCTCCCAGAGGTCCATTGT	GAGCTCAGAGGGTCTCCAGGTAACA
15852	CTTTATCCCAGAAATGGTGACCGGT	GAAATAGGGTCTTTACCACTGGCCA
16655	ACTATCTACTCCCAGTAGTGACGCG	TGATAGATGAGGGTCATCACTGCGC
18080	GTCTGCCGACCCACCGTTTATGTTT	CAGACGGCTGGGTGGCAAATACAAA
19099	GGACACACACCCACGTGTAAACACA	CCTGTGTGTGGGTGCACATTTGTGT
19994	AAGACCTACCCACGTCCGACATGGT	TTCTGGATGGGTGCAGGCTGTACCA
21717	GTACGCTTAGGCCAGTCTTGACCAG	CATGCGAATCCGGTCAGAACTGGTC
27227	GAAGGTCTTCCCGTTGTTCGCTCCA	CTTCCAGAAGGGCAACAAGCGAGGT
27604	GAACTTCCGTCCCTGCACTGAAAGG	CTTGAAGGCAGGGACGTGACTTTCC
29415	CCGAATCTCCCTCTGTGTAGAGTCT	GGCTTAGAGGGAGACACATCTCAGA
36768	TTACTAGACGTTCCAGAGTCAGGGG	AATGATCTGCAAGGTCTCAGTCCCC
39687	GATCCTTTCCACTCGCGCTAGAGCG	CTAGGAAAGGTGAGCGCGATCTCGC
41366	CGCCGCAGTCCACCGCCGACGGCGT	GCGGCGTCAGGTGGCGGCTGCCGCA
42955	CTCTCCGTGTCCAAAGTTCTGTGTA	GAGAGGCACAGGTTTCAAGACACAT
49089	AGTCCAGACCCTTCGTGACTGGTCG	TCAGGTCTGGGAAGCACTGACCAGC
53130	ATAAGAGACCCTCACTGAGTCACGG	TATTCTCTGGGAGTGACTCAGTGCC
53947	AGGTCCGACCCTCTCACGAGTGGAT	TCCAGGCTGGGAGAGTGCTCACCTA
55338	GTACACACAGGCCTTCACACACGGG	CATGTGTGTCCGGAAGTGTGTGCCC
58129	AGAGTTTCCCTAAAGTTCTACGACA	TCTCAAAGGGATTTCAAGATGCTGT
58782	GTCACGCCTCGCCTCAGCCAAGACC	CAGTGCGGAGCGGAGTCGGTTCTGG
59746	GGACCGGGCCTACCACGACCGAGGT	CCTGGCCCGGATGGTGCTGGCTCCA
60909	ACGACCAGCGCCTAGACGACATGGA	TGCTGGTCGCGGATCTGCTGTACCT
64432	ACTCCGTCCTCCTTTCTGGATGAAG	TGAGGCAGGAGGAAAGACCTACTTC
65832	GTTACGGACCTCCTCACATCGGCAG	CAATGCCTGGAGGAGTGTAGCCGTC
72889	GGTTCGGTGTCCTCGAATCGTGTCA	CCAAGCCACAGGAGCTTAGCACAGT
74978	GGTCTCCACGTCCTCGTTCAAGTGT	CCAGAGGTGCAGGAGCAAGTTCACA
75770	CTTCTTGTCCTAACCGGTCTACGCA	GAAGAACAGGATTGGCCAGATGCGT
76500	TTTAAGCTCCTACCGGATAGAGTGT	AAATTCGAGGATGGCCTATCTCACA
89931	AATCCTACACCACTCCTCTTCGACG	TTAGGATGTGGTGAGGAGAAGCTGC

100396	AGACCACACACCTTTGACTGCCACC	TCTGGTGTGTGGAAACTGACGGTGG
125863	AATCCGGTCCGACATCGACCAGGAG	TTAGGCCAGGCTGTAGCTGGTCCTC
128031	CCGCACGACTCCGACTTTTACCGTA	GGCGTGCTGAGGCTGAAAATGGCAT
128748	AAGAGTTCCCGTTATTTCAATCCGT	TTCTCAAGGGCAATAAAGTTAGGCA
128806	CGATTGGCCGTTAAACTATGGTTTC	GCTAACCGGCAATTTGATACCAAAG
130619	GTTTTTACCCGTCCTCGTGTCACTG	CAAAAATGGGCAGGAGCACAGTGAC
144225	ACAACAACACCGTCCTCGTGAGGTC	TGTTGTTGTGGCAGGAGCACTCCAG
185975	TCCGTCGCTGGGTGATGGAACATGA	AGGCAGCGACCCACTACCTTGTACT
196417	CCGGTCGTTGGTTGAGTGTTTATGA	GGCCAGCAACCAACTCACAAATACT
223602	ATTCCCAGGACACCACCAGAGGGCT	TAAGGGTCCTGTGGTGGTCTCCCGA
229451	ATCCGGTTAGGGAGTGTGTCCAATT	TAGGCCAATCCCTCACACAGGTTAA
231682	CGAGGACAGTAGGAACGGAGAACCC	GCTCCTGTCATCCTTGCCTCTTGGG
242908	TCTTGAAGAGGTCCCGCGACCGTGT	AGAACTTCTCCAGGGCGCTGGCACA
249198	TCAAGAACTAGGTCGCGACGAGGGT	AGTTCTTGATCCAGCGCTGCTCCCA
252213	GCGCGGCCCGGCTGGGCGTAGAGGG	CGCGCCGGGCCGACCCGCATCTCCC
295450	CCCGTCTTGCCTCGATAGGTAGGTC	GGGCAGAACGGAGCTATCCATCCAG
306673	GCCACTGCGGCTAGGACACTCGTAA	CGGTGACGCCGATCCTGTGAGCATT
327300	CTCTCAATGCGCTTTCCTCAGGAGG	GAGAGTTACGCGAAAGGAGTCCTCC
468772	ACGACGCAGGCAACTTCGTTGGCGG	TGCTGCGTCCGTTGAAGCAACCGCC
529042	GTCCGGACGGCAGATATCAGATACC	CAGGCCTGCCGTCTATAGTCTATGG
561044	GCACGTCACCAACCTTCGTAGTCGA	CGTGCAGTGGTTGGAAGCATCAGCT
588830	CGTATCTACAAACGGAGGAGAACCT	GCATAGATGTTTGCCTCCTCTTGGA
604042	AACTACTTCCACAGTGTTGCCGTTC	TTGATGAAGGTGTCACAACGGCAAG
604967	GTCCATCTCCACACTGGGGTCCTGA	CAGGTAGAGGTGTGACCCCAGGACT
616095	GTCCTACCACCACTAGTTGCACGGG	CAGGATGGTGGTGATCAACGTGCCC
622161	GACCCTCTGACACCCACTAGGAGGT	CTGGGAGACTGTGGGTGATCCTCCA
622702	GATAACCCACACAACATTTGTCTTC	CTATTGGGTGTGTTGTAAACAGAAG
639146	ACAAACAGACACGAAGATTTTCCAG	TGTTTGTCTGTGCTTCTAAAAGGTC
669436	CGGTCCGTCGGATATCCTTATCATT	GCCAGGCAGCCTATAGGAATAGTAA
708420	CGATCGGGTGAGGTGTCTAAAAACT	GCTAGCCCACTCCACAGATTTTTGA
751418	NA	NA
752527	ATTCCCACGATACGCGAGTCAGAGG	TAAGGGTGCTATGCGCTCAGTCTCC
772367	GCAAAGGGACACACTCCACCACGGT	CGTTTCCCTGTGTGAGGTGGTGCCA
883312	GTTCTCTGTACGTATTGTGCAAAAT	CAAGAGACATGCATAACACGTTTTA
906039	GTAAATAACTTGTTCGATCGGACAA	CATTTATTGAACAAGCTAGCCTGTT
939909	ACCTAGAGTCCTTTCGACGGTCGTA	TGGATCTCAGGAAAGCTGCCAGCAT
1020364	AGAGACGGGTTCCACTCCCTTGAGT	TCTCTGCCCAAGGTGAGGGAACTCA
1059015	CGACGTACAAGTATCAGTAGGTGGA	GCTGCATGTTCATAGTCATCCACCT
1072725	AAGAATTTCGTGGTGTAGTTGGAAT	TTCTTAAAGCACCACATCAACCTTA

1099142	ACATAGTGTCCTCTTTGGTCGTCCC	TGTATCACAGGAGAAACCAGCAGGG
1331569	CCCGGTGTCTAGTCCACGAAGACGT	GGGCCACAGATCAGGTGCTTCTGCA
1354360	GGAAGAGGTCTACTGCACCGACAGT	CCTTCTCCAGATGACGTGGCTGTCA

TABLE 22

Affymetrix Exon ID B	Transcript Cluster ID	SEQ Name	Strand	Strand Start	Strand Stop
16650657	16650657	---	---	---	---
16650745	16650745	---	---	---	---
16651179	16651179	---	---	---	---
16651711	16651711	---	---	---	---
16651915	16651915	---	---	---	---
16651933	16651933	---	---	---	---
16652239	16652239	---	---	---	---
16652289	16652289	---	---	---	---
16652527	16652527	---	---	---	---
16652597	16652597	---	---	---	---
16653327	16653327	---	---	---	---
16655117	16655117	---	---	---	---
16655411	16655411	---	---	---	---
16656923	16656923	---	---	---	---
16657593	16657572	chr1	+	911095	911203
16657854	16657848	chr1	+	1543079	1543119
16658040	16658023	chr1	+	2426362	2426386
16658687	16658674	chr1	+	9671844	9671904
16659314	16659251	chr1	+	12439570	12439594
16659467	16659459	chr1	+	13922361	13922421
16659653	16659650	chr1	+	15860772	15860796
16660293	16660282	chr1	+	20411334	20411363
16660567	16660555	chr1	+	22924244	22924268
16660942	16660933	chr1	+	25889465	25889547
16661236	16661206	chr1	+	26883177	26883201
16662358	16662357	chr1	+	35661576	35661663
16662955	16662945	chr1	+	40431586	40431686
16663887	16663871	chr1	+	44684284	44684308
16666083	16666082	chr1	+	71413125	71413151
16667412	16667385	chr1	+	95712525	95712665
16667429	16667427	chr1	+	95978079	95978160

16675846	16675844	chr1	+	201804083	201804107
16676222	16676217	chr1	+	203738776	203738809
16676511	16676498	chr1	+	205569535	205569588
16676715	16676693	chr1	+	207245602	207245626
16677217	16677201	chr1	+	212274092	212274116
16679760	16679759	chr1	+	248100578	248100658
16680781	16680770	chr1	-	2979261	2979594
16684441	16684439	chr1	-	31934171	31934242
16685867	16685866	chr1	-	41154797	41157855
16685996	16685986	chr1	-	42915653	42915677
16691349	16691333	chr1	-	116311348	116311413
16696420	16696416	chr1	-	173019898	173019989
16697659	16697654	chr1	-	198906415	198906539
16698835	16698816	chr1	-	208219352	208219376
16702313	16702311	chr10	+	7830190	7830214
16708599	16708579	chr10	+	104125274	104125298
16723812	16723803	chr11	+	41857963	41857987
16730164	16730157	chr11	+	93803602	93803707
16733477	16733473	chr11	+	130058031	130058055
16740437	16740412	chr11	-	65315216	65315240
16754738	16754729	chr12	+	81537188	81537212
16756959	16756923	chr12	+	110788494	110788518
16764284	16764238	chr12	-	49504637	49504661
16783655	16783644	chr14	+	39648245	39648280
16784915	16784909	chr14	+	60733933	60733991
16787392	16787364	chr14	+	90485693	90485717
16787649	16787642	chr14	+	93359618	93359819
16792584	16792550	chr14	-	50296038	50296062
16793638	16793632	chr14	-	61447572	61447600
16801591	16801577	chr15	+	59752184	59752276
16802685	16802681	chr15	+	72102896	72102961
16804744	16804716	chr15	+	90768778	90768802
16810304	16810298	chr15	-	62936970	62937310
16819053	16819052	chr16	+	55358040	55358655
16844154	16844137	chr17	-	37557842	37557872
16851838	16851824	chr18	+	29797774	29797878
16851883	16851866	chr18	+	32409010	32409034
16890974	16890970	chr2	+	219524492	219524516
16900045	16900044	chr2	-	88529113	88529181

16900226	16900225	chr2	-	95512287	95512384
16900670	16900657	chr2	-	97613582	97613606
16907908	16907904	chr2	-	213768128	213768160
16918801	16918797	chr20	-	34214399	34214423
16922251	16922243	chr21	+	34655474	34655536
16930003	16929994	chr22	+	38363654	38363678
16939185	16939184	chr3	+	38323792	38323817
16944985	16944982	chr3	+	126006929	126006965
16945570	16945543	chr3	+	130345367	130345391
16950391	16950390	chr3	-	8406218	8406333
16956502	16956486	chr3	-	84911918	84911942
16957913	16957906	chr3	-	120360496	120360520
16964029	16964027	chr4	+	1801084	1801233
17088090	17088084	chr9	+	114409409	114409538

[0083] Several suitable statistical methods may be employed to compare the measured expression levels of genes from the plurality of genes listed in Tables 1-6 to control ranges disclosed herein. Non-limiting examples of suitable statistical methods that can be used for statistical analysis in the detection methods disclosed herein include the group consisting of Fisher Discriminant analysis (FDA), Diagonal linear discriminant analysis (DLDA), Linear discriminant analysis (LDA), linear discriminant analysis based on partial least-squares (PLSLDA), partial least squares random Forest (PLSRF), orthogonal discriminant analysis (QDA), Random Forest (RF), or a combination thereof. Examples of suitable statistical methods are listed in Table 1, for example Support Vector Machine, Quadratic Discriminant analysis, and Fisher's Discriminant analysis (FDA). It is noted that FDA has been shown to provide accurate results for both male and female subjects.

Table 7

Table: Overview of the classification models provided via CMA [2, 3-14].

Method name	Package	Reference
Component wise Boosting	CMA	Bühlmann and Yu [2003]
Elastic Net	glmpath	Zhou and Hastie [2004]
Flexible Discriminant Analysis	mgcv	Ripley [1996]
Tree-based Boosting	gbm	Friedman [2001]
k-nearest neighbours	class	Ripley [1996]
Lasso	glmpath	Young-Park and Hastie [2007]
Feed-Forward Neural Networks	nnet	Ripley [1996]
Probalistic nearest neighbours	CMA	-
Penalized Logistic Regression	CMA	Zhu [1996]
Probabilistic Neural Networks	CMA	Specht [1990]
PAM	CMA	Tibshirani et al [2002]
Shrinkage Discriminant Analysis	CMA	-
Support Vector Machine	e1071	Schölkopf and Smola [2002]
Diagonal Discriminant Analysis	CMA	McLachlan[1992]
Fisher's Discriminant Analysis	CMA	Ripley [1996]
Linear Discriminant Analysis	MASS	McLachlan[1992]
Partial Least Squares	plsgenomics	Boulesteix and Strimmer [2007]
,, + Random Forest	plsgenomics	Boulesteix and Strimmer [2007]
,, + logistic regression	plsgenomics	Boulesteix and Strimmer [2007]
Quadratic Discriminant Analysis	MASS	McLachlan[1992]
Random Forest	randomForest	Breiman [2001]

The Bioconductor library 'CMA' is used to make the prediction models and execute the validations [1,2]. For the validation, a 10-fold cross validation is executed. In addition, the calculations (model generation and validation) are repeated 5 times to improve the validation measures.

Detecting a condition comprising perfusion shortage or a risk thereof at an early stage

[0084] Conventional biomarkers in the field of cardiology or other areas where ischemia can cause serious conditions that are available to date have merely detected myocardial muscle damage after severe ischemia, but fail to detect subtle ischemia (a.k.a., angina pectoris) without muscle damage. Ischemia without muscle damage constitutes the vast majority of the cardiovascular patients in the normal cardiology outpatient clinic. Described in accordance with methods, kits, compositions, and uses of some embodiments herein are biomarkers of myocardial and cerebrovascular ischemia (or any other ischemic disease) in the absence of acute myo- or tissue necrosis (including, but not limited to, angina pectoris, transient ischemic (cerebrovascular) accident, microvascular disease and/or cerebrovascular accident). Further, in certain aspects, the present disclosure presents methods comprising obtaining said biological sample from a subject that has or is at risk for having a condition

comprising perfusion shortage, wherein said perfusion shortage is at an early stage and has not caused any detectable tissue damage and assaying expression levels of two or more genes (nucleotide or protein biomarker) from a plurality of identified genes (nucleotide or protein biomarker) to generate an output comprising said expression levels indicative of said subject's having or risk of having said condition comprising perfusion shortage.

[0085] It is contemplated that methods, compositions, kits, and uses of some embodiments can detect conditions comprising perfusion shortage such as neoangiogenesis or ischemia, even when the subject presents minimal to no symptoms of the condition. In some embodiments, the subject may not present symptoms of any of ischemic cardiovascular disease, microangiopathy in cardiovascular disease (such as diastolic heart failure), hypertrophic cardiomyopathy, cardiovascular pathology with relative ischemia (such as hypertrophic CMP, ischemic heart failure, and/or congenital cardiac disease), ischemic cerebrovascular disease (including CVA/ TIA, and/or vascular dementia), ischemic peripheral artery disease, venous disease, orthopedic disease, sepsis, inflammation, lymphatic disease, ophthalmological disease associated with ischemia and/or neoangiogenesis (such as neoangiogenesis in retinopathy), diabetic macro and microangiopathy, oncological pathology (including solid tumors, metastatic disease), endothelial dysfunction in cardiovascular and peripheral artery disease, ophthalmology (such as neoangiogenesis in retinopathy), diabetic macro and microangiopathy, oncological pathology (such as solid tumors and/or metastatic disease), endothelial dysfunction in cardiovascular and peripheral artery disease, nephrological disease associated with ischemia and/or neoangiogenesis, gynecological disease, orthopedic disease, lung disease (such as COPD, emphysema, lung fibrosis, cystic fibrosis, lung cancer, pulmonary interstitial disease, and/or monitoring pre- and post-lung transplantation, pulmonary emboli), cerebrovascular disease (for example, stroke, TIA, microvascular dementia, and emboli such as pulmonary emboli), deep venous thrombosis, inadequate ventilation/ oxygenation of a mechanically ventilated subject, a gastrointestinal disorder (such as Crohn's disease, colitis ulcerosa), a neurodegenerative disease (such as Parkinson's disease or multiple sclerosis), erectile dysfunction, sport injury, frailty, shock (such as post-resuscitation shock), arterial and venous diseases, disease related to lymphangiogenic disease, vascular remodeling including lymphangiogenic metastatic disease, arteriovenous malformation, arterial remodeling, or venous thrombosis, or a combination of two or more of

the listed items. In some embodiments, the subject may present symptoms of any of ischemic diseases disclosed herein or any other ischemic diseases.

Measuring or detecting expression levels of selected genes

[0086] As used herein "gene products" refer to DNA molecules, RNA molecules (such as mRNAs), particular splice variants, corresponding (translated) peptides, and/or specific downstream signaling cascades (for example, phosphorylation, acetylation, methylation, ubiquitination, SUMOylation, degradation, or subcellular localization of downstream signal transduction pathway molecules), or any combination of two or more of the listed items (any of these items may be referred to as biomarkers). Genes as disclosed herein can be measured or detected by measuring a portion of DNA molecules, RNA molecules (such as mRNAs), particular splice variants, or corresponding (translated) peptides corresponding to a particular gene from the identified set of genes. Gene products/genes that are differently expressed in ischemia and non-ischemia subjects as described herein may also be referred to as "biomarkers." For nucleic acid gene products/genes (or nucleic acids encoding gene products/genes), it will be appreciated that the reverse transcript of a gene product/gene also provides suitable information about the gene product. Accordingly, gene product/gene can refer to either strand of a nucleic acid (e.g., the sense or antisense strand), and thus encompasses the reverse complement of a nucleic acid strand as well as the strand itself, in any reading frame on either strand.

[0087] In methods, compositions, kits, and uses of some embodiments, the specified gene products can identify diseases comprising perfusion shortage (such as ischemic episodes and neoangiogenesis processes) based on expression levels of these gene products/genes, such as DNA molecules, RNA molecules (e.g., mRNAs), particular splice variants, corresponding (translated) peptides, and/or specific downstream signaling cascades (which can be measured, for example, based on phosphorylation, ubiquitination, SUMOylation, transcription, degradation, or subcellular localization of downstream signal transduction pathway molecules), or any combination of two or more of the listed items. In some embodiments, the gene products comprise nucleic acids that are part of the genes selected from Tables 1-6. In some embodiments, the gene products comprise nucleic acids that may be used to detect the expression levels of genes selected from Tables 1-6. In some embodiments, the gene products

comprise peptide sequences that are encode from the genes selected from Tables 1-6. In some embodiments, the gene products comprise peptides that can detect expression levels of protein or fragments thereof encoded by the genes selected from Tables 1-6. In some embodiments, the gene products comprise nucleic acids or peptide sequences encoded therefrom selected from any of SEQ ID NOs: 1-5103 (or a peptide sequence encoded therefrom), Genes Number 1-9280 (or a peptide sequence encoded therefrom), or nucleic acids comprising at least 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 consecutive nucleotides thereof (including ranges between any two of the listed values), or peptides encoded by any of these nucleic acids. It has been observed that RNAs or peptides of each of **Tables 1, 3, and 5** are differentially expressed in hematopoietic EPCs or fractions or secretions thereof of females, and that RNAs or peptides of each of **Tables 2, 4, and 6** are differentially expressed in hematopoietic EPCs or fractions or secretions thereof of males. As such, in some embodiments, for example for female subjects the gene products comprise nucleic acids or peptides selected from any of **Tables 1, 3, and 5**, or nucleic acids comprising at least 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 consecutive nucleotides thereof (including ranges between any two of the listed values), or peptides encoded by any of these nucleic acids. In some embodiments, for example for male subjects the gene products comprise nucleic acids or peptides selected from any **Tables 2, 4, and 6**, or nucleic acids comprising at least 2, 3, 4, 5, 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 consecutive nucleotides thereof (including ranges between any two of the listed values), or peptides encoded by any of these nucleic acids.

[0088] Transcriptomics refers to global analysis of RNA expression and may elucidate genes and molecular pathways involved in biological processes. Genes showing similarities in expression pattern may be functionally related and fall under the same genetic control mechanism. Furthermore, it will be appreciated that transcriptomics can identify particular splice variants, and that splice variants can also be useful as biomarkers, as transcripts may be spliced differently under different conditions. Furthermore, it will be appreciated that transcriptomics can identify gene products such as peptides that are also useful

as biomarkers, since relative levels of transcripts can correlate with, and predict, relative levels of peptides. Using transcriptomics technology, specific expression patterns of gene products have been identified, which were up-regulated under hypoxic conditions in patients with conditions comprising perfusion shortage, such as (but not limited to) myocardial ischemia (due to oxygen deprivation in the heart, which may also be referred to as angina pectoris), peripheral artery ischemia, cerebrovascular ischemia (stroke and TIA), & retinal ischemia (See Example 2 and Tables 1-6). Without being limited by theory, this altered regulation is suggestive for their involvement in a physiological ischemia-driven neoangiogenesis response.

[0089] Levels of gene products/genes (which may also be referred to herein as "levels of expression of genes/gene products" or "expression levels of genes/gene products" or "levels of biomarkers" or "levels of expression of biomarkers" or "expression levels of biomarkers", including variations of these root terms) may be detected in accordance with methods, compositions, kits, and uses using suitable art-recognized methods. Methods, compositions, kits, and uses of some embodiments utilize gene expression profiling to identify biomarkers that exhibit differential gene expression (of DNA sequences/RNA oligonucleotide sequences) and hence DNA/RNA molecular biomarkers, as well as corresponding splice variants, peptides, and/or downstream signal transduction markers. It is noted that for a given nucleic acid sequence, a peptide may be translated from the +1, +2, or +3 position on either the sense or the antisense strand. Accordingly, a peptide corresponding to a given nucleic acid will be understood to encompass translational initiation at position +1, +2, or +3 on either of the sense or antisense stands.

[0090] It is contemplated that any suitable detection platform for DNA, RNA, peptide, and/or signal transduction biomarkers can be used in accordance with methods, compositions, uses, and kits of embodiments herein. The detection platform may have sufficient sensitivity to discriminate between levels of gene products, such as nucleic acids or peptides of any of SEQ ID NOs: 1-5103 or Genes Number 1-9280, as described herein, or corresponding peptides. For example, the detection of the peptide biomarkers or small molecules may be performed by for example, (but not limited to) ELISA, (quantitative) western blot analysis, mass spectrometry, flow cytometry, immunohistochemistry, and/or protein array, or a combination of two or more of any of the listed items. In some embodiments, ChipArray technology is used to detect expression levels of genes/genes products as described

herein. In some embodiments, other technologies can be used to determine differential gene expression with sufficient sensitivity to form the basis for this assay. In some embodiments, a molecular biomarker profile can be detected irrespective of the underlying (current or future) platform, provided the technology has sufficient sensitivity to pick up this low-level differential expression. These may include (but are not limited to) qRT PCR analysis, (quantitative) Northern Blot analysis, microarray analysis, Luminex technology, Multiplexing, SAGE, RNASeq, whole transcriptome analysis, or a combination of any of these listed items. The detected expression levels of gene products in accordance with methods, compositions, kits, and uses of embodiments herein may be compared to a control range. As used herein a "control range" has its ordinary and customary meaning as would be understood by one of ordinary skill in the art in view of this disclosure. It refers to a range of expression levels of a gene/gene product in a sample of a subject that does not have the condition comprising neoangiogenesis or ischemia, for example a healthy subject. It will be appreciated that a control range can be determined experimentally (for example by detecting gene expression levels in a sample of a healthy subject or by using standard samples having gene expression levels indicative of an absence of the condition indicates a level of expression of the gene product outside of the control range) or can be obtained from an electronically or optically stored set of values (for example, from a database of control ranges). By way of example, a control range may be provided as a numerical range, or a confidence interval around a specified value. In some embodiments, an expression level of a gene product exceeds the upper limit of a control range and indicates a presence or risk of the condition comprising neoangiogenesis and/or ischemia. By way of example, expression levels of genes/gene products that are indicative of a presence or risk of the condition comprising neoangiogenesis and/or ischemia are shown in Tables 1-6. In some embodiments, if an expression level of a gene product is greater than or equal to a value in an ischemia patient of Tables 1, 3, and 5 and/or Table 2, 4, and 6, a presence or risk of the condition comprising neoangiogenesis and/or ischemia is determined. In some embodiments, the gene product does not comprise the product of any of Hspg2, Cyb5b, Adora2a, LDLRAD2, or Lgmn. In some embodiments, the gene product does not comprise the product of any of Sox18, Sox7, HO1, ETS2, Rab5, Rock2, Rin3, Crip2, Kcnh2, Plvap, TNFAIP8L1, STAB1, C10orf10, Cingulin like 1, ExoC3I, CCBE1, KIAA1462, 1200015N20Rik, Agtrl-1, DLL4, or HEY1.

[0091] In some embodiments, one or more of a copy number of the at least two specified different gene products, an expression level of the at least two specified different gene products are detected, or an activity level of the at least two specified different gene products is detected.

[0092] In the method of some embodiments, the specified different gene products comprise DNA or RNA comprising one or more exons that individually or in combination comprise a sequence of Table 3 or Table 4.

[0093] The methods, compositions, kits, and uses of some embodiments (which may comprise an array as described herein) can be used for side-by-side comparison between different (anti-ischemic) therapies to demonstrate superiority or non-inferiority (in for instance clinical trials as a surrogate end-point marker). Likewise, methods, compositions, uses, kits of some embodiments may be useful, and exhibit alike properties in diseases where (the lack of or excess) tissue perfusion plays a substantial pathogenetic role or determines therapy responsiveness, including (but not limited to) oncological disease (for instance hematological metastatic disease, solid tumors), diabetic vascular complications (macro and microangiopathy), diastolic heart failure, ophthalmic neoangiogenesis disease, and renal disease, including combinations of two or more of any of the listed items. The methods, compositions, kits, and uses may comprise an array as described herein.

[0094] In some embodiments (for example, methods, compositions, kits, and uses as described herein), the expression levels of genes/gene products are assessed as levels of DNA, RNA, peptide, or any combinations thereof. The expression levels of DNA or RNA can be assessed for example by (but not limited to) cDNA chip array analysis, quantitative PCR (qPCR, such as quantitative RT PCR), microarray analysis, multiplexing, Luminex analysis, nucleic acid sequencing, northern blot analysis, comparative genomic hybridization (CGH), and/or fluorescent in situ hybridization (FISH), genomic high throughput sequencing, nanostring, massive parallel signature sequencing (MPSS), serial analysis of gene expression (SAGE), or a combination of two or more of the listed items. Further, the expression levels of peptides can be assessed for example by (but not limited to) enzyme-linked immunosorbent assay (ELISA), protein sequencing, mass spectrometry (such as MALDI TOF, QTOF, or SELDI TOF), quantitative western blot analysis, and peptide barcoding, or a combination of two or more of the listed items. In methods, compositions, kits, and uses of some embodiments,

the expression levels of genes/gene products are assessed for example by (but not limited to) cDNA chip array analysis, quantitative PCR (qPCR, such as quantitative RT PCR), microarray analysis, multiplexing, Luminex analysis, nucleic acid sequencing, northern blot analysis, comparative genomic hybridization (CGH), and/or fluorescent in situ hybridization (FISH), genomic high throughput sequencing, nanostring, massive parallel signature sequencing (MPSS), serial analysis of gene expression (SAGE), enzyme-linked immunosorbent assay (ELISA), protein sequencing, mass spectrometry (such as MALDI TOF, QTOF, or SELDI TOF), quantitative western blot analysis, and peptide barcoding, or a combination of two or more of the listed items. In some embodiments, the expression levels of the one or more gene products are assessed by detecting the presence in the samples of a polynucleotide molecule encoding the target or a portion of the polynucleotide molecule. In some embodiments, the polynucleotide molecule is a mRNA, cDNA, or functional variants or fragments thereof. Optionally, the detecting can further comprise amplifying the polynucleotide molecule. In some embodiments, the expression level of the one or more gene products is assessed by annealing a nucleic acid probe with the sample of the polynucleotide encoding the one or more targets or a portion of the polynucleotide molecule under stringent hybridization conditions. In some embodiments, the expression level of the gene products is assessed by detecting the presence in the samples of a protein of the target, a peptide, or protein fragment thereof comprising the protein. In some embodiments, the presence of the protein, peptide or protein fragment gene products is detected via mass spectrometry or using a reagent which specifically binds to the protein, peptide or protein fragment thereof. Examples of suitable reagents include, but are not limited to an antibody (as used herein, “antibody” encompasses full-length antibodies, as well as derivatives and binding fragments thereof, for example Fabs, scFvs, minibodies, diabodies, triabodies, and the like) and/or an aptamer (such as a nucleic acid or peptide aptamer). It will be appreciated that gene activity can be modulated by directly or indirectly targeting a gene product. For example, gene activity can be enhanced or increased by increasing the copy number of a gene product (or a nucleic acid encoding the gene product), by increasing the stability of a gene product (or a nucleic acid encoding the gene product), and/or by changing the location of a gene product (for example by translocating a gene product to a location where it acts, or translocating an mRNA or a ribosome). For example, gene activity can be inhibited of decreased by decreasing the copy number of a gene product (or a

nucleic acid encoding the gene product), by decreasing the stability of a gene product (or a nucleic acid encoding the gene product), and/or by changing the location of a gene product (for example by sequestering a gene product or a nucleic acid encoding a gene product, or targeting a peptide gene product to a proteasome). In some embodiments, the expression level of the gene product is assessed by determining the magnitude of modulation of the activity or expression level of downstream targets of the gene product. In some embodiments, for example, an at least a 5%, 10%, 15%, or 20%, increase or an at least 5%, 10%, 15%, or 20%, decrease between the copy number, level of expression, or level of activity of the one or more downstream targets in the subject sample relative to the copy number, level of expression, or level of activity of the one or more downstream targets in a control sample indicates a level of expression of the gene product outside of the control range. In some embodiments, for example, a less-than 20%, 15%, 10%, or 5% increase or a less-than 20%, 15%, 10%, or 5% decrease between the copy number, level of expression, or level of activity of the one or more downstream targets in the subject sample relative to the copy number, level of expression, or level of activity of the one or more downstream targets in a control sample indicates a level of expression of the gene product within the control range. In methods, compositions, kits, and uses of some embodiments, expression levels of the specified different gene products are detected. For example, detection can be for example (but not limited to) any of cDNA chip array analysis, quantitative PCR (qPCR) such as quantitative RT PCR, microarray analysis, comparative genomic hybridization (CGH), fluorescent in situ hybridization (FISH), multiplexing, Luminex analysis, nucleic acid sequencing, northern blot analysis, (genomic) high throughput sequencing, nanostring, massive parallel signature sequencing (MPSS), serial analysis of gene expression (SAGE), enzyme-linked immunosorbent assay (ELISA), protein sequencing, mass spectrometry (such as MALDI TOF, QTOF, or SELDI TOF), quantitative western blot analysis, and peptide barcoding, Affymetrix arrays, GeneChip arrays, tiling arrays, anti-sense arrays, spotted DNA arrays, SNP arrays, expression arrays, or a combination thereof. In methods, compositions, kits, and uses of some embodiments, the expression levels of gene products are assessed for example (but not limited), by microarray analysis, qPCR, high-throughput sequencing, CGH, and/or FISH.

[0095] In some embodiments, an agent for detecting target mRNA, genomic DNA, or fragments thereof is a labeled nucleic acid probe capable of hybridizing to target mRNA,

genomic DNA, or fragments thereof. The nucleic acid probe can be, for example, full-length target nucleic acid, or a portion thereof, such as an oligonucleotide of at least 5, 6, 7, 8, 9, 10, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29 30, 31, 32, 33, 34, 35, 40, 45, 50, 60, 70, 80, 90, 100, 150, 200, 250, or 500, or a range defined by any two of the preceding values (such as 10-40, 10-30, 10-25, 15-40, 15-30, 15-25, 20-40, 20-30, or 20-25) nucleotides in length and sufficient to specifically hybridize under stringent conditions well known to a skilled artisan to target mRNA or genomic DNA. Other suitable probes for use in the diagnostic assays of the disclosure are described herein. It will be appreciated that a "probe" can comprise or consist essentially of or consist of a primer of a primer pair. In some embodiments, the nucleic acid probe is designed to detect transcript variants (e.g., different splice forms) of a gene. Optionally, any nucleic acid probe as described herein can further comprise a detectable moiety, for example a fluorophore, enzyme, radiolabel, quantum dot, or a nucleic acid barcode. Examples of fluorophores include, but are not limited to xanthene dyes, e.g., fluorescein and rhodamine dyes, such as fluorescein isothiocyanate (FITC), 2-[ethylamino)-3-(ethylimino)-2-7-dimethyl-3H-xanthen-9-yl]benzoic acid ethyl ester monohydrochloride (R6G)(emits a response radiation in the wavelength that ranges from about 500 to 560 nm), 1,1,3,3,3',3'-Hexamethylindodicarbocyanine iodide (HIDC) (emits a response radiation in the wavelength that ranged from about 600 to 660 nm), 6-carboxyfluorescein (commonly known by the abbreviations FAM and F), 6-carboxy-2',4',7',4,7-hexachlorofluorescein (HEX), 6-carboxy-4',5'-dichloro-2',7'-dimethoxyfluorescein (JOE or J), N,N,N',N'-tetramethyl-6-carboxyrhodamine (TAMRA or T), 6-carboxy-X-rhodamine (ROX or R), 5-carboxyrhodamine-6G (R6G5 or G5), 6-carboxyrhodamine-6G (R6G6 or G6), and rhodamine 110; cyanine dyes, e.g. Cy3, Cy5 and Cy7 dyes; coumarins, e.g., umbelliferone; benzimide dyes, e.g. Hoechst 33258; phenanthridine dyes, e.g. Texas Red; ethidium dyes; acridine dyes; carbazole dyes; phenoxazine dyes; porphyrin dyes; polymethine dyes, e.g. cyanine dyes such as Cy3 (emits a response radiation in the wavelength that ranges from about 540 to 580 nm), Cy5 (emits a response radiation in the wavelength that ranges from about 640 to 680 nm), etc; BODIPY dyes and quinoline dyes. Specific fluorophores of interest include: Pyrene, Coumarin, Diethylaminocoumarin, FAM, Fluorescein Chlorotriazinyl, Fluorescein, R110, Eosin, JOE, R6G, HIDC, Tetramethylrhodamine, TAMRA, Lissamine, ROX, Napthofluorescein, Texas Red, Napthofluorescein, Cy3, and Cy5, CalFluorOrange.

[0096] As used herein "probe" refers to a nucleic acid that hybridizes to a target nucleic acid sequence. For example, the probe may be immobilized on a substrate and may hybridize with (and capture) a target nucleic acid. For example, the probe may be part of a primer pair as described herein, or may be used for quantification in conjunction with nucleic acid amplification, for example in qPCR. For example, the probe may comprise a detectable moiety such as a fluorophore, or a fluorophore-quencher pair, such as in a TaqMan probe. In some embodiments, detection of the levels of expression of gene products (such as peptides, or RNA's such as miRNAs, non-coding RNAs, coding RNAs, and mRNAs) involves the use of a probe/primer in a polymerase chain reaction (PCR) (see, e.g., U.S. Patents 4,683,195 and 4,683,202), such as anchor PCR or RACE PCR, or, in some embodiments, in a ligation chain reaction (LCR) (see, e.g., Landrigan et al. (1988) Science 241 : 1077- 1080; and Nakazawa et al. (1994) Proc. Natl. Acad. Sci. USA 91 :360-364), the latter of which can be particularly useful for detecting point mutations in one or more targets gene (see Abravaya et al. (1995) Nucleic Acids Res. 23:675-682). This method can include the steps of collecting a sample of cells from a subject, isolating nucleic acid (e.g., genomic DNA, mRNA, cDNA, small RNA, mature miRNA, pre-miRNA, pri-miRNA, miRNA*, anti-miRNA, or a miRNA binding site, or a variant thereof) from the cells of the sample, contacting the nucleic acid sample with one or more primers which specifically hybridize to one or more targets gene of the disclosure, including the target genes selected from Tables 1-6, or fragments thereof, under conditions such that hybridization and amplification of the target gene (if present) occurs, and detecting the presence or absence of an amplification product, or detecting the size of the amplification product and comparing the length to a control sample. It is anticipated that PCR and/or LCR may be desirable to use as a preliminary amplification step in conjunction with any of the techniques used for detecting levels of gene products as described herein.

[0097] In some embodiments, expression levels of the specified different genes/gene products are detected. In some embodiments, detecting expression levels of the specified different genes/gene products comprises a technique selected from the group, but not limited to, consisting of cDNA chip array analysis, quantitative (RT) PCR, microarray analysis, multiplexing, Luminex analysis, nucleic acid sequencing, northern blot analysis, genomic high throughput sequencing, nanostring, massive parallel signature sequencing (MPSS), and serial analysis of gene expression (SAGE), or a combination of two or more of

the listed items. Optionally, the detecting method comprises a technique selected from the group consisting of, but not limited to, enzyme-linked immunosorbent assay (ELISA), protein sequencing, mass spectrometry (such as MALDI TOF, QTOF, or SELDI TOF), quantitative western blot analysis, and peptide barcoding, or a combination of two or more of the listed items.

[0098] In some embodiments, detecting expression levels of the specified different genes/gene products comprises detecting transcript levels, detecting peptide levels, or detecting signal transduction activity for each of the specified different gene products.

[0099] In some embodiments, detecting expression levels of the specified different genes/gene products comprises contacting the sample with a probe that hybridizes to at least a portion of a transcript of a gene, the transcript comprising any of nucleotide sequences listed in Tables 3 and 4,or an antibody that binds specifically to a peptide listed in Tables 3 and 4. At least a portion of the peptide can be encoded by a nucleotide sequence selected from Tables 3 and 4, and the method can comprise for example (but not limited to), protein sequencing, mass spectrometry (such as MALDI TOF, QTOF, or SELDI TOF), or peptide barcoding.

[00100] In some embodiments, detecting expression levels of the specified different genes/gene products comprises contacting the sample with a probe that hybridizes to at least a portion of a transcript of a gene, the transcript comprising any of nucleotide sequences listed in Tables 3 and 4.

[00101] In some embodiments, detecting expression levels of the specified different genes/gene products comprises contacting the sample with an antibody that binds specifically to a peptide. At least a portion of the peptide can be encoded by a sequence selected from peptide sequences listed in Tables 3 and 4.

[00102] In some embodiments, detecting expression levels of the specified different genes/gene products comprises peptide analysis, for example (but not limited to), protein sequencing, mass spectrometry (such as MALDI TOF, QTOF, or SELDI TOF), or peptide barcoding.

[00103] In some embodiments, detecting expression levels of the specified different genes/gene products comprises one or more of contacting the sample with a probe that hybridizes to at least a portion of a transcript of a gene (the transcript comprising any of nucleotide sequences listed in Tables 3 and 4) and/or an antibody that binds specifically to a

peptide (in which at least a portion of the peptide is encoded by a sequence selected from Tables 3 and 4); and/or, for example (but not limited to) protein sequencing, mass spectrometry (such as MALDI TOF, QTOF, or SELDI TOF), or peptide barcoding.

[00104] In some embodiments, detecting expression levels of the specified different genes/gene products comprises contacting the sample with at least two probes that each hybridize to at least a portion of a transcript of a gene, the transcript comprising any of nucleotide sequences listed in Tables 3 and 4, or at least two antibodies (or protein ligands) that each bind specifically to a peptide, in which at least a portion of the peptide is encoded by a sequence selected from Tables 3 and 4.

[00105] In some embodiments, detecting expression levels of the specified different genes/gene products comprises contacting the sample with at least two probes that each hybridize to at least a portion of a transcript of a gene or the reverse complement thereof, the transcript comprising any of nucleotide sequences listed in Tables 3 and 4.

[00106] In some embodiments, detecting expression levels of the specified different genes/gene products comprises contacting the sample with at least two antibodies (or protein ligands) that each bind specifically to a peptide, in which at least a portion of the peptide is encoded by a sequence selected from Tables 3 and 4.

[00107] In some embodiments, detecting expression levels of the specified different genes/gene products comprises contacting the sample with at least 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, or 35 but no more than 40 (or 20 or 15 or 14) probes that each hybridize to at least a portion of a gene product (such as a transcript of a gene) comprising any of nucleotide sequences listed in Tables 3 and 4; and/or at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, or 35 but no more than 40(or 20 or 15 or 14) antibodies (or protein ligands) that each bind specifically to a peptide, wherein at least a portion of the peptide is encoded by a sequence selected from Tables 3 and 4.

[00108] In some embodiments, detecting expression levels of the specified different genes/gene products comprises contacting the sample with at least 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, or 35 but no more than 40 (or 20 or 15 or 14) probes that each hybridize to at least a portion of gene product (such as a transcript of a gene), comprising any of nucleotide sequences listed in Tables 3 and 4.

[00109] In some embodiments, detecting expression levels of the specified different genes/gene products comprises contacting the sample with at least 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, or 35 but no more than 40 (or 20 or 15 or 14) antibodies (or protein ligands) that each bind specifically to a peptide, wherein at least a portion of the peptide is encoded by a sequence selected from Tables 3 and 4.

[00110] In some embodiments, detecting expression levels of the specified different genes/gene products comprises contacting the sample with (a) for a female subject, a set of at least 6, but no more than 60 (for example, 6-14, 6-15, 6-20, 6-25, 6-30, 6-35, 6-40, 6-50, 6-60, 8-14, 8-15, 8-20, 8-25, 8-30, 8-35, 8-40, 8-50, 8-60, 9-10, 9-14, 9-15, 9-16, 9-20, 9-40, 9-50, 9-60, 10-14, 10-15, 10-20, 10-25, 10-30, 10-35, 10-40, 10-50, or 10-60) different nucleic acid probes that each hybridize to at least a portion of a gene product (such as a transcript of a gene) comprising any of nucleotide sequences listed in Table 3, (b) for a male subject, a set of at least 6, but no more than 40 (for example, 6-14, 6-15, 6-20, 6-25, 6-30, 6-35, 6-40, 8-14, 8-15, 8-20, 8-25, 8-30, 8-35, 8-40, 9-10, 9-14, 9-15, 9-16, 9-20, 9-40, 10-14, 10-15, 10-20, 10-25, 10-30, 10-35, or 10-40) different nucleic acid probes and/or primer pairs that each hybridize to at least a portion of a transcript of a gene or the reverse complement thereof, the transcript comprising any of nucleotide sequences listed in Table 4, (c) for a female subject, a set of at least 6, but no more than 12 (for example, 6-12, 6-10, 6-8, 8-12, 8-10, or 10-12) different antibodies (or protein ligands) that each bind specifically to a peptide encoded by sequences selected from Table 3, and/or (d) for a male subject, a set of at least 14, but no more than 20 (or a set of no more than 15) different antibodies (or protein ligands) that each bind specifically to a peptide encoded by sequences selected from Table 4. In some embodiments, the same numerical range of gene products is detected for male and female subjects.

[00111] In some embodiments, for a female subject, detecting expression levels of the specified different genes/gene products comprises contacting the sample with a set of at least 6, but no more than 40, 30, or 20 different nucleic acid probes and/or primer pairs that each hybridize to at least a portion of a transcript of a gene or the reverse complement thereof, the transcript comprising any of nucleotide sequences listed in Tables 3.

[00112] In some embodiments, for a male subject, detecting expression levels of the specified different genes/gene products comprises contacting the sample with a set of at least 10, but no more than 40, 30, or 20 different nucleic acid probes and/or primer pairs that each

hybridize to at least a portion of a transcript of a gene or the reverse complement thereof, the transcript comprising any of nucleotide sequences listed in Table 4.

[00113] In some embodiments, for a female subject, detecting expression levels of the specified different genes/gene products comprises contacting the sample with a set of at least 10, but no more than 40, 30, or 20 different antibodies (or protein ligands) that each bind specifically to a peptide encoded by sequences selected from Table 3.

[00114] In some embodiments, for a male subject, detecting expression levels of the specified different genes/gene products comprises contacting the sample with set of at least 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, or 35 but no more than 40 different antibodies that each bind specifically to a peptide encoded by sequences selected from Table 4. In some embodiments, for a male subject, detecting expression levels of the specified different genes/gene products comprises contacting the sample with set of at least 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, or 35 but no more than 40 different antibodies (or protein ligands) that each bind specifically to a peptide encoded by sequences selected from Table 4.

[00115] In some embodiments, for a female subject, detecting expression levels of the specified different genes/gene products comprises contacting the sample with one or more of a set of at least 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, or 35 but no more than 40 different nucleic acid probes (for example, a part of primer pairs, or for capture on an array) that each hybridize to at least a portion of a transcript of a gene or the reverse complement thereof, the transcript comprising any of nucleotide sequences listed in Table 3, and/or a set of at least 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, or 35 but no more than 40 different antibodies (or protein ligands) that each bind specifically to a peptide encoded by sequences selected from Table 3.

[00116] In some embodiments, for a male subject, detecting expression levels of the specified different genes/gene products comprises contacting the sample with one or more of a set of at least 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 but no more than 40 different nucleic acid probes and/or primer pairs that each hybridize to at least a portion of a transcript of a gene or the reverse complement thereof, the transcript comprising any of nucleotide sequences listed in Table 4, and/or a set of at least 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20, but no more than 40 different antibodies (or protein ligands) that each bind specifically to a peptide encoded by

sequences selected from Table 4. In some embodiments, for a male subject, detecting expression levels of the specified different genes/gene products comprises contacting the sample with one or more of a set of at least 8, 9, 10, 11, 12, 13, or 14, but no more than 15 different nucleic acid probes and/or primer pairs that each hybridize to at least a portion of a transcript of a gene or the reverse complement thereof, the transcript comprising any of sequences selected from Table 4, and/or a set of at least 8, 9, 10, 11, 12, 13, or 14, but no more than 15 different antibodies (or protein ligands) that each bind specifically to a peptide encoded by sequences selected from Table 4.

[00117] In some embodiments, for a female subject, detecting expression levels of the specified different genes/gene products comprises contacting the sample with a set of at least 6, 7, 8, 9, 10, or 11, but no more than 12 (for example, 6-12, 6-10, 6-8, 8-12, 8-10, or 10-12) different nucleic acid probes and/or primer pairs that each hybridize to at least a portion of a transcript of a gene or the reverse complement thereof, the transcript comprising any of nucleotide sequences listed in Table 3. Optionally, detecting expression levels of the specified different genes/gene products comprises contacting the sample with a set of at least 6, 7, 8, 9, 10, 11, or 12, but no more than 12 (for example, 6-12, 6-10, 6-8, 8-12, 8-10, or 10-12) different antibodies (or protein ligands) that each bind specifically to a peptide encoded by sequences selected from Table 3.

[00118] In some embodiments, for a male subject, detecting expression levels of the specified different genes/gene products comprises contacting the sample with a set of at least 10, 11, 12, 13 ,14, 15, 16, 17, 18, or 19, but no more than 20 (or no more than 15) different nucleic acid probes and/or primer pairs that each hybridize to at least a portion of a transcript of a gene or the reverse complement thereof from Tables 2, 4, and 6. Optionally, detecting expression levels of the specified different genes/gene products comprises contacting the sample with a set of at least 10, 11, 12, 13 ,14, 15, 16, 17, 18, or 19, but no more than 20 (or no more than 15) different antibodies (or protein ligands) that each bind specifically to a peptide encoded by sequences selected from Tables 2, 4, and 6.

Subjects having or at risk of having conditions comprising neoangiogenesis and/or ischemia

[00119] As used herein, a subject is referred to a mammal, including, for example, a murine, porcine, bovine, equine, canine, and/or feline mammals. In some embodiments, a

subject is a non-human primate. In some embodiments, the subject is a human. In some embodiments, the subject is a healthy subject. In some embodiments, the subject is a mammal with a cardiac disease or a cardiovascular condition. In some embodiments the subject is a mammal at risk of having a cardiac disease or a cardiovascular condition. In some embodiments, the subject is at risk of ischemia. In some embodiments, the subject is a mammal with a cardiovascular condition characterized by perfusion shortage, or at a risk thereof. In some embodiments, the subject has a cardiac disease. In some embodiments the subject has a disease, or a cardiovascular condition characterized by oxygen insufficiency related to a cardiovascular event.

[00120] It is contemplated that methods, compositions, kits, and uses of embodiments herein can be used to detect any art-recognized condition comprising neoangiogenesis or ischemia or the risk thereof. Additionally, methods, compositions, kits, and uses comprising a therapeutic compound and/or medical intervention as described herein can be used to inhibit, ameliorate, delay the onset of, reduce the likelihood of, treat, or prevent any art-recognized condition comprising neoangiogenesis or ischemia.

[00121] In certain embodiments, a subject may be diagnosed with one of the diseases or conditions listed here. Alternatively, a subject may be given an output/report that the subject is at risk of having one of the diseases or conditions listed herein. “Disease” and “condition” comprising perfusion shortage are used interchangeably herein. Examples of conditions (or diseases) comprising perfusion shortage include ischemic diseases (such as for example (but not limited to) cardiovascular ischemic disease such as angina pectoris, silent myocardial ischemia, microvascular cardiovascular disease, myocardial infarction, TIA, stroke, minimal vessel dementia, peripheral artery disease) and disease with a perfusion component (for example (but not limited to), cancer, diabetes, and ophthalmologic diseases). By way of example, cancer can comprise perfusion components such as tumor vascularization and/or hematological or lymphogenic metastasis (and thus can be characterized as a disease comprising a perfusion shortage or deficiency and neoangiogenesis (tumor angiogenesis)). By way of example, diabetes, in which there can be challenges in providing blood to the extremities can be characterized as a perfusion shortage or retinal neoangiogenesis. By way of example, ophthalmologic conditions for example (but not limited to) retinal neoangiogenesis can be characterized as a neoangiogenesis. By way of example,

gynecological conditions such as placental buildup during a menstrual cycle can be characterized as a perfusion shortage. Accordingly, examples of conditions or diseases comprising perfusion shortage include, but are not limited to, ischemic cardiovascular disease, microangiopathy in cardiovascular disease (such as diastolic heart failure), hypertrophic cardiomyopathy, cardiovascular pathology with relative ischemia (such as hypertrophic CMP, ischemic heart failure, and/or congenital cardiac disease), myocardial infarction, ischemic cerebrovascular disease (including CVA/ TIA, and/or vascular dementia), ischemic peripheral artery disease, venous disease, orthopedic disease, sepsis, inflammation, lymphatic disease, ophthalmological disease associated with ischemia and/or neoangiogenesis (such as neoangiogenesis in retinopathy), diabetic macro- and microangiopathy, oncological pathology (including solid tumors (tumor angiogenesis), metastatic disease), endothelial dysfunction in cardiovascular and peripheral artery disease, ophthalmology (such as neoangiogenesis in retinopathy), diabetic macro- and microangiopathy, oncological pathology (such as solid tumors and/or metastatic disease), endothelial dysfunction in cardiovascular and peripheral artery disease, nephrological disease associated with ischemia and/or neoangiogenesis, gynecological disease, orthopedic disease, lung disease (for example (but not limited to) COPD, emphysema, lung fibrosis, cystic fibrosis, lung cancer, pulmonary interstitial disease, and/or monitoring pre- and post-lung transplantation, pulmonary emboli), cerebrovascular disease (for example, stroke, TIA, microvascular dementia), and emboli (such as pulmonary emboli, deep venous thrombosis), inadequate ventilation/ oxygenation of a mechanically ventilated subject, inflammatory disease, auto-immune disease (with an ischemic component) or gastrointestinal disorders (for example (but not limited to) Crohn's disease, colitis ulcerosa), neurodegenerative disease (for example (but not limited to) Parkinson's disease or multiple sclerosis), erectile dysfunction, sport injury, frailty, shock, post-reanimation, and post-resuscitation, or a combination of two or more of the listed items. In some embodiments, the condition comprising perfusion shortage comprises a diseases or processes related to vascular remodeling including, but not limited to, arterial and venous diseases, as well as diseases related to lymphangiogenic disease, or vascular remodeling including (but not limited to) lymphangiogenic metastatic disease, arteriovenous malformation, arterial remodeling, and/or venous thrombosis, and/or placental development (e.g., to monitor menstrual cycle). In some embodiments, the disease or condition comprising perfusion shortage comprises (but not

limited to) ischemic cardiovascular disease, microangiopathy in cardiovascular disease (such as diastolic heart failure), hypertrophic cardiomyopathy, cardiovascular pathology with relative ischemia (such as hypertrophic CMP, ischemic heart failure, and/or congenital cardiac disease), ischemic cerebrovascular disease (including CVA/ TIA, and/or vascular dementia), ischemic peripheral artery disease, venous disease, orthopedic disease, sepsis, inflammation, lymphatic disease, ophthalmological disease associated with ischemia and/or neoangiogenesis (such as neoangiogenesis in retinopathy), diabetic macro and microangiopathy, oncological pathology (including solid tumors, metastatic disease), endothelial dysfunction in cardiovascular and peripheral artery disease, ophthalmology (such as neoangiogenesis in retinopathy), diabetic macro and microangiopathy, oncological pathology (such as solid tumors and/or metastatic disease), endothelial dysfunction in cardiovascular and peripheral artery disease, nephrological disease associated with ischemia and/or neoangiogenesis, gynecological disease, orthopedic disease, lung disease (such as COPD, emphysema, lung fibrosis, cystic fibrosis, lung cancer, pulmonary interstitial disease, and/or monitoring pre- and post-lung transplantation, pulmonary emboli), cerebrovascular disease (for example, stroke, TIA, microvascular dementia), and emboli (such as pulmonary emboli, deep venous thrombosis), inadequate ventilation/ oxygenation of a mechanically ventilated subject, inflammatory disease and/or auto-immune disease (with an ischemic component) or gastrointestinal disorder (including (but not limited to) Crohn's disease, Colitis Ulcerosa), neurodegenerative disease (including (but not limited to) Parkinson's disease or multiple sclerosis), erectile dysfunction, sport injury, frailty, shock (such as post-resuscitation shock), arterial and venous diseases, disease related to lymphangiogenic disease, vascular remodeling including lymphangiogenic metastatic disease, arteriovenous malformation, arterial remodeling, or venous thrombosis, or a combination of two or more of any of the listed items.

[00122] In the method of some embodiments, the condition comprising perfusion shortage is selected from the group consisting of ischemic cardiovascular disease, microangiopathy in cardiovascular disease (such as diastolic heart failure), hypertrophic cardiomyopathy, cardiovascular pathology with relative ischemia (such as hypertrophic CMP, ischemic heart failure, and/or congenital cardiac disease), ischemic cerebrovascular disease (including CVA/ TIA, and/or vascular dementia), ischemic peripheral artery disease, venous disease, orthopedic disease, sepsis, inflammation, lymphatic disease, ophthalmological disease

associated with ischemia and/or neoangiogenesis (including (but not limited to) neoangiogenesis in retinopathy), diabetic macro and microangiopathy, oncological pathology (including solid tumors, metastatic disease), endothelial dysfunction in cardiovascular and peripheral artery disease, ophthalmology (such as neoangiogenesis in retinopathy), diabetic macro and microangiopathy, oncological pathology (including (but not limited) solid tumors and/or metastatic disease), endothelial dysfunction in cardiovascular and peripheral artery disease, nephrological disease associated with ischemia and/or neoangiogenesis, gynecological disease, orthopedic disease, lung disease (including (but not limited to) COPD, emphysema, lung fibrosis, cystic fibrosis, lung cancer, pulmonary interstitial disease, and/or monitoring pre- and post-lung transplantation), pulmonary emboli or deep venous thrombosis), cerebrovascular disease (including (but not limited to), stroke, TIA, microvascular dementia, and emboli such as pulmonary emboli), deep venous thrombosis, inadequate ventilation/ oxygenation of a mechanically ventilated subject, inflammatory disease and/or auto-immune disease (with an ischemic component), gastrointestinal disorders (including (but not limited) Crohn's disease, colitis ulcerosa), neurodegenerative disease (including (but not limited) Parkinson's disease or multiple sclerosis), erectile dysfunction, sport injury, frailty, shock (such as post-resuscitation shock), arterial and venous diseases, disease related to lymphangiogenic disease, vascular remodeling including lymphangiogenic metastatic disease, arteriovenous malformation, arterial remodeling, or venous thrombosis, or a combination of two or more of the listed items.

[00123] In some embodiments, the condition comprising perfusion shortage comprises cardiovascular pathology with relative or absolute ischemia comprises congenital disease with significant or persistent shunting, such as open foramen ovale, ductus botalli, and/or ventricular shunt, or Eisenmenger syndrome/disease.

[00124] In some embodiments, the condition comprising perfusion shortage comprises relative or absolute ischemia. Without being limited by theory, ischemia can refer to decreased supply of oxygen and/or increased demand for oxygen. In some embodiments, ischemia due to increased demand for oxygen may occur due to, for instance, due to hypertrophy, inflammation or increased metabolism or sepsis

[00125] In some embodiments, the relative ischemia comprises cardiovascular disease with an increased demand for oxygen for instance but not limited to hypertrophic

myocardium or and local and/or systemic increased oxygen demand (including but not limited to inflammation).

[00126] In some embodiments, a subject has at least one risk factor for having a condition comprising perfusion shortage, wherein said risk factor is selected from the group consisting of high blood pressure; glucose intolerance; family history of cardiovascular disease, hypercholesterolemia, or dyslipidemia ; aging; smoking; physical inactivity; obesity; previous cardiovascular disease; diagnosis of diabetes mellitus, kidney disease, peripheral artery disease, or metabolic syndrome; gender; high low density lipoprotein (LDL) level; high cholesterol level; and specific DNA polymorphism associated with higher cardiovascular risk.

Medical monitoring and intervention

[00127] In some embodiments, the method further comprises correlating the detected levels of the specified different gene products to a severity of the condition comprising perfusion shortage or a likelihood of developing the condition, thereby ascertaining a severity or risk of the condition. The correlating can be used to quantify the condition or the risk of the condition. By way of example, if the condition comprising perfusion shortage is present, or there is a risk of the condition, the subject can be recommended for a medical intervention or an invasive or resource-intensive monitoring as described herein (e.g., invasive angiography, advanced imaging, nuclear imaging, MSCT, MRI analysis, or tissue biopsy)) as described herein. Example medical interventions include, but are not limited to, initiation or modulation of pharmacotherapy or anti-ischemic medical intervention (including (but not limited to) percutaneous and/or surgical revascularization), and/or modulating the local (or general) perfusion and oxygenation. In some embodiments, the medical intervention is provided to the subject. In some embodiments, the subject receives the medical intervention. In some embodiments, the correlating can be performed after a medical intervention, for example to determine efficacy of the medical intervention, monitor disease progression, and/or to select further medical management or medical interventions.

[00128] In some embodiments, the method further comprises identifying a previous condition comprising perfusion shortage (such as an ischemic or neoangiogenesis episode), diagnosing the subject as having the condition, determining the subject to be at risk of the condition, prognosticating an outcome in the subject, predicting a response of the subject to a

medical intervention or pharmacotherapy, selecting a medical intervention for the subject (for example, by way of a surrogate marker), selecting a dose and/or frequency of a medical intervention, validating a candidate medical intervention, measuring a response to a candidate medical intervention, measuring and monitoring a subject's ischemic disease progression or remission, and/or monitoring a subject's response to a medical intervention or pharmacotherapy based on the detected levels of the specified different gene products. For example, levels of the specified gene products outside of (e.g., exceeding the upper limit of) the control ranges can indicate that the subject has the condition, or is at risk for the condition.

[00129] In some embodiments, the method comprises recommending the subject for an anti- or pro-ischemic medical intervention and/or anti- or pro-neoangiogenesis medical intervention or the modification of the therapy when the expression levels of the specified different gene products are outside of the control ranges. Any suitable surgical and/or percutaneous procedure to treat a condition comprising ischemia and/or neoangiogenesis is contemplated. The medical intervention can be one that is approved by, and/or meets guidelines set by a local health specialist organisation, or by a professional or government organization, for example the Food and Drug Administration, or the European Medicines Agency.

[00130] In some embodiments, the method comprises providing an assessment of a severity of said subject's perfusion shortage, based on the output. In some embodiments, the output further comprises providing a prognosis report of said subject's perfusion shortage. In some embodiments, providing a prognosis report may be based on the determination of expression levels of two or more genes (nucleotide or protein biomarkers) from a plurality of the identified genes (nucleotide or protein biomarkers) described herein. In some embodiments, providing a prognosis report may be based on the determination of expression levels of two or more genes (nucleotide or protein biomarkers) from a plurality of the identified genes (nucleotide or protein biomarkers) that are specific for a female in case the subject is a female. In some embodiments, providing a prognosis report may be based on the determination of expression levels of two or more genes (nucleotide or protein biomarkers) from a plurality of the identified genes (nucleotide or protein biomarkers) that are specific for a male in case the subject is a male. In some embodiments, providing a prognosis report may be based on the determination of expression levels of two or more genes (nucleotide or protein biomarkers)

from a plurality of the identified genes (nucleotide or protein biomarkers) that are specific for a male or a female in case the subject is a male or a female respectively, depending on the degree of difference of the expression levels of said two or more genes (nucleotide or protein biomarkers) in the subject with respect to a control value.

[00131] In some embodiments, a control value is the respective value in a control for example, an individual of the same gender as the subject, without a cardiovascular risk of having ischemia. A control value may be a baseline value for the level of each of the two or more genes in the subject prior to a cardiovascular event in the subject.

[00132] In some embodiments, said output may further comprise providing a response report of said subject upon, during, and/or after a medical intervention or modulation of pharmacotherapy. In some embodiments, said output may further comprise providing a monitoring report. The monitoring report may comprise monitoring the subject before or after receiving a medical intervention or modulation of pharmacotherapy. In some embodiments, the monitoring may occur periodically from the date of obtaining the samples to generate the output, and continue for a variable period of time, or as determined by a medical practitioner. In some embodiments, the monitoring may occur periodically for 2 months or more, for 4 months or more for 6 months or more, for 8 months or more, for 10 months or more, for 12 months or more for 14 months or more, for 16 months or more, for 18 months or more, for 20 months or more, for 22 months or more, or for 24 months, or more from the time the date of obtaining the samples to generate the output. In some embodiments, the monitoring may occur periodically for 36 months or more. In some embodiments, the monitoring may occur periodically for 48 months or more.

[00133] In some embodiments, the monitoring may occur once every 2 weeks, or once every 3 weeks, or once every 4 weeks, or once every 6 weeks, or once every 8 weeks, or once every 10 weeks, or once every 12 weeks, or once every 14 weeks, or once every 16 weeks, or once every 18 weeks, or once every 20 weeks, or once every 22 weeks, or once every 24 weeks.

[00134] In some embodiments, the method further comprises providing a treatment to said subject, wherein said subject has or is at risk of having a condition comprising perfusion shortage, at least in part based on said output. In some embodiments, providing a treatment comprises administering an anti- or pro-ischemic medical intervention and/or anti-

or pro- neoangiogenesis medical intervention, and/or additional diagnostic analysis (e.g., biopsy) to the subject (or recommending administering an anti- or pro-ischemic medical intervention and/or anti- or pro- neoangiogenesis medical intervention, and/or additional diagnostic analysis (e.g., biopsy) to the subject) when the expression levels of the specified different gene products are outside of the control ranges. For example, in some embodiments, if the expression levels of the specified different gene products exceed the control ranges, and an anti-ischemic medical intervention or anti-neoangiogenesis medical intervention is provided.

[00135] In the method of some embodiments, the medical intervention comprises pharmacotherapy, radiotherapy or a surgical or percutaneous procedure, or a combination of two or more of the listed items. In the method of some embodiments, the medical intervention targets one or more of the at least two specified different gene products. In the method of some embodiments, the medical intervention or pharmacotherapy comprises (but is not limited to) an anti-ischemic medical intervention, for example a beta-blocker, a calcium antagonist, nitrates, thrombolysis, thrombectomy, bypass surgery, or a percutaneous coronary procedure. In some embodiments, the medical intervention comprises administering a pharmaceutical composition including but not limited to beta-blockers, calcium channels antagonists, nitrates, aspirin, cholesterol-lowering compounds, angiotensin-converting enzyme (ACE) inhibitors, and ranolazine. In some embodiments, the medical intervention comprises administering a pharmaceutical composition selected from the group consisting of (but not limited to) beta-blockers, calcium channels antagonists, nitrates, aspirin, cholesterol-lowering compounds, angiotensin-converting enzyme (ACE) inhibitors, and ranolazine. In some embodiments, the medical intervention comprises (but not limited to) one or more of atenolol, nadolol, metoprolol, propranolol, carteolol, carvedilol, labetolol, oxprenolol, penbutolol, pindolol, sotalol, timolol, benazepril, captopril, cilazapril, enalapril, enalaprilat, fosinopril, imidapril, lisinopril, moexipril, perindopril, quinapril, ramipril, trandolapril, candesartan, eprosartan, irbesartan, losartan, olmesartan, telmisartan, valsartan, aspirin, diclofenac; diflunisal, etodolac, fenoprofen, flurbiprofen, ibuprofen, indomethacin, ketoprofen; Ketorolac, meclofenamate, mefenamic acid, meloxicam, nabumetone, naproxen, oxaprozin, piroxicam, salsalate, sulindac, tolmetin, a COX-2 inhibitor (comprises celecoxib rofecoxib, etoricoxib, valdecoxib, parecoxib, meloxicam or lumiracoxib), ranolazine, nitrates, such as isosorbide mononitrate,

isosorbide dinitrate (ISDN), andarine, ethylestrenol, mesterolone, methandrostenolone, methenolone, methyltestosterone, oxandrolone, oxymetholone stanozolol, boldenone, hexoxymestrolum, methandrostenolone, methenolone enanthate, nandrolone decanoate, nandrolone phenproprionate, stanozolol, stenbolone, testosterone cypionate, testosterone enanthate, testosteron, testosterone nicotinate, therobolin, trenbolone, trenbolone, trophobolene, a natural oil or fatty acid, e.g., comprising an omega-3 fatty acid, a fish oil, a long-chain polyunsaturated fatty acid, an n-3 and/or n-6 highly unsaturated fatty acid, eicosapentaenoic acid (EPA), docosahexaenoic acid (DHA), calcium channel blocker, such as Nifidipine, Amlodipine, Diltiazem, Felodipine, Isradipine, Nicardipine, Nisoldipine, Verapamil, or a combination thereof. In some embodiments, the pharmaceutical composition may be packaged for administration intravenously, topically, orally, by inhalation, by infusion, by injection, intraperitoneally, intramuscularly, subcutaneously, intra-aurally, for intra-articular administration, for intra-mammary administration, for topical administration or for absorption through epithelial or mucocutaneous linings.

[00136] In the method of some embodiments, the medical intervention comprises a modulator of nucleic acid or protein expression comprising at least one of nucleotide or peptide sequences listed in Tables 3 and 4. In some embodiments, the medical intervention can target one or more genes (nucleotide or protein targets) listed in Tables 1-6. In some embodiments, the medical intervention may comprise a protein, a small molecule or a nucleic acid that can modulate the expression of the target genes comprising one or more genes (nucleotide or protein targets) listed in Tables 1-3.

[00137] In the method of some embodiments, the medical intervention comprises modulating the function of a gene listed in Tables 1-6. For example, modulating can comprise inhibiting the function of the gene product or enhancing the function of the gene product. Inhibiting (or reducing) can comprise, for example, (but not limited to) inhibiting transcription or translation, destabilizing or degrading a nucleic acid encoding the gene product or the gene product itself, changing the location of a nucleic acid encoding the gene product or the gene product itself, or forming a complex with the gene product. Enhancing (or increasing) can comprise, for example (but not limited to), inducing or increasing transcription or translation, stabilizing a nucleic acid encoding the gene product or the gene product itself, changing the

location of a nucleic acid encoding the gene product or the gene product itself, or forming a complex with the gene product.

[00138] In some cases, the medical intervention comprises using nucleotides or peptides listed in Tables 3 and 4 or nucleotides or peptides derived from genes listed in Tables 1-6 as therapeutic targets. Suitable technologies may be used to direct to these therapeutic targets to modulate gene functions.

[00139] In some embodiments, the method further comprises ceasing or modulating the medical intervention and/or monitoring (or recommending ceasing or modulating the medical intervention and/or monitoring) when the expression levels of the specified different gene products are within the control ranges. For example, modulating can comprise adaptation of dose or frequency, or change of pharmacotherapy/ intervention. It is contemplated that some kinds of patient monitoring can be invasive and/or resource-intensive (which, for shorthand, may collectively be referred to as "invasive monitoring"). Therefore, it can be advantageous to use methods, compositions, kits and uses as described herein to determine that the subject is at-risk before performing more invasive or resource-intensive analysis. In the method, composition, kit, or use of some embodiments, the invasive or resource-intensive monitoring comprises (but is not limited to) invasive angiography, advanced imaging, nuclear imaging, MSCT, MRI analysis, tissue biopsy, or monitoring of mechanical ventilation. Accordingly, in some embodiments, the method comprises determining the subject to be at risk for the condition, and further comprises invasive or resource-intensive monitoring after the subject has been determined to be at-risk. For example, in some embodiments, monitoring is performed for adequate ventilation and oxygenation of a mechanically ventilated patient, such as a patient in the CCU, ICU, and/or during surgery. In the method, composition, kit, or use of some embodiments, detecting a condition comprising perfusion shortage (or risk thereof) as described herein can be used in combination with a therapy for a condition comprising perfusion shortage as for example, a companion diagnostic. By way of example, the companion diagnostic can be used as a "gatekeeper" assay for the initiation of therapy, for modulation of therapy (e.g., reduction or increase of dose and/or frequency), efficacy analysis, and to monitor disease progression and remission. Accordingly, in some embodiments, the method of detecting a condition comprising perfusion shortage (or risk thereof) comprises determining whether or not to initiation therapy (based on whether the

subject has or is at risk of a condition comprising perfusion shortage), for modulation of therapy (e.g., reduction or increase of dose and/or frequency), efficacy analysis, and to monitor disease progression.

[00140] In some embodiments, the subject may be monitored for, in addition to the monitoring aspects contemplated in the preceding sections, a condition or an event related to any one or more of: a trauma, condition or disease comprising: a chronic Systemic Inflammatory Response State (SIRS); chronic systemic inflammatory stress; burns, chronic obstructive pulmonary disease; congestive heart failure; chronic kidney disease; surgery; cancer (and cancer metastasis (hematologic or lymphogenic metastasis); sepsis; ageing; acute respiratory distress syndrome; acute lung injury; infection; a CNS disorder or injury; anemia; immunosuppression; insulin resistance; anorexia; anxiety; sleep disturbances; weakness; fatigue; gastrointestinal distress; sleep disturbances; wake disturbances; pain; listlessness; shortness of breath; lethargy; depression; malaise; or, a combination thereof. In one embodiment, the trauma, condition or disease comprises a maladaptive nutritional state secondary to the SIRS. In one embodiment, the maladaptive nutritional state comprises cachexia, and optionally the cachexia comprises cachexia secondary to cancer. In one embodiment, the CNS disorder comprises Parkinson's disease or Alzheimer's disease. In some embodiments, at least based in part on response report, prognosis report, or both, further comprising ceasing said medical intervention or pharmacotherapy.

Kits

[00141] In some embodiments, a kit is described. The kit can comprise (i) at least two different nucleic acid probes that hybridize to a portion of a transcript comprising sequences selected from Tables 3 and 4 or a reverse complement thereof, in which each of the nucleic acid probes comprises a different detectable moiety; and/or (ii) at least two different antibodies (or protein ligands) that each binds specifically to a peptide, in which at least a portion of the peptide is encoded by a sequence selected from Tables 3 and 4. In some embodiments, the kit consists essentially of or consists of (i) at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, or 19 different nucleic acid probes that hybridize to a portion of a transcript comprising sequences selected from Tables 3 and 4, or (ii) at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, or 19 different antibodies (or protein ligands) that each binds specifically to a peptide, in which at least a portion of the peptide is encoded by a sequence selected from Tables

3 and 4. In some embodiments, the kit consists essentially of or consists of (i) at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, or 19, but no more than 60 different nucleic acid probes that hybridize to a portion of a transcript comprising sequences selected from Tables 3 and 4, or (ii) at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, or 19, but no more than 60 different antibodies (or protein ligands) that each binds specifically to a peptide, in which at least a portion of the peptide is encoded by a sequence selected from Tables 3 and 4. In some embodiments, the kit consists essentially of or consists of (i) at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, or 19, but no more than 40 different nucleic acid probes that hybridize to a portion of a transcript comprising sequences selected from Tables 3 and 4, or (ii) at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, or 19, but no more than 40 different antibodies (or protein ligands) that each binds specifically to a peptide, in which at least a portion of the peptide is encoded by a sequence selected from Tables 3 and 4. In some embodiments, the kit consists essentially of or consists of (i) at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, or 19, but no more than 20 different nucleic acid probes that hybridize to a portion of a transcript comprising sequences selected from Tables 3 and 4. As described herein, a probe may be part of a primer pair, may be for quantifying amplicons in nucleic acid amplification, and/or may be for capturing a nucleic acid on a substrate. In some embodiments, the kit consists essentially of or consists of (ii) at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, or 19, but no more than 20 different antibodies (or protein ligands) that each binds specifically to a peptide, in which at least a portion of the peptide is encoded by a sequence selected from Tables 3 and 4. In some embodiments, the kit consists essentially of or consists of (i) at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, or 19, but no more than 20 different nucleic acid probes that hybridize to a portion of a transcript comprising sequences selected from Tables 3 and 4, or (ii) at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, or 19, but no more than 20 different antibodies (or protein ligands) that each binds specifically to a peptide, in which at least a portion of the peptide is encoded by a sequence selected from Tables 3 and 4. In some embodiments, nucleic acid probes that hybridize to a portion of a transcript comprising sequences selected from Tables 3 and 4 represent at least 50% of the total unique nucleic acid probes in the kit, for example, at least 50%, 60%,70%, 80%, 90%, 95% or 100% of the unique nucleic acid probes in the kit. In some embodiments nucleic acid probes that hybridize to a portion of a transcript comprising

sequences selected from Tables 3 and 4 represent at least 50% of the total unique nucleic acid probes in the kit, for example, at least 50%, 60%,70%, 80%, 90%, 95% or 100% of the unique nucleic acid probes in the kit. In some embodiments, antibodies (or protein ligands) that each bind specifically to a peptide, in which at least a portion of the peptide is encoded by a sequence selected from Tables 3 and 4, represent at least 50% of the total unique antibodies (or protein ligands) in the kit, for example, at least 50%, 60%,70%, 80%, 90%, 95% or 100% of the unique antibodies (or protein ligands) in the kit. In some embodiments, the kit can be for use in any of the methods described herein.

[00142] In some embodiments, the kit comprises at least two different nucleic acid probes or primer pairs that hybridize to a portion of a transcript comprising sequences selected from Tables 3 and 4 or a reverse complement thereof. Each of the nucleic acid probes can comprise a different detectable moiety, for example a fluorophore, a quantum dot, a radiolabel, or an enzyme. In some embodiments, a probe of the kit is a primer of a primer pair as described herein.

[00143] In some embodiments, the kit comprises at least two different antibodies (or protein ligands) that each bind specifically to a peptide. At least a portion of the peptide is encoded by a sequence selected from Tables 3 and 4. Optionally, the antibodies (or protein ligands) can each bind to a sequence encoded by one of Tables 3 and 4.

[00144] In some embodiments, the kit comprises at least two different nucleic acid probes that each hybridize to a portion of a different transcript comprising a sequence selected from SEQ ID NOs: 1-5103, Genes Number 1-9280, or a reverse complement thereof. By way of example, the nucleic acid probes can be parts of primer pairs. By way of example, each of the nucleic acid probes can comprise a different detectable moiety such as a barcode or fluorophore. Optionally, at least two different antibodies (or protein ligands) that each binds specifically to a peptide, on which at least a portion of the peptide is encoded by a sequence selected from Tables 3 and 4.

[00145] In the kit of some embodiments, (a) the nucleic acid probes comprise at least 6 but no more than 12 nucleic acid probes that each hybridize to a portion of a transcript comprising sequences selected from Table 3 or a reverse complement thereof, wherein each of the different nucleic acid probes comprises a different detectable moiety, and/or (b) at least 14 but no more than 40 nucleic acid probes that each hybridize to a portion of a transcript

comprising sequences selected from Table 4 or a reverse complement thereof, wherein each of the different nucleic acid probes comprises a different detectable moiety. In the kit of some embodiments, (c) the at least two different antibodies (or protein ligands) comprise at least 6, but no more than 12 antibodies (or protein ligands) that each binds specifically to a peptide, and at least a portion of the peptide can be encoded by a sequence selected from Table 3, and each of the antibodies (or protein ligands) can comprises a different detectable moiety, and/or (d) the at least two different antibodies (or protein ligands) comprise at least 14, but no more than 20 antibodies (or protein ligands) that each binds specifically to a peptide, and at least a portion of the peptide is encoded by a sequence selected from Table 4, and each of the antibodies (or protein ligands) comprises a different detectable moiety.

[00146] In the kit of some embodiments, the at least two different nucleic acid probes comprise at least 6 but no more than 12 nucleic acid probes that each hybridize to a portion of a transcript comprising sequences selected from Table 3or a reverse complement thereof. Each of the different nucleic acid probes can comprise a different detectable moiety.

[00147] In the kit of some embodiments, the at least two different nucleic acid probes comprise at least 14 but no more than 20 nucleic acid probes that each hybridize to a portion of a transcript comprising sequences selected from Table 4 or a reverse complement thereof. Each of the different nucleic acid probes can comprises a different detectable moiety.

[00148] In the kit of some embodiments, the at least two different antibodies (or protein ligands) comprise at least 6, but no more than 12 antibodies (or protein ligands) that each binds specifically to a peptide, in which at least a portion of the peptide is encoded by a sequence selected from Table 3. Each of the antibodies (or protein ligands) can comprises a different detectable moiety.

[00149] In the kit of some embodiments, the at least two different antibodies (or protein ligands) comprise at least 14, but no more than 20 antibodies (or protein ligands) that each binds specifically to a peptide, wherein at least a portion of the peptide is encoded by a sequence selected from Table 4. Each of the antibodies (or protein ligands) can comprises a different detectable moiety.

[00150] In some embodiments, the kit further comprises (i) a primer pair configured to amplify a transcript comprising a sequence from Table 3, in which at least one of the nucleic acid probes hybridizes to the transcript or portion thereof; or (ii) a primer pair configured to

amplify a transcript comprising a sequence from Table 4, in which at least one of the nucleic acid probes hybridizes to the transcript or portion thereof. For example, the kit can comprise at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, or 19, but no more than 40 different primer pairs that each amplify a different transcript comprising a sequence from Table 3, such as 6-12 primer pairs, or at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, or 19, but no more than 40 different primer pairs that each amplify a different transcript comprising a sequence from Table 3, such as 14-20 primer pairs.

[00151] In some embodiments, the kit further comprises a primer pair configured to amplify a transcript comprising a sequence from Table 3. At least one of the nucleic acid probes as described herein can hybridize to the transcript or portion thereof. For example, the kit can comprise at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, or 19, but no more than 40 different primer pairs that each amplify a different transcript comprising a sequence from Table 3, such as 6-12 primer pairs.

[00152] In some embodiments, the kit further comprises a primer pair configured to amplify a transcript comprising a sequence from Table 4. At least one of the nucleic acid probes hybridizes to the transcript or portion thereof. For example, the kit can comprise at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, or 19, but no more than 40 different primer pairs that each amplify a different transcript comprising a sequence from Table 3, such as 14-20 primer pairs.

[00153] In the kit of some embodiments, the antibodies (or protein ligands) are each immobilized on a separate substrate, each substrate comprising a detectable moiety unique to the antibody immobilized thereon.

[00154] In the kit some embodiments, the kit further comprises an antibody that binds specifically to Flk1, Flt1, Flt4, or any other cell surface marker disclosed herein, or a combination of the listed items, optionally wherein the antibody is immobilized on a substrate. This antibody can be used to isolate Flk1+ cells or other hematopoietic EPCs with other cell surface marker(s) disclosed herein.

[00155] In the kit of some embodiments, the detectable moiety comprises (but is not limited to) a fluorophore, a radiolabel, a nanoparticle (such as a metal nanoparticle), magnetic bead, an enzyme, a quantum dot, or a nucleic acid barcode.

[00156] In the kit of some embodiments, the kit further comprises a reference composition comprising nucleic acids of cells. At least 50% of the nucleic acids can be from mononuclear endothelial stem cells from a peripheral blood sample of a control individual who does not have a perfusion shortage (e.g., ischemia and/or neoangiogenesis).

[00157] In some embodiments, a method of detecting a condition comprising perfusion shortage (such as neoangiogenesis and/or ischemia), or risk thereof in a subject is performed using the reagents of any of the kits or compositions described herein.

Methods of inhibiting, ameliorating, delaying the onset of, reducing the likelihood of, treating, or preventing a condition comprising neoangiogenesis or ischemia

[00158] In some embodiments, a method of inhibiting, ameliorating, delaying the onset of, reducing the likelihood of, treating, or preventing a condition comprising neoangiogenesis or ischemia in a subject in need thereof is provided. The method can comprise administering to the subject a medical intervention comprising an effective amount of a modulator nucleic acid comprising at least one SEQ ID NOs: 1-5103 or Genes Number 1-9280. Optionally, the medical intervention further comprises an additional pharmacotherapy, or a surgical or percutaneous procedure, or a combination of two or more of the listed items. The modulator nucleic acid can be administered by any suitable means, for example, oral, intravenous, intramuscular, subcutaneous, intra-arterial or the like. The modulator nucleic acid can be administered in an amount effect to inhibit, reduce, or prevent or even increase expression, initiate expression or mimic the expression of genes listed in Tables 1-6. It will be appreciated that any method of inhibiting, ameliorating, delaying the onset of, reducing the likelihood of, treating, or preventing a condition comprising neoangiogenesis or ischemia described herein may be performed in conjunction with a method of detecting a condition comprising neoangiogenesis or ischemia as described herein. For example, the condition can be detected, and then the inhibiting, ameliorating, delaying the onset of, reducing the likelihood of, treating, or preventing a condition comprising neoangiogenesis or ischemia can be performed. Conceptually, in some embodiments, the method comprises any method of reducing, inhibiting, or preventing the increase of the expression levels of any of the gene products comprising or encoded at least in part by any of genes listed in Tables 1-6. Without being limited by theory, although the nucleic acids of Tables 1-6 are overexpressed in

conditions comprising perfusion (such as ischemia and/or neoangiogenesis), it is contemplated that the overexpression can represent a component of disease or disease progression, or can represent a response to disease progression. Accordingly, it will be appreciated that a "modulator nucleic acid" can decrease the expression of a gene product, for example if the modulator nucleic acid comprises an antisense RNA, small interfering RNA (siRNA), microRNA (miRNA), short hairpin RNA (shRNA), or CRISPR gRNA. It will also be appreciated that a modulator nucleic acid can increase the expression of a gene product, for example by encoding the gene product. Accordingly, in some embodiments, a modulator nucleic is comprised by an expression vector, such as a lentiviral vector, adenoviral vector, or adeno-associated viral vector. It will be appreciated that a modulator nucleic acid comprises sufficient sequence identity to a target nucleic acid to either enhance activity of the encoded gene product (for example by encoding additional gene product) or to inhibit the encoded gene product (for example, by hybridizing to a target nucleic acid encoding the gene product. Accordingly, a modulator nucleic acid can comprise at least 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, 35, 40, 45, or 50 consecutive nucleotides of a target nucleic acid. In some embodiments, a modulator nucleic acid hybridizes to a target nucleic acid under physiological conditions.

[00159] In the method of some embodiments, (a) if the subject is a female, the modulator nucleic acid comprises at least 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 35, 40, 45, or 50 consecutive nucleotides of one or more of any of Table 3 or an antisense strand thereof (for example, 2-14, 2-15, 2-16, 2-17, 2-18, 2-19, 2-20, 2-40, 4-14, 4-15, 4-20, 4-25, 4-30, 4-35, 4-40, 5-10, 5-14, 5-15, 5-16, 5-17, 5-18, 5-19, 5-20, 5-40, 6-14, 6-15, 6-20, 6-25, 6-30, 6-35, 6-40, 8-14, 8-15, 8-20, 8-25, 8-30, 8-35, 8-40, 9-10, 9-14, 9-15, 9-16, 9-20, 9-40, 10-14, 10-15, 10-20, 10-25, 10-30, 10-35, or 10-40 of sequences listed in Table 3), or (b) if the subject is a male, the modulator nucleic acid comprises at least 5, 10, 15, 20, 25, 30, 35, 40, 45, or 50 consecutive nucleotides of one or more of any at least one of **Tables 2, 4, and 6** or an antisense strand thereof to the subject (for example, 2-14, 2-15, 2-16, 2-17, 2-18, 2-19, 2-20, 2-40, 4-14, 4-15, 4-20, 4-25, 4-30, 4-35, 4-40, 5-10, 5-14, 5-15, 5-16, 5-17, 5-18, 5-19, 5-20, 5-40, 6-14, 6-15, 6-20, 6-25, 6-30, 6-35, 6-40, 8-14, 8-15, 8-20, 8-25, 8-30, 8-35, 8-40, 9-10, 9-14, 9-15, 9-16, 9-20, 9-40, 10-14, 10-15, 10-20, 10-25, 10-30, 10-35, or 10-40 of the listed SEQ ID NO:s). In some embodiments, the same numerical range of gene products is detected for male

and female subjects. In some embodiments, the modulator nucleic acid enhances activity of the gene product. In some embodiments, the modulator nucleic acid inhibits activity of the gene product, for example, comprising an antisense RNA, small interfering RNA (siRNA), microRNA (miRNA), short hairpin RNA (shRNA), or CRISPR gRNA

[00160] In the method of some embodiments, if the subject is a female, the modulator nucleic acid comprises at least one of sequences listed in Table 3 or an antisense strand thereof.

[00161] In the method of some embodiments, if the subject is a male, the modulator nucleic acid comprises at least one of sequences listed in Table 4 or an antisense strand thereof.

[00162] In some embodiments, a method of inhibiting, ameliorating, delaying the onset of, reducing the likelihood of, treating, or preventing a condition comprising perfusion shortage in a subject in need thereof is provided. In some embodiments, the method comprises obtaining a sample of a subject, and obtaining expression levels from the sample of the subject. The expression levels can be of at least two specified different gene products from Tables 1-6. The expression levels of the specified different gene products can be outside of control ranges of expression levels of the specified different gene products. Accordingly, the method can comprise administering a medical intervention for the condition to the subject.

[00163] In the method of some embodiments, the cellular secretion is selected from the group consisting of: cell lysate, blood, plasma, serum, stool, lymph, cerebrospinal fluid, saliva, sputum, tears, sweat, semen, transudate, urine, exudate, tissue biopsy, and synovial fluid. In the method of some embodiments, the cellular secretion is selected from the group consisting of: blood, plasma, serum, stool, lymph, cerebrospinal fluid, saliva, sputum, tears, sweat, semen, transudate, urine, exudate, tissue biopsy, and synovial fluid

[00164] In some embodiments, the method further comprises correlating the detected levels of the specified different gene products to a severity of the condition or a likelihood of developing the condition, thereby ascertaining a severity or risk of the condition.

[00165] In the method of some embodiments, administering the medical intervention to the subject when the expression levels of at least 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, 50, or 60 specified different gene products are outside of the control ranges, including ranges between any two of the listed values, for example, 2-14, 2-15, 2-16, 2-17, 2-18, 2-19, 2-20, 2-40, 20-50, 20-60, 4-14, 4-15, 4-20, 4-25, 4-30, 4-35, 4-40, 4-50, 4-60, 5-10, 5-14, 5-15, 5-16,

5-17, 5-18, 5-19, 5-20, 5-40, 5-50, 5-60, 6-14, 6-15, 6-20, 6-25, 6-30, 6-35, 6-40, 6-50, 6-60, 8-14, 8-15, 8-20, 8-25, 8-30, 8-35, 8-40, 8-50, 8-60, 9-10, 9-14, 9-15, 9-16, 9-20, 9-40, 9-50, 9-60, 10-14, 10-15, 10-20, 10-25, 10-30, 10-35, 10-40, 10-50, or 10-60 specified different gene products.

[00166] In some embodiments, (a) if the subject is female, the method comprises determining the subject to have the condition or a risk thereof in the subject when the expression levels of at least two specified different gene products that each comprise a sequence selected from Table 3 (or peptide sequence encoded therefrom) are outside of the control ranges, and (b) if the subject is male, the method comprises determining the subject to have the condition or a risk thereof in the subject when the expression levels of at least two specified different gene products that each comprise a sequence selected from Table 4 (or peptide sequence encoded therefrom) are outside of the control ranges.

[00167] In some embodiments, if the subject is female, the method comprises determining the subject to have the condition or a risk thereof in the subject when the expression levels of at least two specified different gene products that each comprise a sequence selected from Table 3 (or peptide sequence encoded therefrom) are outside of the control ranges.

[00168] In some embodiments, if the subject is male, the method comprises determining the subject to have the condition or a risk thereof in the subject when the expression levels of at least two specified different gene products that each comprise a sequence selected from Table 4 (or peptide sequence encoded therefrom) are outside of the control ranges.

[00169] In some embodiments, (a) if the subject is female, the method comprises determining the subject to have the condition or risk thereof in the subject when the expression levels of 2-14, 2-15, 2-16, 2-17, 2-18, 2-19, 2-20, 2-40, 20-50, 20-60, 4-14, 4-15, 4-20, 4-25, 4-30, 4-35, 4-40, 4-50, 4-60, 5-10, 5-14, 5-15, 5-16, 5-17, 5-18, 5-19, 5-20, 5-40, 5-50, 5-60, 6-14, 6-15, 6-20, 6-25, 6-30, 6-35, 6-40, 6-50, 6-60, 8-14, 8-15, 8-20, 8-25, 8-30, 8-35, 8-40, 8-50, 8-60, 9-10, 9-14, 9-15, 9-16, 9-20, 9-40, 9-50, 9-60, 10-14, 10-15, 10-20, 10-25, 10-30, 10-35, 10-40, 10-50, or 10-60 specified different gene products that each comprise a sequence selected from Table 3 (or peptide sequence encoded therefrom) are outside of the control ranges, and (b) if the subject is male, the method comprises determining the subject to have

the condition or a risk thereof in the subject when the expression levels of 2-14, 2-15, 2-16, 2-17, 2-18, 2-19, 2-20, 2-40, 4-14, 4-15, 4-20, 4-25, 4-30, 4-35, 4-40, 5-10, 5-14, 5-15, 5-16, 5-17, 5-18, 5-19, 5-20, 5-40, 6-14, 6-15, 6-20, 6-25, 6-30, 6-35, 6-40, 8-14, 8-15, 8-20, 8-25, 8-30, 8-35, 8-40, 9-10, 9-14, 9-15, 9-16, 9-20, 9-40, 10-14, 10-15, 10-20, 10-25, 10-30, 10-35, or 10-40 specified different gene products that each comprise a sequence selected from Table 4 (or peptide sequence encoded therefrom) are outside of the control ranges. In some embodiments, (a) if the subject is female, the method comprises determining the subject to have the condition or risk thereof in the subject when the expression levels of 2-14, 2-15, 2-16, 2-17, 2-18, 2-19, 2-20, 2-40, 4-14, 4-15, 4-20, 4-25, 4-30, 4-35, 4-40, 5-10, 5-14, 5-15, 5-16, 5-17, 5-18, 5-19, 5-20, 5-40, 6-14, 6-15, 6-20, 6-25, 6-30, 6-35, 6-40, 8-14, 8-15, 8-20, 8-25, 8-30, 8-35, 8-40, 9-10, 9-14, 9-15, 9-16, 9-20, 9-40, 10-14, 10-15, 10-20, 10-25, 10-30, 10-35, or 10-40 specified different gene products that each comprise a sequence selected from Table 3 (or peptide sequence encoded therefrom) are outside of the control ranges, and (b) if the subject is male, the method comprises determining the subject to have the condition or a risk thereof in the subject when the expression levels of 2-14, 2-15, 2-16, 2-17, 2-18, 2-19, 2-20, 2-40, 4-14, 4-15, 4-20, 4-25, 4-30, 4-35, 4-40, 5-10, 5-14, 5-15, 5-16, 5-17, 5-18, 5-19, 5-20, 5-40, 6-14, 6-15, 6-20, 6-25, 6-30, 6-35, 6-40, 8-14, 8-15, 8-20, 8-25, 8-30, 8-35, 8-40, 9-10, 9-14, 9-15, 9-16, 9-20, 9-40, 10-14, 10-15, 10-20, 10-25, 10-30, 10-35, or 10-40 specified different gene products that each comprise a sequence selected from Table 4 (or peptide sequence encoded therefrom) are outside of the control ranges. In some embodiments, the same numerical range of gene products is utilized for male and female subjects.

[00170] In some embodiments, if the subject is female, the method comprises determining the subject to have the condition or risk thereof in the subject when the expression levels of 2-14, 2-15, 2-16, 2-17, 2-18, 2-19, 2-20, 2-40, 20-50, 20-60, 4-14, 4-15, 4-20, 4-25, 4-30, 4-35, 4-40, 4-50, 4-60, 5-10, 5-14, 5-15, 5-16, 5-17, 5-18, 5-19, 5-20, 5-40, 5-50, 5-60, 6-14, 6-15, 6-20, 6-25, 6-30, 6-35, 6-40, 6-50, 6-60, 8-14, 8-15, 8-20, 8-25, 8-30, 8-35, 8-40, 8-50, 8-60, 9-10, 9-14, 9-15, 9-16, 9-20, 9-40, 9-50, 9-60, 10-14, 10-15, 10-20, 10-25, 10-30, 10-35, 10-40, 10-50, or 10-60 specified different gene products (or fewer than 60, 40, 30, or 20 specified different gene products) that each comprise a sequence selected from Table 3 (or peptide sequence encoded therefrom) are outside of the control ranges.

[00171] In some embodiments, if the subject is male, the method comprises determining the subject to have the condition or a risk thereof in the subject when the expression levels of only 2-14, 2-15, 2-16, 2-17, 2-18, 2-19, 2-20, 2-40, 4-14, 4-15, 4-20, 4-25, 4-30, 4-35, 4-40, 5-10, 5-14, 5-15, 5-16, 5-17, 5-18, 5-19, 5-20, 5-40, 6-14, 6-15, 6-20, 6-25, 6-30, 6-35, 6-40, 8-14, 8-15, 8-20, 8-25, 8-30, 8-35, 8-40, 9-10, 9-14, 9-15, 9-16, 9-20, 9-40, 10-14, 10-15, 10-20, 10-25, 10-30, 10-35, or 10-40 specified different gene products (or fewer than 40, 30, or 20 specified different gene products) that each comprise a sequence selected from Table 4 (or peptide sequence encoded therefrom) are outside of the control ranges.

[00172] In some embodiments, (a) if the subject is female, the method comprises detecting, from the sample, expression levels of only 10-40 or 10-60 specified different gene products that each comprise a sequence selected from Table 3 (or peptide sequence encoded therefrom), and (b) if the subject is male, the method comprises detecting, from the sample, expression levels of only 10-40 specified different gene products that each comprise a sequence selected from Table 4 (or peptide sequence encoded therefrom).

[00173] In some embodiments, if the subject is female, the method comprises detecting, from the sample, expression levels of only 2-14, 2-15, 2-16, 2-17, 2-18, 2-19, 2-20, 2-40, 20-50, 20-60, 4-14, 4-15, 4-20, 4-25, 4-30, 4-35, 4-40, 4-50, 4-60, 5-10, 5-14, 5-15, 5-16, 5-17, 5-18, 5-19, 5-20, 5-40, 5-50, 5-60, 6-14, 6-15, 6-20, 6-25, 6-30, 6-35, 6-40, 6-50, 6-60, 8-14, 8-15, 8-20, 8-25, 8-30, 8-35, 8-40, 8-50, 8-60, 9-10, 9-14, 9-15, 9-16, 9-20, 9-40, 9-50, 9-60, 10-14, 10-15, 10-20, 10-25, 10-30, 10-35, 10-40, 10-50, or 10-60 specified different gene products (or fewer than 60, 40, 30, or 20 specified different gene products) that each comprise a sequence selected from Table 3 (or peptide sequence encoded therefrom).

[00174] In some embodiments, if the subject is male, the method comprises detecting, from the sample, expression levels of only 2-14, 2-15, 2-16, 2-17, 2-18, 2-19, 2-20, 2-40, 4-14, 4-15, 4-20, 4-25, 4-30, 4-35, 4-40, 5-10, 5-14, 5-15, 5-16, 5-17, 5-18, 5-19, 5-20, 5-40, 6-14, 6-15, 6-20, 6-25, 6-30, 6-35, 6-40, 8-14, 8-15, 8-20, 8-25, 8-30, 8-35, 8-40, 9-10, 9-14, 9-15, 9-16, 9-20, 9-40, 10-14, 10-15, 10-20, 10-25, 10-30, 10-35, or 10-40 specified different gene products (or fewer than 40, 30, or 20 specified different gene products) that each comprise a sequence selected from Table 4 (or peptide sequence encoded therefrom).

[00175] In the method of some embodiments, the medical intervention further comprises pharmacotherapy, or a surgical or percutaneous procedure, or a combination of two or more of the listed items.

[00176] In the method of some embodiments, the medical intervention comprises an anti-ischemic therapy selected from the group consisting of for example (but not limited to) beta-blockers, calcium antagonists, long- or short-acting nitrates, Ranolazine, artery bypass surgery (surgical revascularization), or a percutaneous coronary or arterial procedure, or any medical intervention (including suitable surgical and/or percutaneous procedure) to treat perfusion shortage (such as ischemia and/or neoangiogenesis) approved by, and/or meets guidelines set by a local health specialist organisation, or by a professional or government organization, for example the Food and Drug Administration, or the European Medicines Agency.

[00177] In the method of some embodiments, the medical intervention comprises a modulator nucleic acid or a modulator protein comprising or targeting at least one of genes listed in Tables 1-6 or gene products as described herein.

[00178] In the method of some embodiments, (a) if the subject is a female, the therapy comprises an modulator nucleic acid or a modulator protein comprising or targeting at least one of genes listed in Tables 1, 3, and 5 or gene products to the subject, or (b) if the subject is a male, the therapy comprises an modulator nucleic acid or a modulator protein comprising or targeting at least one of genes listed in Tables 2, 4, 6 or gene products to the subject.

[00179] In the method of some embodiments, the modulator nucleic acid comprises at least one of an antisense RNA, small interfering RNA, or CRISPR gRNA. In the method of some embodiments, the modulator nucleic acid is encoded by an expression vector, for example a lentiviral, adenoviral, or AAV vector for expressing the modulator nucleic acid in order to produce gene product encoded by the modulator nucleic acid (thus increasing activity of the gene product).

[00180] In the method of some embodiments, the subject may not present symptoms of any disease comprising perfusion shortage, such as neoangiogenesis and/or ischemia. For example, the subject may not present symptoms of any of ischemic cardiovascular disease, microangiopathy in cardiovascular disease (for example (but not limited to) diastolic heart failure), hypertrophic cardiomyopathy, cardiovascular pathology with relative ischemia (such

as hypertrophic CMP, ischemic heart failure, and/or congenital cardiac disease), ischemic cerebrovascular disease (for example (but not limited to) CVA/ TIA, and/or vascular dementia), ischemic peripheral artery disease, venous disease, orthopedic disease, sepsis, inflammation, lymphatic disease, ophthalmological disease associated with ischemia and/or neoangiogenesis (for example (but not limited to) neoangiogenesis in retinopathy), diabetic macro and microangiopathy, oncological pathology (for example (but not limited to) solid tumors, metastatic disease), endothelial dysfunction in cardiovascular and peripheral artery disease, ophthalmology (for example (but not limited to) neoangiogenesis in retinopathy), diabetic macro and microangiopathy, oncological pathology (for example (but not limited to) solid tumors and/or metastatic disease), endothelial dysfunction in cardiovascular and peripheral artery disease, nephrological disease associated with ischemia and/or neoangiogenesis, gynecological disease, orthopedic disease, lung disease (for example (but not limited to) COPD, emphysema, lung fibrosis, cystic fibrosis, lung cancer, pulmonary interstitial disease, and/or monitoring pre- and post-lung transplantation, pulmonary emboli), cerebrovascular disease (for example, stroke, TIA, microvascular dementia), and emboli (such as pulmonary emboli, deep venous thrombosis), inadequate ventilation/ oxygenation of a mechanically ventilated subject, an inflammatory and auto-immune disease with an ischemic component, gastrointestinal disorders (for example (but not limited to) Crohn's disease, colitis ulcerosa), a neurodegenerative disease (for example (but not limited to) Parkinson's disease or multiple sclerosis), erectile dysfunction, sport injury, frailty, shock (such as post-resuscitation shock), arterial and venous diseases, disease related to lymphangiogenic disease, vascular remodeling including lymphangiogenic metastatic disease, arteriovenous malformation, arterial remodeling, or venous thrombosis, or a combination of two or more of the listed items. In the method of some embodiments, the subject may present symptoms of any disease comprising perfusion shortage as disclosed herein.

[00181] In the method of some embodiments, the condition comprising perfusion shortage is selected from the group consisting of: ischemic cardiovascular disease, microangiopathy in cardiovascular disease (such as diastolic heart failure), hypertrophic cardiomyopathy, cardiovascular pathology with relative ischemia (such as hypertrophic CMP, ischemic heart failure, and/or congenital cardiac disease), ischemic cerebrovascular disease (for example (but not limited to) CVA/ TIA, and/or vascular dementia), ischemic peripheral

artery disease, venous disease, orthopedic disease, sepsis, inflammation, lymphatic disease, ophthalmological disease associated with ischemia and/or neoangiogenesis (for example (but not limited to) neoangiogenesis in retinopathy), diabetic macro and microangiopathy, oncological pathology (for example (but not limited to) solid tumors, metastatic disease), endothelial dysfunction in cardiovascular and peripheral artery disease, ophthalmology (for example (but not limited to) as neoangiogenesis in retinopathy), diabetic macro and microangiopathy, oncological pathology (for example (but not limited to) as solid tumors and/or metastatic disease), endothelial dysfunction in cardiovascular and peripheral artery disease, nephrological disease associated with ischemia and/or neoangiogenesis, gynecological disease, orthopedic disease, lung disease (for example (but not limited to) COPD, emphysema, lung fibrosis, cystic fibrosis, lung cancer, pulmonary interstitial disease, and/or monitoring pre- and post-lung transplantation, pulmonary emboli), cerebrovascular disease (for example (but not limited to), stroke, TIA, microvascular dementia, and emboli (pulmonary emboli, deep venous thrombosis), inadequate ventilation/ oxygenation of a mechanically ventilated subject, inflammatory disease and auto-immune disease with an ischemic component, gastrointestinal disorders (for example (but not limited to) Crohn's disease, colitis ulcerosa), a neurodegenerative disease (for example (but not limited to) Parkinson's disease or multiple sclerosis), erectile dysfunction, sport injury, frailty, shock (such as post-resuscitation shock), arterial and venous diseases, disease related to lymphangiogenic disease, vascular remodeling including lymphangiogenic metastatic disease, arteriovenous malformation, arterial remodeling, and venous thrombosis, or a combination of two or more of the listed items

[00182] In the method of some embodiments, the condition comprising perfusion shortage comprises cardiovascular pathology with relative or absolute ischemia comprises congenital disease with significant or persistent shunting, such as open foramen ovale, ductus botalli, and/or ventricular shunt, or Eisenmenger syndrome/disease. Without being limited by theory, it is contemplated that the condition can comprise any congenital disease in which ischemia or neoangiogenesis plays an important role in the pathogenesis or determines prognostication or response to therapy

[00183] In the method of some embodiments, the condition comprises relative or absolute ischemia. In some embodiments, ischemia due to increased demand for oxygen may occur due to, for instance, due to hypertrophy, inflammation or increased metabolism or sepsis.

[00184] In the method of some embodiments, the relative ischemia comprises cardiovascular disease with an increased demand for oxygen for instance but not limited to hypertrophic myocardium or and local and/or systemic increased oxygen demand (including but not limited to inflammation).

Additional Embodiments

[00185] In some embodiments, a test to diagnose, measure, quantify and monitor disease comprising perfusion shortage (ischemic periods) in patients is provided. This test may also be used to measure therapy responsiveness in patients, for example anti-ischemic therapy, pro-ischemic therapy, measure neoangiogenesis, and increased tissue perfusion. Further, the test may be used to monitor disease progression or remission for better personalized and adjustable treatment in patients.

[00186] In some embodiments, disclosed herein is the identification of biomarkers that can identify and measure these episodes of oxygen deprivation with great certainty. Disclosed herein are unique diagnostic tests (method of blood processing), unique set of biomarkers, and a specific biostatistical algorithm and reference values to determine abnormal or pathological outcome/values in patients with disease comprising perfusion shortage such as neoangiogenesis (for example, tumor neoangiogenesis, and hematological metastatic disease, or ophthalmologic disease with retinal neoangiogenesis) or ischemia (for example cardiovascular or any other form of ischemic disease) from normal values in subjects without ischemic disease.

[00187] In some embodiments, molecular biomarkers have been identified that are up-regulated in patients having reperfusion shortage (such as ischemic patients) and may be used to diagnose (and quantify) ischemia including silent or transient ischemic episodes in CAD patients, and thus are likely to serve as sensitive biomarkers for the detection of mild ischemia in coronary, cerebrovascular and peripheral artery disease patients (and other ischemic patients). The gene expression patterns involved in the hypoxic response and/or the regulation of vasculogenesis likely represent a specific biomarker (RNA) profile that can be used for the diagnosis of coronary, cerebrovascular and peripheral artery disease.

[00188] The extent of reperfusion shortage (e.g., number and severity of ischemic episodes) may correlate with an incremental biological response and corresponding

upregulation of the molecular biomarkers. Hence, the biomarkers may be used as to quantify ongoing ischemia in patients (using arbitrary units/ scale), for example to quantify the extent of disease comprising perfusion shortage. Further, the biomarkers may also be used to monitor disease progression or remission over time.

[00189] The markers may be upregulated / responding rapidly to ischemic episodes, whereas other may be responding slowly to the hypoxic conditions. The former markers could be useful/ appropriate in the dynamic setting of a hospital in which clinical decision making occurs from hour-to-hour (instantaneously), whereas the latter would be more useful in an outpatient setting (for a general practitioner or for population screening).

[00190] The methods (protocol, biomarkers, reference values and algorithm) of some embodiments disclosed herein may be used for the identification of current and past ischemic events (irrespective of its location (for instance (but not limited to) cerebral, myocardial, claudication) and can be used for the diagnosis of ischemic disease (including, but not limited to cardiovascular disease, cerebrovascular disease and peripheral artery disease).

[00191] The methods (protocol, biomarkers, reference values and algorithm) of some embodiments herein may be used for the identification of current and past ischemic events (irrespective of its location) and may be used for monitor the progression of ischemic disease (including cardiovascular disease, cerebrovascular disease and peripheral artery disease), and to monitor the response (efficacy) to initiated therapy (pharmacotherapy or invasive therapy).

[00192] The methods (protocol, biomarkers, reference values and algorithm) of some embodiments herein may also be used to prognosticate/ predict future outcome in patients with ischemic disease or disease with an important ischemic or neoangiogenesis component (mortality and adverse events) and to predict and measure/quantify the response of patients with ischemic disease (or disease with an important ischemic or neoangiogenesis component) to specific therapy (and therefore can be used to determine medical decision making (patient stratification and companion use of this assay for specific therapies or in depth diagnostic tracts (including more advanced imaging).

[00193]

Examples

[00194] The following examples are non-limiting and other variants within the scope of the art also contemplated.

Example 1 - Isolation of Flk1+ (KDR1) cells.

[00195] KDR1 (also referred to as Flk1, VEGFR2, CD309 or Kdr) is a key marker defining hematopoietic stem cells. Human KDR1+ cells were isolated using immuno-selection by flow cytometry. After a venous blood draw, whole blood is processed by lysis of the erythrocytes, followed by a Ficoll gradient isolation of the mononucleated cells. The Flk1+ (or Flt1+/Flt4+) cell preparation is isolated using an immunoseperation and a proprietary antibody directed against the CD cell surface markers Flk1+ (CD309, KDR1, VEGFR2 or alternatively Flt1+/Flt4+). After cell isolation, the preparation is stored at -80°C for further analysis, or processed for differential gene expression analysis or protein expression using DNAchip analysis, qPCR or any other method for differential expression analysis of nucleotide biomarkers.

Example 2 – Screen for differentially expressed gene products

[00196] A screen was performed for molecular biomarkers (here (RNA) oligonucleotides / candidate regulatory genes) using DNA chip analysis of 244 symptomatic patients with potential (cardiac/ coronary) hypoxic episodes. Circulating KDR1-cells were isolated from blood samples, as these cells are involved in the physiological hypoxic response. Molecular expression patterns were cross-correlated with clinical diagnosis using current standard-of-care/ best-of-care diagnostic tract. In order to increase the accuracy of the diagnoses in this clinical cohort (and reduce the number of false positive/ false negative diagnoses), patients received a 6 month clinical telephone follow-up (and/or review of the clinical follow-up tract): in patients that were originally diagnosed as /allocated to the “angina pectoris excluded group” (no myocardial ischemia detectable), did hence not receive any (anti-ischemic) therapy as follow-up (and should not have shown any progression of ischemic heart disease (i.e. no persistent and/or progressive angina episodes and/or major cardiovascular events (including myocardial infarction). In the case a patient was inadvertently classified as “no myocardial ischemia detectable/ diagnosed”, it should be possible to capture this misclassification (false negative) at 6-month clinical follow-up as the complaints would have deteriorated without appropriate pharmacotherapy or medical intervention. This is expected to

reduce the number of false negative/ inappropriately classified patients (patients with ischemia inadvertently diagnosed as "healthy"). Patients initially diagnosed as ischemic, with initiation of anti-ischemic pharmacotherapy or more invasive intervention should find confirmation of their diagnosis in their response to the specifically initiated pharmacotherapy, or upon invasive imaging and/or therapy (and their respective response to intervention). This should reduce the number of patients with false positive diagnosis. On average the number of initially falsely allocated patients using current standard-of-care diagnostics is estimated to be 16-26%.

[00197] Cross correlation of these clinical data with the molecular data set identified molecular markers (nucleotide probe or peptides) for female patients listed in Table 3 and molecular (nucleotide probe or peptides) markers for male patients that were statistically significantly differentially expressed in the classifier clinical data set. These markers and relative expression levels are shown in Tables 1-6. High throughput computing (i.e. machine learning) comparing different biostatistical analyses of the various combinations of biomarkers (out of the identified pool) showed that a minimal combination of 8 molecular biomarkers in female patients and a minimal combination of 12 biomarkers in male patients is sufficient to identify ischemic patients with the maximal / greatest accuracy in a separate independent patient cohort. This led to the misclassification error (alpha and beta error combined) in male patients of minimal 1.3% and in female patients of <0.05%. The misclassification rate of the current standard-of-care/ best-of-care diagnostic tract involving multiple functional and imaging tests is 16-26%. The analysis of this assay comparing (individual) molecular biomarkers against reference values provided an objective (uniform) classification of the diagnosis of patient with a superior accuracy. The current standard-of-care/ best-of-care diagnostic tract requires the (subjective) interpretation of exercise performances, ECG alterations and imaging phenomena by medical professionals (which is the basis of variability/ inconsistency).

Example 3 – Analyses of differential expression of gene products in female patients

Analyses of differential expression of gene products in samples collected from ischemic female patients were performed using Affymetrix array and/or GeneChip Arrays. For female patients, the expression levels of genes listed in Tables 1, 3, 5 were up-or downregulated in ischemia (compared to non-ischemia controls). The current disclosure shows density plots

of individual arrays and plots of individual arrays after frozen RNA normalization and showing re-analysis of 244 blood samples using Affymetrix Exon 2.0 microarrays. The differently expressed nucleic acids are shown in Tables 1, 3, 5. Accordingly, in accordance with some embodiments herein, it is shown that gene products corresponding to the genes listed in Tables 1, 3, 5 are expressed outside of control ranges in ischemic females.

Example 4 – Analyses of differential expression of gene products in male patients

Analyses of differential expression of gene products in samples collected from ischemic male patients were performed using Affymetrix Exon 2.0 array and/or GeneChip Arrays. For male patients, the genes listed in Tables 2, 4, 6 were up- or downregulated in ischemia (compared to non-ischemia controls). The current disclosure shows density plots of individual arrays and density plots of individual arrays after frozen RNA normalization and showing re-analysis of 244 blood samples using Affymetrix Exon 2.0 microarrays. The differently expressed nucleic acids are shown in Tables 2, 4, 6. Accordingly, in accordance with some embodiments herein, it is shown that gene products corresponding to the genes listed in Tables 2, 4, 6 are expressed outside of control ranges in ischemic males.

Example 5 – Validation Study for female patients

[00198] Validation of detection of conditions comprising ischemia and/or neoangiogenesis was performed for female patients using gene algorithms, exon algorithms and probe algorithms. Data in FIGS. 1-5 show that superior classification (as measured by classification scores) was observed for numbers of variables in Female biopanel ranging from 8-14 nucleotide biomarkers, resulting in an accuracy of >99.9% sensitivity using Fisher Discriminant analysis /Diagonal linear discriminant analysis. FIG. 1 shows a plot of classification scores with fitted curves for probes (gene products) for female patients using different statistical methods according to some embodiments. FIG. 2 shows a plot of classification scores with fitted curves for exons (gene products) for female patients using different statistical methods according to some embodiments. FIG. 3 shows LDA accuracy with fitted curve for exons versus the number of selected variables (gene products) for female patients according to some embodiments. FIGs. 4 and 5 show DLDA misclassification (FIG.

4) and LDA misclassification rate (FIG. 5) with fitted curves for probes versus the number of selected variables (gene products) for female patients according to some embodiments.

[00199] As shown by the data in FIGS. 1 – 5, superior classification (as indicated by high accuracy) was observed when the number of selected variables (number of gene products) for samples from female patients was around >8-10. The data were analyzed using several statistical methods. The data showed an accuracy of >99.9%. The data indicated that several statistical methods can be used for detection/diagnosis of conditions comprising ischemia in female patients with nearly 100% accuracy in accordance with some embodiments herein.

[00200] Table 8 - Table 13 show data for accuracy of detection of ischemic heart disease in female patients. Variables indicated the number of gene products used in the method. The gene products were selected from Table 1, 3, 5.

Table 8

Probe Algorithm Female subjects	No. of gene products	type 1 + type 2 error (%)	Accuracy (100% – type 1 and type 2 error (%))
DLDA	10	1.2	98.9
FDA	10	0.9	99.1
LDA	10	2.3	97.7
PLSLDA	10	1.9	98.1
PLSRF	10	1.0	99.0
QDA	10	0.8	99.2
RF	10	4.7	95.3

Table 9

Exon Algorithm Female subjects	No. of gene products	type 1 + type 2 error (%)	Accuracy (100% – type 1 and type 2 error (%))
DLDA	10	4.2	95.8
FDA	10	2.4	97.6
LDA	10	6.6	93.4
PLSLDA	10	3.2	96.8
PLSRF	10	6.1	93.9
QDA	10	8.7	91.3
RF	10	8.9	91.1

Table 10

Gene Algorithm Female subjects	No. of gene products	type 1 + type 2 error (%)	Accuracy (100% – type 1 and type 2 error (%))
DLDA	10	1.6	98.5
FDA	10	1.4	98.6
LDA	10	2.3	97.7
PLSLDA	10	2.3	97.8
PLSRF	10	3.9	96.1

QDA	10	4.6	95.4
RF	10	5.6	94.4

Table 11

Probe Algorithm Female subjects	No. of gene products	type 1 + type 2 error (%)	Accuracy (100% – type 1 and type 2 error (%))
DLDA	14	1.1	98.9
FDA	14	<0.05	˜100.0
LDA	14	<0.05	˜100.0
PLSLDA	14	1.1	98.9
PLSRF	14	<0.05	˜100.0
QDA	14	<0.05	˜100.0
RF	14	4.3	95.7

Table 12

Exon Algorithm Female subjects	No. of gene products	type 1 + type 2 error (%)	Accuracy (100% – type 1 and type 2 error (%))

DLDA	14	<0.05	˜100.0
FDA	14	1.1	99.0
LDA	14	1.2	98.9
PLSLDA	14	<0.05	˜100.0
PLSRF	14	1.1	98.9
QDA	14	4.1	95.9
RF	14	6.4	93.6

Table 13

Gene Algorithm Female subjects	No. of gene products	type 1 + type 2 error (%)	Accuracy (100% – type 1 and type 2 error (%))
DLDA	14	1.1	˜98.9
FDA	14	3.3	96.7
LDA	14	1.2	98.9
PLSLDA	14	2.3	97.8
PLSRF	14	<0.05	˜100

QDA	14	10.5	89.5
RF	14	5.4	94.6

Example 6 – Validation Study for male patients

[00201] Validation of detection of conditions comprising (cardiac) ischemia was performed for male patients using exon, probe, and gene algorithms.

[00202] Data in FIGs. 6 and 7 show that superior classification (as measured by classification scores) was observed for numbers of variables in male biopanel >15, resulting in a misclassification of 1.7% (or >98.3% sensitivity) using Fisher Discriminant analysis /Diagonal linear discriminant analysis. FIG. 6 shows a plot of classification scores with fitted curves for probes for male patients according to some embodiments. FIG. 7 shows plots of classification scores with fitted curves for genes for male patients according to some embodiments. Accuracy as a measure of how well this binary classification test correctly identifies or excludes a condition, here ischemic heart disease, is defined as the proportion of correct predictions (both true positives and true negatives) among the total number of cases examined or 100% - alpha and beta error. As shown by the data in FIGs. 6 and 7, the optimal number of selected variables (number of gene products) for samples from male patients was >14. The data were analyzed using several statistical methods. The data showed an accuracy of 98.3%. The data indicated that several statistical methods can be used for detection/diagnosis of conditions comprising ischemia in male patients with nearly 100% accuracy in accordance with some embodiments herein.

[00203] **Tables 14 - 16** show data for accuracy of detection of ischemic heart disease in male patients. Variables indicated the number of gene products used in the method. The gene products were selected from Tables 2, 4, 6.

Table 14

Probe Algorithm Male subjects	No. of gene products	type 1 + type 2 error (%)	Accuracy

			(100% – type 1 and type 2 error (%))
DLDA	14	2.9	97.1
FDA	14	1.7	98.3
LDA	14	2.4	97.6
PLSLDA	14	11.3	88.7
PLSRF	14	7.2	92.8
QDA	14	2.4	97.6
RF	14	<0.05	˜100

Table 15

Exon Algorithm Male subjects	No. of gene products	type 1 + type 2 error (%)	Accuracy (100% – type 1 and type 2 error (%))
DLDA	14	6.5	93.5
FDA	14	3.5	96.5
LDA	14	7.8	92.2
PLSLDA	14	2.9	97.1
PLSRF	14	8.3	91.7

QDA	14	7.2	92.8
RF	14	6.4	93.6

Table 16

Genes Algorithm Male subjects	No. of gene products	type 1 + type 2 error (%)	Accuracy (100% – type 1 and type 2 error (%))
DLDA	14	5.6	94.4
FDA	14	10.9	89.1
LDA	**14**	8.3	91.7
PLSLDA	14	8.6	91.4
PLSRF	14	9.2	90.8
QDA	14	7.4	92.6
RF	14	9.0	91.0

Example 7 – Validation study for male and female patients

[00204] Validation of detection of conditions comprising ischemia/ neoangiogenesis was performed for male and female patients using gene algorithms, exon algorithms, and probe algorithms.

[00205] Tables 17 and Table 18 show data for accuracy of detection of ischemic heart disease in male and female patients combined. Variables indicated the number of gene products used in the method. The gene products were selected from Tables 1-6. Depending on the statistical method used, there was an accuracy of 67-75%. These data show that ischemic heart disease in both male and female patients can be accurately detected by methods in accordance with some embodiments herein, with an accuracy of 67% of higher.

Table 17

Exon Algorithm	No. of gene products	type 1 + type 2 error (%))	Accuracy (100% – type 1 and type 2 error (%))
DLDA	24	33.0	67.0
FDA	24	33.5	66.5
LDA	24	30.5	69.5
PLSLDA	24	27.0	73.0
PLSRF	24	31.1	68.9
QDA	24	33.5	66.5
RF	24	26.7	73.3

Table 18

Probe Algorithm	No. of gene products	type 1 + type 2 error (%)	Accuracy (100% – type 1 and type 2 error (%))
DLDA	20	27.2	72.8
FDA	20	24.8	75.2
LDA	20	24.7	75.3
PLSLDA	20	26.7	73.3
PLSRF	20	29.3	70.7
QDA	20	25.4	74.4
RF	20	26.2	73.8

Example 8 – Comparison to MIBI-SPECT tracking

[00206] Blood samples of patients with anginal complaints and scheduled for elective nuclear and CMR (cardiac magnetic resonance imaging) perfusion imaging (MIBI SPECT) are collected. MIBI-SPECT is tracking of radionuclide-labelled molecules to the well-perfused myocardial tissue target tissues and is generally considered to be the gold standard for determination of imaging in the clinic. Initial diagnosis and long-term clinical outcome of these patients are prospectively cross-correlated with expression patterns of molecular biomarkers comprising or encoded by SEQ ID NOs: 1-5103 (or a peptide sequence encoded therefrom), Genes Number 1-9280 (or a peptide sequence encoded therefrom). Cross correlations are made with diagnosis, progression (and prognosis (MACCE events)) and therapy responsiveness.

Example 9 – Accuracy of Diagnosis by proposed MyCor Classifier methods

[00207] In the first analysis of 244 patients, the proof of concept was verified. Data indicated very high rate of correct diagnosis, i.e., in 98.3-99.9% of the patients (without the need for patient selection). The number of false negative and false positives was extremely low, i.e., <0.05-1.7%.

[00208] The current standard-of-care diagnostic tract of ischemic heart disease requires ECG, blood work, exercise test, and nuclear and/or CT(A) scan in a specialised cardiology outpatient clinic. The observed sensitivity of current best-in-class diagnostic is 74-84%.

[00209] Diagnosis based on the proposed MyCor Classifier methods disclosed herein was superior to the current best-in-class diagnostic.

[00210] The methods, compositions, uses, and kit described herein permitted detection with a (simple) blood test. The methods provided a diagnosis (and severity) of ischemic heart disease (angina) with an accuracy > 98-99,9% in an all-comers population (non-selected 'real world' population). No sub-stratification is needed for cardiovascular risk factors. Blood test according to the methods herein outperformed sophisticated imaging techniques like nuclear imaging and CT (angio) scans. Thus, a first-in-class diagnostic blood test for conditions comprising ischemia and/or neoangiogenesis (such as heart disease) is described in some embodiments herein.

Example 10 – BioBank Clinical Validation

[00211] This Example provides further analysis of the first 244 patients. A retrospective analysis of the first 'real world' patients with chest pain showed that the procedural failure of the diagnostic test was 1.3% in the last 200 patients. This study provided a proof-of-principle. Based on the analysis of the data, a classifier of 14 biomarkers had an accuracy of 98-99,9%, and a classifier of 2 biomarkers has an accuracy of 82%. Thus, without being limited by theory, a combination of platforms may be indicated. It is further contemplated that validation of quantification of ischemia (based on the methods, kits, compositions, and uses disclosed herein) would allow one to compare treatments and to continue to monitor patients.

Example 11 – Confirmatory Analysis in Ischemic disease

[00212] In the first ("Proposed MyCor Classifier") analysis of 244 patients (described, for example, in Examples 9 and 10), a proof-of-concept was established (alpha+beta error 0,05-1,7% in non-optimized conditions). No sub-stratification was needed for cardiovascular risk factors.

[00213] In a second analysis/ study, a refined definition of an ischemic patient population is utilized for the assessed population (n=1000). In the second analysis, adjudication is further optimized, biostatistical analysis is further optimized, sub-stratification explored, optimized and standardized (FDA approved) micro array platform are used, cross-correlation with the extend of ischemia on advanced imaging (including MIBI SPECT and coronary angiography) is analysed, and retrospective and prospective analyses are performed. Based on a consideration of the above factors, a sensitivity of >99% is expected to be obtained in all patients.

[00214] Without being limited by theory, preliminary bioinformatics analysis suggest that a classifier can be generated using the blood samples of CAD patients based on in depth bioinformatics (retrospective) analysis of patient cohort by a biostatistician to optimise algorithms, including (but not limited to) Random Forrest plot analysis, (un)-scaled SVM analysis, and Bootstrapping.

[00215] Data annotation is useful for diagnosis based on the current practise in cardiology outpatient clinic involving patient interview, ECG, blood work, bicycle test, MSCT, etc., in clinical follow up at 6 months. It is contemplated that clinical follow up can reduce the false negative and false positive allocated patients in the SOC diagnostic group.

[00216] In contrast, to diagnosis based on the current practice in cardiology outpatient clinic, advanced imaging (including for example myocardial perfusion imaging with MIBI SPECT) has improved sensitivity and specificity as an advanced myocardial perfusion imaging test. Analysis was performed using Affymetrix Exon 2.0 microarray platform and samples of 244 patients re-analysed using expression profiling.

Example 12 – Product Development Status 3

[00217] In an analysis, ischemic RNA and protein signatures are further validated and expanded in a prospective study/registry in a better-defined ischemic patient population (n=5000). Adjudication is further optimized, biostatistical analysis is further optimized, sub-

stratification explored, optimized and standardized (FDA approved) micro array platform are used, cross-correlation with the extend of ischemia on advanced imaging (such as MIBI SPECT, and other myocardial perfusion imaging) is analysed, and retrospective and prospective analyses are performed. Diagnostic platform(s) are identified and optimized, for example, microarray (for validation and reference), Luminex assays, Multiplex assay, qPCR, protein assay (ELISA), Nanostring, or direct sequencing.

Example 13 – Isolation of nucleic acids

[00218] Methods of isolating nucleic acids from cells are well known in the art. For example, methods of isolating nucleic acids from cells using solid phase binding materials without the use of a lysis solution is described in US 2005/0106602 A1, which is hereby incorporated by reference in its entirety. Methods for isolating total RNA from cells are also well known in the art. For example, methods for isolating RNA from cells using an extraction solution comprising formamide is described in US 9,416,357 B2, which is hereby incorporated by reference in its entirety. Several commercially available kits allow for high-throughput analysis-grade nucleic acids to be isolated from cells.

[00219] In some embodiments, the method, use, or composition comprises various steps or features that are present as single steps or features (as opposed to multiple steps or features). For example, in one embodiment, the method comprises detecting the condition or a risk thereof in the subject when the expression levels of the specified different gene products are outside of the control ranges, and further includes inhibiting, ameliorating, delaying the onset of, reducing the likelihood of, treating, or preventing a condition comprising perfusion shortage by administering a medical intervention as described herein. The medical intervention may be provided in a single step or administration, or over a period of time, as is suitable in the art. Multiple features or components may be provided in alternate embodiments. In some embodiments, the method, composition, or use comprises one or more medical interventions. In some embodiments, the medical intervention comprises a modulator (such as an inhibitor or enhancer) of a nucleic acid comprising any of nucleotide sequences selected from Tables 1-6, or a peptide encoded by a nucleic acid comprising any of sequences of Tables 1-6.

Example 14 – Clinical Study of Ischemic Biomarker Analysis In Heart Disease Patients

[00220] This example covers a clinical study for detecting ischemia in patients without myonecrosis. Currently, patients analyzed for chest pain reminiscent of angina pectoris are analyzed using a combination of including ECG, standard blood works, exercise testing, and CT analysis (including calcium imaging and CT angiography) only to result in an adequate diagnosis in 74% of the cases. Even with advanced perfusion imaging, the adequate/ accurate diagnosis of ischemic heart disease does not exceed 84%. In addition, setting up a multi-disciplinary analysis of these complex patients remains a logistical challenge (involving functional testing and imaging, involvement of the dept of cardiology, nuclear medicine, and radiology) and represents a laborious and costly diagnostic track (with disappointing accuracy). In addition, the (extend of) ischemia (or the biological response to ischemia) cannot be readily quantified (or expressed in AU) for use in monitoring of these patients for disease progression or therapy responsiveness.

[00221] Subjects selected for the study will be selected from among adults of at least 18 years of age presenting chest pain or other cardiac related symptoms. Excluded subjects will include those who: (1) received percutaneous coronary intervention (PCI) within the last 6 months, (2) coronary artery bypass graft surgery within the past 6 months, (3) are suspected of acute coronary syndrome (acute myocardial infarction and unstable angina) or are Troponin positive, (4) have prior documented myocardial infarction within 30 days prior to cCTA or between cCTA and ICA, (5) have tachycardia or significant arrhythmia, (6) have a known anaphylactic allergy to iodinated contrast, (7) are pregnant or have unknown pregnancy status as well as childbearing potential, (8) have a body mass index compatible with imaging, (9) requires an emergent procedure, (10) displays evidence of ongoing or active clinical instability, including acute chest pain (sudden onset), cardiogenic shock, unstable blood pressure with systolic blood pressure <90 mmHg, and severe congestive heart failure (NYHA III or IV) or acute pulmonary edema, (11) has any active, serious, life-threatening disease with a life expectancy of less than 2 months, (12) is unable to comply with study procedures.

[00222] The study will enroll patients with angina suspect complaints and will enroll two cohorts of patients. Cohort 1 (evaluate for sensitivity) will include subjects with angina disease and Cohort 2 of controls (evaluate for specificity) will include subjects without angina disease. The sample size of approximate 180 will provide 90% power to establish that the studied ischemic biomarker profile method is superior over the standard method (Standard

Method) at two-sided significance level of 0.05. In the sample size calculation, it is assumed that the sensitivity and specificity are at least 92% for Test Method and no more than 80% for the Control Method.

[00223] The study will enroll at least 75 health subjects without angina disease into Cohort 2. In addition, the study will enroll clinical evaluation subjects who present themselves to the participating sites for clinical evaluation for potential angina disease. It is expected that 30% of them will have angina disease (to be included in Cohort 1 analysis) and 70% of them will not have angina disease (to be included in Cohort 2 analysis). The study will enroll at least 600 clinical evaluation subjects to reach at least 180 Cohort 1 subjects.

[00224] Subjects who are determined to have the disease by the methods of the present study and Standard Methods may be treated (the investigator can decide to follow them without immediate treatment). All other subjects (subjects who are determined to have angina by only one method and subjects who are determined to no having angina by both methods) will be followed without treatment unless the investigator has determined that it is unethical not to treat the subjects based on well documented clinical observations. If the following treatment occurs within 6 months of chest pain, the subject will be stratified to the treatment group.

[00225] A thorough clinical work up which consists of multiple exams and visits to the clinic would be required of the patient, as the next step. An analytical framework presente d in **FIG. 8**, demonstrates the complex decision making involved. For patients, who are suspected of CAD, will undergo invasive coronary angiography furthering their risk of radiation exposure. A test often ordered and completed weeks after initial complaint of chest pain. **FIG. 9** provides a thorough summary of sensitivity and specificity results of invasive tests currently used to diagnosis CAD. Study assessments will be performed at the visits and time points outlined in the Time and Events Schedule **FIG. 10**.

[00226] A total of 1000 subjects will be enrolled. Subjects who provide informed consent will provide blood samples at Baseline (10 ml) and prior to imaging (15 ml). The study site will reach out to the subject at month 6 and 12 and capture prognosis, treatment related and if any, hospitalization details.

[00227] Any subject who voluntarily withdraws consent or is discontinued from the study prior to completion will be considered as withdrawn from the study. Subjects may be

discontinued from the study under any of the following circumstances: (1) cccurrence of intolerable AE, as assessed by the investigator or designee; (2) withdrawal of consent; (3) lost to follow-up; (4) Administrative reasons (e.g., sponsor decision); (5) major violation of the protocol; (6) if, in the opinion of the qualified investigator, it is in the best interest of the subject; (7) non-compliance with study requirements and restrictions. Replacement subjects are to be added at the sponsor's discretion, in agreement with the principal investigator.

[00228] Subjects will undergo phlebotomy and provide a total of 10 ml blood in an sterile RNA stabilizer tube and 5 ml whole blood at Baseline and prior to cardiac imaging. The investigational site will prepare the samples, as instructed, by the sponsor. The investigational site will be store the RNA collected samples in a secured research area at room temperature prior to shipment to the sponsor. The sponsor will work with each clinical site to determine the appropriate shipment schedule.

[00229] Medical histories will be obtained according to the site's SOPs. Medical histories will include demographic data (date of birth, sex, race, and ethnicity); histories of acute, chronic, and infectious disease; surgical and oncologic histories; and any reported conditions affecting major body systems. All findings on medical history will be evaluated by the investigator for clinical significance. All medications (prescription and non-prescription, herbal medications/natural health products, and investigational drugs) taken by the subjects during the 30 days prior to consent will be recorded in the source documentation as medication history. The physical examination, assessing the subject's overall health and physical condition, will be performed according to the site's SOPs. Height, weight, and BMI will be recorded. Vital signs will be measured and managed according to the site's SOPs. Vital signs will consist of systolic and diastolic blood pressure (mmHg), heart rate (bpm), respiratory rate (breaths/min), and oral temperature (°C). Safety 12-lead ECGs will be performed and interpreted according to the site's SOPs or if complete Telemetry is available, data is acceptable. If the following treatment occurs within 6 months of chest pain, the subject will be stratified to treatment group: (1) treatment with beta blockers, antiangina Medications, antihypertensive drug, calcium channel blocker and anticoagulant; (2) angioplasty, coronary stent, cardiac catherization, revascularization, coronary angioplasty; (3) coronary artery bypass surgery and hybrid coronary revascularization.

[00230] All analyses will be performed using SAS version 9.3 or higher, run on the Microsoft Windows Server 2003 R2 operating system.

[00231] While various aspects and embodiments have been disclosed herein, other aspects and embodiments will be apparent to those skilled in the art. The various aspects and embodiments disclosed herein are for purposes of illustration and are not intended to be limiting, with the true scope and spirit being indicated by the following claims.

[00232] For each method of described herein, relevant compositions for use in the method are expressly contemplated, uses of compositions in the method, and, as applicable, methods of making a medicament for use in the method are also expressly contemplated. For example, for methods of inhibiting, ameliorating, delaying the onset of, reducing the likelihood of, treating, or preventing a condition comprising perfusion shortage (or neoangiogenesis), corresponding compositions for use in the corresponding method are also contemplated, as are uses of the corresponding composition to inhibit, ameliorate, delaying the onset of, reduce the likelihood of, treat, or prevent a condition comprising perfusion shortage. In some cases, disclosed nucleotide sequences as medical compounds or targets may be used to promote ischemic conditions, such as in tumor angiogenesis.

[00233] One skilled in the art will appreciate that, for this and other processes and methods disclosed herein, the functions performed in the processes and methods can be implemented in differing order. Furthermore, the outlined steps and operations are only provided as examples, and some of the steps and operations can be optional, combined into fewer steps and operations, or expanded into additional steps and operations without detracting from the essence of the disclosed embodiments.

[00234] With respect to the use of substantially any plural and/or singular terms herein, those having skill in the art can translate from the plural to the singular and/or from the singular to the plural as is appropriate to the context and/or application. The various singular/plural permutations may be expressly set forth herein for sake of clarity.

[00235] It will be understood by those within the art that, in general, terms used herein, and especially in the appended claims (e.g., bodies of the appended claims) are generally intended as "open" terms (e.g., the term "including" should be interpreted as "including but not limited to," the term "having" should be interpreted as "having at least," the term "includes" should be interpreted as "includes but is not limited to," etc.). It will be further

understood by those within the art that if a specific number of an introduced claim recitation is intended, such an intent will be explicitly recited in the claim, and in the absence of such recitation no such intent is present. For example, as an aid to understanding, the following appended claims may contain usage of the introductory phrases “at least one" and "one or more" to introduce claim recitations. However, the use of such phrases should not be construed to imply that the introduction of a claim recitation by the indefinite articles “a“ or "an" limits any particular claim containing such introduced claim recitation to embodiments containing only one such recitation, even when the same claim includes the introductory phrases "one or more" or "at least one" and indefinite articles such as ”a“ or ”an“ (e.g., “a” and/or “an” should be interpreted to mean “at least one” or “one or more”); the same holds true for the use of definite articles used to introduce claim recitations. In addition, even if a specific number of an introduced claim recitation is explicitly recited, those skilled in the art will recognize that such recitation should be interpreted to mean at least the recited number (e.g., the bare recitation of "two recitations," without other modifiers, means at least two recitations, or two or more recitations). Furthermore, in those instances where a convention analogous to “at least one of A, B, and C, etc.” is used, in general such a construction is intended in the sense one having skill in the art would understand the convention (e.g., “ a system having at least one of A, B, and C” would include but not be limited to systems that have A alone, B alone, C alone, A and B together, A and C together, B and C together, and/or A, B, and C together, etc.). In those instances where a convention analogous to “at least one of A, B, or C, etc.” is used, in general such a construction is intended in the sense one having skill in the art would understand the convention (e.g., “ a system having at least one of A, B, or C” would include but not be limited to systems that have A alone, B alone, C alone, A and B together, A and C together, B and C together, and/or A, B, and C together, etc.). It will be further understood by those within the art that virtually any disjunctive word and/or phrase presenting two or more alternative terms, whether in the description, claims, or drawings, should be understood to contemplate the possibilities of including one of the terms, either of the terms, or both terms. For example, the phrase “A or B” will be understood to include the possibilities of “A” or “B” or “A and B.”

[00236] In addition, where features or aspects of the disclosure are described in terms of Markush groups, those skilled in the art will recognize that the disclosure is also thereby described in terms of any individual member or subgroup of members of the Markush group.

[00237] As will be understood by one skilled in the art, for any and all purposes, such as in terms of providing a written description, all ranges disclosed herein also encompass any and all possible subranges and combinations of subranges thereof. Any listed range can be easily recognized as sufficiently describing and enabling the same range being broken down into at least equal halves, thirds, quarters, fifths, tenths, etc. As a non-limiting example, each range discussed herein can be readily broken down into a lower third, middle third and upper third, etc. As will also be understood by one skilled in the art all language such as "up to," "at least," and the like include the number recited and refer to ranges which can be subsequently broken down into subranges as discussed above. For example, "about 5", shall include the number 5. Finally, as will be understood by one skilled in the art, a range includes each individual member. Thus, for example, a group having 1-3 cells refers to groups having 1, 2, or 3 cells. Similarly, a group having 1-5 cells refers to groups having 1, 2, 3, 4, or 5 cells, and so forth.

[00238] From the foregoing, it will be appreciated that various embodiments of the present disclosure have been described herein for purposes of illustration, and that various modifications may be made without departing from the scope and spirit of the present disclosure. Accordingly, the various embodiments disclosed herein are not intended to be limiting, with the true scope and spirit being indicated by the following claims.

Table 1. A set of target genes in female subjects.

Gene Number	Gene Name	Gene Number	Gene Name	Gene Number	Gene Name
1	ASIC4	228	LINC01486	455	LOC100288866
2	LOC644961	229	LINC01502	456	LOC100505940
3	ACBD5	230	LINC00265	457	LOC100506125
4	ACAD10	231	LINC00304	458	LOC100506713
5	ADAMTS1	232	LINC00482	459	LOC100507065
6	ADAMTS17	233	LINC00523	460	LOC100507642
7	ADAMTSL2	234	LINC00870	461	LOC100996660
8	AP1S3	235	LINC00896	462	LOC101926941
9	ADORA1	236	MGAT5B	463	LOC101927029

10	ADGRB2	237	MAP7D2	464	LOC101927230
11	ADIG	238	MRGPRE	465	LOC101927377
12	ARF6	239	MED1	466	LOC101927419
13	ARFGEF2	240	MED4	467	LOC101927479
14	AFG3L2	241	MED7	468	LOC101927503
15	AKR7A2	242	MAGEC3	469	LOC101927542
16	ALG6	243	MBTPS1	470	LOC101927585
17	ALX3	244	MESDC2	471	LOC101927722
18	ASB9	245	MIER3	472	LOC101927735
19	ANKRD2	246	MT1IP	473	LOC101927880
20	LOC101060400	247	MT1M	474	LOC101928765
21	ANKFN1	248	MAT1A	475	LOC101928775
22	ANHX	249	MTHFD1L	476	LOC101928850
23	APOA1	250	MEX3A	477	LOC101929074
24	AQP5	251	MIR1185-1	478	LOC101929239
25	ARHGEF38-IT1	252	MIR1250	479	LOC101929330
26	ARSF	253	MIR1261	480	LOC101929374
27	ABCA6	254	MIR1266	481	LOC101929696
28	ATAD3B	255	MIR1273F	482	LOC283731
29	ATP2B1	256	MIR1289-2	483	LOC284933
30	ATG14	257	MIR1976	484	LOC338667
31	ATG4A	258	MIR215	485	LOC339807
32	ATG4C	259	MIR216B	486	FLJ26245
33	BEST3	260	MIR3115	487	FLJ31662
34	BGN	261	MIR378D1	488	LOC441179
35	BOLA1	262	MIR3907	489	FLJ38668
36	BMP15	263	MIR3928	490	USE1
37	BAI2	264	MIR3944	491	UMOD
38	BAZ1B	265	MIR422A	492	USP12-AS2

39	BRD9	266	MIR4262	493	UTP6
40	BTAF1	267	MIR4489	494	VPS13C
41	C20orf166-AS1	268	MIR4519	495	VPS45
42	CADPS	269	MIR4747	496	VIPR2
43	CDH26	270	MIR4799	497	VAT1L
44	CELSR2	271	MIR532	498	VTI1A
45	CABP1	272	MIR591	499	LOC646513
46	CACNG4	273	MIR802	500	WIPF3
47	CAPN11	274	MIR155HG	501	WDR11
48	CELP	275	MGME1	502	LOC401127
49	CES1P1	276	MPC1L	503	WIPI2
50	CES1P2	277	MRPS21	504	WBSCR16
51	CEACAM5	278	MTIF2	505	XXYLT1-AS2
52	CASP7	279	MAP4K4	506	ZFP3
53	CBLC	280	MRGPRF-AS1	507	ZNRF2P1
54	CD177	281	MRGPRG-AS1	508	ZNRF4
55	CD180	282	MTRNR2L10	509	ZBTB39
56	CLK4	283	LOC100996637	510	ZSCAN10
57	CEBPZOS	284	MYADML2	511	ZSCAN22
58	CEND1	285	MEF2C	512	ZNF226
59	CDC40	286	MYO7A	513	ZNF280C
60	CERS5	287	MYO16	514	ZNF484
61	CLN5	288	MYO18B	515	ZNF512B
62	CHMP4B	289	MYH13	516	ZNF579
63	CCL19	290	NATD1	517	ZNF763
64	LOC440300	291	NECAB3	518	ZNF807
65	CBX5	292	NA	519	ZNF821
66	C1orf106	293	NA	520	ABCC12
67	C1orf64	294	NA	521	ABHD12
68	C10orf32	295	NDUFB9	522	ADAMTS8

69	C10orf71	296	NDUFS1	523	AGRN
70	C10orf91	297	NCR2	524	AMOT
71	C11orf40	298	NCAM1-AS1	525	ANAPC11
72	C19orf45	299	NEUROD1	526	ARHGEF10L
73	C2orf70	300	NOTCH4	527	ATN1
74	C6orf15	301	NCOA6	528	ATP10B
75	C8orf86	302	NUP155	529	ATPIF1
76	C9orf163	303	NUP210P1	530	ATR
77	C9orf85	304	NUDT8	531	BAIAP2L2
78	CCDC177	305	NUTM2F	532	BPIFA1
79	CCDC179	306	NYX	533	BTRC
80	CCDC40	307	NYNRIN	534	C10orf53
81	CCDC54	308	OR2M1P	535	C12orf26
82	COL3A1	309	OR2T3	536	C6orf195
83	COL5A3	310	OR4N4	537	C8orf12
84	COMMD10	311	OR7A10	538	CALCRL
85	C5	312	OR8J1	539	CBS
86	C8A	313	OR9I1	540	CCBL1
87	CBFB	314	OPN5	541	CCDC57
88	CPXCR1	315	OTUD7A	542	CCK
89	CRYGC	316	PPT2	543	CD1C
90	CSMD2	317	PAPLN	544	CDC20B
91	DMTF1	318	PNMA5	545	CDH19
92	CDK5R2	319	PTRH1	546	CES1P1
93	COX6C	320	LOC729739	547	CHST3
94	COX7B2	321	PER2	548	CLCA1
95	CYP2A7	322	PPL	549	CNP
96	CYP2E1	323	PIKFYVE	550	CNTN1
97	CTU1	324	PLTP	551	CNTNAP3
98	DCC	325	PGF	552	COG5

99	DDX19A	326	PKP1	553	COL2A1
100	DDX39B	327	PTN	554	COL6A4P2
101	DFNB31	328	PVRL4	555	COX7A2
102	DOCK7	329	PABPN1L	556	CPT1B
103	DEFB4A	330	PQBP1	557	CSN1S1
104	DDN	331	KCTD6	558	CYFIP1
105	DCSTAMP	332	KCNC3	559	CYP1A2
106	DENR	333	POTEA	560	DCHS2
107	DNASE1L2	334	LOC100130331	561	DCST1
108	DMKN	335	POU3F3	562	DENND5B
109	DESI2	336	PJA1	563	DIO3
110	DHDH	337	PROKR1	564	DNAH7
111	DLGAP1	338	PROKR2	565	DNAJC10
112	DLX5	339	PCSK4	566	DOC2A
113	DNLZ	340	PBOV1	567	EFCAB2
114	DOPEY2	341	PRSS3P2	568	EGFL6
115	DNMBP	342	PRSS57	569	ELK4
116	DNAL4	343	PSMD13	570	ELOVL4
117	EAPP	344	PROC	571	EMID2
118	EBF2	345	PIAS2	572	EPB41L4B
119	ENOX2	346	PRKAG3	573	EPHA6
120	EHBP1	347	PPP1R3C	574	ESRRG
121	ELOVL4	348	PPP1R9A	575	FAM49A
122	EMX1	349	PTK6	576	FASTK
123	ECHDC1	350	PTPLB	577	FLJ41309
124	EFNA5	351	PTPRO	578	FOXN4
125	EPS8L1	352	PTPRU	579	GABRP
126	ETNK2	353	PCDHA6	580	GALNT11
127	EIF3L	354	PSORS1C3	581	GGT3P
128	FBXO28	355	PYDC2	582	GLI2

129	FAM115A	356	PDHA2	583	GOLGB1
130	FAM126A	357	RERG	584	GPC2
131	FAM133B	358	RAC3	585	GRB7
132	FAM204A	359	REG4	586	GRID1
133	FAM66A	360	RCC1	587	GRIP1
134	FAM71A	361	RGS17	588	GRK7
135	FAM83C	362	RAX	589	GTF2IRD1
136	FAM90A25P	363	ARHGEF16	590	HDAC9
137	FAM99A	364	ARHGEF19	591	HNRNPR
138	FSCN2	365	RHOXF1P1	592	HPGDS
139	FADS6	366	RIBC1	593	INPP5K
140	FDX1L	367	RNASE7	594	ITGBL1
141	FATE1	368	RPL15	595	KCNMB1
142	FIBCD1	369	RPS21	596	KDM4C
143	FIBP	370	RPS6	597	KIAA1614
144	FGF11	371	RPLP0	598	KIF18B
145	FGF6	372	RIC8B	599	KIF3B
146	FLNB	373	RNMT	600	KIR2DL4
147	FOXC2	374	RBM23	601	KY
148	FOXD4	375	RBM41	602	LINC00323
149	WI2-2373I1.2	376	RBM46	603	LOC284294
150	FUT3	377	RBMY1A3P	604	LOC550112
151	FXYD7	378	RPL34-AS1	605	LPAR6
152	GFM2	379	SUN2	606	LRRC1
153	GPR125	380	SLFN11	607	LTBP3
154	GPR149	381	SCT	608	MIAT
155	GPR158	382	Sep-02	609	MINA
156	GPR25	383	SERPINA12	610	MKI67IP
157	GPR4	384	SETDB1	611	MMP11
158	GPR6	385	SHBG	612	MRGPRG

159	GAL3ST3	386	LOC101929108	613	MTMR1
160	GAL	387	SCUBE3	614	MTUS2
161	GABRB3	388	SMCO1	615	MUC5B
162	GJA8	389	SKOR2	616	MYO18A
163	GLIPR1	390	SNAR-I	617	MYPN
164	GBA3	391	SNRPD1	618	NAALADL2
165	GPX5	392	SNORD53	619	NBLA00301
166	GYG2	393	SLC16A8	620	NCAPG2
167	GOSR1	394	SLC22A31	621	NKAIN3
168	GOLGA1	395	SLC23A2	622	NMU
169	GUCY1A2	396	SLC25A21	623	NR3C1
170	GUCA2A	397	SLC27A4	624	NRXN2
171	HAND1	398	SLC30A3	625	NUBP1
172	HSPA12B	399	SLC34A1	626	NUPL1
173	HECTD1	400	SLC6A18	627	OLA1
174	HECTD4	401	SLC9C2	628	OLFML2B
175	HNRNPDL	402	SP1	629	PAGE4
176	HIST1H2BA	403	SLA	630	PLEKHA6
177	HIST1H3F	404	SRGAP3-AS3	631	PMM2
178	HIST1H4J	405	SOX9	632	PRRX1
179	HOXA7	406	ST3GAL4	633	PRSS33
180	HUNK	407	ST3GAL5	634	PTPLA
181	HMMR	408	STMN2	635	PTPRD
182	HSD17B8	409	SAMD10	636	PTS
183	HCRT	410	SYNGR3	637	PYROXD1
184	IGFL3	411	SYCE1	638	QRFPR
185	IGHV1-2	412	TRBV30	639	QTRTD1
186	IGHV1-58	413	TBX18	640	RAPGEF4
187	IGLV6-57	414	TBX20	641	RARA
188	IGDCC4	415	TLX3	642	RASA2

189	INHBE	416	TTBK1	643	RASGEF1B
190	INSL6	417	TBC1D24	644	RASL11B
191	IGFALS	418	TBX5-AS1	645	RASSF5
192	ICE2	419	TEX13B	646	RHBDD1
193	IL13	420	THUMPD2	647	RHOXF2
194	INA	421	TDG	648	RPL8
195	IQSEC3	422	TCAP	649	SEC16B
196	JAZF1	423	TLK2	650	SEMA6A
197	KLK6	424	TRAPPC13	651	SEPSECS
198	KLK8	425	TCEANC	652	SHMT1
199	KRT16P2	426	TCEAL1	653	SLC22A6
200	KRT39	427	TFAP2E	654	SLC44A4
201	KRT81	428	TF	655	SLC6A3
202	KRTAP13-1	429	TKTL1	656	SMARCB1
203	KRTAP4-4	430	TMED6	657	SP8
204	KIF4A	431	TMEM168	658	SPECC1L
205	LAMB4	432	TMEM38B	659	SPEG
206	LAMP5-AS1	433	TMEM62	660	STIP1
207	LCE4A	434	TMEM8C	661	STK36
208	LAMTOR5	435	TRIM71	662	SUCLG2
209	LTBP3	436	TRMU	663	TBCB
210	LURAP1	437	TNNI3	664	TESK1
211	LRRC38	438	TUBAL3	665	TGM4
212	LEUTX	439	TNFRSF8	666	THY1
213	LRPPRC	440	TP73	667	TLK1
214	LRRIQ1	441	TTYH1	668	TMEM168
215	LRTM1	442	U2AF1L4	669	TMEM247
216	LGI1	443	U2SURP	670	TNNT2
217	LARS	444	USP7	671	TRPV4
218	LIG4	445	UBE2V2	672	TXNDC11

219	LMCD1	446	UBE2DNL	673	TXNDC15
220	LHX2	447	UFM1	674	UROC1
221	LCN12	448	B3GNT6	675	VARS2
222	LCN15	449	UNC5A	676	VAV3
223	LINC01104	450	LOC100128364	677	WSCD1
224	LINC01121	451	LOC100130093	678	ZIC3
225	LINC01186	452	LOC100130872	679	ZNF135
226	LINC01314	453	LOC100131372	680	ZNF33B
227	LINC01387	454	LOC100133331		

Table 2 – A set of target genes in male subjects.

Gene Number	Gene Name	Gene Number	Gene Name	Gene Number	Gene Name
681	ZBTB11-AS1	972	LOC284009	1263	AKAP17A
682	SNORD115-2	973	C17orf89	1264	PCDH11Y
683	SNORD115-37	974	MAMSTR	1265	FAM103A1
684	SNORD115-24	975	EMC10	1266	PARP9
685	SNORA11B	976	WDR62	1267	TRAPPC9
686	MIR876	977	MCHR1	1268	HYAL3
687	MIR942	978	LOC284825	1269	CASP5
688	MIR708	979	IGHD2-21	1270	TTTY11
689	COL4A2-AS2	980	IGHD2-15	1271	RAB34
690	LOC100130373	981	EOGT	1272	NACAP1
691	LOC100130548	982	OR2V2	1273	SPOP
692	NFYC-AS1	983	C8orf31	1274	ZMYND12
693	MIR181A1HG	984	IGLV10-54	1275	HSDL2
694	LOC100131496	985	IGLV3-12	1276	EIF1AD
695	LINC00240	986	SNX24	1277	LLPH
696	LOC100133669	987	ARHGAP35	1278	BRMS1L
697	NA	988	SCG3	1279	SYVN1

698	BCL2L11	989	HOOK2	1280	TUBB6
699	FAR2P2	990	PYCR2	1281	C22orf23
700	MED16	991	RPA4	1282	GTPBP3
701	ERVV-2	992	GYPE	1283	SUV420H2
702	KRTAP21-3	993	SLC39A3	1284	USMG5
703	LOC100289230	994	H3F3B	1285	POMGNT2
704	LOC100289283	995	HBA2	1286	MASTL
705	MIR513C	996	HBB	1287	MIR22HG
706	MIR1468	997	HELLS	1288	IFITM1
707	MIR1538	998	ANXA5	1289	HAT1
708	MIR1275	999	CXXC1	1290	SHANK3
709	MIR1912	1000	CDR2L	1291	KIAA1656
710	MIR1302-7	1001	FOXA2	1292	LRRCC1
711	MIR1231	1002	HNF4A	1293	KIAA1755
712	MIR1238	1003	HNRNPF	1294	DENR
713	MIR1179	1004	HNRNPK	1295	NPFF
714	MIR1301	1005	SNORD56B	1296	MARCO
715	MIR1197	1006	HPN	1297	KRT38
716	MIR1908	1007	HPRT1	1298	JRKL
717	MIR1237	1008	ERAS	1299	PAGE1
718	MIR2116	1009	HSD17B1	1300	PABPC4
719	CSN1S2BP	1010	KRTAP20-1	1301	SUCLA2
720	MIR3148	1011	KRTAP20-2	1302	DPM1
721	MIR4280	1012	LOC339166	1303	SYNGAP1
722	MIR3116-1	1013	ZFP69	1304	CDC123
723	MIR3129	1014	LOC340074	1305	SGPL1
724	MIR4275	1015	NRBP2	1306	DDX18
725	MIR4326	1016	KIAA1875	1307	BUD31
726	MIR3125	1017	IDI1	1308	HIST1H3F
727	MIR4254	1018	OR2T8	1309	CHRNA6

728	LINC00673	1019	FIGLA	1310	KLHL6
729	MIR3926-2	1020	PAQR9	1311	SYT8
730	MIR3678	1021	IFNGR1	1312	BRSK2
731	MIR548Z	1022	IGFBP1	1313	ZNF622
732	MIR3657	1023	RTN4RL2	1314	MAP7
733	MIR3935	1024	KRTAP10-10	1315	ZFAND2A
734	LOC100505478	1025	AQP1	1316	PAGE5
735	LINC01364	1026	IL13RA1	1317	RGN
736	FAM212B-AS1	1027	NANOGNB	1318	PDLIM1
737	LOC100506371	1028	PDX1	1319	BTF3L4
738	C16orf95	1029	KCNA3	1320	DYRK1B
739	LOC100506730	1030	KCNA5	1321	VAPB
740	LOC100507419	1031	TPTE2P6	1322	RCSD1
741	LOC100507507	1032	LHFPL3	1323	RAB11B
742	LINC00837	1033	C9orf50	1324	SLIT2
743	MIR4686	1034	SLC27A1	1325	GRAP2
744	MIR378D1	1035	KCNJ10	1326	MUC16
745	MIR3689F	1036	TRIM74	1327	CGB8
746	MIR4756	1037	LINC00162	1328	MED21
747	MIR3529	1038	KCNS3	1329	EPSTI1
748	MIR4475	1039	KIR2DL3	1330	NCR2
749	MIR4499	1040	KRTAP12-3	1331	PAGE4
750	MIR550A3	1041	KRTAP5-1	1332	CYTIP
751	MIR4425	1042	C10orf99	1333	NCOR2
752	MIR4492	1043	CC2D2B	1334	RNF7
753	MIR4784	1044	RPRML	1335	MTFR1
754	MIR4732	1045	MFSD2B	1336	CD59
755	MIR4684	1046	LRRC14B	1337	TMEM63A
756	MIR4691	1047	OR52N2	1338	ATP2C2
757	MIR4773-2	1048	LAMA4	1339	MAP3K8

758	MIR4429	1049	LIPE	1340	TGFBI
759	MIR4442	1050	LINC00200	1341	LOC284825
760	HTT-AS	1051	DKFZp667F0711	1342	LOC284628
761	CERS6-AS1	1052	LINC00668	1343	OR1J2
762	LINC00507	1053	ZNF880	1344	LOC100129724
763	RNU6-81P	1054	LOC400756	1345	MTA3
764	FGF14-AS1	1055	ASB18	1346	DDX39B
765	SLC9A9-AS1	1056	LRRD1	1347	RGL3
766	LOC100996345	1057	LDLRAD2	1348	ZMYND8
767	CYYR1-AS1	1058	SOHLH1	1349	DDB1
768	LOC100996635	1059	LYN	1350	C6orf15
769	DHRS9	1060	MIR127	1351	SLC25A3
770	CDK4	1061	MIR188	1352	SLC39A13
771	LOC101927053	1062	MIR210	1353	COL8A1
772	PDZRN3-AS1	1063	MIR181A1	1354	OR51S1
773	LOC101927314	1064	MIR26B	1355	MFSD2B
774	LOC101927483	1065	MIR296	1356	KCNMB2
775	MEOX2-AS1	1066	MIR9-1	1357	PAPPA2
776	LINC01186	1067	MIR98	1358	CD2
777	NA	1068	MIR99B	1359	TRBV20OR9-2
778	GBAT2	1069	MIR17HG	1360	C5orf51
779	LINC01214	1070	MAFG	1361	ZNF783
780	LOC101928101	1071	MAN2A2	1362	PHKA1-AS1
781	LOC101928118	1072	MAS1	1363	CALD1
782	NA	1073	MAX	1364	USP12-AS1
783	LOC101928195	1074	MGST3	1365	TMEM191A
784	LINC01280	1075	MLF1	1366	LOC100507009
785	LINC01488	1076	MLH1	1367	IPO9
786	LOC101928385	1077	LOC440910	1368	INSIG1
787	LOC101928399	1078	SMIM4	1369	VARS2

788	TCONS_00029157	1079	SUGT1P1	1370	EFNA1
789	LOC101928509	1080	RPS26P11	1371	U2AF1
790	LOC101928579	1081	MYBPH	1372	DAD1
791	LOC101928668	1082	MYO10	1373	SALL4
792	LOC101928668	1083	NASP	1374	NUPL1
793	LINC01450	1084	NDUFA1	1375	SALL4
794	NA	1085	NDUFB9	1376	LBH
795	LOC101928823	1086	NDUFS1	1377	MTPAP
796	LOC101928880	1087	NFIL3	1378	WNT7A
797	LOC101928919	1088	NKX3-1	1379	PFDN6
798	LINC01262	1089	NOS1	1380	PFDN6
799	LOC101929031	1090	NRGN	1381	COL6A3
800	LOC101929159	1091	RNASE12	1382	SSB
801	NA	1092	MIR375	1383	RND3
802	LOC101929236	1093	MIR380	1384	CPNE1
803	LOC101929284	1094	OXTR	1385	SLC23A1
804	LOC101929432	1095	DUOX2	1386	TRPC7
805	LOC101929468	1096	RRP15	1387	KIF13B
806	LOC101929497	1097	TXNDC11	1388	HAVCR2
807	LOC101929636	1098	RPS27L	1389	SDCBP
808	PSMD14	1099	NMD3	1390	PTDSS2
809	GPA33	1100	KLHL5	1391	ADCK5
810	ZNF267	1101	SBDS	1392	TTYH2
811	CDO1	1102	RPL26L1	1393	MAP2K3
812	CHERP	1103	EGFL7	1394	GLYAT
813	IFI44	1104	PCYT1A	1395	PTDSS2
814	RGS14	1105	CDC40	1396	NOP2
815	FUT9	1106	POMP	1397	PITPNA
816	GMEB1	1107	UBE2J1	1398	LGR5
817	RFPL2	1108	CWC15	1399	RPAP3

818	IFI44L	1109	UFC1	1400	LOC100506792
819	MAPRE2	1110	ATP6V1H	1401	PITX2
820	MAPRE2	1111	ERGIC3	1402	FGFR1
821	SLC27A5	1112	RBMX2	1403	EPOR
822	CHD1	1113	SF3B6	1404	PAFAH2
823	C9orf9	1114	PFDN4	1405	SLC26A4
824	RABL2B	1115	SERPINB8	1406	SLC5A5
825	RABL2A	1116	PIK3C2G	1407	AMT
826	FSTL1	1117	TLR9	1408	PMS1
827	MRPL3	1118	FAM193B	1409	TSC2
828	BIRC8	1119	DDIT4	1410	CYP51A1
829	KLHL2	1120	EGLN1	1411	OR5A2
830	GLB1L3	1121	NUTM2F	1412	CHD3
831	GPR182	1122	FAM20A	1413	FSD2
832	GPN1	1123	DNAJC25	1414	NTRK3
833	CHRM5	1124	HEATR3	1415	SPTB
834	SMIM12	1125	EPN3	1416	GLTPaD1
835	LRRC37B	1126	KANSL3	1417	TOM1L2
836	SMYD4	1127	CEP72	1418	TOM1L2
837	TBCB	1128	VIMP	1419	SCNN1G
838	CKM	1129	ZC3H15	1420	CAMSAP3
839	RAB3C	1130	THSD1	1421	LAMA4
840	KLHDC3	1131	EIF2AK2	1422	MYBBP1A
841	RPL39L	1132	PSMA2	1423	TTC24
842	OR52M1	1133	PSMA4	1424	STK32A
843	CLK3	1134	PSME2	1425	MDGA2
844	CLTB	1135	MIR362	1426	TMC6
845	JDP2	1136	MIR412	1427	SULF1
846	PRSS30P	1137	MIR494	1428	ALDH3A1
847	SNX20	1138	MIR520C	1429	STRA6

848	PCP2	1139	MIR516B2	1430	MYADML2
849	SHE	1140	MIR502	1431	KRTAP21-3
850	DMBX1	1141	MIR508	1432	THEMIS
851	EDARADD	1142	ERMN	1433	IYD
852	FITM2	1143	PRR12	1434	ARG2
853	C20orf144	1144	RANBP10	1435	SLC6A2
854	COMP	1145	ZNF492	1436	NPNT
855	GLYCTK	1146	SH3RF1	1437	ECHDC2
856	SNTN	1147	FBRSL1	1438	GOLGB1
857	UBLCP1	1148	SQRDL	1439	EDA
858	TMEM68	1149	RET	1440	FAT2
859	APOOL	1150	EXOC4	1441	IGSF1
860	OTUD6A	1151	TGIF2	1442	BAI1
861	CRP	1152	RPL3L	1443	BICD1
862	RNF113B	1153	RPL28	1444	COL11A1
863	DYNLL2	1154	MIR487A	1445	CPA2
864	CRYGD	1155	RPS6KA3	1446	DRP2
865	NA	1156	BCORL1	1447	EGR1
866	CST1	1157	SCN4B	1448	ID1
867	TMC8	1158	CCL5	1449	INSL4
868	CSTB	1159	SDCBP	1450	KIR2DL4
869	CREB3L4	1160	FAM204A	1451	PBX2
870	SLC35F3	1161	RRAGC	1452	PRSS8
871	CCDC140	1162	XYLT2	1453	REV3L
872	CTSL	1163	ACOT6	1454	SNAI2
873	WDSUB1	1164	IRF2BPL	1455	XPNPEP2
874	NCBP2-AS2	1165	POPDC3	1456	ZNF267
875	SH3D19	1166	LINC00535	1457	POLRMT
876	TEX28	1167	CCT6P1	1458	CXCL11
877	MGC32805	1168	TSG1	1459	SYT1

878	FEZF1-AS1	1169	ZNF862	1460	SFN
879	CRYGN	1170	NA	1461	ARIH2
880	ESCO2	1171	BLVRA	1462	CHERP
881	ZNF645	1172	GZF1	1463	CLP1
882	CYP51A1	1173	ATG3	1464	RASGRF2
883	DAB1	1174	NARFL	1465	RBBP6
884	TMEM30B	1175	CSMD1	1466	RBBP6
885	ZCCHC12	1176	SGSH	1467	TRH
886	DNMT3A	1177	GGT8P	1468	ZDHHC1
887	DRP2	1178	NDST4	1469	GHITM
888	HBEGF	1179	NA	1470	ZNF638
889	DUSP5	1180	EBF2	1471	MICAL2
890	DVL2	1181	SI	1472	MTFR1
891	E4F1	1182	EFTUD1P1	1473	NUP93
892	EGR2	1183	SIPA1	1474	CUL9
893	ABCA2	1184	SKI	1475	MLC1
894	FLJ23867	1185	SLC5A4	1476	ANGEL1
895	ZNF385C	1186	FOXD4L6	1477	ARHGEF18
896	CDY2B	1187	SPAG11A	1478	PVRL3
897	SENP5	1188	PCP4L1	1479	TXNDC11
898	EPS8	1189	SLC9A2	1480	LSR
899	EVI2B	1190	SLN	1481	TRMT6
900	EVPL	1191	LYNX1	1482	CERCAM
901	EXTL1	1192	MIR539	1483	NR2E3
902	ALCAM	1193	MIR376A2	1484	A4GALT
903	EZH2	1194	CAPN15	1485	ATAD2B
904	ABCD1	1195	SPAG1	1486	MIOX
905	F12	1196	FOXL2	1487	POMGNT1
906	FAH	1197	SPRR3	1488	EXD3
907	OR5A2	1198	SQLE	1489	CXorf57

908	CCDC89	1199	SRI	1490	THSD1
909	FABP5P3	1200	SCARNA2	1491	DDIT4
910	FOXK1	1201	SCARNA16	1492	TRMT13
911	DKFZP586I1420	1202	TACR1	1493	DMAP1
912	FGF4	1203	SNORD66	1494	SLC12A9
913	FGF14	1204	SNORD84	1495	EPHA8
914	DIP2C	1205	SNORD91A	1496	KCTD16
915	ATG2A	1206	SNORD97	1497	PRX
916	WDR43	1207	TCF3	1498	BCAN
917	DIP2A	1208	MIR550A2	1499	NXN
918	ATP11B	1209	MIR552	1500	NARFL
919	NUP210	1210	MIR563	1501	IL25
920	EXOC6B	1211	MIR591	1502	FUNDC2
921	ARC	1212	TCF19	1503	CENPM
922	SCFD1	1213	TNP1	1504	CHAC1
923	SIN3B	1214	MIR660	1505	IQCA1
924	FMR1	1215	DNAJC7	1506	TREML2
925	USP22	1216	LOC727710	1507	ACSF2
926	SASH1	1217	SDHAP3	1508	DNAJC5
927	SZT2	1218	LOC729224	1509	SLC19A3
928	CRTC1	1219	FAHD2CP	1510	PBX4
929	MED13L	1220	MRS2P2	1511	HORMAD1
930	GRIP1	1221	LOC729739	1512	HOOK3
931	SEC61G	1222	SEC14L6	1513	MAP1LC3A
932	SCRIB	1223	MEIS1-AS3	1514	BOC
933	POLA2	1224	TMEM258	1515	BIRC8
934	GABARAPL1	1225	NELFA	1516	LRRCC1
935	DEFB108B	1226	WNT9A	1517	TMEM54
936	DEFB110	1227	ZNF41	1518	NALCN
937	DEFB113	1228	SNORD113-3	1519	PKD1L2

938	FTH1P3	1229	SNORD113-5	1520	CNTROB
939	PROSER2	1230	SNORD113-8	1521	TBX5
940	C19orf26	1231	SNORD114-3	1522	CABLES1
941	CDRT15L2	1232	SNORD114-9	1523	LIPH
942	HEATR9	1233	SNORD114-18	1524	TMC8
943	ALS2CL	1234	SNORD114-27	1525	FGD5
944	ASPM	1235	SNORD114-30	1526	C1GALT1C1
945	GEMIN5	1236	MIR758	1527	SPPL2B
946	SYF2	1237	MIR668	1528	SVEP1
947	RWDD3	1238	MIR769	1529	SYT9
948	GARS	1239	MIR766	1530	ANGPTL5
949	INTS1	1240	ZNF134	1531	FAM83C
950	OR2F1	1241	PPDPF	1532	KRTAP20-1
951	GATA2	1242	OR5H2	1533	COQ6
952	PLA2G2D	1243	CERS4	1534	E2F6
953	GBP2	1244	OGFOD2	1535	LHFPL3
954	GCNT1	1245	LIN28A	1536	AOX2P
955	AGO1	1246	CLMP	1537	SNHG15
956	MYEOV	1247	NEK11	1538	SERPINA13
957	OR7A5	1248	DCAKD	1539	LINC00200
958	OR1J2	1249	GGNBP2	1540	LINC00111
959	SNORA70	1250	GPR157	1541	HTA
960	SNORD14A	1251	BRD3	1542	MIR99B
961	B3GAT1	1252	EFHC2	1543	MIR494
962	ZNF330	1253	CXXC4	1544	MIR758
963	PCDH11X	1254	PBX4	1545	MIR1912
964	GNAI3	1255	CPTP	1546	CSN1S2BP
965	GP9	1256	SSPN	1547	MIR3657
966	BCL9L	1257	TUBB1	1548	MIR3935
967	OTOGL	1258	NPRL3	1549	HTT-AS1

968	SLC46A3	1259	COIL	1550	TRIM46
969	EWSAT1	1260	OR2B2	1551	CENPJ
970	LINC00927	1261	SF3A2	1552	LOC100507049
971	C16orf54	1262	NRIP1		

Table 3:

SEQ ID NO:	***Code PSC***	***biomarker nucleotide seq target Probe***	***biomarker nucleotide seq target mRNA***
SEQ ID NO: 1	**2102**	ATCAGAGGCAGTTAAGATCCAATGT	TAGTCTCCGTCAATTCTAGGTTACA
SEQ ID NO: 2	**8673**	AAGTATAGACGCCCCGTCTCTGCCT	TTCATATCTGCGGGGCAGAGACGGA
SEQ ID NO: 3	**11464**	CTTTATCCCATTTTCGACGTGCCCG	GAAATAGGGTAAAAGCTGCACGGGC
SEQ ID NO: 4	**16663**	CTGAGACTCCCAGTACGCGGATCGT	GACTCTGAGGGTCATGCGCCTAGCA
SEQ ID NO: 5	**21817**	ACTCTCTTGCCAGTCGAACCTCGTG	TGAGAGAACGGTCAGCTTGGAGCAC
SEQ ID NO: 6	**24286**	NA	NA
SEQ ID NO: 7	**25439**	CGTGTAAATCCCACCGTACCGGAGA	GCACATTTAGGGTGGCATGGCCTCT
SEQ ID NO: 8	**29371**	AGGCACACTCCCAAGTTCCGGTTCG	TCCGTGTGAGGGTTCAAGGCCAAGC
SEQ ID NO: 9	**30491**	AGGCCTGTCCCAACTCCATCGAGAG	TCCGGACAGGGTTGAGGTAGCTCTC
SEQ ID NO: 10	**31618**	AGTGCCTGTCCCTATCTCCAAACGG	TCACGGACAGGGATAGAGGTTTGCC
SEQ ID NO: 11	**32943**	CTGTTCTCGTCCCTCGGTGTAGGAC	GACAAGAGCAGGGAGCCACATCCTG
SEQ ID NO: 12	**33806**	TCCGGAATCCAGAAGATAACAGTCT	AGGCCTTAGGTCTTCTATTGTCAGA
SEQ ID NO: 13	**36050**	GTTACGGTTTCCAGTCAGATCCAGG	CAATGCCAAAGGTCAGTCTAGGTCC
SEQ ID NO: 14	**40648**	ACCATACTTCCACGACCGGTGTCGG	TGGTATGAAGGTGCTGGCCACAGCC
SEQ ID NO: 15	**44512**	CCGCCGTCGTCCAATTCCTGTGAAA	GGCGGCAGCAGGTTAAGGACACTTT
SEQ ID NO: 16	**48445**	GTATAATGACCCTTATTTACTCCAG	CATATTACTGGGAATAAATGAGGTC
SEQ ID NO: 17	**52624**	AGTCTACGGTCCCTCCTATTTCGTC	TCAGATGCCAGGGAGGATAAAGCAG

SEQ ID NO: 18	**53091**	CTACAACTCCCTCGTGTAAACACAA	GATGTTGAGGGAGCACATTTGTGTT
SEQ ID NO: 19	**53355**	ACGACTGTTCCCTCTTAGTGGTGTC	TGCTGACAAGGGAGAATCACCACAG
SEQ ID NO: 20	**59716**	ACGTCGGTGACCCTAAGTCGAAGGG	TGCAGCCACTGGGATTCAGCTTCCC
SEQ ID NO: 21	**62038**	ACAAGAGATCCTGACCCTCTTCGAC	TGTTCTCTAGGACTGGGAGAAGCTG
SEQ ID NO: 22	**65216**	AAAGACGTCTCCTTTGCCCTACCAA	TTTCTGCAGAGGAAACGGGATGGTT
SEQ ID NO: 23	**65253**	CTCAGGATCCTGGTAGACCCGAGAC	GAGTCCTAGGACCATCTGGGCTCTG
SEQ ID NO: 24	**66201**	GGGCTCTCTCCTTCACCAGTCGATT	CCCGAGAGAGGAAGTGGTCAGCTAA
SEQ ID NO: 25	**71233**	ATTCCGGTCCTGTCTCTCAAATTAC	TAAGGCCAGGACAGAGAGTTTAATG
SEQ ID NO: 26	**88970**	AGGTGCCACCAGTCCATGTACTACG	TCCACGGTGGTCAGGTACATGATGC
SEQ ID NO: 27	**89503**	GGAATAAACCACTAAACTCGGAGAC	CCTTATTTGGTGATTTGAGCCTCTG
SEQ ID NO: 28	**98630**	GAGGTGACAGTACCACCCGAGGACA	CTCCACTGTCATGGTGGGCTCCTGT
SEQ ID NO: 29	**112599**	GTTCTTTCTACCTACCCTTTTGAGG	CAAGAAAGATGGATGGGAAAACTCC
SEQ ID NO: 30	**121129**	CCGAGTTTCCGATATCTTTATGGTG	GGCTCAAAGGCTATAGAAATACCAC
SEQ ID NO: 31	**143577**	AACGGTGCACCGTGTCGGAAGGTTT	TTGCCACGTGGCACAGCCTTCCAAA
SEQ ID NO: 32	**149915**	AGGTCTTGGGAGTTCTTATTAGGGA	TCCAGAACCCTCAAGAATAATCCCT
SEQ ID NO: 33	**151536**	TTAGGACCGGGGTATCGGACTCCCT	AATCCTGGCCCCATAGCCTGAGGGA
SEQ ID NO: 34	**156137**	ATAAATAGGGCTAGAAACTTGTGGT	TATTTATCCCGATCTTTGAACACCA
SEQ ID NO: 35	**175079**	AAAACAGTGGCAGGTCTTAGTGACC	TTTTGTCACCGTCCAGAATCACTGG
SEQ ID NO: 36	**179722**	ATCCGACATGGACCGCGTCTCCGGA	TAGGCTGTACCTGGCGCAGAGGCCT
SEQ ID NO: 37	**196695**	ATTTTTGGTGGATGACCGATGGTAC	TAAAAACCACCTACTGGCTACCATG
SEQ ID NO: 38	**200539**	ACGTCAATTGGTCATAAACTCCAGA	TGCAGTTAACCAGTATTTGAGGTCT
SEQ ID NO: 39	**202647**	AAATTGTGGTTGAGTCGTTCTCTAG	TTTAACACCAACTCAGCAAGAGATC
SEQ ID NO: 40	**232609**	AGAGTCCCTAGGATCACAGACCATC	TCTCAGGGATCCTAGTGTCTGGTAG

SEQ ID NO: 41	**235679**	GACTTAGTAGAAGGTTTTCTAAAGA	CTGAATCATCTTCCAAAAGATTTCT
SEQ ID NO: 42	**239356**	AGCTCCAGAGGTTCACCCTGTTTGG	TCGAGGTCTCCAAGTGGGACAAACC
SEQ ID NO: 43	**239483**	ACAGGTGAAGGTCTTTTCTCGGCGG	TGTCCACTTCCAGAAAAGAGCCGCC
SEQ ID NO: 44	**241691**	CATGTATACGAGGTGGAATTGGAAC	GTACATATGCTCCACCTTAACCTTG
SEQ ID NO: 45	**243938**	TTGGTACTGAGGTAAACAGTCAGAC	AACCATGACTCCATTTGTCAGTCTG
SEQ ID NO: 46	**279663**	ATATAAAACGGTAGCGAGTGGGCTT	TATATTTTGCCATCGCTCACCCGAA
SEQ ID NO: 47	**433854**	TTACCGGAGAAGAGCTAAGACGTTG	AATGGCCTCTTCTCGATTCTGCAAC
SEQ ID NO: 48	**449476**	CTCCAAGAAGTTTGAGGCCCGTATT	GAGGTTCTTCAAACTCCGGGCATAA
SEQ ID NO: 49	**508151**	GTCAGGTATTACAACATCAATGCCT	CAGTCCATAATGTTGTAGTTACGGA
SEQ ID NO: 50	**617278**	ATAACGCCCACTACTACTGTCCGAG	TATTGCGGGTGATGATGACAGGCTC
SEQ ID NO: 51	**680209**	ATACTGACTAAGAACGGCAACTCTG	TATGACTGATTCTTGCCGTTGAGAC
SEQ ID NO: 52	**854711**	CTGGTTTTTACTGTCCCGTTTCGCT	GACCAAAAATGACAGGGCAAAGCGA
SEQ ID NO: 53	**1279720**	GTTATTATTTATTCCCACTGCCCGA	CAATAATAAATAAGGGTGACGGGCT
SEQ ID NO: 54	**1326871**	TTGTGTACCCTAGATCCCTGACAGT	AACACATGGGATCTAGGGACTGTCA
SEQ ID NO: 55	**1263398**	CGTAAACGCCGTCGAGATGGTGACT	GCATTTGCGGCAGCTCTACCACTGA
SEQ ID NO: 56	**318029**	CCCAGGAGCAGTGGCAAACTCAGCT	GGGTCCTCGTCACCGTTTGAGTCGA
SEQ ID NO: 57	**229049**	CTCCTCCTAGGGCTGAAGGAAGGTG	GAGGAGGATCCCGACTTCCTTCCAC
SEQ ID NO: 58	**1184708**	GTCGGAGAAGAGTCAGCCAGAAAAG	CAGCCTCTTCTCAGTCGGTCTTTTC
SEQ ID NO: 59	**1244296**	ATCACAACAGTCTACTCGGTGAGTG	TAGTGTTGTCAGATGAGCCACTCAC
SEQ ID NO: 60	**457526**	TTGGTCGCCAATGACTCAAGTCGGT	AACCAGCGGTTACTGAGTTCAGCCA
SEQ ID NO: 61	**1195242**	GTGTTCAATCGTTGTATGTTCGTGT	CACAAGTTAGCAACATACAAGCACA
SEQ ID NO: 62	**393731**	ATTATCGTAAATGCATCACCGTCTT	TAATAGCATTTACGTAGTGGCAGAA
SEQ ID NO: 63	**1012148**	ATACCAGGTTCCAATCACTTTCAGG	TATGGTCCAAGGTTAGTGAAAGTCC

SEQ ID NO: 64	**1399727**	GTAGGATTCACGTACCACCGGAGTC	CATCCTAAGTGCATGGTGGCCTCAG
SEQ ID NO: 65	**1317798**	ATCAATACTCTATCTGCGCGTGGTG	TAGTTATGAGATAGACGCGCACCAC
SEQ ID NO: 66	**600514**	ATAGGACCCACCGTGTCAGGTAGGT	TATCCTGGGTGGCACAGTCCATCCA
SEQ ID NO: 67	**1363886**	ATGGAAGGTAAATGATCGACCCACT	TACCTTCCATTTACTAGCTGGGTGA
SEQ ID NO: 68	**1171486**	CTAGAATTGTGACTACAGAGCCCGT	GATCTTAACACTGATGTCTCGGGCA
SEQ ID NO: 69	**177608**	CTTTTATGGAACGTACTCTGGTGAC	GAAAATACCTTGCATGAGACCACTG
SEQ ID NO: 70	**402976**	AGAAGTAGTGAATCTGAGAGGTCGC	TCTTCATCACTTAGACTCTCCAGCG
SEQ ID NO: 71	**1278306**	AGACGAGTGTGTTAAAAGGGTCGTC	TCTGCTCACACAATTTTCCCAGCAG
SEQ ID NO: 72	**657765**	NA	NA
SEQ ID NO: 73	**56439**	AGGGTAGGCCTCCGGTACGATTACA	TCCCATCCGGAGGCCATGCTAATGT
SEQ ID NO: 74	**807258**	NA	NA
SEQ ID NO: 75	**454924**	AGGAAAGAAGTACGGAAGAGTAACG	TCCTTTCTTCATGCCTTCTCATTGC
SEQ ID NO: 76	**202177**	GGCCTAGAGTGGTTCCCTGAGGACC	CCGGATCTCACCAAGGGACTCCTGG
SEQ ID NO: 77	**515371**	GTGTATTCTAACATCGTGGTCGTCG	CACATAAGATTGTAGCACCAGCAGC
SEQ ID NO: 78	**638470**	ACTAAATGTACACGTCGTTGTTACC	TGATTTACATGTGCAGCAACAATGG
SEQ ID NO: 79	**800996**	GTCACCAGGGACGTAGGCCTCCCTC	CAGTGGTCCCTGCATCCGGAGGGAG
SEQ ID NO: 80	**153891**	CCTTGGGGCACCTATAATACGTCGC	GGAACCCCGTGGATATTATGCAGCG
SEQ ID NO: 81	**1155348**	AGCCGAAGAGTTCGCCGTTCACCGA	TCGGCTTCTCAAGCGGCAAGTGGCT
SEQ ID NO: 82	**1034779**	CGGGGTTTCTTCTGTAGACCACCCA	GCCCCAAAGAAGACATCTGGTGGGT
SEQ ID NO: 83	**459487**	AGGACTCCCAATAAACACGGTGTGG	TCCTGAGGGTTATTTGTGCCACACC
SEQ ID NO: 84	**963529**	GTGAACCTGTCTTGTCAGTCCGTCG	CACTTGGACAGAACAGTCAGGCAGC
SEQ ID NO: 85	**937694**	GTACGTCCTCCCTTTTCAGGTCATG	CATGCAGGAGGGAAAAGTCCAGTAC
SEQ ID NO: 86	**241716**	ACTTAAAGAGGTGCTAGACGCGTCC	TGAATTTCTCCACGATCTGCGCAGG

SEQ ID NO: 87	**838241**	CTACGTGTAGTTTTCGTATCGGGGT	GATGCACATCAAAAGCATAGCCCCA
SEQ ID NO: 88	**214577**	AAGTACCCGAGGCAGTTCCTCTTGA	TTCATGGGCTCCGTCAAGGAGAACT
SEQ ID NO: 89	**863010**	CCAACTCATTTGTAACCGTTCGACA	GGTTGAGTAAACATTGGCAAGCTGT
SEQ ID NO: 90	**205026**	AGGGGTATGGTATGATTCATTGAGT	TCCCCATACCATACTAAGTAACTCA
SEQ ID NO: 91	**879245**	CAATCCTATTTAGGTTGCTGATCGG	GTTAGGATAAATCCAACGACTAGCC
SEQ ID NO: 92	**1398922**	CTCTGTGTAGGTACTTAAACGCTAC	GAGACACATCCATGAATTTGCGATG
SEQ ID NO: 93	**207243**	TATTTGAAGGGTAGACCTCGTCCGG	ATAAACTTCCCATCTGGAGCAGGCC
SEQ ID NO: 94	**939284**	GTAAAAGACCTTTGTGTATTAGCAT	CATTTTCTGGAAACACATAATCGTA
SEQ ID NO: 95	**989830**	AAGGACTTCTGGACGAGCGTGTGAC	TTCCTGAAGACCTGCTCGCACACTG
SEQ ID NO: 96	**421339**	CGGAAAAAGCTGTGGTCTCTCAAGT	GCCTTTTTCGACACCAGAGAGTTCA
SEQ ID NO: 97	**937274**	ACCGTTCCCTTTGGTCATGAGGGGT	TGGCAAGGGAAACCAGTACTCCCCA
SEQ ID NO: 98	**854718**	AGAGGCTCTTTACCCTTCGTCTTTC	TCTCCGAGAAATGGGAAGCAGAAAG
SEQ ID NO: 99	**394142**	ACTCAACAAATGTCGGGTGGTCCTC	TGAGTTGTTTACAGCCCACCAGGAG
SEQ ID NO: 100	**1113006**	AAGGGGTACTCCCTCTCCGTGACCT	TTCCCCATGAGGGAGAGGCACTGGA
SEQ ID NO: 101	**780830**	AGTGTACCAGGACTCTGTTGTATGT	TCACATGGTCCTGAGACAACATACA
SEQ ID NO: 102	**436876**	CCACCTCGAAGAGGGCCCTTCGGTG	GGTGGAGCTTCTCCCGGGAAGCCAC
SEQ ID NO: 103	**103631**	ACCAATGACCTTGGGAAGCAGACGT	TGGTTACTGGAACCCTTCGTCTGCA
SEQ ID NO: 104	**1220647**	ATAATAATGTCCGTATGAAACCTCG	TATTATTACAGGCATACTTTGGAGC
SEQ ID NO: 105	**790219**	GTATCAGAGACGAGACAGCAAAGTG	CATAGTCTCTGCTCTGTCGTTTCAC
SEQ ID NO: 106	**52442**	ATCTACTCCCCTACCCAATTGTCTT	TAGATGAGGGGATGGGTTAACAGAA
SEQ ID NO: 107	**250045**	NA	NA
SEQ ID NO: 108	**832985**	GTAATTTCTTTGGATCTGGTAGTAG	CATTAAAGAAACCTAGACCATCATC
SEQ ID NO: 109	**1092796**	ATTGACATCTCCCATAGCTGACGTT	TAACTGTAGAGGGTATCGACTGCAA

SEQ ID NO: 110	**648413**	GAAACGGCGGAAGCACCAGTGGCCT	CTTTGCCGCCTTCGTGGTCACCGGA
SEQ ID NO: 111	**250016**	AAGAAGACCGGGTGCTTCCGGACCC	TTCTTCTGGCCCACGAAGGCCTGGG
SEQ ID NO: 112	**965989**	AACTACTATCTCTTATTGCAGGTGG	TTGATGATAGAGAATAACGTCCACC
SEQ ID NO: 113	**1227356**	GACTAACCGGGTCTGAATCCACCCA	CTGATTGGCCCAGACTTAGGTGGGT
SEQ ID NO: 114	**552104**	GTAGTTCTTGACAGAGGGTCCGTCG	CATCAAGAACTGTCTCCCAGGCAGC
SEQ ID NO: 115	**984051**	CAAAGACCTGAGTTTCCCACGAGGA	GTTTCTGGACTCAAAGGGTGCTCCT
SEQ ID NO: 116	**1205010**	CGACCACCTCGTGAACTCTGTATGA	GCTGGTGGAGCACTTGAGACATACT
SEQ ID NO: 117	**1223832**	CTGCCTCTGTCACGTCGGGACGCGT	GACGGAGACAGTGCAGCCCTGCGCA
SEQ ID NO: 118	**870307**	NA	NA
SEQ ID NO: 119	**747123**	CTGTACCCGTCGATAAACATTTTAC	GACATGGGCAGCTATTTGTAAAATG
SEQ ID NO: 120	**166927**	ATCTGTTCGGGACGGACTCTTCTAC	TAGACAAGCCCTGCCTGAGAAGATG
SEQ ID NO: 121	**616515**	GAGATCACATCACTGCATCCCTCGG	CTCTAGTGTAGTGACGTAGGGAGCC
SEQ ID NO: 122	**1244467**	GGTCAAAGTAGTCTTTAGTGCAAGT	CCAGTTTCATCAGAAATCACGTTCA
SEQ ID NO: 123	**178668**	TACGTGTTCCTGGAGGCTGACGTGC	ATGCACAAGGACCTCCGACTGCACG
SEQ ID NO: 124	**733825**	CGTCGTCGCCGAGAGTATCATCATC	GCAGCAGCGGCTCTCATAGTAGTAG
SEQ ID NO: 125	**829061**	GGTCCTCCTTTTCTCGAGCCAGTTG	CCAGGAGGAAAAGAGCTCGGTCAAC
SEQ ID NO: 126	**391658**	CCGACTAAAATTGTCCTTTCCAACT	GGCTGATTTTAACAGGAAAGGTTGA
SEQ ID NO: 127	**427566**	CTGTCAAAAGAAAGTCACCTAACCT	GACAGTTTTCTTTCAGTGGATTGGA
SEQ ID NO: 128	**127879**	CCCGGGTCCGAGGTAATAACTATAT	GGGCCCAGGCTCCATTATTGATATA
SEQ ID NO: 129	**486349**	CAGTACAGACCATCAAGTAGACGGT	GTCATGTCTGGTAGTTCATCTGCCA
SEQ ID NO: 130	**1160676**	CTCCAGGGTGGTCATCTCAAGAACT	GAGGTCCCACCAGTAGAGTTCTTGA
SEQ ID NO: 131	**884637**	CTCAACGTTTGGTAGCCTGTTCCCG	GAGTTGCAAACCATCGGACAAGGGC
SEQ ID NO: 132	**581804**	NA	NA

SEQ ID NO: 133	**1010241**	CTTCACGAGTACTGAGGGTTAGACG	GAAGTGCTCATGACTCCCAATCTGC
SEQ ID NO: 134	**309429**	ATGTGGCGTGCTGGGTAAAAATACC	TACACCGCACGACCCATTTTTATGG
SEQ ID NO: 135	**1170693**	TCCGTTGTTGTGACTCTGAGGAGGA	AGGCAACAACACTGAGACTCCTCCT
SEQ ID NO: 136	**169484**	ATCTAATATGGGTGTTTGTCGTGAC	TAGATTATACCCACAAACAGCACTG
SEQ ID NO: 137	**1137858**	NA	NA
SEQ ID NO: 138	**960864**	ATACTTTTCTTCGTAGTGTGACGTC	TATGAAAAGAAGCATCACACTGCAG
SEQ ID NO: 139	**900370**	AGAAAATTGACCCTTCGTGTAAAGT	TCTTTTAACTGGGAAGCACATTTCA
SEQ ID NO: 140	**1180658**	ATATGTCTCGTGTGTAGAGTACCCG	TATACAGAGCACACATCTCATGGGC
SEQ ID NO: 141	**115056**	CGCCGGCCCGCTGCCCGCGGCCTCG	GCGGCCGGGCGACGGGCGCCGGAGC
SEQ ID NO: 142	**1242378**	GTTCACCCTAGTCATGACGGGAAGA	CAAGTGGGATCAGTACTGCCCTTCT
SEQ ID NO: 143	**1244006**	AAATGATAGTCTTCTGGTCGTGTCC	TTTACTATCAGAAGACCAGCACAGG
SEQ ID NO: 144	**140894**	ATGAAGGACCGACTTATAACCGGTA	TACTTCCTGGCTGAATATTGGCCAT
SEQ ID NO: 145	**398392**	GTATCGACCACAATCCTCTCACTGA	CATAGCTGGTGTTAGGAGAGTGACT
SEQ ID NO: 146	**310782**	ACTGTAGACTCGTGCTGTTCCGATC	TGACATCTGAGCACGACAAGGCTAG
SEQ ID NO: 147	**646093**	TAAGTCAGGGAAGTGTCCTGTGCAC	ATTCAGTCCCTTCACAGGACACGTG
SEQ ID NO: 148	**817529**	GAGACGGAGGTTTGCCTAAGCCCTA	CTCTGCCTCCAAACGGATTCGGGAT
SEQ ID NO: 149	**191193**	GTTCTCTTGGGTCTAGTCGTTCCGT	CAAGAGAACCCAGATCAGCAAGGCA
SEQ ID NO: 150	**473876**	GGGGGCTCAAGCCGCGCTGGGCTCG	CCCCCGAGTTCGGCGCGACCCGAGC
SEQ ID NO: 151	**389947**	GAAATAGAGTAAACTTGACTCCCTC	CTTTATCTCATTTGAACTGAGGGAG
SEQ ID NO: 152	**939494**	ATTTGTCCTTTGAGCCGTGCCCCGT	TAAACAGGAAACTCGGCACGGGGCA
SEQ ID NO: 153	**177777**	CTTTCATGGATGTTCCGAGTGTCCT	GAAAGTACCTACAAGGCTCACAGGA
SEQ ID NO: 154	**13579**	GGAGAGACTCCCAGGCTCCCGGGCG	CCTCTCTGAGGGTCCGAGGGCCCGC
SEQ ID NO: 155	**646397**	ACGTAACTCGTGGAAGACCCTGCCC	TGCATTGAGCACCTTCTGGGACGGG

SEQ ID NO: 156	**1029128**	CTTCTTTTCACCATTCAGGAGTCGA	GAAGAAAAGTGGTAAGTCCTCAGCT
SEQ ID NO: 157	**1312014**	ATTATTCACTAATGCACCGGAGGGT	TAATAAGTGATTACGTGGCCTCCCA
SEQ ID NO: 158	**853971**	AGACCTCCTTTAGGTGGTCGTCCAC	TCTGGAGGAAATCCACCAGCAGGTG
SEQ ID NO: 159	**119393**	AGGCTCTACCCGAGGTGGAACTAGA	TCCGAGATGGGCTCCACCTTGATCT
SEQ ID NO: 160	**189739**	TCAGTGGTGGGTCTTTAACAGGCTC	AGTCACCACCCAGAAATTGTCCGAG
SEQ ID NO: 161	**22861**	CTCTCTCCTCCACCCCCCTCTTCGC	GAGAGAGGAGGTGGGGGGAGAAGCG
SEQ ID NO: 162	**897801**	AAAGTTTTGAGTTCCCTGACGGTCG	TTTCAAAACTCAAGGGACTGCCAGC
SEQ ID NO: 163	**861160**	CTACTTCAATTTATTCGTTTCCATG	GATGAAGTTAAATAAGCAAAGGTAC
SEQ ID NO: 164	**409503**	CCGGATTAATGTCCGTGATTGACAC	GGCCTAATTACAGGCACTAACTGTG
SEQ ID NO: 165	**871670**	TCATGTACACGATTTCTTCACCCGT	AGTACATGTGCTAAAGAAGTGGGCA
SEQ ID NO: 166	**496895**	CGTTTAAGTCATTGCGTCCGTGGTT	GCAAATTCAGTAACGCAGGCACCAA
SEQ ID NO: 167	**170269**	AAATTCTGGGGTTCTGTTTAGTGGT	TTTAAGACCCCAAGACAAATCACCA
SEQ ID NO: 168	**228035**	AGTTTAAGAGGACTGAAGTGCGGAC	TCAAATTCTCCTGACTTCACGCCTG
SEQ ID NO: 169	**343592**	CCGAAACCGCTGACGCGATGAGGGC	GGCTTTGGCGACTGCGCTACTCCCG
SEQ ID NO: 170	**98414**	GTCCGAGGAGTACCACTAGAAGGGT	CAGGCTCCTCATGGTGATCTTCCCA
SEQ ID NO: 171	**847702**	ACTCACGCGGTTTCAAGTTGTTCGG	TGAGTGCGCCAAAGTTCAACAAGCC
SEQ ID NO: 172	**572108**	GTCTCACTCAGAACATCACCCTTTT	CAGAGTGAGTCTTGTAGTGGGAAAA
SEQ ID NO: 173	**966784**	GTTATTTGTCTTAGTAGTATCGTCA	CAATAAACAGAATCATCATAGCAGT
SEQ ID NO: 174	**86152**	AGCATGAACCAGGAGGTGACCCGTT	TCGTACTTGGTCCTCCACTGGGCAA
SEQ ID NO: 175	**893740**	GTACAGTTCCGTTGCGAATAACCGG	CATGTCAAGGCAACGCTTATTGGCC
SEQ ID NO: 176	**1046962**	GTATGACTTCATCCCTTGTTCTGGT	CATACTGAAGTAGGGAACAAGACCA
SEQ ID NO: 177	**732965**	CTTTTGTAGAGTCCGCAGTAGTTGA	GAAAACATCTCAGGCGTCATCAACT
SEQ ID NO: 178	**1234766**	CGAATGCAGTCCGTTGTTTGAGTTT	GCTTACGTCAGGCAACAAACTCAAA

SEQ ID NO: 179	**531804**	AAAATTCAGGTTCCATGGTAGACGG	TTTTAAGTCCAAGGTACCATCTGCC
SEQ ID NO: 180	**928672**	GTACCCACCATGTTTGTCCATCTGT	CATGGGTGGTACAAACAGGTAGACA
SEQ ID NO: 181	**330493**	CCGAGCCTGCGTGGAAGGCGCTTCC	GGCTCGGACGCACCTTCCGCGAAGG
SEQ ID NO: 182	**206283**	CCAAAGTGGTATAGGGTGACAGACA	GGTTTCACCATATCCCACTGTCTGT
SEQ ID NO: 183	**889233**	ATTCTTCTTGGACTCTTGTGTACTC	TAAGAAGAACCTGAGAACACATGAG
SEQ ID NO: 184	**374416**	GTCTACAAAGAAATCGACTCTGTGT	CAGATGTTTCTTTAGCTGAGACACA
SEQ ID NO: 185	**892717**	ACAACTTGTTGGCAGTCGGACCGAG	TGTTGAACAACCGTCAGCCTGGCTC
SEQ ID NO: 186	**167058**	TTTGATTGGGTGTATGACGGGAACC	AAACTAACCCACATACTGCCCTTGG
SEQ ID NO: 187	**976043**	ACGTGACGGAACTTAAGGTAGACAT	TGCACTGCCTTGAATTCCATCTGTA
SEQ ID NO: 188	**325916**	CGAGCGCGGGCGGAAACAATCAAAG	GCTCGCGCCCGCCTTTGTTAGTTTC
SEQ ID NO: 189	**949597**	GGTTCCACGCTTTTCTTGATCGACG	CCAAGGTGCGAAAAGAACTAGCTGC
SEQ ID NO: 190	**587378**	CACGGTTGTAACTCCCTCCGCGTAG	GTGCCAACATTGAGGGAGGCGCATC
SEQ ID NO: 191	**1275401**	AGATGCTTTAACAGAAGACCCGGAC	TCTACGAAATTGTCTTCTGGGCCTG
SEQ ID NO: 192	**1180471**	GTATCGCCAGTGTGTAGACGTAGTG	CATAGCGGTCACACATCTGCATCAC
SEQ ID NO: 193	**541995**	CTAGACGGCCAGTATGACACGGCGG	GATCTGCCGGTCATACTGTGCCGCC
SEQ ID NO: 194	**420240**	ACAGAAGTAAAGCTTTGTGTCGGGT	TGTCTTCATTTCGAAACACAGCCCA
SEQ ID NO: 195	**208375**	ATGTTGAAGGGGTTTAGCTCTGTTC	TACAACTTCCCCAAATCGAGACAAG
SEQ ID NO: 196	**1216874**	TCTCCCGTCGGTCCTTCATGTACTA	AGAGGGCAGCCAGGAAGTACATGAT
SEQ ID NO: 197	**225018**	ACGGTCACAGAGGAATTATGAAGAA	TGCCAGTGTCTCCTTAATACTTCTT
SEQ ID NO: 198	**999430**	CTTAGTACTTCTGTTTCCTGGTCGC	GAATCATGAAGACAAAGGACCAGCG
SEQ ID NO: 199	**194569**	GTCGAGTTGGGGTACTTGAGTCACA	CAGCTCAACCCCATGAACTCAGTGT
SEQ ID NO: 200	**425083**	AACGGCGGAAGCACCAGTGGCCTTG	TTGCCGCCTTCGTGGTCACCGGAAC
SEQ ID NO: 201	**470488**	CATTAATCAATATTGCTTTAAGTAT	GTAATTAGTTATAACGAAATTCATA

SEQ ID NO: 202	**904322**	ATGTACTTTTGTGCCGTTGAGGTCC	TACATGAAAACACGGCAACTCCAGG
SEQ ID NO: 203	**318229**	CGCACTTGAGCAACGACTTCGGTTT	GCGTGAACTCGTTGCTGAAGCCAAA
SEQ ID NO: 204	**862638**	GTAACACGCAATTGTCACCGAGTCT	CATTGTGCGTTAACAGTGGCTCAGA
SEQ ID NO: 205	**988384**	GGAACGTCTTCTGCGGCATGCTCCA	CCTTGCAGAAGACGCCGTACGAGGT
SEQ ID NO: 206	**864453**	ATTGTATAATTCTTGAACCTCCTCC	TAACATATTAAGAACTTGGAGGAGG
SEQ ID NO: 207	**510658**	GTTATTCGAGTACAAGGGTAGGTCA	CAATAAGCTCATGTTCCCATCCAGT
SEQ ID NO: 208	**104933**	GTTCTACAAGACCTTTCCTCGGCGC	CAAGATGTTCTGGAAAGGAGCCGCG
SEQ ID NO: 209	**576724**	ACCAAGGTAACACCTTTGTGACCGT	TGGTTCCATTGTGGAAACACTGGCA
SEQ ID NO: 210	**719845**	TGTCACCACTGAGTAGTCTCCCGCT	ACAGTGGTGACTCATCAGAGGGCGA
SEQ ID NO: 211	**864726**	CTTTAGACATTGACCGGCACTATTT	GAAATCTGTAACTGGCCGTGATAAA
SEQ ID NO: 212	**17140**	TTGATTCCCACTCTGGTTCTGGATA	AACTAAGGGTGAGACCAAGACCTAT
SEQ ID NO: 213	**1350424**	AAATGTCCTACCTTCGTTCAGTCGG	TTTACAGGATGGAAGCAAGTCAGCC
SEQ ID NO: 214	**191706**	ACTTGGCGGGTCAGAAACTGGACTC	TGAACCGCCCAGTCTTTGACCTGAG
SEQ ID NO: 215	**440529**	ATCTGGCTAAGAAATCGAAGGACGT	TAGACCGATTCTTTAGCTTCCTGCA
SEQ ID NO: 216	**789471**	CCGCTGTGTAGACAGGATGATCTCT	GGCGACACATCTGTCCTACTAGAGA
SEQ ID NO: 217	**811399**	GAATATGACCGACTTTTTTGAAACG	CTTATACTGGCTGAAAAAACTTTGC
SEQ ID NO: 218	**912758**	ACACCGATAGTTGTCATCTAGACCA	TGTGGCTATCAACAGTAGATCTGGT
SEQ ID NO: 219	**1025895**	AATATGTTTCAGTTTCGGAGGGTCG	TTATACAAAGTCAAAGCCTCCCAGC
SEQ ID NO: 220	**731798**	ACTTAACTAAGAGTGTCCCGGACGA	TGAATTGATTCTCACAGGGCCTGCT
SEQ ID NO: 221	**290773**	CTTCATAGGCAATGTCGACCGCTGC	GAAGTATCCGTTACAGCTGGCGACG
SEQ ID NO: 222	**837720**	CTCCAATTTCGGCTGTCGTCGTCAA	GAGGTTAAAGCCGACAGCAGCAGTT
SEQ ID NO: 223	**775055**	GTACATCGGCTGACAAGGTTGAGAA	CATGTAGCCGACTGTTCCAACTCTT
SEQ ID NO: 224	**862096**	AGTTATACGAATTGTGACCCGGTGC	TCAATATGCTTAACACTGGGCCACG

SEQ ID NO: 225	**951484**	AGACGACGTCCCTTATTCTTGAAAG	TCTGCTGCAGGGAATAAGAACTTTC
SEQ ID NO: 226	**429070**	GTAAATCCAAGAAGTGACCCTGACA	CATTTAGGTTCTTCACTGGGACTGT
SEQ ID NO: 227	**1326860**	CTGAAGTACCTAGGTTATTCGTGCT	GACTTCATGGATCCAATAAGCACGA
SEQ ID NO: 228	**241752**	GACTCTAGTACTGAGGTTTAATTCT	CTGAGATCATGACTCCAAATTAAGA
SEQ ID NO: 229	**779813**	NA	NA
SEQ ID NO: 230	**1131191**	CTTCTCCGGTTTTTAGTAGTCGACT	GAAGAGGCCAAAAATCATCAGCTGA
SEQ ID NO: 231	**187197**	GCCTCCGCGGGTGGTACTTCATCCA	CGGAGGCGCCCACCATGAAGTAGGT
SEQ ID NO: 232	**546526**	GTAACTTGAACAGGTTTAACCACCC	CATTGAACTTGTCCAAATTGGTGGG
SEQ ID NO: 233	**1390384**	AGAAGCTGACGTAGAAAAGGATCAA	TCTTCGACTGCATCTTTTCCTAGTT
SEQ ID NO: 234	**533355**	CTCTGCATCAGGTCCGACTCCATGT	GAGACGTAGTCCAGGCTGAGGTACA
SEQ ID NO: 235	**55004**	CTAGGTCGGCCTTCACTGTTTTTCT	GATCCAGCCGGAAGTGACAAAAAGA
SEQ ID NO: 236	**394182**	GTTTACTCGCAATTTGTGGGTTAGT	CAAATGAGCGTTAAACACCCAATCA
SEQ ID NO: 237	**103742**	GTATATTAGGACCTTTGCTGAGGTT	CATATAATCCTGGAAACGACTCCAA
SEQ ID NO: 238	**416958**	ACAAAAAAGGTGTAGTATGACAGGT	TGTTTTTTCCACATCATACTGTCCA
SEQ ID NO: 239	**26450**	GTAGTTCAATCCCACTCAGTAGGGC	CATCAAGTTAGGGTGAGTCATCCCG
SEQ ID NO: 240	**603514**	NA	NA
SEQ ID NO: 241	**489219**	ATCTGTGGCATCGTGTACGAGTTTG	TAGACACCGTAGCACATGCTCAAAC
SEQ ID NO: 242	**501666**	CTCTCGAAACAAAAATGAAGTCTGT	GAGAGCTTTGTTTTTACTTCAGACA
SEQ ID NO: 243	**535783**	ATTGAGGTCAGAACATGAACAGTGT	TAACTCCAGTCTTGTACTTGTCACA
SEQ ID NO: 244	**464840**	TTGACGGTCCAACCCTTTAAGGAGC	AACTGCCAGGTTGGGAAATTCCTCG
SEQ ID NO: 245	**1341684**	AGACCACCTATACCTCGTCTTGAGG	TCTGGTGGATATGGAGCAGAACTCC
SEQ ID NO: 246	**1251330**	GCAATCGTCTGTCGTTTTGTACTTT	CGTTAGCAGACAGCAAAACATGAAA
SEQ ID NO: 247	**512235**	CCGAAAACATGGTCCAGTAAGAAAT	GGCTTTTGTACCAGGTCATTCTTTA

SEQ ID NO: 248	**711651**	GGATCCATGAGAAGAACAAACAGTT	CCTAGGTACTCTTCTTGTTTGTCAA
SEQ ID NO: 249	**448395**	TTTCCGTAGAAGTTGGTTGTCCGTT	AAAGGCATCTTCAACCAACAGGCAA
SEQ ID NO: 250	**1337367**	AGGGCTTTACACAGACCAGGGTTTC	TCCCGAAATGTGTCTGGTCCCAAAG
SEQ ID NO: 251	**663077**	AGTCTTTCGTGAATTCTGTCGGTGA	TCAGAAAGCACTTAAGACAGCCACT
SEQ ID NO: 252	**13580**	AATAACACCCAGTCGAACCGCCGGT	TTATTGTGGGTCAGCTTGGCGGCCA
SEQ ID NO: 253	**1001194**	ACTTCTAATCTGTGGAAGGGACCGA	TGAAGATTAGACACCTTCCCTGGCT
SEQ ID NO: 254	**292368**	ACCGTTACGGGCACTACCACGGCGG	TGGCAATGCCCGTGATGGTGCCGCC
SEQ ID NO: 255	**628760**	ATAGCTTAGACACTTCGGCGACAGA	TATCGAATCTGTGAAGCCGCTGTCT
SEQ ID NO: 256	**476048**	AAGAACTTCAACAGAATGTTAGTGG	TTCTTGAAGTTGTCTTACAATCACC
SEQ ID NO: 257	**828036**	ACAATTATTTGGTCCCGCCCACTGT	TGTTAATAAACCAGGGCGGGTGACA
SEQ ID NO: 258	**917007**	AGACAGATCATGGTGTCCAGTACTC	TCTGTCTAGTACCACAGGTCATGAG
SEQ ID NO: 259	**445845**	ACTCCTCGTAAAGTGTCCAGTGCGG	TGAGGAGCATTTCACAGGTCACGCC
SEQ ID NO: 260	**918400**	ACATGGCGATGGACCCGCTTCGCGA	TGTACCGCTACCTGGGCGAAGCGCT
SEQ ID NO: 261	**242112**	AAGTCTCCGAGGTTGTAAAGTCTGT	TTCAGAGGCTCCAACATTTCAGACA
SEQ ID NO: 262	**833985**	AAAAACTTTGACGACCTACTCAAGT	TTTTTGAAACTGCTGGATGAGTTCA
SEQ ID NO: 263	**829425**	AGAGGAGTCTTTTTGCATCAACAGG	TCTCCTCAGAAAAACGTAGTTGTCC
SEQ ID NO: 264	**913655**	ATCGAGTCGAGTTGTACCTAAGTGG	TAGCTCAGCTCAACATGGATTCACC
SEQ ID NO: 265	**413753**	ATTGGATAATAACACGTCGTCCGGA	TAACCTATTATTGTGCAGCAGGCCT
SEQ ID NO: 266	**779572**	AGTCCATAGGACTGGGTGCCAGAAC	TCAGGTATCCTGACCCACGGTCTTG
SEQ ID NO: 267	**712555**	ACATAGTTTGAGACGGAGCCTTTCC	TGTATCAAACTCTGCCTCGGAAAGG
SEQ ID NO: 268	**673977**	CTCTTGTGTGATAAGGTCTTGTCTC	GAGAACACACTATTCCAGAACAGAG
SEQ ID NO: 269	**495410**	CTAAGACGTCTCATGACTCCACCGT	GATTCTGCAGAGTACTGAGGTGGCA
SEQ ID NO: 270	**1025836**	AGTTGAATTCATGTTTTGTGCTGCT	TCAACTTAAGTACAAAACACGACGA

SEQ ID NO: 271	**611383**	GTCCACCACTCACATCACGGGTTGT	CAGGTGGTGAGTGTAGTGCCCAACA
SEQ ID NO: 272	**841691**	AGTGGGGTTTTTCTCCCGGACTCAC	TCACCCCAAAAAGAGGGCCTGAGTG
SEQ ID NO: 273	**445870**	AGTTGTCCAAGTTACAGTTCCCACA	TCAACAGGTTCAATGTCAAGGGTGT
SEQ ID NO: 274	**717200**	CTTTGAGGAGTATTTAGAGTCGTCG	GAAACTCCTCATAAATCTCAGCAGC
SEQ ID NO: 275	**507885**	TTTAAAGACAAGGACGAGCTACGCC	AAATTTCTGTTCCTGCTCGATGCGG
SEQ ID NO: 276	**320125**	CACGCTCAAGCTCCGGTTGTGGACC	GTGCGAGTTCGAGGCCAACACCTGG
SEQ ID NO: 277	**1269863**	AAGTTCCCGTCGTCTGCACTACCAA	TTCAAGGGCAGCAGACGTGATGGTT
SEQ ID NO: 278	**216801**	TGAGGTCAAGGATCCCGCCCACGTC	ACTCCAGTTCCTAGGGCGGGTGCAG
SEQ ID NO: 279	**506048**	AAAAAGACAACTACCCTATTCTGGA	TTTTTCTGTTGATGGGATAAGACCT
SEQ ID NO: 280	**497246**	ATTATAGTGTCATTGTGTTTGTCCG	TAATATCACAGTAACACAAACAGGC
SEQ ID NO: 281	**275198**	GTACCCGTAGGTCGGTACTTACACC	CATGGGCATCCAGCCATGAATGTGG
SEQ ID NO: 282	**716073**	NA	NA
SEQ ID NO: 283	**265773**	CCGACGTGGTCGGACGGACGACTCA	GGCTGCACCAGCCTGCCTGCTGAGT
SEQ ID NO: 284	**674645**	GTCATCACTTGATACTACCATGGTC	CAGTAGTGAACTATGATGGTACCAG
SEQ ID NO: 285	**161199**	NA	NA
SEQ ID NO: 286	**695802**	GTTCCGGTAAGATAGTGAACGGAGA	CAAGGCCATTCTATCACTTGCCTCT
SEQ ID NO: 287	**1366028**	TAATTGGTGTAAAGTACGTAGAGGT	ATTAACCACATTTCATGCATCTCCA
SEQ ID NO: 288	**1003627**	ATCTGGTCACTGGAAACGACACGGG	TAGACCAGTGACCTTTGCTGTGCCC
SEQ ID NO: 289	**462246**	ATTTGTCCAAGCAAGAACCGCGGTG	TAAACAGGTTCGTTCTTGGCGCCAC
SEQ ID NO: 290	**456080**	ATGGAACTAAGTATTCCTTCGGGGT	TACCTTGATTCATAAGGAAGCCCCA
SEQ ID NO: 291	**759542**	GATCCTCCCGAGTAAGGTCTGTGTC	CTAGGAGGGCTCATTCCAGACACAG
SEQ ID NO: 292	**1222654**	CTAGTAACGTCTGTCCCGGAGGTAT	GATCATTGCAGACAGGGCCTCCATA
SEQ ID NO: 293	**628680**	CGAACAGGACACTGGTGCCCTCTCT	GCTTGTCCTGTGACCACGGGAGAGA

SEQ ID NO: 294	**282392**	CTATCTTCGACGGTTCCAGACCCGA	GATAGAAGCTGCCAAGGTCTGGGCT
SEQ ID NO: 295	**764630**	CCTTACGTCGACGAGTAGACAACCC	GGAATGCAGCTGCTCATCTGTTGGG
SEQ ID NO: 296	**112896**	CTTCACACCAGGAGCTGAGGTTCCG	GAAGTGTGGTCCTCGACTCCAAGGC
SEQ ID NO: 297	**270651**	ACGCATTTCGGTTTGCTGCCGTCGT	TGCGTAAAGCCAAACGACGGCAGCA
SEQ ID NO: 298	**556715**	CTTCAAACAGTATCCTTCCCGTCGG	GAAGTTTGTCATAGGAAGGGCAGCC
SEQ ID NO: 299	**196190**	TCCCGACCTGGTAGTTCCGAAATCA	AGGGCTGGACCATCAAGGCTTTAGT
SEQ ID NO: 300	**211956**	NA	NA
SEQ ID NO: 301	**1182810**	TTTCGTGAGAGTGGGTCCATCGTTC	AAAGCACTCTCACCCAGGTAGCAAG
SEQ ID NO: 302	**1127464**	TCCAGGGGTTTAGGACTTTTACGTG	AGGTCCCCAAATCCTGAAAATGCAC
SEQ ID NO: 303	**1323092**	GCCTCGTCGTCACTAAGGTCGAAGT	CGGAGCAGCAGTGATTCCAGCTTCA
SEQ ID NO: 304	**1086976**	GCGTTAGCTGCTCCACTTAGTGACA	CGCAATCGACGAGGTGAATCACTGT
SEQ ID NO: 305	**858896**	AATTTACGTTTATCTGGTGAGTGTT	TTAAATGCAAATAGACCACTCACAA
SEQ ID NO: 306	**826483**	GACGTCCATTTTGCGGCGCGGACCC	CTGCAGGTAAAACGCCGCGCCTGGG
SEQ ID NO: 307	**831119**	NA	NA
SEQ ID NO: 308	**72245**	AGTTTCCGTCCTTTCCGACTCCGGA	TCAAAGGCAGGAAAGGCTGAGGCCT
SEQ ID NO: 309	**405782**	CCCGTGAAATAGACGGACTAGTCTA	GGGCACTTTATCTGCCTGATCAGAT
SEQ ID NO: 310	**851677**	ATACGGATTTTAATAGTTTCAGGGG	TATGCCTAAAATTATCAAAGTCCCC
SEQ ID NO: 311	**403186**	NA	NA
SEQ ID NO: 312	**952377**	CGAATTACCTTACCTTGTGACGAGG	GCTTAATGGAATGGAACACTGCTCC
SEQ ID NO: 313	**846079**	ATTTTACGTTTTGGGTCCAACCCGT	TAAAATGCAAAACCCAGGTTGGGCA
SEQ ID NO: 314	**1036173**	AGATCAGCTTCTTCGGTGAACCAGG	TCTAGTCGAAGAAGCCACTTGGTCC
SEQ ID NO: 315	**763720**	GTAAGAAAACGAGTACGCCTACCCT	CATTCTTTTGCTCATGCGGATGGGA
SEQ ID NO: 316	**388000**	TCCCTCTAGTAAAGTGATGACCTAC	AGGGAGATCATTTCACTACTGGATG

SEQ ID NO: 317	**537928**	TCCGGTATCCAGTATCGACTCTTCA	AGGCCATAGGTCATAGCTGAGAAGT
SEQ ID NO: 318	**1144626**	AACAGGACTGTTCGACCACCCTCGA	TTGTCCTGACAAGCTGGTGGGAGCT
SEQ ID NO: 319	**1371715**	GTTTCAGTCGTAGTAATACCAGGCT	CAAAGTCAGCATCATTATGGTCCGA
SEQ ID NO: 320	**220735**	TTCACACCAGGAGCTGAGGTTCCGT	AAGTGTGGTCCTCGACTCCAAGGCA
SEQ ID NO: 321	**1033537**	ATTAAGTTTCTTGAGCCGTGTCGTG	TAATTCAAAGAACTCGGCACAGCAC
SEQ ID NO: 322	**924130**	GTAACTCCAGATGATACATGATCAG	CATTGAGGTCTACTATGTACTAGTC
SEQ ID NO: 323	**308084**	CGGTCTGGGCTACCTCGCTCGTGGC	GCCAGACCCGATGGAGCGAGCACCG
SEQ ID NO: 324	**1000577**	AGTTTTATCTGTGTCCCTTCCGGTA	TCAAAATAGACACAGGGAAGGCCAT
SEQ ID NO: 325	**1049901**	GTGTGAAAACTCATCACTCCCGGAC	CACACTTTTGAGTAGTGAGGGCCTG
SEQ ID NO: 326	**740314**	AAAGTGGTCGAAGCGTGTCTGAAAG	TTTCACCAGCTTCGCACAGACTTTC
SEQ ID NO: 327	**500571**	GTCAAAGAACAAGGGTAGGCATACC	CAGTTTCTTGTTCCCATCCGTATGG
SEQ ID NO: 328	**698390**	TGGTGTTGTAGATCGTCTCTTAGTG	ACCACAACATCTAGCAGAGAATCAC
SEQ ID NO: 329	**773187**	AGTCGGCCGGACACATGTGCTTCAG	TCAGCCGGCCTGTGTACACGAAGTC
SEQ ID NO: 330	**1221496**	AGTTCTGATGTCCAGGGTCGTTCGT	TCAAGACTACAGGTCCCAGCAAGCA
SEQ ID NO: 331	**1231840**	GACAACATTAGTCAACATTTGTGGT	CTGTTGTAATCAGTTGTAAACACCA
SEQ ID NO: 332	**1223694**	ATTCCCTGTCAAAAGAAAGTCACCT	TAAGGGACAGTTTTCTTTCAGTGGA
SEQ ID NO: 333	**1026306**	AGTCGAGACTTTCAGGCCAAGGTTT	TCAGCTCTGAAAGTCCGGTTCCAAA
SEQ ID NO: 334	**369436**	GTTTCATCAAACTTCACACCGGACG	CAAAGTAGTTTGAAGTGTGGCCTGC
SEQ ID NO: 335	**430238**	ACCGGTGTCAAGAAATGGTGTCTAA	TGGCCACAGTTCTTTACCACAGATT
SEQ ID NO: 336	**851896**	CTCATCATTTATTCGGAGTCGGGGA	GAGTAGTAAATAAGCCTCAGCCCCT
SEQ ID NO: 337	**930638**	CACTGCGGATGTTGGTCTATTATTT	GTGACGCCTACAACCAGATAATAAA
SEQ ID NO: 338	**516083**	ACACGTTTAGACATGGTGGTTCCAC	TGTGCAAATCTGTACCACCAAGGTG
SEQ ID NO: 339	**229510**	CCAGTCTTAGGGGTAGTAGTGTTTT	GGTCAGAATCCCCATCATCACAAAA

SEQ ID NO: 340	**738248**	GTTTCCACGCGAACATTGCGAGGTG	CAAAGGTGCGCTTGTAACGCTCCAC
SEQ ID NO: 341	**93763**	GATTTCGTTACCCTTGTCATCTTCA	CTAAAGCAATGGGAACAGTAGAAGT
SEQ ID NO: 342	**649967**	AGTCTTAGGGAACTCGACCGATTCA	TCAGAATCCCTTGAGCTGGCTAAGT
SEQ ID NO: 343	**1224667**	AGAGGATCTGTCACTGTGTCTTTCA	TCTCCTAGACAGTGACACAGAAAGT
SEQ ID NO: 344	**273712**	CATCAAGTCGGTCGGTCAGTGTAAC	GTAGTTCAGCCAGCCAGTCACATTG
SEQ ID NO: 345	**477197**	AGGAGGACTCAACCGGAGATTTTGG	TCCTCCTGAGTTGGCCTCTAAAACC
SEQ ID NO: 346	**979244**	GTTTCCCTACTTCCCAGGCGAGAGT	CAAAGGGATGAAGGGTCCGCTCTCA
SEQ ID NO: 347	**829240**	ACTCCCCTTTTGATGACCTCGAGGA	TGAGGGGAAAACTACTGGAGCTCCT
SEQ ID NO: 348	**1272737**	TCTTTTATTAATGTCGCCCGCGCCC	AGAAAATAATTACAGCGGGCGCGGG
SEQ ID NO: 349	**720633**	GACCAAAAGAGGGTAGATTTATGAT	CTGGTTTTCTCCCATCTAAATACTA
SEQ ID NO: 350	**817226**	TTATCGTTGCGACGGAAGGCCTTCT	AATAGCAACGCTGCCTTCCGGAAGA
SEQ ID NO: 351	**1116818**	NA	NA
SEQ ID NO: 352	**710854**	ACTAACCGAGTGAGGCGTCTGGCAC	TGATTGGCTCACTCCGCAGACCGTG
SEQ ID NO: 353	**812913**	AGTTCAAGCGACTTCTGTCACGGTG	TCAAGTTCGCTGAAGACAGTGCCAC
SEQ ID NO: 354	**1140564**	AGAACGTCATGTTTGGTCCGTCTGG	TCTTGCAGTACAAACCAGGCAGACC
SEQ ID NO: 355	**1403202**	ATTGTTACAGTACGTGGTCCCACTA	TAACAATGTCATGCACCAGGGTGAT
SEQ ID NO: 356	**236942**	ATAAAGAAGGTGTCGGGAGCTGATT	TATTTCTTCCACAGCCCTCGACTAA
SEQ ID NO: 357	**820375**	CCAAGTAGTCGACGTGAAGGGCATC	GGTTCATCAGCTGCACTTCCCGTAG
SEQ ID NO: 358	**113117**	AGTATCTCGAGTACCTGTGGGACCT	TCATAGAGCTCATGGACACCCTGGA
SEQ ID NO: 359	**466136**	GGTTTTGCAAAGTGTGTTTAGTCCA	CCAAAACGTTTCACACAAATCAGGT
SEQ ID NO: 360	**563126**	GCCGTCGCGGAACCCTGTTTTTTGT	CGGCAGCGCCTTGGGACAAAAAACA
SEQ ID NO: 361	**705223**	ATCCTGAGGAGACAACAATCCGGTA	TAGGACTCCTCTGTTGTTAGGCCAT
SEQ ID NO: 362	**1229464**	CCGTGGACGGTCTTTATGAAGCTTC	GGCACCTGCCAGAAATACTTCGAAG

SEQ ID NO: 363	**949977**	CTTTGGCTTAATCCTTCTCCGGTAC	GAAACCGAATTAGGAAGAGGCCATG
SEQ ID NO: 364	**1326134**	ACATACTCCCTAGGTTCTCTGTAGT	TGTATGAGGGATCCAAGAGACATCA
SEQ ID NO: 365	**357443**	CGACCGTAGTAAAATACCACCCGGA	GCTGGCATCATTTTATGGTGGGCCT
SEQ ID NO: 366	**96768**	GTTAGTGGTTACCATTCACCGTCGA	CAATCACCAATGGTAAGTGGCAGCT
SEQ ID NO: 367	**945783**	AGATGAACCTTCAGTCCCAAGAGTT	TCTACTTGGAAGTCAGGGTTCTCAA
SEQ ID NO: 368	**365842**	TTAGTTCTAAAACATGTGAGTAGTA	AATCAAGATTTTGTACACTCATCAT
SEQ ID NO: 369	**983019**	GGCCGACCCTGGTGCAGAAGTCCCT	CCGGCTGGGACCACGTCTTCAGGGA
SEQ ID NO: 370	**1251919**	AGCTGCAGGTCGTGTTACCGAAGTC	TCGACGTCCAGCACAATGGCTTCAG
SEQ ID NO: 371	**294308**	TCCTACGAGAGGCACGACTCAGGCG	AGGATGCTCTCCGTGCTGAGTCCGC
SEQ ID NO: 372	**305873**	NA	NA
SEQ ID NO: 373	**524504**	TCTGAAACCAGCGAAATGTCACAGT	AGACTTTGGTCGCTTTACAGTGTCA
SEQ ID NO: 374	**956547**	ATAGCGGTTCTTGTTGTTCCAGGGT	TATCGCCAAGAACAACAAGGTCCCA
SEQ ID NO: 375	**1304380**	CTAACTTATTAGTTTGTGTATAGGG	GATTGAATAATCAAACACATATCCC
SEQ ID NO: 376	**592243**	AGACAGAGGTAACGATGGTAGGATC	TCTGTCTCCATTGCTACCATCCTAG
SEQ ID NO: 377	**1300444**	AAAGGTTTAGATCGAGGTTGTTGGA	TTTCCAAATCTAGCTCCAACAACCT
SEQ ID NO: 378	**1080745**	GAGACCCGATATCGTGTGTCCCGGT	CTCTGGGCTATAGCACACAGGGCCA
SEQ ID NO: 379	**876302**	AATTCTGATTAATATTTCAATGTCG	TTAAGACTAATTATAAAGTTACAGC
SEQ ID NO: 380	**1363175**	AGTACTTGAGGTAAGTTTGTATACG	TCATGAACTCCATTCAAACATATGC
SEQ ID NO: 381	**529732**	CCTCGACTCCAGACAGTTTTGTGCT	GGAGCTGAGGTCTGTCAAAACACGA
SEQ ID NO: 382	**737545**	CGAATTGCGAATACCTCTCCGTCTA	GCTTAACGCTTATGGAGAGGCAGAT
SEQ ID NO: 383	**330419**	GCGATCGGCGGCGTTGTTTCAAACT	CGCTAGCCGCCGCAACAAAGTTTGA
SEQ ID NO: 384	**1273354**	ACCCTCTCTTAAAGCTCCGAAACGT	TGGGAGAGAATTTCGAGGCTTTGCA
SEQ ID NO: 385	**109841**	ACGTGGTCCACCTACAGCATGACAC	TGCACCAGGTGGATGTCGTACTGTG

SEQ ID NO: 386	**779616**	NA	NA
SEQ ID NO: 387	**471589**	CGAATCTTCAAGGTAATTCGGTATT	GCTTAGAAGTTCCATTAAGCCATAA
SEQ ID NO: 388	**583611**	TCGAGACGAGGAACTCCTACCCGGC	AGCTCTGCTCCTTGAGGATGGGCCG
SEQ ID NO: 389	**764030**	CTTCCACACGAGACCAAATGATGGT	GAAGGTGTGCTCTGGTTTACTACCA
SEQ ID NO: 390	**1229869**	CCTTCGAGGTCTCGAGGCGCAGGCT	GGAAGCTCCAGAGCTCCGCGTCCGA
SEQ ID NO: 391	**732986**	AAATTAAGAGTAGTAAGGAGTCAGG	TTTAATTCTCATCATTCCTCAGTCC
SEQ ID NO: 392	**670590**	GTTGTTTGGATACGACCCTCGGACT	CAACAAACCTATGCTGGGAGCCTGA
SEQ ID NO: 393	**552909**	CTTGTTTACAGAGAGGAGTTTACCC	GAACAAATGTCTCTCCTCAAATGGG
SEQ ID NO: 394	**1304833**	CAGTGATAGTTAGTCCGTGGACGAC	GTCACTATCAATCAGGCACCTGCTG
SEQ ID NO: 395	**213744**	CCAAAAGGCGACACTCCTAGACGGG	GGTTTTCCGCTGTGAGGATCTGCCC
SEQ ID NO: 396	**1396643**	AATAATCGGTACAGGGTAGAGACCA	TTATTAGCCATGTCCCATCTCTGGT
SEQ ID NO: 397	**205919**	AGTTCCGGTGGTACGACAAAGAGTC	TCAAGGCCACCATGCTGTTTCTCAG
SEQ ID NO: 398	**1123629**	CCTCCAACTCGGTCGTAACACAGTG	GGAGGTTGAGCCAGCATTGTGTCAC
SEQ ID NO: 399	**1035986**	NA	NA
SEQ ID NO: 400	**739807**	GTCTGCCTCGCGAAAGGCCCTCTGT	CAGACGGAGCGCTTTCCGGGAGACA
SEQ ID NO: 401	**796279**	AGGAATAGTGACGATGTTCCCATCC	TCCTTATCACTGCTACAAGGGTAGG
SEQ ID NO: 402	**589879**	CACCAGAAACGCGTCCCGGGTACGA	GTGGTCTTTGCGCAGGGCCCATGCT
SEQ ID NO: 403	**670857**	CGTGGTTTGATTATCCTACGTTTGA	GCACCAAACTAATAGGATGCAAACT
SEQ ID NO: 404	**796378**	CTTTCTTAGACTACTCGAAGTGATC	GAAAGAATCTGATGAGCTTCACTAG
SEQ ID NO: 405	**408409**	CTGCTCGTGAATATAGTCTGTTGTC	GACGAGCACTTATATCAGACAACAG
SEQ ID NO: 406	**98186**	GTTCTAGTTACTACCATCGGGACCT	CAAGATCAATGATGGTAGCCCTGGA
SEQ ID NO: 407	**248090**	ATTCTTTAGGTCAGTCATTTGTCGG	TAAGAAATCCAGTCAGTAAACAGCC
SEQ ID NO: 408	**1163394**	ATTTAAGGTGACGACTGGAGACCCT	TAAATTCCACTGCTGACCTCTGGGA

SEQ ID NO: 409	**489115**	NA	NA
SEQ ID NO: 410	**1357488**	ACGTTAGTACTATCTACTACTTCTC	TGCAATCATGATAGATGATGAAGAG
SEQ ID NO: 411	**561041**	AGGGTGCAACCACGTCCAGTATGTC	TCCCACGTTGGTGCAGGTCATACAG
SEQ ID NO: 412	**923790**	CTTTGACGATGAAGACGCAATGCGC	GAAACTGCTACTTCTGCGTTACGCG
SEQ ID NO: 413	**735961**	NA	NA
SEQ ID NO: 414	**92269**	GGTATTTGACCACGCAGGAGCCCAA	CCATAAACTGGTGCGTCCTCGGGTT
SEQ ID NO: 415	**479508**	GATTGGGTCAAGTCCTAGTTCTTCC	CTAACCCAGTTCAGGATCAAGAAGG
SEQ ID NO: 416	**1030314**	GGAATCTATTCACTGTCGTGTGAGG	CCTTAGATAAGTGACAGCACACTCC
SEQ ID NO: 417	**414294**	GTTGTCTCAAAGGTTTAAGGGTAAG	CAACAGAGTTTCCAAATTCCCATTC
SEQ ID NO: 418	**616296**	GTTACTTTCCACTAGAGACGCCGAG	CAATGAAAGGTGATCTCTGCGGCTC
SEQ ID NO: 419	**518906**	ACTCATGTCACATAGTGAGAACCAG	TGAGTACAGTGTATCACTCTTGGTC
SEQ ID NO: 420	**370699**	AGGACCTGAAATCACCGTTTGAGTC	TCCTGGACTTTAGTGGCAAACTCAG
SEQ ID NO: 421	**628084**	GAGCATAGTGACACTCTGATGTTCG	CTCGTATCACTGTGAGACTACAAGC
SEQ ID NO: 422	**187291**	AGAAAGTCGGGTTAGGTGATTCCTC	TCTTTCAGCCCAATCCACTAAGGAG
SEQ ID NO: 423	**151601**	AGTCTTGTAGGGGTGTATTAGTTAC	TCAGAACATCCCCACATAATCAATG
SEQ ID NO: 424	**417264**	AATGAAAAGGTGAGTAGTCGGCCGC	TTACTTTTCCACTCATCAGCCGGCG
SEQ ID NO: 425	**813613**	AGTAAAGTTACGACTCAGGTGACCG	TCATTTCAATGCTGAGTCCACTGGC
SEQ ID NO: 426	**4326**	CTAATTCCCCCCGTGCCGTCTACAT	GATTAAGGGGGGCACGGCAGATGTA
SEQ ID NO: 427	**143344**	CTCGGGCGACCGACACGATTGTTAC	GAGCCCGCTGGCTGTGCTAACAATG
SEQ ID NO: 428	**1329910**	CGATTCCTCTAGTGTCGTTCTAATT	GCTAAGGAGATCACAGCAAGATTAA
SEQ ID NO: 429	**1157884**	ATGTGAGCTAGTTTTTCACGGCCTG	TACACTCGATCAAAAAGTGCCGGAC
SEQ ID NO: 430	**431431**	CCCGGAAAGACTGTGAGGGAACGTC	GGGCCTTTCTGACACTCCCTTGCAG
SEQ ID NO: 431	**440371**	GTTTCGGTAGTAAGGGTATCGGCAT	CAAAGCCATCATTCCCATAGCCGTA

SEQ ID NO: 432	**1257794**	CTTGCCCGTCCTCTCGGGACAGGGG	GAACGGGCAGGAGAGCCCTGTCCCC
SEQ ID NO: 433	**827345**	ATCATATTTTGTGTCCTCGGTGAAC	TAGTATAAAACACAGGAGCCACTTG
SEQ ID NO: 434	**1116186**	GTGGTCTGACACTCTAGTTACGGTT	CACCAGACTGTGAGATCAATGCCAA
SEQ ID NO: 435	**1248596**	GGTTCTGATGTCGAAAGAGGTCTAC	CCAAGACTACAGCTTTCTCCAGATG
SEQ ID NO: 436	**259804**	AGACGGCCGCGGACAACTTCTCGAC	TCTGCCGGCGCCTGTTGAAGAGCTG
SEQ ID NO: 437	**1101920**	ATTCTCCCTCTATGATTTTCTCTGA	TAAGAGGGAGATACTAAAAGAGACT
SEQ ID NO: 438	**972707**	CTTACCTGACTTTTCCTGTTGTGGG	GAATGGACTGAAAAGGACAACACCC
SEQ ID NO: 439	**757712**	CCGTTGATCGAGGACTTCGTATTGC	GGCAACTAGCTCCTGAAGCATAACG
SEQ ID NO: 440	**885289**	GTTATGTTTTGGACGACGTATCCAG	CAATACAAAACCTGCTGCATAGGTC
SEQ ID NO: 441	**827495**	CTACATGTTTTGTGAGGAGCCTTCG	GATGTACAAAACACTCCTCGGAAGC
SEQ ID NO: 442	**83320**	AAGTAGGGACCCGTTCCTCTCCAGC	TTCATCCCTGGGCAAGGAGAGGTCG
SEQ ID NO: 443	**931683**	ACAGAGTCCATGTCTTCAAATTACG	TGTCTCAGGTACAGAAGTTTAATGC
SEQ ID NO: 444	**489974**	TGTAGGAGCCATAGCAGGTGGTCCC	ACATCCTCGGTATCGTCCACCAGGG
SEQ ID NO: 445	**874870**	GTGGTTGGATTATTTATCCGGTTTA	CACCAACCTAATAAATAGGCCAAAT
SEQ ID NO: 446	**1381951**	CTATTCGGAGTAGGAGCCTTTTGGT	GATAAGCCTCATCCTCGGAAAACCA
SEQ ID NO: 447	**682319**	GTAGTTGATAAGAACACCGTCGGTC	CATCAACTATTCTTGTGGCAGCCAG
SEQ ID NO: 448	**84230**	ACTGGTGTACGACCCTAGACCCGAC	TGACCACATGCTGGGATCTGGGCTG
SEQ ID NO: 449	**872839**	TCTTTATACAGTTAAGCTTTAAAAA	AGAAATATGTCAATTCGAAATTTTT
SEQ ID NO: 450	**193890**	NA	NA
SEQ ID NO: 451	**87752**	GACTCTTCACACCAGGAGCTGAGGT	CTGAGAAGTGTGGTCCTCGACTCCA
SEQ ID NO: 452	**1075071**	TTCCAGTGTTCGTCGACCGGCTCTA	AAGGTCACAAGCAGCTGGCCGAGAT
SEQ ID NO: 453	**259008**	GAACCCAGCGGACCAGACACTTCGG	CTTGGGTCGCCTGGTCTGTGAAGCC
SEQ ID NO: 454	**1335417**	ATTTAATTACCACGAGACGACCCTG	TAAATTAATGGTGCTCTGCTGGGAC

SEQ ID NO: 455	**186250**	CCCATGGGTGTATGTATGTTCCGTA	GGGTACCCACATACATACAAGGCAT
SEQ ID NO: 456	**486992**	AGCGTGGGCATTGCGCAGCCCCGGA	TCGCACCCGTAACGCGTCGGGGCCT
SEQ ID NO: 457	**961015**	GTGTGACACTCTCTTCTGGACCACC	CACACTGTGAGAGAAGACCTGGTGG
SEQ ID NO: 458	**1047087**	AGTCGAAAATCCGATCTTTATCTTC	TCAGCTTTTAGGCTAGAAATAGAAG
SEQ ID NO: 459	**1383472**	CTTTTACACGTAAGGCTCGATTCCC	GAAAATGTGCATTCCGAGCTAAGGG
SEQ ID NO: 460	**957749**	GGAAATTCTTCACTAACTAGGTAAG	CCTTTAAGAAGTGATTGATCCATTC
SEQ ID NO: 461	**535491**	TCGAGTGACACGTCAGGGTCGTCGT	AGCTCACTGTGCAGTCCCAGCAGCA
SEQ ID NO: 462	**976524**	AAAGCGGACTTACTTTTTCCTGAGT	TTTCGCCTGAATGAAAAAGGACTCA
SEQ ID NO: 463	**209610**	GAATATCTCAGGGTCCGTGGTAAGG	CTTATAGAGTCCCAGGCACCATTCC
SEQ ID NO: 464	**472669**	GGTGGTAGATCAAACCTAACAAGTT	CCACCATCTAGTTTGGATTGTTCAA
SEQ ID NO: 465	**567246**	NA	NA
SEQ ID NO: 466	**1263144**	CTAACCTACCGTCTTAGACCTAGAT	GATTGGATGGCAGAATCTGGATCTA
SEQ ID NO: 467	**1358792**	ACGCCATGTCGTACTTTGGGTGGTC	TGCGGTACAGCATGAAACCCACCAG
SEQ ID NO: 468	**465107**	GGTCGGGTCCAACAGTCGCTACTAT	CCAGCCCAGGTTGTCAGCGATGATA
SEQ ID NO: 469	**608361**	GTTTTTCTCACCACTACTTGTCTCC	CAAAAAGAGTGGTGATGAACAGAGG
SEQ ID NO: 470	**938351**	GTCCTAATCCTTTTGGCGGTGTCGA	CAGGATTAGGAAAACCGCCACAGCT
SEQ ID NO: 471	**279725**	ACCGACCAACGGTCGGGTGGATCCA	TGGCTGGTTGCCAGCCCACCTAGGT
SEQ ID NO: 472	**1230816**	AGGAGTTTGTCTACTTTAGCCCGTA	TCCTCAAACAGATGAAATCGGGCAT
SEQ ID NO: 473	**1217953**	ACGACTCATCGGTCATCGGACTGCG	TGCTGAGTAGCCAGTAGCCTGACGC
SEQ ID NO: 474	**1347752**	TTGGTACCCTACAGAATCCTTCTCC	AACCATGGGATGTCTTAGGAAGAGG
SEQ ID NO: 475	**724163**	TCTCCGTGTAGAGAGGGTCAGACCC	AGAGGCACATCTCTCCCAGTCTGGG
SEQ ID NO: 476	**1083316**	GGTACCCGACCTCCAGTTTCCAGTG	CCATGGGCTGGAGGTCAAAGGTCAC
SEQ ID NO: 477	**496316**	ATGTAGGGTCATGTTTACGTAGGAA	TACATCCCAGTACAAATGCATCCTT

SEQ ID NO: 478	**424384**	TCTGTAGAAGAAGGTTCCTTGGAAC	AGACATCTTCTTCCAAGGAACCTTG
SEQ ID NO: 479	**799870**	CCGTTATTGACGTTATAGGAACAGA	GGCAATAACTGCAATATCCTTGTCT
SEQ ID NO: 480	**489918**	CTACCATGCATAAACTGGTTTCGTC	GATGGTACGTATTTGACCAAAGCAG
SEQ ID NO: 481	**949857**	ATTTCTACCTTAGCATTTTGAGTTA	TAAAGATGGAATCGTAAAACTCAAT
SEQ ID NO: 482	**390897**	CTCAGGTCAATGTTCCACCTTGATC	GAGTCCAGTTACAAGGTGGAACTAG
SEQ ID NO: 483	**509097**	CTCCATATACAACGTCCTAGGTCCT	GAGGTATATGTTGCAGGATCCAGGA
SEQ ID NO: 484	**717204**	TCCGACCCTGAGTTCACGCCGGGGT	AGGCTGGGACTCAAGTGCGGCCCCA
SEQ ID NO: 485	**830590**	TATACTTTATTTCGGGTGTCATTTC	ATATGAAATAAAGCCCACAGTAAAG
SEQ ID NO: 486	**204661**	AATTTTGGTAGGTGATTTACTGACT	TTAAAACCATCCACTAAATGACTGA
SEQ ID NO: 487	**559128**	ATTAGGAAACCGTCACTTTTGGGAC	TAATCCTTTGGCAGTGAAAACCCTG
SEQ ID NO: 488	**736325**	AGGTCGCACCGAAACTCAACGTCGC	TCCAGCGTGGCTTTGAGTTGCAGCG
SEQ ID NO: 489	**519454**	GGTCACACCGACATAACTACCTTCG	CCAGTGTGGCTGTATTGATGGAAGC
SEQ ID NO: 490	**1267806**	CTTCACCGACGTCTGAGGTATCTCC	GAAGTGGCTGCAGACTCCATAGAGG
SEQ ID NO: 491	**899544**	AAGGAAGTTGAACCCACCAGTCCCT	TTCCTTCAACTTGGGTGGTCAGGGA
SEQ ID NO: 492	**374962**	GTCCAGGTCGAAATGAGAAGGGTTC	CAGGTCCAGCTTTACTCTTCCCAAG
SEQ ID NO: 493	**1326017**	CCACAGACCTAGGTTCCAGCGGTGC	GGTGTCTGGATCCAAGGTCGCCACG
SEQ ID NO: 494	**617712**	GTTATTATTCACTGGGTCCCTCTGA	CAATAATAAGTGACCCAGGGAGACT
SEQ ID NO: 495	**918524**	ACGGTAAAGATGATAGGTTCATGAT	TGCCATTTCTACTATCCAAGTACTA
SEQ ID NO: 496	**186584**	ATTGTTAGGGTTTACACGTACGTGG	TAACAATCCCAAATGTGCATGCACC
SEQ ID NO: 497	**421864**	AAAATGAAGGGTGCGCGTAGACCGT	TTTTACTTCCCACGCGCATCTGGCA
SEQ ID NO: 498	**1004946**	ACCGAGCCACTGAGCGACCGATCCA	TGGCTCGGTGACTCGCTGGCTAGGT
SEQ ID NO: 499	**269379**	AAGTCCAGCGGTACCTTAGTCGTGT	TTCAGGTCGCCATGGAATCAGCACA
SEQ ID NO: 500	**1059852**	GAAAACTACATCTGTCCATGGAGTC	CTTTTGATGTAGACAGGTACCTCAG

SEQ ID NO: 501	**793446**	ACATACTCTAAGACTTCCGGGACCT	TGTATGAGATTCTGAAGGCCCTGGA
SEQ ID NO: 502	**1092743**	GTCGGAACTAGTCTCCTAGGGGCAA	CAGCCTTGATCAGAGGATCCCCGTT
SEQ ID NO: 503	**388412**	AATCGGGTAAACTTCTCTTCGGTGT	TTAGCCCATTTGAAGAGAAGCCACA
SEQ ID NO: 504	**323848**	CTGACAGACGTAGCTTCCGGGACTA	GACTGTCTGCATCGAAGGCCCTGAT
SEQ ID NO: 505	**308240**	CTCTTGTCGTGCTGAAGAGGTAATG	GAGAACAGCACGACTTCTCCATTAC
SEQ ID NO: 506	**888472**	ACAAGATCTTGGTCTGGAATTGACT	TGTTCTAGAACCAGACCTTAACTGA
SEQ ID NO: 507	**1209731**	CCGCTCCACGTGAAGCGCCGCAGTG	GGCGAGGTGCACTTCGCGGCGTCAC
SEQ ID NO: 508	**94242**	NA	NA
SEQ ID NO: 509	**198027**	CAACCACTGGTTGTAAGATCTAGAA	GTTGGTGACCAACATTCTAGATCTT
SEQ ID NO: 510	**166650**	ACTTCTTAGGGACGAGTGTTCCTTA	TGAAGAATCCCTGCTCACAAGGAAT
SEQ ID NO: 511	**82304**	CTAGACAGGACCCAAGTCGGTTCCC	GATCTGTCCTGGGTTCAGCCAAGGG
SEQ ID NO: 512	**770917**	ATTTAGTCGGACAGTTCTTCCTTCC	TAAATCAGCCTGTCAAGAAGGAAGG
SEQ ID NO: 513	**588199**	GTTCTACAGTACGTAACTGAAGAGA	CAAGATGTCATGCATTGACTTCTCT
SEQ ID NO: 514	**978611**	TTTTTCTACTTTGCGTAGTACTTAA	AAAAAGATGAAACGCATCATGAATT
SEQ ID NO: 515	**338536**	CTCGGAGCCGCCGTTTTTGGTCGCC	GAGCCTCGGCGGCAAAAACCAGCGG
SEQ ID NO: 516	**336569**	CCGCCCCGCCGCGCGGTTCCCGGCC	GGCGGGGCGGCGCGCCAAGGGCCGG
SEQ ID NO: 517	**1272583**	GGATATGTTTAAAGCGACCCGTCCC	CCTATACAAATTTCGCTGGGCAGGG
SEQ ID NO: 518	**592968**	GCAAGACGACGTAACGAAAACGCGT	CGTTCTGCTGCATTGCTTTTGCGCA
SEQ ID NO: 519	**203964**	TCAGGTCTAGTGGTGTCTTGGCCTT	AGTCCAGATCACCACAGAACCGGAA
SEQ ID NO: 520	**5133**	NA	NA
SEQ ID NO: 521	**278210**	ATTAGGAGACGGACAGACACAAGAG	TAATCCTCTGCCTGTCTGTGTTCTC
SEQ ID NO: 522	**529823**	CTTCTACTGCAGAAGAAACGACCGC	GAAGATGACGTCTTCTTTGCTGGCG
SEQ ID NO: 523	**1215346**	CCGTTTGGTCCTACGAACCACTGGG	GGCAAACCAGGATGCTTGGTGACCC

SEQ ID NO: 524	**193310**	CTGTAGGAGGGTAATATATCAGTTC	GACATCCTCCCATTATATAGTCAAG
SEQ ID NO: 525	**1265385**	ATTAAGGTCGTCTTCTGACTAGTGG	TAATTCCAGCAGAAGACTGATCACC
SEQ ID NO: 526	**23063**	CAGAGTGGCCACAAGAAAAAGAGTC	GTCTCACCGGTGTTCTTTTTCTCAG
SEQ ID NO: 527	**1257960**	TCCCTCGGCGTCACGGAAGCGGAGT	AGGGAGCCGCAGTGCCTTCGCCTCA
SEQ ID NO: 528	**1014295**	CTTTACTTTCCACCCTCTCGTTAGA	GAAATGAAAGGTGGGAGAGCAATCT
SEQ ID NO: 529	**872561**	GACAACAAGATTCAATTAGCCAAAC	CTGTTGTTCTAAGTTAATCGGTTTG
SEQ ID NO: 530	**545519**	ATCGGCACTCAGTAGTCGTCTGTTG	TAGCCGTGAGTCATCAGCAGACAAC
SEQ ID NO: 531	**442850**	GAAGCTGGAAGTATCCAGACGACAA	CTTCGACCTTCATAGGTCTGCTGTT
SEQ ID NO: 532	**431449**	CTTTTCAAGAGAGGAACGCGTCGGT	GAAAAGTTCTCTCCTTGCGCAGCCA
SEQ ID NO: 533	**118682**	GTCACAACGCCCGAACTCGTTCTGG	CAGTGTTGCGGGCTTGAGCAAGACC
SEQ ID NO: 534	**1255816**	AGACATCCAGTCGAACTTTAGTAGT	TCTGTAGGTCAGCTTGAAATCATCA
SEQ ID NO: 535	**843412**	TGTACAGGGTTTGAGTACGTCTGTA	ACATGTCCCAAACTCATGCAGACAT
SEQ ID NO: 536	**1030174**	AGACTGGGTTCAGCTAGGCCACTCA	TCTGACCCAAGTCGATCCGGTGAGT
SEQ ID NO: 537	**399283**	CTACCTACGGAATGAATTGGGACGA	GATGGATGCCTTACTTAACCCTGCT
SEQ ID NO: 538	**957822**	CTCTCATCTCTTTCTTGTTTCTTTA	GAGAGTAGAGAAAGAACAAAGAAAT
SEQ ID NO: 539	**909468**	NA	NA
SEQ ID NO: 540	**1147856**	CTTCAATGTTATGCGACAAGGGTAG	GAAGTTACAATACGCTGTTCCCATC
SEQ ID NO: 541	**306238**	TGTCCAAGGCTCCTTGTCGGTCGTG	ACAGGTTCCGAGGAACAGCCAGCAC
SEQ ID NO: 542	**1142832**	AAAGTTATGTTCCTCTGCCAGACCG	TTTCAATACAAGGAGACGGTCTGGC
SEQ ID NO: 543	**663711**	CCATAAGTGAACTACATAGAGGTCG	GGTATTCACTTGATGTATCTCCAGC
SEQ ID NO: 544	**77655**	AGGGAAACCCGGTCCATTAGGATAT	TCCCTTTGGGCCAGGTAATCCTATA
SEQ ID NO: 545	**1107517**	CTCATGAACTCCATCCACGCGGGTA	GAGTACTTGAGGTAGGTGCGCCCAT
SEQ ID NO: 546	**419968**	CCAGAGTCAAGGTTCGGAAGTAGAA	GGTCTCAGTTCCAAGCCTTCATCTT

SEQ ID NO: 547	**919186**	CTCCGGTAATGATCTATCAGACTAA	GAGGCCATTACTAGATAGTCTGATT
SEQ ID NO: 548	**1284902**	ATGCGACTCATAAACCGGTTCAGCG	TACGCTGAGTATTTGGCCAAGTCGC
SEQ ID NO: 549	**1020656**	AAAAGTGTTCCCAGTATTTACGGTC	TTTTCACAAGGGTCATAAATGCCAG
SEQ ID NO: 550	**175693**	ATACGACAGTATGGATTATGTGATA	TATGCTGTCATACCTAATACACTAT
SEQ ID NO: 551	**628018**	GGTGTGGAACACTACGTCTTACGGG	CCACACCTTGTGATGCAGAATGCCC
SEQ ID NO: 552	**240512**	CTAAAGGAGGTTGCACGGTGCAAGA	GATTTCCTCCAACGTGCCACGTTCT
SEQ ID NO: 553	**1318884**	CTATCAGTTCTATGAAAAGTCGGTG	GATAGTCAAGATACTTTTCAGCCAC
SEQ ID NO: 554	**449655**	GTACTGGTCTAGAAGTTATACTCCC	CATGACCAGATCTTCAATATGAGGG
SEQ ID NO: 555	**964497**	GACCCATTCTTACATTGAGGAAACC	CTGGGTAAGAATGTAACTCCTTTGG
SEQ ID NO: 556	**429149**	NA	NA
SEQ ID NO: 557	**829043**	GAAACCCTTTTTGTCCATACCGTAA	CTTTGGGAAAAACAGGTATGGCATT
SEQ ID NO: 558	**851717**	ATCCCGTTTTAACTTGACGCGTCGG	TAGGGCAAAATTGAACTGCGCAGCC
SEQ ID NO: 559	**1165878**	CTCGGTAGCGGTGATGTCCACTACT	GAGCCATCGCCACTACAGGTGATGA
SEQ ID NO: 560	**902979**	ACCAAACTTGTTTTGGGTGACGTAA	TGGTTTGAACAAAACCCACTGCATT
SEQ ID NO: 561	**200296**	CTATCGACCTGGTCCGCCGTAGACG	GATAGCTGGACCAGGCGGCATCTGC
SEQ ID NO: 562	**256336**	AGGTTCCCGGAGTTAAGAGACGAAA	TCCAAGGGCCTCAATTCTCTGCTTT
SEQ ID NO: 563	**838530**	TGAAATCTTTCCCTCCCTAACGGTC	ACTTTAGAAAGGGAGGGATTGCCAG
SEQ ID NO: 564	**692967**	CTTCCTCAGATCTTATACAAGTCGT	GAAGGAGTCTAGAATATGTTCAGCA
SEQ ID NO: 565	**656853**	CTCGGTAATGAAGTTCTAGTAGCTC	GAGCCATTACTTCAAGATCATCGAG
SEQ ID NO: 566	**113258**	AAACTCCCTCAGATAACAATTTGAT	TTTGAGGGAGTCTATTGTTAAACTA
SEQ ID NO: 567	**1019287**	GTCAATGGTTCCATACTTCAGCCAG	CAGTTACCAAGGTATGAAGTCGGTC
SEQ ID NO: 568	**1053442**	ATTAGTCACATCAGGGTCTGGACCC	TAATCAGTGTAGTCCCAGACCTGGG
SEQ ID NO: 569	**86531**	CTAGCCACACCAGTTTACCGTGACG	GATCGGTGTGGTCAAATGGCACTGC

SEQ ID NO: 570	**188520**	NA	NA
SEQ ID NO: 571	**634461**	AGTCCTACTGCACGTCTTTTTACCC	TCAGGATGACGTGCAGAAAAATGGG
SEQ ID NO: 572	**87437**	CGGTCTTCACCATCGTATACGGGTA	GCCAGAAGTGGTAGCATATGCCCAT
SEQ ID NO: 573	**594662**	ACGAGTTCGAAACGTAGGTGGTCGA	TGCTCAAGCTTTGCATCCACCAGCT
SEQ ID NO: 574	**805126**	ACCTTAAGAGACGTCCGGCGATCGT	TGGAATTCTCTGCAGGCCGCTAGCA
SEQ ID NO: 575	**248872**	ACTAAAGGTAGGTTGGTCTCTAGAA	TGATTTCCATCCAACCAGAGATCTT
SEQ ID NO: 576	**476904**	CCGTGACTGTCAAAGAAGATCTCTG	GGCACTGACAGTTTCTTCTAGAGAC
SEQ ID NO: 577	**31912**	ATCTGGGTCCCGACGACAAACAGCC	TAGACCCAGGGCTGCTGTTTGTCGG
SEQ ID NO: 578	**511005**	AAATACAGTACAAGGGTGGAGCTCC	TTTATGTCATGTTCCCACCTCGAGG
SEQ ID NO: 579	**286737**	GAGGCCGAGGCCCTAGTCCGAACCG	CTCCGGCTCCGGGATCAGGCTTGGC
SEQ ID NO: 580	**267576**	CCCAACCGGTGTCAAGCGGCGAAGT	GGGTTGGCCACAGTTCGCCGCTTCA
SEQ ID NO: 581	**855456**	GTTTCATGTTTAGGGTTCTCGGAAG	CAAAGTACAAATCCCAAGAGCCTTC
SEQ ID NO: 582	**675579**	AGTCTGAAAGAAGTCCCTAAAAATA	TCAGACTTTCTTCAGGGATTTTTAT
SEQ ID NO: 583	**1259409**	ATAAGTATTCGTCAACCCGTCTGGG	TATTCATAAGCAGTTGGGCAGACCC
SEQ ID NO: 584	**1346470**	CCAGGTATTACGACCACCCGTTTCA	GGTCCATAATGCTGGTGGGCAAAGT
SEQ ID NO: 585	**154298**	CGCACGCAGGGCTGCATAGTCTGAG	GCGTGCGTCCCGACGTATCAGACTC
SEQ ID NO: 586	**517399**	ACTCGGGTAGACATCTCTGTGTTTG	TGAGCCCATCTGTAGAGACACAAAC
SEQ ID NO: 587	**264238**	CTTTGGCGGTGTAAAAAGTCCGACT	GAAACCGCCACATTTTTCAGGCTGA
SEQ ID NO: 588	**1272893**	ATCCATTTAATTCGATCGGTAAGGA	TAGGTAAATTAAGCTAGCCATTCCT
SEQ ID NO: 589	**181578**	TTCGGCGTCTGGACGTGTCAGTCAG	AAGCCGCAGACCTGCACAGTCAGTC
SEQ ID NO: 590	**484179**	GTCTTTTACCATCTCTGGTTTTCTG	CAGAAAATGGTAGAGACCAAAAGAC
SEQ ID NO: 591	**488061**	AGTGACGCGTGCATGACCACTGGGT	TCACTGCGCACGTACTGGTGACCCA
SEQ ID NO: 592	**589367**	CCCTTACAACGGGAGTAATGACCGT	GGGAATGTTGCCCTCATTACTGGCA

SEQ ID NO: 593	**870621**	TTGTACGGTGATTCGGACTCAGCAC	AACATGCCACTAAGCCTGAGTCGTG
SEQ ID NO: 594	**1180835**	ACAAACAAGTGCTGAAGGTCGGCCA	TGTTTGTTCACGACTTCCAGCCGGT
SEQ ID NO: 595	**1373206**	CTGTCTAGGTAGTATAGGGCCGTTT	GACAGATCCATCATATCCCGGCAAA
SEQ ID NO: 596	**524353**	CACCACGTACCAGGAGTCTTTGAGG	GTGGTGCATGGTCCTCAGAAACTCC
SEQ ID NO: 597	**219007**	CTTCTTAAGGATCGGTTGTTCGTGA	GAAGAATTCCTAGCCAACAAGCACT
SEQ ID NO: 598	**470746**	ATGACATTCAAAACGGATTTAAGGT	TACTGTAAGTTTTGCCTAAATTCCA
SEQ ID NO: 599	**211198**	CTAGTAGAGTCAGGGCTACAGTACC	GATCATCTCAGTCCCGATGTCATGG
SEQ ID NO: 600	**953667**	CCATTACCTTACTCCGACTGAAGGA	GGTAATGGAATGAGGCTGACTTCCT
SEQ ID NO: 601	**748865**	TGAAGATGACGAACCCAGTGACTGT	ACTTCTACTGCTTGGGTCACTGACA
SEQ ID NO: 602	**915795**	NA	NA
SEQ ID NO: 603	**110359**	ATGTGTATTACCTGATCTGGGACGA	TACACATAATGGACTAGACCCTGCT
SEQ ID NO: 604	**366130**	CTCAAAAAACTTGGGTAGACTCGGC	GAGTTTTTTGAACCCATCTGAGCCG
SEQ ID NO: 605	**1386072**	TGGAGGAGTCGTATCTTTTGGTGTC	ACCTCCTCAGCATAGAAAACCACAG
SEQ ID NO: 606	**978623**	CGGTCTATTACTTCTACGCTGGCTT	GCCAGATAATGAAGATGCGACCGAA
SEQ ID NO: 607	**69122**	GTGAAATTCCTCGTACCGGTGTCGG	CACTTTAAGGAGCATGGCCACAGCC
SEQ ID NO: 608	**416004**	CGACACCGTAAAGGTTTGTAGGTTT	GCTGTGGCATTTCCAAACATCCAAA
SEQ ID NO: 609	**1353482**	ACCGCCGCGACTACATTGACGACTG	TGGCGGCGCTGATGTAACTGCTGAC
SEQ ID NO: 610	**803755**	ACATACCGCAGACGCTCAATAGGAG	TGTATGGCGTCTGCGAGTTATCCTC
SEQ ID NO: 611	**821403**	GTATACTCTTCTACGACGCTCTGGT	CATATGAGAAGATGCTGCGAGACCA
SEQ ID NO: 612	**522791**	CTCTGGTCCAGGACGAGATCGCCAA	GAGACCAGGTCCTGCTCTAGCGGTT
SEQ ID NO: 613	**120759**	NA	NA
SEQ ID NO: 614	**992881**	AGACTAATCTCTGAAACCGTGCACA	TCTGATTAGAGACTTTGGCACGTGT
SEQ ID NO: 615	**811744**	ATACTTAACCGACTGCTCTGGGTGG	TATGAATTGGCTGACGAGACCCACC

SEQ ID NO: 616	**832825**	CTAGTATTTTTCCAAGTCTCCCACC	GATCATAAAAAGGTTCAGAGGGTGG
SEQ ID NO: 617	**650241**	NA	NA
SEQ ID NO: 618	**301149**	CGACACACGTTGCACGTCTCAGGGT	GCTGTGTGCAACGTGCAGAGTCCCA
SEQ ID NO: 619	**119696**	CGTGGAGACCCGAGTTTCGCCAAAC	GCACCTCTGGGCTCAAAGCGGTTTG
SEQ ID NO: 620	**692006**	NA	NA
SEQ ID NO: 621	**942856**	AGGTCGGCCTTCACTGTTTTTCTGT	TCCAGCCGGAAGTGACAAAAAGACA
SEQ ID NO: 622	**874005**	TTATAAACATTATGCTATATCAATG	AATATTTGTAATACGATATAGTTAC
SEQ ID NO: 623	**659162**	CTATACTACTACTGAAGGGGTGACT	GATATGATGATGACTTCCCCACTGA
SEQ ID NO: 624	**1380776**	ATAGACTTCTGTAGTCGTGCCTGGT	TATCTGAAGACATCAGCACGGACCA
SEQ ID NO: 625	**105522**	CGCGCCGAGACCTGACCATTTACTA	GCGCGGCTCTGGACTGGTAAATGAT
SEQ ID NO: 626	**487420**	CCTAGAGGCATCTATGCGCGGTGGG	GGATCTCCGTAGATACGCGCCACCC
SEQ ID NO: 627	**1115351**	ACGTCGGACTCACTCTCGTACTCTG	TGCAGCCTGAGTGAGAGCATGAGAC
SEQ ID NO: 628	**84773**	ACTCTTCACACCAGGAGCTGAGGTT	TGAGAAGTGTGGTCCTCGACTCCAA
SEQ ID NO: 629	**926346**	GGACCTTTATGGTCTGGTACAGAAT	CCTGGAAATACCAGACCATGTCTTA
SEQ ID NO: 630	**996725**	TTTACACACCTGTTTTTGGGTACCG	AAATGTGTGGACAAAAACCCATGGC
SEQ ID NO: 631	**384566**	ACCCTCTTAAAGAAAAAGTAGGCCT	TGGGAGAATTTCTTTTTCATCCGGA
SEQ ID NO: 632	**951080**	CTAGGAGTCCTTAGCACTGTCCTGT	GATCCTCAGGAATCGTGACAGGACA
SEQ ID NO: 633	**1036449**	CATTCATTCTGCATCCGTAGAGGTA	GTAAGTAAGACGTAGGCATCTCCAT
SEQ ID NO: 634	**202393**	TGTATATTGTGGTAGGTGTGATTGT	ACATATAACACCATCCACACTAACA
SEQ ID NO: 635	**103697**	AGAAGGGACCTTTGGAGTTACGCCG	TCTTCCCTGGAAACCTCAATGCGGC
SEQ ID NO: 636	**281921**	CTTCTAAACGGTCTGCGAGTATTAC	GAAGATTTGCCAGACGCTCATAATG
SEQ ID NO: 637	**1052211**	NA	NA
SEQ ID NO: 638	**764653**	GACAAGAGCTACGAGTCCCGCGCCA	CTGTTCTCGATGCTCAGGGCGCGGT

SEQ ID NO: 639	**1299336**	GTTCTGAAGTTAGGACTTGTTGTCG	CAAGACTTCAATCCTGAACAACAGC
SEQ ID NO: 640	**1049573**	AGTCGGTACGACATCCTTCTTAGGG	TCAGCCATGCTGTAGGAAGAATCCC
SEQ ID NO: 641	**161480**	ATCATTGGGAGTGTCGAGCAACCAC	TAGTAACCCTCACAGCTCGTTGGTG
SEQ ID NO: 642	**49443**	CGGCCTCCCTGGAAGACGACTCGGT	GCCGGAGGGACCTTCTGCTGAGCCA
SEQ ID NO: 643	**1238844**	ATACTTCCAGTCAAGTCAGGGTGGT	TATGAAGGTCAGTTCAGTCCCACCA
SEQ ID NO: 644	**1082844**	GACACCCTGCTCGACTTTCTGAACA	CTGTGGGACGAGCTGAAAGACTTGT
SEQ ID NO: 645	**175504**	CGGGACGAGTGGCGTCCGGTGGTGG	GCCCTGCTCACCGCAGGCCACCACC
SEQ ID NO: 646	**488611**	CCGGAGGCATCGGTGACGTCGAAAA	GGCCTCCGTAGCCACTGCAGCTTTT
SEQ ID NO: 647	**930831**	GGAAGTAAATGTCTCACCCGTCGGG	CCTTCATTTACAGAGTGGGCAGCCC
SEQ ID NO: 648	**284919**	AGAAGTGGGCCCTCCTCGCGGTAAG	TCTTCACCCGGGAGGAGCGCCATTC
SEQ ID NO: 649	**979582**	GCAAAACGTACTTCTGTGACGTCGT	CGTTTTGCATGAAGACACTGCAGCA
SEQ ID NO: 650	**971805**	AGGTTCGACACTTCTTCGCACAGGG	TCCAAGCTGTGAAGAAGCGTGTCCC
SEQ ID NO: 651	**589223**	ATTCTACCAACGGTCCTACAGCGGA	TAAGATGGTTGCCAGGATGTCGCCT
SEQ ID NO: 652	**904162**	GGACTGGATTGTTTCGTTACCTAAG	CCTGACCTAACAAAGCAATGGATTC
SEQ ID NO: 653	**182222**	GTTATTAGTGTGGAACCTCCTTGGA	CAATAATCACACCTTGGAGGAACCT
SEQ ID NO: 654	**1057832**	AAGAGCAGTATCAGCACTCTCCACT	TTCTCGTCATAGTCGTGAGAGGTGA
SEQ ID NO: 655	**329724**	GCCAATTGCGTGAGACATGGACCTA	CGGTTAACGCACTCTGTACCTGGAT
SEQ ID NO: 656	**412388**	TTACCTTGTAATATTCGACGTCCTG	AATGGAACATTATAAGCTGCAGGAC
SEQ ID NO: 657	**473820**	AGTCGTACGCATCAAGGTTCTTCGG	TCAGCATGCGTAGTTCCAAGAAGCC
SEQ ID NO: 658	**98923**	AGTCACCTAACCTTAGATTTTACCG	TCAGTGGATTGGAATCTAAAATGGC
SEQ ID NO: 659	**198759**	CCGTGACGCTGGTGATTTTGACATT	GGCACTGCGACCACTAAAACTGTAA
SEQ ID NO: 660	**353756**	NA	NA
SEQ ID NO: 661	**895943**	GATTACCATTGATACATCGGTGTAG	CTAATGGTAACTATGTAGCCACATC

SEQ ID NO: 662	**619558**	NA	NA
SEQ ID NO: 663	**863435**	CAACCTCATTTGTGGGCGCCGTATC	GTTGGAGTAAACACCCGCGGCATAG
SEQ ID NO: 664	**1046277**	TGTTTCAATCCCAACTACCCTGGTC	ACAAAGTTAGGGTTGATGGGACCAG
SEQ ID NO: 665	**562235**	CCGGCACAACCGTTCTGCGGAGTAG	GGCCGTGTTGGCAAGACGCCTCATC
SEQ ID NO: 666	**904102**	ATCTACGTTTTGTTTGTTATCTCCG	TAGATGCAAAACAAACAATAGAGGC
SEQ ID NO: 667	**1215641**	GAGGTTCAGGTCATTATTGTTGTTC	CTCCAAGTCCAGTAATAACAACAAG
SEQ ID NO: 668	**533565**	ATGGTGGTCAGCTTCAACATCGCCC	TACCACCAGTCGAAGTTGTAGCGGG
SEQ ID NO: 669	**1242353**	ATCATAGTAAGTCTTAACGGGCCTA	TAGTATCATTCAGAATTGCCCGGAT

Table 4:

SEQ ID NO:	Code PSC	biomarker nucleotide seq target Probe	biomarker target mRNA
670	**1673**	GACCGGGTGTTGGTGCGGCTATTAC	CTGGCCCACAACCACGCCGATAATG
SEQ ID NO: 671	**6351**	AGAAGGAGCCCGACCAGGTTCTACC	TCTTCCTCGGGCTGGTCCAAGATGG
SEQ ID NO: 672	**6767**	GTGGTGGTGCCCACTGTGGTCCTAC	CACCACCACGGGTGACACCAGGATG
SEQ ID NO: 673	**6774**	CTGTGTGTGCCCTTCACAAGAGGTT	GACACACACGGGAAGTGTTCTCCAA
SEQ ID NO: 674	**9512**	CTCGGCGCCCAGCTGCGTGCGTGCA	GAGCCGCGGGTCGACGCACGCACGT
SEQ ID NO: 675	**11081**	GGAGACTCTCCCAAAGGAACCATAG	CCTCTGAGAGGGTTTCCTTGGTATC
SEQ ID NO: 676	**15750**	CTCGAGTCTCCCAGAGGTCCATTGT	GAGCTCAGAGGGTCTCCAGGTAACA
SEQ ID NO: 677	**15852**	CTTTATCCCAGAAATGGTGACCGGT	GAAATAGGGTCTTTACCACTGGCCA
SEQ ID NO: 678	**16655**	ACTATCTACTCCCAGTAGTGACGCG	TGATAGATGAGGGTCATCACTGCGC
SEQ ID NO: 679	**18080**	GTCTGCCGACCCACCGTTTATGTTT	CAGACGGCTGGGTGGCAAATACAAA
SEQ ID NO: 680	**19099**	GGACACACACCCACGTGTAAACACA	CCTGTGTGTGGGTGCACATTTGTGT
SEQ ID NO: 681	**19994**	AAGACCTACCCACGTCCGACATGGT	TTCTGGATGGGTGCAGGCTGTACCA
SEQ ID NO: 682	**21717**	GTACGCTTAGGCCAGTCTTGACCAG	CATGCGAATCCGGTCAGAACTGGTC
SEQ ID NO: 683	**27227**	GAAGGTCTTCCCGTTGTTCGCTCCA	CTTCCAGAAGGGCAACAAGCGAGGT
SEQ ID NO: 684	**27604**	GAACTTCCGTCCCTGCACTGAAAGG	CTTGAAGGCAGGGACGTGACTTTCC
SEQ ID NO: 685	**29415**	CCGAATCTCCCTCTGTGTAGAGTCT	GGCTTAGAGGGAGACACATCTCAGA
SEQ ID NO: 686	**36768**	TTACTAGACGTTCCAGAGTCAGGGG	AATGATCTGCAAGGTCTCAGTCCCC
SEQ ID NO: 687	**39687**	GATCCTTTCCACTCGCGCTAGAGCG	CTAGGAAAGGTGAGCGCGATCTCGC
SEQ ID NO: 688	**41366**	CGCCGCAGTCCACCGCCGACGGCGT	GCGGCGTCAGGTGGCGGCTGCCGCA
SEQ ID NO: 689	**42955**	CTCTCCGTGTCCAAAGTTCTGTGTA	GAGAGGCACAGGTTTCAAGACACAT

SEQ ID NO: 690	**49089**	AGTCCAGACCCTTCGTGACTGGTCG	TCAGGTCTGGGAAGCACTGACCAGC
SEQ ID NO: 691	**53130**	ATAAGAGACCCTCACTGAGTCACGG	TATTCTCTGGGAGTGACTCAGTGCC
SEQ ID NO: 692	**53947**	AGGTCCGACCCTCTCACGAGTGGAT	TCCAGGCTGGGAGAGTGCTCACCTA
SEQ ID NO: 693	**55338**	GTACACACAGGCCTTCACACACGGG	CATGTGTGTCCGGAAGTGTGTGCCC
SEQ ID NO: 694	**58129**	AGAGTTTCCCTAAAGTTCTACGACA	TCTCAAAGGGATTTCAAGATGCTGT
SEQ ID NO: 695	**58782**	GTCACGCCTCGCCTCAGCCAAGACC	CAGTGCGGAGCGGAGTCGGTTCTGG
SEQ ID NO: 696	**59746**	GGACCGGGCCTACCACGACCGAGGT	CCTGGCCCGGATGGTGCTGGCTCCA
SEQ ID NO: 697	**60909**	ACGACCAGCGCCTAGACGACATGGA	TGCTGGTCGCGGATCTGCTGTACCT
SEQ ID NO: 698	**64432**	ACTCCGTCCTCCTTTCTGGATGAAG	TGAGGCAGGAGGAAAGACCTACTTC
SEQ ID NO: 699	**65832**	GTTACGGACCTCCTCACATCGGCAG	CAATGCCTGGAGGAGTGTAGCCGTC
SEQ ID NO: 700	**72889**	GGTTCGGTGTCCTCGAATCGTGTCA	CCAAGCCACAGGAGCTTAGCACAGT
SEQ ID NO: 701	**74978**	GGTCTCCACGTCCTCGTTCAAGTGT	CCAGAGGTGCAGGAGCAAGTTCACA
SEQ ID NO: 702	**75770**	CTTCTTGTCCTAACCGGTCTACGCA	GAAGAACAGGATTGGCCAGATGCGT
SEQ ID NO: 703	**76500**	TTTAAGCTCCTACCGGATAGAGTGT	AAATTCGAGGATGGCCTATCTCACA
SEQ ID NO: 704	**89931**	AATCCTACACCACTCCTCTTCGACG	TTAGGATGTGGTGAGGAGAAGCTGC
SEQ ID NO: 705	**100396**	AGACCACACACCTTTGACTGCCACC	TCTGGTGTGTGGAAACTGACGGTGG
SEQ ID NO: 706	**125863**	AATCCGGTCCGACATCGACCAGGAG	TTAGGCCAGGCTGTAGCTGGTCCTC
SEQ ID NO: 707	**128031**	CCGCACGACTCCGACTTTTACCGTA	GGCGTGCTGAGGCTGAAAATGGCAT
SEQ ID NO: 708	**128748**	AAGAGTTCCCGTTATTTCAATCCGT	TTCTCAAGGGCAATAAAGTTAGGCA
SEQ ID NO: 709	**128806**	CGATTGGCCGTTAAACTATGGTTTC	GCTAACCGGCAATTTGATACCAAAG
SEQ ID NO: 710	**130619**	GTTTTTACCCGTCCTCGTGTCACTG	CAAAAATGGGCAGGAGCACAGTGAC

SEQ ID NO: 711	**144225**	ACAACAACACCGTCCTCGTGAGGTC	TGTTGTTGTGGCAGGAGCACTCCAG
SEQ ID NO: 712	**185975**	TCCGTCGCTGGGTGATGGAACATGA	AGGCAGCGACCCACTACCTTGTACT
SEQ ID NO: 713	**196417**	CCGGTCGTTGGTTGAGTGTTTATGA	GGCCAGCAACCAACTCACAAATACT
SEQ ID NO: 714	**223602**	ATTCCCAGGACACCACCAGAGGGCT	TAAGGGTCCTGTGGTGGTCTCCCGA
SEQ ID NO: 715	**229451**	ATCCGGTTAGGGAGTGTGTCCAATT	TAGGCCAATCCCTCACACAGGTTAA
SEQ ID NO: 716	**231682**	CGAGGACAGTAGGAACGGAGAACCC	GCTCCTGTCATCCTTGCCTCTTGGG
SEQ ID NO: 717	**242908**	TCTTGAAGAGGTCCCGCGACCGTGT	AGAACTTCTCCAGGGCGCTGGCACA
SEQ ID NO: 718	**249198**	TCAAGAACTAGGTCGCGACGAGGGT	AGTTCTTGATCCAGCGCTGCTCCCA
SEQ ID NO: 719	**252213**	GCGCGGCCCGGCTGGGCGTAGAGGG	CGCGCCGGGCCGACCCGCATCTCCC
SEQ ID NO: 720	**295450**	CCCGTCTTGCCTCGATAGGTAGGTC	GGGCAGAACGGAGCTATCCATCCAG
SEQ ID NO: 721	**306673**	GCCACTGCGGCTAGGACACTCGTAA	CGGTGACGCCGATCCTGTGAGCATT
SEQ ID NO: 722	**327300**	CTCTCAATGCGCTTTCCTCAGGAGG	GAGAGTTACGCGAAAGGAGTCCTCC
SEQ ID NO: 723	**468772**	ACGACGCAGGCAACTTCGTTGGCGG	TGCTGCGTCCGTTGAAGCAACCGCC
SEQ ID NO: 724	**529042**	GTCCGGACGGCAGATATCAGATACC	CAGGCCTGCCGTCTATAGTCTATGG
SEQ ID NO: 725	**561044**	GCACGTCACCAACCTTCGTAGTCGA	CGTGCAGTGGTTGGAAGCATCAGCT
SEQ ID NO: 726	**588830**	CGTATCTACAAACGGAGGAGAACCT	GCATAGATGTTTGCCTCCTCTTGGA
SEQ ID NO: 727	**604042**	AACTACTTCCACAGTGTTGCCGTTC	TTGATGAAGGTGTCACAACGGCAAG
SEQ ID NO: 728	**604967**	GTCCATCTCCACACTGGGGTCCTGA	CAGGTAGAGGTGTGACCCCAGGACT
SEQ ID NO: 729	**616095**	GTCCTACCACCACTAGTTGCACGGG	CAGGATGGTGGTGATCAACGTGCCC
SEQ ID NO: 730	**622161**	GACCCTCTGACACCCACTAGGAGGT	CTGGGAGACTGTGGGTGATCCTCCA
SEQ ID NO: 731	**622702**	GATAACCCACACAACATTTGTCTTC	CTATTGGGTGTGTTGTAAACAGAAG

SEQ ID NO: 732	**639146**	ACAAACAGACACGAAGATTTTCCAG	TGTTTGTCTGTGCTTCTAAAAGGTC
SEQ ID NO: 733	**669436**	CGGTCCGTCGGATATCCTTATCATT	GCCAGGCAGCCTATAGGAATAGTAA
SEQ ID NO: 734	**708420**	CGATCGGGTGAGGTGTCTAAAAACT	GCTAGCCCACTCCACAGATTTTTGA
SEQ ID NO: 735	**751418**	NA	NA
SEQ ID NO: 736	**752527**	ATTCCCACGATACGCGAGTCAGAGG	TAAGGGTGCTATGCGCTCAGTCTCC
SEQ ID NO: 737	**772367**	GCAAAGGGACACACTCCACCACGGT	CGTTTCCCTGTGTGAGGTGGTGCCA
SEQ ID NO: 738	**883312**	GTTCTCTGTACGTATTGTGCAAAAT	CAAGAGACATGCATAACACGTTTTA
SEQ ID NO: 739	**906039**	GTAAATAACTTGTTCGATCGGACAA	CATTTATTGAACAAGCTAGCCTGTT
SEQ ID NO: 740	**939909**	ACCTAGAGTCCTTTCGACGGTCGTA	TGGATCTCAGGAAAGCTGCCAGCAT
SEQ ID NO: 741	**1020364**	AGAGACGGGTTCCACTCCCTTGAGT	TCTCTGCCCAAGGTGAGGGAACTCA
SEQ ID NO: 742	**1059015**	CGACGTACAAGTATCAGTAGGTGGA	GCTGCATGTTCATAGTCATCCACCT
SEQ ID NO: 743	**1072725**	AAGAATTTCGTGGTGTAGTTGGAAT	TTCTTAAAGCACCACATCAACCTTA
SEQ ID NO: 744	**1099142**	ACATAGTGTCCTCTTTGGTCGTCCC	TGTATCACAGGAGAAACCAGCAGGG
SEQ ID NO: 745	**1331569**	CCCGGTGTCTAGTCCACGAAGACGT	GGGCCACAGATCAGGTGCTTCTGCA
SEQ ID NO: 746	**1354360**	GGAAGAGGTCTACTGCACCGACAGT	CCTTCTCCAGATGACGTGGCTGTCA
SEQ ID NO: 747	**3786**	ACCCGGTATGCCATCATAAATCAAC	TGGGCCATACGGTAGTATTTAGTTG
SEQ ID NO: 748	**4793**	NA	NA
SEQ ID NO: 749	**9787**	GGGACAACGCCCACTCCGCCGACGA	CCCTGTTGCGGGTGAGGCGGCTGCT
SEQ ID NO: 750	**9950**	GAAGCACGTCGCCCAGTCAATTAGA	CTTCGTGCAGCGGGTCAGTTAATCT
SEQ ID NO: 751	**12347**	CTGACCGACCCAAGAGTCAACCTCG	GACTGGCTGGGTTCTCAGTTGGAGC
SEQ ID NO: 752	**13624**	ATCGGAACCCATGTGTGTGTAGGAA	TAGCCTTGGGTACACACACATCCTT

SEQ ID NO: 753	**14494**	GCCGGGACCCAGACCAACCACTTCG	CGGCCCTGGGTCTGGTTGGTGAAGC
SEQ ID NO: 754	**15728**	GTGGTTTCCCAGCACCGACGACTGT	CACCAAAGGGTCGTGGCTGCTGACA
SEQ ID NO: 755	**15827**	AGTCTCCGTCCCAGTACCTCCAAGG	TCAGAGGCAGGGTCATGGAGGTTCC
SEQ ID NO: 756	**16875**	GAGGGGCCCACACTCGTACCATCTT	CTCCCCGGGTGTGAGCATGGTAGAA
SEQ ID NO: 757	**18211**	NA	NA
SEQ ID NO: 758	**18634**	AGGGGTCCCACTGCCGACGACACTT	TCCCCAGGGTGACGGCTGCTGTGAA
SEQ ID NO: 759	**19902**	ACCACAACCCACGTAGGACGCGGTG	TGGTGTTGGGTGCATCCTGCGCCAC
SEQ ID NO: 760	**21086**	GCGCCGCGCGCCAGCTGCCAGCCAG	CGCGGCGCGCGGTCGACGGTCGGTC
SEQ ID NO: 761	**21136**	ATCCGCCGCCAAGCAGGGCGAGGTA	TAGGCGGCGGTTCGTCCCGCTCCAT
SEQ ID NO: 762	**21187**	ACCACTACTGCCAGGGTGATCCTTG	TGGTGATGACGGTCCCACTAGGAAC
SEQ ID NO: 763	**21644**	NA	NA
SEQ ID NO: 764	**22341**	CATACGCCGCCAGCCGGATGGGGGC	GTATGCGGCGGTCGGCCTACCCCCG
SEQ ID NO: 765	**22349**	GGCACGCCGCCATCGACAAGAAGAG	CCGTGCGGCGGTAGCTGTTCTTCTC
SEQ ID NO: 766	**22657**	ATACGCCACGCCACATGCAAGACGG	TATGCGGTGCGGTGTACGTTCTGCC
SEQ ID NO: 767	**22823**	GGATCGCCGCCACTGAAAAAACCGC	CCTAGCGGCGGTGACTTTTTTGGCG
SEQ ID NO: 768	**22883**	CGCGCGCCGCCAGCTTGCACCACCC	GCGCGCGGCGGTCGAACGTGGTGGG
SEQ ID NO: 769	**22897**	ATGGACACGCCAACACGCCGCAAGA	TACCTGTGCGGTTGTGCGGCGTTCT
SEQ ID NO: 770	**22899**	AGAGACACCGCCACCGAATCGTGAG	TCTCTGTGGCGGTGGCTTAGCACTC
SEQ ID NO: 771	**22984**	TAAAGGGCCACACACCGCACTGTAC	ATTTCCCGGTGTGTGGCGTGACATG
SEQ ID NO: 772	**23224**	GTGTGGTGTGCCACCGGAAAAAGTC	CACACCACACGGTGGCCTTTTTCAG
SEQ ID NO: 773	**23356**	GGTTAATGCCACCACCGACAACATG	CCAATTACGGTGGTGGCTGTTGTAC

SEQ ID NO: 774	**23644**	GACCACCACGCCACGACGAGTAGTT	CTGGTGGTGCGGTGCTGCTCATCAA
SEQ ID NO: 775	**23680**	TCGTGCACGGCCACACTCGGCAAGG	AGCACGTGCCGGTGTGAGCCGTTCC
SEQ ID NO: 776	**23821**	AGTACCGACCGCCACTCTAGAAGGT	TCATGGCTGGCGGTGAGATCTTCCA
SEQ ID NO: 777	**23994**	AGGGTTCGCCACACCACACCTGGAG	TCCCAAGCGGTGTGGTGTGGACCTC
SEQ ID NO: 778	**24164**	GTCGTGTGTCGTGCCACTCAGCGTA	CAGCACACAGCACGGTGAGTCGCAT
SEQ ID NO: 779	**24218**	GAGTTACTCCGCCACGACGTCAAAG	CTCAATGAGGCGGTGCTGCAGTTTC
SEQ ID NO: 780	**24329**	GAAACCGTTCCCGATGCCACCTCAA	CTTTGGCAAGGGCTACGGTGGAGTT
SEQ ID NO: 781	**28089**	CGTCGACTCGTTCCCGTTCGAAAGC	GCAGCTGAGCAAGGGCAAGCTTTCG
SEQ ID NO: 782	**28642**	TCCTCTGCTCCCTCGGGTTGTACAA	AGGAGACGAGGGAGCCCAACATGTT
SEQ ID NO: 783	**28683**	TGGGTCACTCCCGTACACCGACGTG	ACCCAGTGAGGGCATGTGGCTGCAC
SEQ ID NO: 784	**29743**	ATAGTGGGTCCCTTATGCATTGGTC	TATCACCCAGGGAATACGTAACCAG
SEQ ID NO: 785	**29858**	NA	NA
SEQ ID NO: 786	**29884**	AAAGAGACTCCCACGACCACGGTAG	TTTCTCTGAGGGTGCTGGTGCCATC
SEQ ID NO: 787	**30745**	GTCCCACGGTCCCAAGAACATGAAA	CAGGGTGCCAGGGTTCTTGTACTTT
SEQ ID NO: 788	**31206**	TCTGCCTGTCCCACGCACGGGAGTA	AGACGGACAGGGTGCGTGCCCTCAT
SEQ ID NO: 789	**32495**	GAACCCGCGTCCCACGAGTCGAAGA	CTTGGGCGCAGGGTGCTCAGCTTCT
SEQ ID NO: 790	**32504**	GAATTCCGTCCCGTAGACCTCGATA	CTTAAGGCAGGGCATCTGGAGCTAT
SEQ ID NO: 791	**33863**	GTGTGTCCGACGTCCCGTTCTCCGA	CACACAGGCTGCAGGGCAAGAGGCT
SEQ ID NO: 792	**38185**	TCGACGGACCTCCAGGGCGTCATCT	AGCTGCCTGGAGGTCCCGCAGTAGA
SEQ ID NO: 793	**38997**	ACCCAGACTCCAACGAGGTGTAGAC	TGGGTCTGAGGTTGCTCCACATCTG
SEQ ID NO: 794	**39417**	NA	NA

SEQ ID NO: 795	**39990**	GGTCCCGACTCCACTAAGACGATGG	CCAGGGCTGAGGTGATTCTGCTACC
SEQ ID NO: 796	**40354**	GTCACAGTGTTCCACACCGAACTCG	CAGTGTCACAAGGTGTGGCTTGAGC
SEQ ID NO: 797	**40681**	GCTGTCTATATCCACACACACATGT	CGACAGATATAGGTGTGTGTGTACA
SEQ ID NO: 798	**40972**	CTCCGTCGTATCCACAGGTGTTCGA	GAGGCAGCATAGGTGTCCACAAGCT
SEQ ID NO: 799	**41363**	NA	NA
SEQ ID NO: 800	**41556**	AGGACGCTGTCCAAGTCCATCCGGC	TCCTGCGACAGGTTCAGGTAGGCCG
SEQ ID NO: 801	**41747**	AACACGCGTCTCCACCACGGCCCGG	TTGTGCGCAGAGGTGGTGCCGGGCC
SEQ ID NO: 802	**41778**	AGTCGAGGCTCCACTACGGTCTCGG	TCAGCTCCGAGGTGATGCCAGAGCC
SEQ ID NO: 803	**42086**	ACGAAGAAGTCCAGGCGCAAGAGCG	TGCTTCTTCAGGTCCGCGTTCTCGC
SEQ ID NO: 804	**42700**	CCCACGGTCCAGGAGTTTATTCTTC	GGGTGCCAGGTCCTCAAATAAGAAG
SEQ ID NO: 805	**43130**	TGTCCGCCGTCCACCCACGAAAGGA	ACAGGCGGCAGGTGGGTGCTTTCCT
SEQ ID NO: 806	**44103**	TGGCGCACGTCCAGCCGAGCGCAGA	ACCGCGTGCAGGTCGGCTCGCGTCT
SEQ ID NO: 807	**44290**	GCGCCGCAGTCCACCGCCGACGGCG	CGCGGCGTCAGGTGGCGGCTGCCGC
SEQ ID NO: 808	**44292**	ACGCCACCGTCCACAGTGTCGGTTT	TGCGGTGGCAGGTGTCACAGCCAAA
SEQ ID NO: 809	**44883**	CGTCCGAACGTCCACAGGGCACGGG	GCAGGCTTGCAGGTGTCCCGTGCCC
SEQ ID NO: 810	**45156**	ACAGCGCCGTCCATGTGGACGTCCA	TGTCGCGGCAGGTACACCTGCAGGT
SEQ ID NO: 811	**45276**	CTGTACCTCGTCCATCAGTGTCGGT	GACATGGAGCAGGTAGTCACAGCCA
SEQ ID NO: 812	**45312**	TCTGACGTCCGTCCAGTCTCCAGGG	AGACTGCAGGCAGGTCAGAGGTCCC
SEQ ID NO: 813	**45406**	CACACACACGTCCATGTATATGTGT	GTGTGTGTGCAGGTACATATACACA
SEQ ID NO: 814	**45583**	ATCGAAGACGTCCACCACGACCTAG	TAGCTTCTGCAGGTGGTGCTGGATC
SEQ ID NO: 815	**45684**	GTGCTTCCGTCCACCATATTTAGTG	CACGAAGGCAGGTGGTATAAATCAC

SEQ ID NO: 816	**45798**	ACGGTTACACGTCCACACACAGGTC	TGCCAATGTGCAGGTGTGTGTCCAG
SEQ ID NO: 817	**48085**	ACCACCGACCCTTTTATTCCTAGGG	TGGTGGCTGGGAAAATAAGGATCCC
SEQ ID NO: 818	**49278**	CGACCCGACCCTTAAGTATCTGTGG	GCTGGGCTGGGAATTCATAGACACC
SEQ ID NO: 819	**51312**	ACCCTCGACCCTGAGCGTTTGGAGT	TGGGAGCTGGGACTCGCAAACCTCA
SEQ ID NO: 820	**52044**	AGTCTCCGACCCTCGCTTCGTCACG	TCAGAGGCTGGGAGCGAAGCAGTGC
SEQ ID NO: 821	**55102**	TGTGTGGTGCCTCTTCTAAACCTAT	ACACACCACGGAGAAGATTTGGATA
SEQ ID NO: 822	**55790**	GTGTGTGTGTGCCTTACACTCTCCC	CACACACACACGGAATGTGAGAGGG
SEQ ID NO: 823	**55963**	AAAGGGCCTGAACGACGACCGACCG	TTTCCCGGACTTGCTGCTGGCTGGC
SEQ ID NO: 824	**56155**	ATGTCGTGGCCTGTGTTTCAATACG	TACAGCACCGGACACAAAGTTATGC
SEQ ID NO: 825	**57291**	CGAGACCGCGCCTCTCTTAGCCTCA	GCTCTGGCGCGGAGAGAATCGGAGT
SEQ ID NO: 826	**57662**	ACCGACCACGCCTGTAGTCTTGTAT	TGGCTGGTGCGGACATCAGAACATA
SEQ ID NO: 827	**59621**	ACGTTCCTACCCTACAAGTCTTCTT	TGCAAGGATGGGATGTTCAGAAGAA
SEQ ID NO: 828	**65472**	ATCCGTCCTCCTGTTTAAGTTCACT	TAGGCAGGAGGACAAATTCAAGTGA
SEQ ID NO: 829	**65603**	CATTTATCCTGTGGTGTACGTATTC	GTAAATAGGACACCACATGCATAAG
SEQ ID NO: 830	**67226**	ACGCCACACTCCTCTACTTAAGGGT	TGCGGTGTGAGGAGATGAATTCCCA
SEQ ID NO: 831	**70445**	GTGTGACCCGTCCTCTCCCAATTTG	CACACTGGGCAGGAGAGGGTTAAAC
SEQ ID NO: 832	**72360**	CGACGAGGGTCCTCCGTCCGTTTAT	GCTGCTCCCAGGAGGCAGGCAAATA
SEQ ID NO: 833	**73820**	AGATTGGTCCTAACGGAGTCACAGG	TCTAACCAGGATTGCCTCAGTGTCC
SEQ ID NO: 834	**73862**	ATCTCACCGTCCTCGTGTCGGATTC	TAGAGTGGCAGGAGCACAGCCTAAG
SEQ ID NO: 835	**74172**	TCAGTGACCGTCCTCGTTGGAAGTG	AGTCACTGGCAGGAGCAACCTTCAC
SEQ ID NO: 836	**74611**	ATTCCCGTCCTCAGGGTACTACTCT	TAAGGGCAGGAGTCCCATGATGAGA

SEQ ID NO: 837	**76275**	AACTAGAATCCTACGGCCCACGGGT	TTGATCTTAGGATGCCGGGTGCCCA
SEQ ID NO: 838	**78024**	ATAATTCACCACGACCATTTTTCTC	TATTAAGTGGTGCTGGTAAAAAGAG
SEQ ID NO: 839	**79015**	CACACACACACCCAGATGTATGTGT	GTGTGTGTGTGGGTCTACATACACA
SEQ ID NO: 840	**80190**	TTACCGTCGTCACCCATTGCGAAGG	AATGGCAGCAGTGGGTAACGCTTCC
SEQ ID NO: 841	**80215**	CACGCACACACCCACCCACGCGTAA	GTGCGTGTGTGGGTGGGTGCGCATT
SEQ ID NO: 842	**80721**	GGTCCTACGTCACCCGATAATCGGT	CCAGGATGCAGTGGGCTATTAGCCA
SEQ ID NO: 843	**81088**	CGCGGACACACCCACGTGTAAACAC	GCGCCTGTGTGGGTGCACATTTGTG
SEQ ID NO: 844	**81224**	AACACACACACCCACGTGTAAACAC	TTGTGTGTGTGGGTGCACATTTGTG
SEQ ID NO: 845	**81235**	GACACACACACACCCAGATGTATGT	CTGTGTGTGTGTGGGTCTACATACA
SEQ ID NO: 846	**81241**	CACACAGACACCCAGACGCGTGTAT	GTGTGTCTGTGGGTCTGCGCACATA
SEQ ID NO: 847	**81345**	TCCCACCGACCACGAGCATAGATGT	AGGGTGGCTGGTGCTCGTATCTACA
SEQ ID NO: 848	**81397**	AACTAACACACCCACGGGGTAAAGA	TTGATTGTGTGGGTGCCCCATTTCT
SEQ ID NO: 849	**82134**	TGGGTGACACCCGACGTACGACACG	ACCCACTGTGGGCTGCATGCTGTGC
SEQ ID NO: 850	**82415**	CCACGGGACCCACAGTCGAGGTCAT	GGTGCCCTGGGTGTCAGCTCCAGTA
SEQ ID NO: 851	**82422**	GCCTTGGACCCACGTAAAGTAAGTA	CGGAACCTGGGTGCATTTCATTCAT
SEQ ID NO: 852	**82975**	TGAGTCCAGACCCAACCGATGTTTC	ACTCAGGTCTGGGTTGGCTACAAAG
SEQ ID NO: 853	**83511**	TACGACCCCGACCCACAAGGCGGGA	ATGCTGGGGCTGGGTGTTCCGCCCT
SEQ ID NO: 854	**83611**	ACCCTACCGACCCAAAAGATCAGAG	TGGGATGGCTGGGTTTTCTAGTCTC
SEQ ID NO: 855	**84490**	ATGTCTGATTCATGTATTTGAAGGT	TACAGACTAAGTACATAAACTTCCA
SEQ ID NO: 856	**84697**	ACGTTCCCGACCCTACTTACGAAGA	TGCAAGGGCTGGGATGAATGCTTCT
SEQ ID NO: 857	**85924**	ATGCCGAACCAAGACGGACCTGCGT	TACGGCTTGGTTCTGCCTGGACGCA

SEQ ID NO: 858	**86540**	AGTAGTCACCACCAACATATGGTTG	TCATCAGTGGTGGTTGTATACCAAC
SEQ ID NO: 859	**88139**	GTTAAAAACCACCACCGCTGTTAGG	CAATTTTTGGTGGTGGCGACAATCC
SEQ ID NO: 860	**88266**	AGTCCGACGACACCATGGTCCCGTA	TCAGGCTGCTGTGGTACCAGGGCAT
SEQ ID NO: 861	**89352**	GTCTTCGTCACACCAGAGCGTTCAA	CAGAAGCAGTGTGGTCTCGCAAGTT
SEQ ID NO: 862	**89494**	GTTCCGCAACCACCGCCAACGTCGC	CAAGGCGTTGGTGGCGGTTGCAGCG
SEQ ID NO: 863	**89548**	TCGTCGGCACACCACATCGAGTCGT	AGCAGCCGTGTGGTGTAGCTCAGCA
SEQ ID NO: 864	**89683**	TTGAACCACCACAGGCACTCGGAGC	AACTTGGTGGTGTCCGTGAGCCTCG
SEQ ID NO: 865	**89735**	AAAAGAACCACTCACTACCAGTAGG	TTTTCTTGGTGAGTGATGGTCATCC
SEQ ID NO: 866	**89893**	GAACACACACACCACGTCGAGGCGG	CTTGTGTGTGTGGTGCAGCTCCGCC
SEQ ID NO: 867	**90734**	GTAAGGACACACCACCTACCGTTGT	CATTCCTGTGTGGTGGATGGCAACA
SEQ ID NO: 868	**91845**	NA	NA
SEQ ID NO: 869	**91990**	CGTCTCCCGACCAATGTCTTCGGGG	GCAGAGGGCTGGTTACAGAAGCCCC
SEQ ID NO: 870	**92992**	NA	NA
SEQ ID NO: 871	**93730**	ACGTTACCCGACCACACTTGTCAAG	TGCAATGGGCTGGTGTGAACAGTTC
SEQ ID NO: 872	**94043**	CCTAGTCGACGACCAGACACCAGGT	GGATCAGCTGCTGGTCTGTGGTCCA
SEQ ID NO: 873	**94156**	GTGTCCTTCGACCACTGCCGCTACT	CACAGGAAGCTGGTGACGGCGATGA
SEQ ID NO: 874	**94159**	CGTCACCCGACCACGGTGGGGCTTG	GCAGTGGGCTGGTGCCACCCCGAAC
SEQ ID NO: 875	**94163**	TTAGTCCCGACCACACTATACAGGT	AATCAGGGCTGGTGTGATATGTCCA
SEQ ID NO: 876	**94185**	GGAGACACAGACCACACACCTGGGG	CCTCTGTGTCTGGTGTGTGGACCCC
SEQ ID NO: 877	**94187**	AGGTATCAGACCACACACACGTCTT	TCCATAGTCTGGTGTGTGTGCAGAA
SEQ ID NO: 878	**94205**	ATTTCCGACCACGAGTCCTTTGGAG	TAAAGGCTGGTGCTCAGGAAACCTC

SEQ ID NO: 879	**94261**	ACAACAGAGACCACCACGACGTACA	TGTTGTCTCTGGTGGTGCTGCATGT
SEQ ID NO: 880	**94327**	GTTCCACCTACCCAACAACGGGTGA	CAAGGTGGATGGGTTGTTGCCCACT
SEQ ID NO: 881	**94333**	GAAGCCCTACCCAACACTCCAGAGT	CTTCGGGATGGGTTGTGAGGTCTCA
SEQ ID NO: 882	**94878**	CGCTCCCGACCACGAAGACGGGTAG	GCGAGGGCTGGTGCTTCTGCCCATC
SEQ ID NO: 883	**94982**	TGATTCTACGACCACCACACGGTGT	ACTAAGATGCTGGTGGTGTGCCACA
SEQ ID NO: 884	**95220**	AGATGACACGACCACACCGCAGTAT	TCTACTGTGCTGGTGTGGCGTCATA
SEQ ID NO: 885	**95266**	AGTTCCATACCCACACGACACGAGG	TCAAGGTATGGGTGTGCTGTGCTCC
SEQ ID NO: 886	**95467**	ACACACATTACCACACACATCACCA	TGTGTGTAATGGTGTGTGTAGTGGT
SEQ ID NO: 887	**95502**	GGTACCTACCTACCCGACTGAGCAT	CCATGGATGGATGGGCTGACTCGTA
SEQ ID NO: 888	**95786**	CTCGACACACGTACCCGAAGAGGGG	GAGCTGTGTGCATGGGCTTCTCCCC
SEQ ID NO: 889	**97255**	AATCATTACCATCCGACGACTACCG	TTAGTAATGGTAGGCTGCTGATGGC
SEQ ID NO: 890	**100876**	CGTCACACTCACCTTTTCATTACTT	GCAGTGTGAGTGGAAAAGTAATGAA
SEQ ID NO: 891	**101169**	ACACACGTCCACCTGCAAGGAAAGT	TGTGTGCAGGTGGACGTTCCTTTCA
SEQ ID NO: 892	**101216**	AGGTCCCACCTGACGACGCACATGA	TCCAGGGTGGACTGCTGCGTGTACT
SEQ ID NO: 893	**101373**	CGATCGCTCACCTTTCGTCCGGAGA	GCTAGCGAGTGGAAAGCAGGCCTCT
SEQ ID NO: 894	**102481**	ATGTCACCACCTGTCCGTAGGTTCG	TACAGTGGTGGACAGGCATCCAAGC
SEQ ID NO: 895	**103824**	GTGTGTCCTCACCTCACCTGCAGGA	CACACAGGAGTGGAGTGGACGTCCT
SEQ ID NO: 896	**105726**	GTTATCGTCTGACCTGTCCTTCTAT	CAATAGCAGACTGGACAGGAAGATA
SEQ ID NO: 897	**106034**	CGGACCCGACCTGGATACACAAGAT	GCCTGGGCTGGACCTATGTGTTCTA
SEQ ID NO: 898	**106049**	GTCACACTCGTAGACCTGGATCCCG	CAGTGTGAGCATCTGGACCTAGGGC
SEQ ID NO: 899	**106772**	CCGACCACGACCTGAAGTAGTTGCG	GGCTGGTGCTGGACTTCATCAACGC

SEQ ID NO: 900	**108420**	GACCGTCCAACCTACGAACTACTTT	CTGGCAGGTTGGATGCTTGATGAAA
SEQ ID NO: 901	**109037**	GGCCACCGACCTAAGTGTTTCTGAA	CCGGTGGCTGGATTCACAAAGACTT
SEQ ID NO: 902	**110082**	ACATCCGACGACCTAGCGTTCACGT	TGTAGGCTGCTGGATCGCAAGTGCA
SEQ ID NO: 903	**112010**	AGAACGGAACCGCCGGGTCGGGCGA	TCTTGCCTTGGCGGCCCAGCCCGCT
SEQ ID NO: 904	**112043**	CGTCTCTACCTACCTAAGCTACGTT	GCAGAGATGGATGGATTCGATGCAA
SEQ ID NO: 905	**112299**	CCCTACCTACCTGAGGCTCGTGGGA	GGGATGGATGGACTCCGAGCACCCT
SEQ ID NO: 906	**112405**	TGATGAGTCGTACCTTTGTTCTACT	ACTACTCAGCATGGAAACAAGATGA
SEQ ID NO: 907	**112471**	TCACCACCACCGGACTGAAGAGTAC	AGTGGTGGTGGCCTGACTTCTCATG
SEQ ID NO: 908	**112726**	CACGCCGCCCGGGCATTCAAGCGGA	GTGCGGCGGGCCCGTAAGTTCGCCT
SEQ ID NO: 909	**113835**	TGACCGTCCACCGTGTATCCACTGG	ACTGGCAGGTGGCACATAGGTGACC
SEQ ID NO: 910	**113889**	NA	NA
SEQ ID NO: 911	**114267**	AGAACCGACCCGGAGAACCGTCTTT	TCTTGGCTGGGCCTCTTGGCAGAAA
SEQ ID NO: 912	**114596**	ACCCTGTCCCGGAAGGCTTACCACA	TGGGACAGGGCCTTCCGAATGGTGT
SEQ ID NO: 913	**115476**	AGAACCACCCGCACGGACGTAGTGA	TCTTGGTGGGCGTGCCTGCATCACT
SEQ ID NO: 914	**115692**	AGCAGCCGCCGCTCGTCTAGGACTT	TCGTCGGCGGCGAGCAGATCCTGAA
SEQ ID NO: 915	**116207**	CCGCCGGCCGCCTGCCGCAGCCCCT	GGCGGCCGGCGGACGGCGTCGGGGA
SEQ ID NO: 916	**116232**	AAGTTCACGCCGCACACGCGGTTCG	TTCAAGTGCGGCGTGTGCGCCAAGC
SEQ ID NO: 917	**116645**	GTCCAAGACCCGCAAGAGGTCCCGG	CAGGTTCTGGGCGTTCTCCAGGGCC
SEQ ID NO: 918	**116784**	GAATCCCACCGACCACGAGCATAGA	CTTAGGGTGGCTGGTGCTCGTATCT
SEQ ID NO: 919	**116846**	NA	NA
SEQ ID NO: 920	**116887**	TTGACACCGTCCGTCCCGGAACAGG	AACTGTGGCAGGCAGGGCCTTGTCC

SEQ ID NO: 921	**117048**	CTACGGAGGCCGGTTCTTCAGAAAC	GATGCCTCCGGCCAAGAAGTCTTTG
SEQ ID NO: 922	**117289**	ATCCACAGCCGCAGGACGTCCACCG	TAGGTGTCGGCGTCCTGCAGGTGGC
SEQ ID NO: 923	**118097**	GTAAAGTGCCCGACGCCCACCGAAA	CATTTCACGGGCTGCGGGTGGCTTT
SEQ ID NO: 924	**118248**	CCTACGACCCCGACCCACAAGGCGG	GGATGCTGGGGCTGGGTGTTCCGCC
SEQ ID NO: 925	**118436**	ATACTCCGACCCGATTTATTAGACG	TATGAGGCTGGGCTAAATAATCTGC
SEQ ID NO: 926	**118920**	CTGCCGACCCGAACTATTGTGTGAG	GACGGCTGGGCTTGATAACACACTC
SEQ ID NO: 927	**119438**	GCCACGGCCCGAGCGCCGCAGGGGC	CGGTGCCGGGCTCGCGGCGTCCCCG
SEQ ID NO: 928	**120030**	TCCCGACACCCGAGACGTCGGAGGT	AGGGCTGTGGGCTCTGCAGCCTCCA
SEQ ID NO: 929	**120219**	GGACGACAACCCGACGCAAAGGATC	CCTGCTGTTGGGCTGCGTTTCCTAG
SEQ ID NO: 930	**120608**	CGACTCGTTCCCGACTCGTTTGTTT	GCTGAGCAAGGGCTGAGCAAACAAA
SEQ ID NO: 931	**120722**	AAATAACCCGACCACGTTTTCGTTA	TTTATTGGGCTGGTGCAAAAGCAAT
SEQ ID NO: 932	**120737**	AACTAAGACCCGACCACGTTAAAGA	TTGATTCTGGGCTGGTGCAATTTCT
SEQ ID NO: 933	**121874**	AACCACCACCGCTGTTAGGGTTGTT	TTGGTGGTGGCGACAATCCCAACAA
SEQ ID NO: 934	**122456**	GAAATAAGCCGACACACCGTCACCG	CTTTATTCGGCTGTGTGGCAGTGGC
SEQ ID NO: 935	**123760**	CAAAGATCCGGTTAGGGAGTGTGTC	GTTTCTAGGCCAATCCCTCACACAG
SEQ ID NO: 936	**123895**	CCGCCGTCTCCGGTTCATGAGATCG	GGCGGCAGAGGCCAAGTACTCTAGC
SEQ ID NO: 937	**124971**	GTTTCCATCCGCACGACACGACGAG	CAAAGGTAGGCGTGCTGTGCTGCTC
SEQ ID NO: 938	**125063**	TTTTGGTCCGCGCACGCCGCTGCAG	AAAACCAGGCGCGTGCGGCGACGTC
SEQ ID NO: 939	**126402**	GTGTTCTCCTCCGAAGGCCTCATCG	CACAAGAGGAGGCTTCCGGAGTAGC
SEQ ID NO: 940	**126524**	ACAGGCCTCCGAGGCACGACGACGG	TGTCCGGAGGCTCCGTGCTGCTGCC
SEQ ID NO: 941	**126959**	TCGTTCCATCCGACCGAGAGGTTGT	AGCAAGGTAGGCTGGCTCTCCAACA

SEQ ID NO: 942	**126992**	GTGGTGTGTGCCGTCAACTCCACCA	CACCACACACGGCAGTTGAGGTGGT
SEQ ID NO: 943	**127550**	CGTTTCCGTCCGATTTGAACCAGAT	GCAAAGGCAGGCTAAACTTGGTCTA
SEQ ID NO: 944	**128152**	ATTTTCTCCGACGACAAGTTAGGGT	TAAAAGAGGCTGCTGTTCAATCCCA
SEQ ID NO: 945	**128274**	GTCCGCACGACTCCGACTTTTACCG	CAGGCGTGCTGAGGCTGAAAATGGC
SEQ ID NO: 946	**128869**	AGGACCGACCCGTCTCAGGATTCGT	TCCTGGCTGGGCAGAGTCCTAAGCA
SEQ ID NO: 947	**129272**	AACTCATCCCGTGTAGGTTGTGTAT	TTGAGTAGGGCACATCCAACACATA
SEQ ID NO: 948	**129574**	CCGTCCTCCCGTTCTAGAGAGTTTA	GGCAGGAGGGCAAGATCTCTCAAAT
SEQ ID NO: 949	**131084**	GACCACCGCGCCGTCCTGGGAGGCC	CTGGTGGCGCGGCAGGACCCTCCGG
SEQ ID NO: 950	**131104**	GTATCTCATCCCGTCGTCCCTGGAA	CATAGAGTAGGGCAGCAGGGACCTT
SEQ ID NO: 951	**132909**	GTGTTTCCGCCGTCCGTGTCCTGAC	CACAAAGGCGGCAGGCACAGGACTG
SEQ ID NO: 952	**134480**	GACGATCGCGCTCCGTCCGTTAATG	CTGCTAGCGCGAGGCAGGCAATTAC
SEQ ID NO: 953	**135692**	AACTCCCTCCGTCCATAGTACGTTA	TTGAGGGAGGCAGGTATCATGCAAT
SEQ ID NO: 954	**135816**	GTACTCGGCAGTCCGTAGCCCGGAA	CATGAGCCGTCAGGCATCGGGCCTT
SEQ ID NO: 955	**136132**	GTGAAATCGTCCGTGTGTTATTTAC	CACTTTAGCAGGCACACAATAAATG
SEQ ID NO: 956	**137084**	ACCTCACCGTCCGTCAAGAGGAGAT	TGGAGTGGCAGGCAGTTCTCCTCTA
SEQ ID NO: 957	**137086**	ACCACTTCGTCCGTCACAGAGACGA	TGGTGAAGCAGGCAGTGTCTCTGCT
SEQ ID NO: 958	**137351**	AGACGACACGACTCCGTACTTCTGT	TCTGCTGTGCTGAGGCATGAAGACA
SEQ ID NO: 959	**137926**	NA	NA
SEQ ID NO: 960	**138033**	ATTTTACACCGGTCCGTGTGTCCGA	TAAAATGTGGCCAGGCACACAGGCT
SEQ ID NO: 961	**138287**	CCACGAGAACCGGACAAGGGAACTG	GGTGCTCTTGGCCTGTTCCCTTGAC
SEQ ID NO: 962	**138629**	NA	NA

SEQ ID NO: 963	**139007**	ACAGAGACGACACCGGACTTGTGAC	TGTCTCTGCTGTGGCCTGAACACTG
SEQ ID NO: 964	**139248**	CCACTAGGACCGGTAGACACGACAC	GGTGATCCTGGCCATCTGTGCTGTG
SEQ ID NO: 965	**139810**	GTCCAGCCACCGACGAGAGAGGCTT	CAGGTCGGTGGCTGCTCTCTCCGAA
SEQ ID NO: 966	**139819**	ACCCACCACCGACCCATCTCTACGA	TGGGTGGTGGCTGGGTAGAGATGCT
SEQ ID NO: 967	**139826**	CTCGAAAACCGACACGACATTACTT	GAGCTTTTGGCTGTGCTGTAATGAA
SEQ ID NO: 968	**139916**	AATCCCACCGACCACGAGCATAGAT	TTAGGGTGGCTGGTGCTCGTATCTA
SEQ ID NO: 969	**140150**	AGTGCACCACCGACAACCTAGAAGT	TCACGTGGTGGCTGTTGGATCTTCA
SEQ ID NO: 970	**140231**	GGGACTGTCACCGACACCGCAAGAA	CCCTGACAGTGGCTGTGGCGTTCTT
SEQ ID NO: 971	**140303**	CGTCCCAACCGACACGAAGAAGAGA	GCAGGGTTGGCTGTGCTTCTTCTCT
SEQ ID NO: 972	**140431**	CTATGATAACCGAACCGAAGCTCGT	GATACTATTGGCTTGGCTTCGAGCA
SEQ ID NO: 973	**140582**	AAAACAACCGACCACGTGTAGCGGC	TTTTGTTGGCTGGTGCACATCGCCG
SEQ ID NO: 974	**140589**	GTAAGGGAACCGACCACGACCAGGA	CATTCCCTTGGCTGGTGCTGGTCCT
SEQ ID NO: 975	**140797**	ATGTGGTCACCGACTCAGCGTTCAG	TACACCAGTGGCTGAGTCGCAAGTC
SEQ ID NO: 976	**141116**	GGGTCACCACCGACAACGATCGAAG	CCCAGTGGTGGCTGTTGCTAGCTTC
SEQ ID NO: 977	**141165**	AGACTTCGCACCGACACTTAAGGTG	TCTGAAGCGTGGCTGTGAATTCCAC
SEQ ID NO: 978	**141366**	GAGACCACGACACCGAATTGTAAGT	CTCTGGTGCTGTGGCTTAACATTCA
SEQ ID NO: 979	**141728**	GCGGCCAACCGACCAGTGTCTACAT	CGCCGGTTGGCTGGTCACAGATGTA
SEQ ID NO: 980	**141764**	AATGTCGCACCGACTACGACGAGGA	TTACAGCGTGGCTGATGCTGCTCCT
SEQ ID NO: 981	**141905**	AGAAGTCGCACCGACGCACGTCTAC	TCTTCAGCGTGGCTGCGTGCAGATG
SEQ ID NO: 982	**142232**	GTAATTTCACCGACGACGAGTAAGT	CATTAAAGTGGCTGCTGCTCATTCA
SEQ ID NO: 983	**142864**	GAACGACAACGACCGATACTACACT	CTTGCTGTTGCTGGCTATGATGTGA

SEQ ID NO: 984	**143097**	AAGTCCAACCGTTCCCGGTGGAGCC	TTCAGGTTGGCAAGGGCCACCTCGG
SEQ ID NO: 985	**143787**	ACACTCCACACCGTGCCGCAGACAC	TGTGAGGTGTGGCACGGCGTCTGTG
SEQ ID NO: 986	**144427**	CCGACGACCACCGTCGGCACCAGTA	GGCTGCTGGTGGCAGCCGTGGTCAT
SEQ ID NO: 987	**145773**	TCCGCAGACACCGTCACGCAGGGGA	AGGCGTCTGTGGCAGTGCGTCCCCT
SEQ ID NO: 988	**146863**	NA	NA
SEQ ID NO: 989	**147237**	GGCGGTACCGGGGTTGGTGTGTGAC	CCGCCATGGCCCCAACCACACACTG
SEQ ID NO: 990	**147544**	CACATGTGGGGGTGTGTTCCGATTC	GTGTACACCCCCACACAAGGCTAAG
SEQ ID NO: 991	**148053**	AAATTCGGGGTGTGGGAACCTCTAC	TTTAAGCCCCACACCCTTGGAGATG
SEQ ID NO: 992	**148230**	NA	NA
SEQ ID NO: 993	**149105**	TCTATCCGTGGGGTCGGTACCTCGT	AGATAGGCACCCCAGCCATGGAGCA
SEQ ID NO: 994	**149219**	CTTGTTGGGGTGTGCTCCGTCACCA	GAACAACCCCACACGAGGCAGTGGT
SEQ ID NO: 995	**151637**	ACCCGCACGGGGCTCGACGCCAACA	TGGGCGTGCCCCGAGCTGCGGTTGT
SEQ ID NO: 996	**153038**	GTGGTCACGGGGCACACACCCTTCG	CACCAGTGCCCCGTGTGTGGGAAGC
SEQ ID NO: 997	**153557**	CTCCGTGACGGGGTGACCACACGAC	GAGGCACTGCCCCACTGGTGTGCTG
SEQ ID NO: 998	**153558**	ATTCCCGGGATTCCGACACGACAGG	TAAGGGCCCTAAGGCTGTGCTGTCC
SEQ ID NO: 999	**153569**	AGAACTGGGGCTTCTCCTACCACGC	TCTTGACCCCGAAGAGGATGGTGCG
SEQ ID NO: 1000	**153877**	AGGTCCAGGGCCTCATCACCACTGT	TCCAGGTCCCGGAGTAGTGGTGACA
SEQ ID NO: 1001	**153913**	ACCACTGGGGCACCACCGTCGCACC	TGGTGACCCCGTGGTGGCAGCGTGG
SEQ ID NO: 1002	**155549**	ACCTGAAGGGCTTTTTCTTCGACCG	TGGACTTCCCGAAAAAGAAGCTGGC
SEQ ID NO: 1003	**155818**	CCCACCGGGCGCACACAGACACACA	GGGTGGCCCGCGTGTGTCTGTGTGT
SEQ ID NO: 1004	**155968**	CGGCCCGGGCGTAAAAACGAGCCTT	GCCGGGCCCGCATTTTTGCTCGGAA

SEQ ID NO: 1005	**156898**	CGAACCACGGGCACACCAGTGACGT	GCTTGGTGCCCGTGTGGTCACTGCA
SEQ ID NO: 1006	**157354**	GTCACTGGCGGGCTATCTTTCTCCT	CAGTGACCGCCCGATAGAAAGAGGA
SEQ ID NO: 1007	**158307**	ACCCTCGGGGAAATACCCGACCGGT	TGGGAGCCCCTTTATGGGCTGGCCA
SEQ ID NO: 1008	**164776**	AGTGTTGTCGGGACACACCAGGGTC	TCACAACAGCCCTGTGTGGTCCCAG
SEQ ID NO: 1009	**166722**	GACCTCCACGGGACACACGGTGTTT	CTGGAGGTGCCCTGTGTGCCACAAA
SEQ ID NO: 1010	**166723**	CCTCCACGGGACACAGGTCGTCGTG	GGAGGTGCCCTGTGTCCAGCAGCAC
SEQ ID NO: 1011	**166977**	TTGCGTTTGGGGTGCGACGCTCCTC	AACGCAAACCCCACGCTGCGAGGAG
SEQ ID NO: 1012	**167419**	TTCCTCGTTGGGGTGCGTATCCACC	AAGGAGCAACCCCACGCATAGGTGG
SEQ ID NO: 1013	**167637**	CACTCTTTGGGGTGGTAGTGGAACC	GTGAGAAACCCCACCATCACCTTGG
SEQ ID NO: 1014	**167838**	ACTGAACTTGGGTTGGTGTCTGACC	TGACTTGAACCCAACCACAGACTGG
SEQ ID NO: 1015	**168831**	AAGACTATTGGGTGGTGGTACCTGT	TTCTGATAACCCACCACCATGGACA
SEQ ID NO: 1016	**168872**	NA	NA
SEQ ID NO: 1017	**169433**	CTTTGTATGGGAGTCTGGTTCACAC	GAAACATACCCTCAGACCAAGTGTG
SEQ ID NO: 1018	**172189**	AGTGTTGGTGGGCTATGGTGCTGCA	TCACAACCACCCGATACCACGACGT
SEQ ID NO: 1019	**172637**	CGAGGTAGGTGGGTCTCAGACCCTC	GCTCCATCCACCCAGAGTCTGGGAG
SEQ ID NO: 1020	**172828**	TTTGTGGTGGCGTGATACTAATCGG	AAACACCACCGCACTATGATTAGCC
SEQ ID NO: 1021	**173270**	GCAGGTGGTGGGGACTGTTATCCTC	CGTCCACCACCCCTGACAATAGGAG
SEQ ID NO: 1022	**173689**	NA	NA
SEQ ID NO: 1023	**174543**	CTCGGTGTGTGGGTAATATTCTTTA	GAGCCACACACCCATTATAAGAAAT
SEQ ID NO: 1024	**174591**	NA	NA
SEQ ID NO: 1025	**174600**	AGTAGGTGGTGGGTACTTCTCCGTA	TCATCCACCACCCATGAAGAGGCAT

SEQ ID NO: 1026	**174624**	CTAAGTGTGTGGGTTACGTGTCTCT	GATTCACACACCCAATGCACAGAGA
SEQ ID NO: 1027	**174748**	TCCTGTGTGTGGGTCCGGTCTCCCT	AGGACACACACCCAGGCCAGAGGGA
SEQ ID NO: 1028	**175266**	ACGTGGTGGTGGCTCCCGAACTACA	TGCACCACCACCGAGGGCTTGATGT
SEQ ID NO: 1029	**175734**	NA	NA
SEQ ID NO: 1030	**178419**	CTTTATATGGAGTCGTGTGGTCTTC	GAAATATACCTCAGCACACCAGAAG
SEQ ID NO: 1031	**178963**	GTGTGTGTGTTGGACTCCCTCCCGA	CACACACACAACCTGAGGGAGGGCT
SEQ ID NO: 1032	**180242**	GTTTGTGGTGGAATGATACTTCGAC	CAAACACCACCTTACTATGAAGCTG
SEQ ID NO: 1033	**180769**	AGGTATCGGTGGACGCCTCCGCCTT	TCCATAGCCACCTGCGGAGGCGGAA
SEQ ID NO: 1034	**182321**	TATCGTGAGTGTGGATCCAAGGTTC	ATAGCACTCACACCTAGGTTCCAAG
SEQ ID NO: 1035	**182327**	GTGGGTGGTGGACTGACCCTAAACC	CACCCACCACCTGACTGGGATTTGG
SEQ ID NO: 1036	**183200**	ACTACACGAGTGTGGAGTCCTTACT	TGATGTGCTCACACCTCAGGAATGA
SEQ ID NO: 1037	**183228**	CTGTGTGGTGGACTTCACTGAGCCC	GACACACCACCTGAAGTGACTCGGG
SEQ ID NO: 1038	**183427**	AGATCTGCGGGTGTGGCACTCCCGA	TCTAGACGCCCACACCGTGAGGGCT
SEQ ID NO: 1039	**184001**	CGGTACCGGGGTTGGTGTGTGACCC	GCCATGGCCCCAACCACACACTGGG
SEQ ID NO: 1040	**184202**	GTCGGCGTTGTGGACGTCGACATCC	CAGCCGCAACACCTGCAGCTGTAGG
SEQ ID NO: 1041	**184251**	TTACCCTGGGTTGGTGGAGTACCAC	AATGGGACCCAACCACCTCATGGTG
SEQ ID NO: 1042	**185290**	GTTTGCTGGGTGGTGACATATTCAC	CAAACGACCCACCACTGTATAAGTG
SEQ ID NO: 1043	**185586**	CTGTGTTGGGTGGTGGTACCCTCAG	GACACAACCCACCACCATGGGAGTC
SEQ ID NO: 1044	**185602**	TTGGCGTGGGTTTGTGACGACCCAT	AACCGCACCCAAACACTGCTGGGTA
SEQ ID NO: 1045	**185974**	CACTATTGGGTGGTGGTAACCTGGT	GTGATAACCCACCACCATTGGACCA
SEQ ID NO: 1046	**186359**	NA	NA

SEQ ID NO: 1047	**186694**	GGAAATGGGTGTGTCTGCGACTTCC	CCTTTACCCACACAGACGCTGAAGG
SEQ ID NO: 1048	**186751**	CTTACGTTGGGTGAGTGTTTTATTT	GAATGCAACCCACTCACAAAATAAA
SEQ ID NO: 1049	**186902**	CATGGTGGGTGTGTTCCTCCTAGCC	GTACCACCCACACAAGGAGGATCGG
SEQ ID NO: 1050	**187006**	GTCCACATGGGTGTGTGACCTCTGT	CAGGTGTACCCACACACTGGAGACA
SEQ ID NO: 1051	**187101**	TTCGGAGTGGGTGTGTTCAGTCAAC	AAGCCTCACCCACACAAGTCAGTTG
SEQ ID NO: 1052	**187404**	AGGGACTACGGGTGTCGTGCTCTTT	TCCCTGATGCCCACAGCACGAGAAA
SEQ ID NO: 1053	**187451**	ACGCCCAGGGTGACTTTACGCGCGT	TGCGGGTCCCACTGAAATGCGCGCA
SEQ ID NO: 1054	**187665**	CTTCCTGGGTGTGTTCTTAAGATCG	GAAGGACCCACACAAGAATTCTAGC
SEQ ID NO: 1055	**189499**	TTAGTGTGGGGTCTTTGTCAGAGCT	AATCACACCCCAGAAACAGTCTCGA
SEQ ID NO: 1056	**190140**	GGTTGTGTGGGTCTCACGTTACCTA	CCAACACACCCAGAGTGCAATGGAT
SEQ ID NO: 1057	**192117**	AAACCTGGGTCGGTGTGTTTGTCCT	TTTGGACCCAGCCACACAAACAGGA
SEQ ID NO: 1058	**192303**	GTCCAGACACGGGTCTTTCCTCTGA	CAGGTCTGTGCCCAGAAAGGAGACT
SEQ ID NO: 1059	**192555**	NA	NA
SEQ ID NO: 1060	**193209**	CTGTGTCTGGGTATCTTCGCTCGAA	GACACAGACCCATAGAAGCGAGCTT
SEQ ID NO: 1061	**193235**	CAGGTGTCGGGTCATAGATGTCTCC	GTCCACAGCCCAGTATCTACAGAGG
SEQ ID NO: 1062	**193785**	GTCGGTAGGTGGGTAAGTCACTCCA	CAGCCATCCACCCATTCAGTGAGGT
SEQ ID NO: 1063	**194302**	AGTGTGAGTGGGTACGAAAATGTAC	TCACACTCACCCATGCTTTTACATG
SEQ ID NO: 1064	**194400**	NA	NA
SEQ ID NO: 1065	**196006**	AATCCACTGGTGGTGGGGTTCCAGT	TTAGGTGACCACCACCCCAAGGTCA
SEQ ID NO: 1066	**196040**	NA	NA
SEQ ID NO: 1067	**196416**	CTTTGTTGGTTGCTGGTCATGTTCT	GAAACAACCAACGACCAGTACAAGA

SEQ ID NO: 1068	**196598**	CAAGTTTGGTTGTCGCTGTTATCGG	GTTCAAACCAACAGCGACAATAGCC
SEQ ID NO: 1069	**197136**	CTATCGTTTGGTGTGAGCCGTGTCC	GATAGCAAACCACACTCGGCACAGG
SEQ ID NO: 1070	**197704**	GACTACGACTACGATGGTTGCGACG	CTGATGCTGATGCTACCAACGCTGC
SEQ ID NO: 1071	**198410**	NA	NA
SEQ ID NO: 1072	**198589**	TCCCTTATGGTGTGTCTGACGGGCC	AGGGAATACCACACAGACTGCCCGG
SEQ ID NO: 1073	**199145**	CCGCACCTGGTCGAACCGCCGACGT	GGCGTGGACCAGCTTGGCGGCTGCA
SEQ ID NO: 1074	**199718**	CATGTGTCTGGTGTGTTACACGGTG	GTACACAGACCACACAATGTGCCAC
SEQ ID NO: 1075	**200191**	CCAAGTACTGGTGGTGCCTGAACGG	GGTTCATGACCACCACGGACTTGCC
SEQ ID NO: 1076	**200345**	GGGTCGGTTGGTCTAGTTGACTTAT	CCCAGCCAACCAGATCAACTGAATA
SEQ ID NO: 1077	**200403**	ACTTCGGTGTGGTGCGATGCCAGAC	TGAAGCCACACCACGCTACGGTCTG
SEQ ID NO: 1078	**201098**	GTGGTCACGGTGGTGCAGTCCCAGG	CACCAGTGCCACCACGTCAGGGTCC
SEQ ID NO: 1079	**201172**	NA	NA
SEQ ID NO: 1080	**201271**	GGTGGTTGTGGTTAACACGTCACCT	CCACCAACACCAATTGTGCAGTGGA
SEQ ID NO: 1081	**201584**	TTTGTGGTGGTGACGTTTGCCAAGT	AAACACCACCACTGCAAACGGTTCA
SEQ ID NO: 1082	**201762**	TCGCTTAGGTGGTGCTTGTTGAAGA	AGCGAATCCACCACGAACAACTTCT
SEQ ID NO: 1083	**201968**	CAGATGGTGGTGAAACTTTTCTACC	GTCTACCACCACTTTGAAAAGATGG
SEQ ID NO: 1084	**202279**	CCTCGTATGTGGTGGTGAGGACACA	GGAGCATACACCACCACTCCTGTGT
SEQ ID NO: 1085	**202285**	CTACGAACGGTGGTGGGTTACTACT	GATGCTTGCCACCACCCAATGATGA
SEQ ID NO: 1086	**202326**	ACAGGTGGTGGTCTTCCTTGGGTAA	TGTCCACCACCAGAAGGAACCCATT
SEQ ID NO: 1087	**202358**	ATGTTTGTGGTGCTCTGTCAAATCC	TACAAACACCACGAGACAGTTTAGG
SEQ ID NO: 1088	**202382**	CGTGTCGTTGTGGTTCTTAGGTGAA	GCACAGCAACACCAAGAATCCACTT

SEQ ID NO: 1089	**202479**	ACCGGGTGTGGTGTCCTCTTCCCGC	TGGCCCACACCACAGGAGAAGGGCG
SEQ ID NO: 1090	**202524**	ATAATAGGTGGTTGTGGTCATGCAC	TATTATCCACCAACACCAGTACGTG
SEQ ID NO: 1091	**202545**	GTACCCGTTGTGGTGTGACGAACAT	CATGGGCAACACCACACTGCTTGTA
SEQ ID NO: 1092	**202728**	TAGTGGTGGTGGTTACTGCTACGAT	ATCACCACCACCAATGACGATGCTA
SEQ ID NO: 1093	**202776**	TTATCGTCAGTGGTGGTGTTATACG	AATAGCAGTCACCACCACAATATGC
SEQ ID NO: 1094	**202777**	CCTTCTAGTGGTGGTGTCAGTTGTC	GGAAGATCACCACCACAGTCAACAG
SEQ ID NO: 1095	**203034**	ACTCAACGTGTGGTTTGTGTCCGAC	TGAGTTGCACACCAAACACAGGCTG
SEQ ID NO: 1096	**203190**	ACCCGTTTGGTATGTGATTGAACCC	TGGGCAAACCATACACTAACTTGGG
SEQ ID NO: 1097	**203335**	CATTTGTGGTGTGACGTGAACTTGG	GTAAACACCACACTGCACTTGAACC
SEQ ID NO: 1098	**203350**	CGTGCTTGTGGTGGCGTCTGTTCCC	GCACGAACACCACCGCAGACAAGGG
SEQ ID NO: 1099	**203404**	TACCGACGGGTGGTGCGTTATCTAC	ATGGCTGCCCACCACGCAATAGATG
SEQ ID NO: 1100	**203499**	ATTTTGTGGTGGTCTCGTGTTCACT	TAAAACACCACCAGAGCACAAGTGA
SEQ ID NO: 1101	**203523**	ACACATCACGTGGTGTGTGCAAACC	TGTGTAGTGCACCACACACGTTTGG
SEQ ID NO: 1102	**203548**	ACTGTGTTGTGGTGTCTAGAGTCTC	TGACACAACACCACAGATCTCAGAG
SEQ ID NO: 1103	**203595**	CGCGTTTGTGGTCGTCTTAGTGTCC	GCGCAAACACCAGCAGAATCACAGG
SEQ ID NO: 1104	**203717**	ACTCGCGACTGTGGTGTGGTACCAA	TGAGCGCTGACACCACACCATGGTT
SEQ ID NO: 1105	**203740**	CTAAGCGTGTGGTGTTGGTCTTTCT	GATTCGCACACCACAACCAGAAAGA
SEQ ID NO: 1106	**203794**	ATGTTGCGTGGTTTTGAGCGCCCTA	TACAACGCACCAAAACTCGCGGGAT
SEQ ID NO: 1107	**204121**	CTCACTCGACGTGGTTCAAGGTCTC	GAGTGAGCTGCACCAAGTTCCAGAG
SEQ ID NO: 1108	**204315**	GTGGTCGTAGTTGGTATTTTGGATC	CACCAGCATCAACCATAAAACCTAG
SEQ ID NO: 1109	**204326**	GGCCGTGGTGGTCTTCAGTCCTTTT	CCGGCACCACCAGAAGTCAGGAAAA

SEQ ID NO: 1110	**205206**	ATGGTGGTGGTACCATACCTGTCAA	TACCACCACCATGGTATGGACAGTT
SEQ ID NO: 1111	**205711**	GTAGGTGGTCGTGGTACCTCACAGT	CATCCACCAGCACCATGGAGTGTCA
SEQ ID NO: 1112	**206165**	AGACATCAAGGCCAAGGGCAACTCG	TCTGTAGTTCCGGTTCCCGTTGAGC
SEQ ID NO: 1113	**206204**	ACGTGTGAGGTGGTACAGTACATCT	TGCACACTCCACCATGTCATGTAGA
SEQ ID NO: 1114	**206227**	CGTCGGGTGTGGTAGACTATGACAC	GCAGCCCACACCATCTGATACTGTG
SEQ ID NO: 1115	**208340**	ATCTTGTAAGGGTGGTGGTACTCCA	TAGAACATTCCCACCACCATGAGGT
SEQ ID NO: 1116	**212155**	TGACTCAACAGGCACCACCACAGGT	ACTGAGTTGTCCGTGGTGGTGTCCA
SEQ ID NO: 1117	**212916**	CTGTGTGTGAGGCTCATTAAACCAC	GACACACACTCCGAGTAATTTGGTG
SEQ ID NO: 1118	**213037**	GCACCTCAAGGCGAAACTGACACCG	CGTGGAGTTCCGCTTTGACTGTGGC
SEQ ID NO: 1119	**215679**	ACGAACCAGAGGGCCAAGGTCACAC	TGCTTGGTCTCCCGGTTCCAGTGTG
SEQ ID NO: 1120	**215855**	CTTGGAGAGGGCACTCGACGACCCT	GAACCTCTCCCGTGAGCTGCTGGGA
SEQ ID NO: 1121	**218149**	GTTTCCGAAGGAATCCACGCGCCGA	CAAAGGCTTCCTTAGGTGCGCGGCT
SEQ ID NO: 1122	**221409**	ACGACCCACAGGATCCAATTCTAGG	TGCTGGGTGTCCTAGGTTAAGATCC
SEQ ID NO: 1123	**222070**	ACACGTACACACAGGAACCGGCTTA	TGTGCATGTGTGTCCTTGGCCGAAT
SEQ ID NO: 1124	**226797**	ATAGACACCGAGGATCACCGTCGGA	TATCTGTGGCTCCTAGTGGCAGCCT
SEQ ID NO: 1125	**227073**	ACATCAAGAGGAGTCGTAATCGTGA	TGTAGTTCTCCTCAGCATTAGCACT
SEQ ID NO: 1126	**227969**	CCAGACACGAGGAGGAGATTCACCC	GGTCTGTGCTCCTCCTCTAAGTGGG
SEQ ID NO: 1127	**230496**	TGCTCCGCGTAGGAGTGAAGAGCCT	ACGAGGCGCATCCTCACTTCTCGGA
SEQ ID NO: 1128	**232301**	CGACGAGTATTAGGACCGGGTCCAT	GCTGCTCATAATCCTGGCCCAGGTA
SEQ ID NO: 1129	**233370**	CGGTAAGACTAGGAGGTGCGACCAC	GCCATTCTGATCCTCCACGCTGGTG
SEQ ID NO: 1130	**233785**	ATAGGAGAAGGTTTTCAGAGAATCC	TATCCTCTTCCAAAAGTCTCTTAGG

SEQ ID NO: 1131	**235352**	ACAGACGAAAGGTTAGTGGCCACGA	TGTCTGCTTTCCAATCACCGGTGCT
SEQ ID NO: 1132	**237003**	AGTCTCAGTAAGGTGTGTGTCCCAA	TCAGAGTCATTCCACACACAGGGTT
SEQ ID NO: 1133	**238190**	CGGTGTCCAGGTGTTGCAAGTAGTC	GCCACAGGTCCACAACGTTCATCAG
SEQ ID NO: 1134	**238366**	CTTTCCAGGTGTGTGGAGAGCCAAT	GAAAGGTCCACACACCTCTCGGTTA
SEQ ID NO: 1135	**238389**	ACTGTTCTCAGGTGTGTGACTTCTT	TGACAAGAGTCCACACACTGAAGAA
SEQ ID NO: 1136	**238514**	ATTTATCAGGTGTGTGTCGTTCTCC	TAAATAGTCCACACACAGCAAGAGG
SEQ ID NO: 1137	**239205**	ACACGTCCGCAGGTCTTCCACTTTT	TGTGCAGGCGTCCAGAAGGTGAAAA
SEQ ID NO: 1138	**239621**	ACTACACACACAGGTCAGTTGACGG	TGATGTGTGTGTCCAGTCAACTGCC
SEQ ID NO: 1139	**242306**	ACCTGTTGAGGTGTTTTGTGTCGAA	TGGACAACTCCACAAAACACAGCTT
SEQ ID NO: 1140	**242462**	GCTCCACCGAGGTTCTTACGGAGTA	CGAGGTGGCTCCAAGAATGCCTCAT
SEQ ID NO: 1141	**249844**	TCTTCTCCCGGGCTTGCGTGCGAGG	AGAAGAGGGCCCGAACGCACGCTCC
SEQ ID NO: 1142	**250357**	CCACCCCGGGCACGCAGCACCGCCG	GGTGGGGCCCGTGCGTCGTGGCGGC
SEQ ID NO: 1143	**250469**	CCGTCCACCGGGGTCAATATGTGTG	GGCAGGTGGCCCCAGTTATACACAC
SEQ ID NO: 1144	**251863**	CTCTCCGCCGGGTTAGAAGACTCTA	GAGAGGCGGCCCAATCTTCTGAGAT
SEQ ID NO: 1145	**252484**	TACACCGACACCGGGGTATCGACGC	ATGTGGCTGTGGCCCCATAGCTGCG
SEQ ID NO: 1146	**252515**	GATTGGTCCGGCAGCGACCGACCGT	CTAACCAGGCCGTCGCTGGCTGGCA
SEQ ID NO: 1147	**253092**	CTCACACGGCGGGTCTAACAATGGT	GAGTGTGCCGCCCAGATTGTTACCA
SEQ ID NO: 1148	**253539**	TTCCCGTCCGGCGAGGAACCTCGAG	AAGGGCAGGCCGCTCCTTGGAGCTC
SEQ ID NO: 1149	**254357**	AGCACTTGCGGCGTGTGTACCAACA	TCGTGAACGCCGCACACATGGTTGT
SEQ ID NO: 1150	**255874**	NA	NA
SEQ ID NO: 1151	**256213**	AAAACACCGGAACCAACAGGTCAGC	TTTTGTGGCCTTGGTTGTCCAGTCG

SEQ ID NO: 1152	**257069**	AGTTGGTGCGGATTTCTCCTTTCTT	TCAACCACGCCTAAAGAGGAAAGAA
SEQ ID NO: 1153	**257180**	CTCCTCTCCGGACCGGAAACAGAGT	GAGGAGAGGCCTGGCCTTTGTCTCA
SEQ ID NO: 1154	**257378**	CTCACACCCGGACAAAGTCAGTAGT	GAGTGTGGGCCTGTTTCAGTCATCA
SEQ ID NO: 1155	**258113**	ACACACACAGCGGACGATCCATAAA	TGTGTGTGTCGCCTGCTAGGTATTT
SEQ ID NO: 1156	**258189**	CTCCAAGCGGAAAACGTGCGTGCCA	GAGGTTCGCCTTTTGCACGCACGGT
SEQ ID NO: 1157	**259991**	TTCAACATCGGCGACGACGGGACCA	AAGTTGTAGCCGCTGCTGCCCTGGT
SEQ ID NO: 1158	**260464**	AAGTTGATCGGGACACACCTTTTCT	TTCAACTAGCCCTGTGTGGAAAAGA
SEQ ID NO: 1159	**260507**	CTATCTGTTCGGGTGTGTTCCTTCG	GATAGACAAGCCCACACAAGGAAGC
SEQ ID NO: 1160	**261666**	TTTTCGTGTCGGGTGTCGCACCGAG	AAAAGCACAGCCCACAGCGTGGCTC
SEQ ID NO: 1161	**262477**	CCGGTGTGTCGGGTTTCTCCGACCA	GGCCACACAGCCCAAAGAGGCTGGT
SEQ ID NO: 1162	**263369**	AGGTCGTGTTCGGATGGTTCACTAC	TCCAGCACAAGCCTACCAAGTGATG
SEQ ID NO: 1163	**264689**	TTGGTCTGCGGTTTCGATCTTTCCC	AACCAGACGCCAAAGCTAGAAAGGG
SEQ ID NO: 1164	**265582**	CACTCGACCCGGTTCCACTTTAAGA	GTGAGCTGGGCCAAGGTGAAATTCT
SEQ ID NO: 1165	**271201**	AGAACTGTGTCGGTGGGTCCCACCA	TCTTGACACAGCCACCCAGGGTGGT
SEQ ID NO: 1166	**272154**	TCACCGTTTCGGTGTGGGTCGATGA	AGTGGCAAAGCCACACCCAGCTACT
SEQ ID NO: 1167	**272726**	ATTACTGGTCGGTCTGGCAACCCTG	TAATGACCAGCCAGACCGTTGGGAC
SEQ ID NO: 1168	**272908**	ACAGGTGTGTCGGTATCGTTAGGTC	TGTCCACACAGCCATAGCAATCCAG
SEQ ID NO: 1169	**273043**	GTTGGACTGTCGGTGATTTATCACC	CAACCTGACAGCCACTAAATAGTGG
SEQ ID NO: 1170	**273195**	AAACTGGTCGGTGGTTCTAAAGGTC	TTTGACCAGCCACCAAGATTTCCAG
SEQ ID NO: 1171	**274034**	CGTTTCGGTCGGTGTATATGTGTAC	GCAAAGCCAGCCACATATACACATG
SEQ ID NO: 1172	**275178**	AGAAAGAACGGCTCCGACCGCAGCC	TCTTTCTTGCCGAGGCTGGCGTCGG

SEQ ID NO: 1173	**275653**	CACACCCACGGGAAGGGTCACTGGT	GTGTGGGTGCCCTTCCCAGTGACCA
SEQ ID NO: 1174	**275658**	AAAGGTAACGGCGACCTCGTCCGTC	TTTCCATTGCCGCTGGAGCAGGCAG
SEQ ID NO: 1175	**276301**	TCTTACACGACACGGCAGACACGGG	AGAATGTGCTGTGCCGTCTGTGCCC
SEQ ID NO: 1176	**276860**	GGACCCGACACGGAACCTCCGAGTG	CCTGGGCTGTGCCTTGGAGGCTCAC
SEQ ID NO: 1177	**276871**	ATCCGACCACGGTAAATCTTTACTG	TAGGCTGGTGCCATTTAGAAATGAC
SEQ ID NO: 1178	**277540**	CGGACACACACGGAAAGGACCGTAG	GCCTGTGTGTGCCTTTCCTGGCATC
SEQ ID NO: 1179	**277616**	GTACAACTCCGACGGCGTACTCCGG	CATGTTGAGGCTGCCGCATGAGGCC
SEQ ID NO: 1180	**278061**	GTACCACACACACGGAACATCTAGG	CATGGTGTGTGTGCCTTGTAGATCC
SEQ ID NO: 1181	**278460**	TGTGTGCTTGCTTGTTTGCTTCAGT	ACACACGAACGAACAAACGAAGTCA
SEQ ID NO: 1182	**279024**	TAGGACCCGACGGACTCGAAAGGTC	ATCCTGGGCTGCCTGAGCTTTCCAG
SEQ ID NO: 1183	**279323**	GACGACACCCTACGGGACGAGGAAC	CTGCTGTGGGATGCCCTGCTCCTTG
SEQ ID NO: 1184	**279723**	CCCATACACGGTGTGGTGGGTCCTC	GGGTATGTGCCACACCACCCAGGAG
SEQ ID NO: 1185	**279794**	GACACACACGGTACGGGTCTAACTT	CTGTGTGTGCCATGCCCAGATTGAA
SEQ ID NO: 1186	**281430**	TGTGAACCACGGTCCCAGGGCTCGT	ACACTTGGTGCCAGGGTCCCGAGCA
SEQ ID NO: 1187	**281858**	CTGGTGAACGGTCCCACGACTCATC	GACCACTTGCCAGGGTGCTGAGTAG
SEQ ID NO: 1188	**283589**	GGCCGCCGGCCACCGTGGTGTGTAT	CCGGCGGCCGGTGGCACCACACATA
SEQ ID NO: 1189	**286443**	CAAAAGGCCCAGCACCGTCGTAGGA	GTTTTCCGGGTCGTGGCAGCATCCT
SEQ ID NO: 1190	**286872**	CGGGCCGGCCACCGCGCAGCCAGAC	GCCCGGCCGGTGGCGCGTCGGTCTG
SEQ ID NO: 1191	**287004**	AAAAGAGGCCTCGACTCCGCGTTTC	TTTTCTCCGGAGCTGAGGCGCAAAG
SEQ ID NO: 1192	**287416**	GGGGCACGGCCACCGACGCCAAGTA	CCCCGTGCCGGTGGCTGCGGTTCAT
SEQ ID NO: 1193	**289033**	ATGTCCCGGCCTCAATTCTACTCAG	TACAGGGCCGGAGTTAAGATGAGTC

SEQ ID NO: 1194	**290488**	GTACCTTAGGGCAGGACCACAGACA	CATGGAATCCCGTCCTGGTGTCTGT
SEQ ID NO: 1195	**290768**	GTTCTAAAGGCATGTGTGTGCTCAC	CAAGATTTCCGTACACACACGAGTG
SEQ ID NO: 1196	**292002**	TGAGAGTCAGGCACCGACCTCATCT	ACTCTCAGTCCGTGGCTGGAGTAGA
SEQ ID NO: 1197	**292250**	TCAGCGCCGGCAACCACAGGAGTCG	AGTCGCGGCCGTTGGTGTCCTCAGC
SEQ ID NO: 1198	**293300**	ACTAGGCGGGCACACTATCGTTGTC	TGATCCGCCCGTGTGATAGCAACAG
SEQ ID NO: 1199	**293357**	TTACTCCACGGCACGGGTACACAAG	AATGAGGTGCCGTGCCCATGTGTTC
SEQ ID NO: 1200	**293479**	GTCTTTTGGCACACTCGGGCAAACC	CAGAAAACCGTGTGAGCCCGTTTGG
SEQ ID NO: 1201	**293948**	AGAGACACCGGCACACACAACGTAC	TCTCTGTGGCCGTGTGTGTTGCATG
SEQ ID NO: 1202	**294054**	GTCGGACGCAGGCACAGACGTAGAC	CAGCCTGCGTCCGTGTCTGCATCTG
SEQ ID NO: 1203	**294157**	AGTCACTCTGGCACGCACTTTCGAC	TCAGTGAGACCGTGCGTGAAAGCTG
SEQ ID NO: 1204	**294419**	TCCTCGGACGGCACAACAGTGTCGC	AGGAGCCTGCCGTGTTGTCACAGCG
SEQ ID NO: 1205	**294525**	TGGTGTGTATGCCTGGTTAGCGGCA	ACCACACATACGGACCAATCGCCGT
SEQ ID NO: 1206	**294683**	CTAAACCGGCACACTCCGAGTCGGA	GATTTGGCCGTGTGAGGCTCAGCCT
SEQ ID NO: 1207	**294721**	CGACACCGACGGCACGCACAGATAA	GCTGTGGCTGCCGTGCGTGTCTATT
SEQ ID NO: 1208	**294871**	GACTACGACAGACGGCACGCTCCAG	CTGATGCTGTCTGCCGTGCGAGGTC
SEQ ID NO: 1209	**295235**	CGTGGGTGTGCCGAAACCTAAAACA	GCACCCACACGGCTTTGGATTTTGT
SEQ ID NO: 1210	**295889**	GACGTCGCCTATGCCTGCCGATCAC	CTGCAGCGGATACGGACGGCTAGTG
SEQ ID NO: 1211	**296170**	CGCCGGCTGCCACCACATGACTCGC	GCGGCCGACGGTGGTGTACTGAGCG
SEQ ID NO: 1212	**296184**	CTCCTCCTGCCTGTGGGACTCGAGG	GAGGAGGACGGACACCCTGAGCTCC
SEQ ID NO: 1213	**296404**	CTATTAGAGTGCCTGTGTGTCATTC	GATAATCTCACGGACACACAGTAAG
SEQ ID NO: 1214	**296421**	TGTGTGTGGTGCCTCTTCTAAACCT	ACACACACCACGGAGAAGATTTGGA

SEQ ID NO: 1215	**296565**	TGGTGTGTCTGCCAGTCTCTCCAGT	ACCACACAGACGGTCAGAGAGGTCA
SEQ ID NO: 1216	**296973**	GAGTTACTCGACTGCCTCCTCGTGT	CTCAATGAGCTGACGGAGGAGCACA
SEQ ID NO: 1217	**297952**	TGTCGTGTGTCGTGCCACTCAGCGT	ACAGCACACAGCACGGTGAGTCGCA
SEQ ID NO: 1218	**298063**	TCGTGCGTCTCGTGCCGCTAGACGC	AGCACGCAGAGCACGGCGATCTGCG
SEQ ID NO: 1219	**298802**	ACTCGTGCGCTGCAGTGTTTAATGG	TGAGCACGCGACGTCACAAATTACC
SEQ ID NO: 1220	**298965**	AACGGCGTGTGCAGCGTGCACCAGA	TTGCCGCACACGTCGCACGTGGTCT
SEQ ID NO: 1221	**298980**	AGATCCTTGCGACCTCCTGGAACCG	TCTAGGAACGCTGGAGGACCTTGGC
SEQ ID NO: 1222	**300542**	GCCGCCGCTGCACGTCACGTAGTGG	CGGCGGCGACGTGCAGTGCATCACC
SEQ ID NO: 1223	**301687**	CTGGTGCGTGCATAGAGAACTCTTT	GACCACGCACGTATCTCTTGAGAAA
SEQ ID NO: 1224	**301774**	CCTAGTGTGTGCAGTGACAGAAAGC	GGATCACACACGTCACTGTCTTTCG
SEQ ID NO: 1225	**302075**	GTGTGTACGATGTGCACAAGGAAAA	CACACATGCTACACGTGTTCCTTTT
SEQ ID NO: 1226	**303562**	TCGGTGGTGGCTTTCAAGACTCGTC	AGCCACCACCGAAAGTTCTGAGCAG
SEQ ID NO: 1227	**304039**	CTTGTGTGGCTTTCTATCCGGACTG	GAACACACCGAAAGATAGGCCTGAC
SEQ ID NO: 1228	**305284**	CAGAAGGGCTCACGCCGCCACGTTG	GTCTTCCCGAGTGCGGCGGTGCAAC
SEQ ID NO: 1229	**306035**	CGTGGTGCGTGCTACCGACAAAGAA	GCACCACGCACGATGGCTGTTTCTT
SEQ ID NO: 1230	**306317**	CTCCAAGGCTCACGAGACGCCTGAG	GAGGTTCCGAGTGCTCTGCGGACTC
SEQ ID NO: 1231	**306859**	CCACTACGGGCTAAAGTACGGGTCC	GGTGATGCCCGATTTCATGCCCAGG
SEQ ID NO: 1232	**307309**	GCCCATCGTGCTTGTGGTGGCGTCT	CGGGTAGCACGAACACCACCGCAGA
SEQ ID NO: 1233	**307508**	AATCTACTTGCGTGCGACTGTGCAT	TTAGATGAACGCACGCTGACACGTA
SEQ ID NO: 1234	**309542**	ACTACCACTACTGCTTCCGGGGTCG	TGATGGTGATGACGAAGGCCCCAGC
SEQ ID NO: 1235	**309630**	CGTTCGTGGTGCTTGTTCGACTGTA	GCAAGCACCACGAACAAGCTGACAT

SEQ ID NO: 1236	**309722**	ATACTGAGTGTGCTGTGGTCATCAG	TATGACTCACACGACACCAGTAGTC
SEQ ID NO: 1237	**310412**	CGGTAAAAGCCCTGACCACCACATA	GCCATTTTCGGGACTGGTGGTGTAT
SEQ ID NO: 1238	**310622**	ACTTGTGTGTGCTCGAGGAACCACC	TGAACACACACGAGCTCCTTGGTGG
SEQ ID NO: 1239	**311199**	CTTCTACACGTGCTAGTCGAGCGAC	GAAGATGTGCACGATCAGCTCGCTG
SEQ ID NO: 1240	**313170**	GCCTGCCAGCCTCTTCCGTCATCCA	CGGACGGTCGGAGAAGGCAGTAGGT
SEQ ID NO: 1241	**313391**	TGCGCGCCAGCCCGCCGGCGCCGGC	ACGCGCGGTCGGGCGGCCGCGGCCG
SEQ ID NO: 1242	**313697**	GGCCGCCAGCCAGCCGTGCACGGGC	CCGGCGGTCGGTCGGCACGTGCCCG
SEQ ID NO: 1243	**313826**	CGCGCCGCAGCCGAGCTCTCCGCCG	GCGCGGCGTCGGCTCGAGAGGCGGC
SEQ ID NO: 1244	**314636**	CGCACCGCAGCCGCGCGCCGAGGCC	GCGTGGCGTCGGCGCGCGGCTCCGG
SEQ ID NO: 1245	**314646**	CCCGCGCAGCCGCCATTGAGGACTT	GGGCGCGTCGGCGGTAACTCCTGAA
SEQ ID NO: 1246	**316647**	TAGTGTGTGTCAGCAGATTCTGTGC	ATCACACACAGTCGTCTAAGACACG
SEQ ID NO: 1247	**316720**	CGTAACGAAAGCACATTTAATACAT	GCATTGCTTTCGTGTAAATTATGTA
SEQ ID NO: 1248	**317049**	ACCGACCACGAGCATAGATGTTTTT	TGGCTGGTGCTCGTATCTACAAAAA
SEQ ID NO: 1249	**317428**	GGTCGACACGACAGCATGAGTATGT	CCAGCTGTGCTGTCGTACTCATACA
SEQ ID NO: 1250	**318046**	ACTTCTTCAGCACGCCACGAGGTGT	TGAAGAAGTCGTGCGGTGCTCCACA
SEQ ID NO: 1251	**318047**	CTCCCGCAGCACGAACACGAAGTCG	GAGGGCGTCGTGCTTGTGCTTCAGC
SEQ ID NO: 1252	**318400**	CTACCTACCTAGCATGTGGAACGGA	GATGGATGGATCGTACACCTTGCCT
SEQ ID NO: 1253	**318735**	AGATCCGTAGAGCACACTCGCCTGA	TCTAGGCATCTCGTGTGAGCGGACT
SEQ ID NO: 1254	**318923**	GCCGTCCACGAGCAGGAGTCTCTTC	CGGCAGGTGCTCGTCCTCAGAGAAG
SEQ ID NO: 1255	**318986**	TCCTACGCGACGAGCAGCCGGACTA	AGGATGCGCTGCTCGTCGGCCTGAT
SEQ ID NO: 1256	**319714**	GTCGCACGCATAGCCTTGCCGACGC	CAGCGTGCGTATCGGAACGGCTGCG

SEQ ID NO: 1257	**321658**	GGTCGCGACTCAGCTCCAACTGTCC	CCAGCGCTGAGTCGAGGTTGACAGG
SEQ ID NO: 1258	**321709**	CTACCCTAAGCTTGTGCGTTCGTGT	GATGGGATTCGAACACGCAAGCACA
SEQ ID NO: 1259	**323758**	CCGCCGCCGCGGAAAGGTTATACCG	GGCGGCGGCGCCTTTCCAATATGGC
SEQ ID NO: 1260	**323857**	AGACATAAGAGCTCGGTAGACGACA	TCTGTATTCTCGAGCCATCTGCTGT
SEQ ID NO: 1261	**323891**	GCGGGGTGTGCGGCCGGAAAAGACG	CGCCCCACACGCCGGCCTTTTCTGC
SEQ ID NO: 1262	**323951**	CGACCGAAGAGCTCTTTATAAGCCG	GCTGGCTTCTCGAGAAATATTCGGC
SEQ ID NO: 1263	**325339**	CTTCGGGGCGGTGTTACAGTACACT	GAAGCCCCGCCACAATGTCATGTGA
SEQ ID NO: 1264	**327761**	CGCAGTGTTGCGTGCATGAGGCTCA	GCGTCACAACGCACGTACTCCGAGT
SEQ ID NO: 1265	**327871**	AAACTTTGCGGTGTGTCGGCTCCGC	TTTGAAACGCCACACAGCCGAGGCG
SEQ ID NO: 1266	**328030**	GCAAGTTAGGCGACCCGACGACACC	CGTTCAATCCGCTGGGCTGCTGTGG
SEQ ID NO: 1267	**328482**	TTCACCAGGCGACACCGAAGAGAGG	AAGTGGTCCGCTGTGGCTTCTCTCC
SEQ ID NO: 1268	**328548**	AGCCAGTGGCGACACCGACGCCAGT	TCGGTCACCGCTGTGGCTGCGGTCA
SEQ ID NO: 1269	**328552**	TCGAAGCGGTGCGTGTGCCGATCCC	AGCTTCGCCACGCACACGGCTAGGG
SEQ ID NO: 1270	**328973**	GGGACATGTGCGGTGGTTTTACTAC	CCCTGTACACGCCACCAAAATGATG
SEQ ID NO: 1271	**329077**	NA	NA
SEQ ID NO: 1272	**329196**	CCTGTGGTGCGCTGCGGCAGCCCTG	GGACACCACGCGACGCCGTCGGGAC
SEQ ID NO: 1273	**329941**	TCCGACGACACTGCGCGTTGAGATC	AGGCTGCTGTGACGCGCAACTCTAG
SEQ ID NO: 1274	**330744**	GTTCGTGTAACTGCGAGGACTGATA	CAAGCACATTGACGCTCCTGACTAT
SEQ ID NO: 1275	**330978**	ACGTCCAGGGCGTCACGGACAAGAG	TGCAGGTCCCGCAGTGCCTGTTCTC
SEQ ID NO: 1276	**331248**	CTCCCGTGGCGTGTGGTACGTCCCA	GAGGGCACCGCACACCATGCAGGGT
SEQ ID NO: 1277	**331628**	CTGTCTTGTGCGTGTAAAGAGACGC	GACAGAACACGCACATTTCTCTGCG

SEQ ID NO: 1278	**331806**	ACCTGTTCTGCGTGCCGTGTCTGTA	TGGACAAGACGCACGGCACAGACAT
SEQ ID NO: 1279	**331817**	CGGTCGTGGTGCGTGCTACCGACAA	GCCAGCACCACGCACGATGGCTGTT
SEQ ID NO: 1280	**331848**	CCGCGGCGTGCGTACCTGACACAAG	GGCGCCGCACGCATGGACTGTGTTC
SEQ ID NO: 1281	**331995**	ATCCACTACTGCGTCGAGAACCCGG	TAGGTGATGACGCAGCTCTTGGGCC
SEQ ID NO: 1282	**332410**	CGACAGGTGTGCGTCTACATGGGCT	GCTGTCCACACGCAGATGTACCCGA
SEQ ID NO: 1283	**332502**	CTCGTGGATGCGTGGTCTGTAAAAT	GAGCACCTACGCACCAGACATTTTA
SEQ ID NO: 1284	**332729**	CGACTAAGGTGCGTACCGTGCTTTT	GCTGATTCCACGCATGGCACGAAAA
SEQ ID NO: 1285	**332747**	TCGCTGAGGTGCGTGAGTTCCATCA	AGCGACTCCACGCACTCAAGGTAGT
SEQ ID NO: 1286	**332821**	CCTTGTGTGCGTGTCAAAGACGGAC	GGAACACACGCACAGTTTCTGCCTG
SEQ ID NO: 1287	**332920**	CCCTCGGTGCGTGTGTTACGCGCAC	GGGAGCCACGCACACAATGCGCGTG
SEQ ID NO: 1288	**332992**	GGTTCCGCTGCGTGCCGTGCATTTA	CCAAGGCGACGCACGGCACGTAAAT
SEQ ID NO: 1289	**333279**	ACCGCGCGTCGTGCGTAAGCTACTA	TGGCGCGCAGCACGCATTCGATGAT
SEQ ID NO: 1290	**333395**	CTTTTGTGCGTCCTGTTGTGACTAC	GAAAACACGCAGGACAACACTGATG
SEQ ID NO: 1291	**333430**	ATGTACGAGTGTGCGTATCCGACAC	TACATGCTCACACGCATAGGCTGTG
SEQ ID NO: 1292	**333642**	AACTTCGGTGCGTGAGGACTTCTTG	TTGAAGCCACGCACTCCTGAAGAAC
SEQ ID NO: 1293	**333795**	GCTTCTACTACGTGCGTGTCCTCCA	CGAAGATGATGCACGCACAGGAGGT
SEQ ID NO: 1294	**334171**	TGTAGACTGTGTGCGTACACTTGCG	ACATCTGACACACGCATGTGAACGC
SEQ ID NO: 1295	**334307**	TATTGTGTGAGCGTAGAAGGTACCG	ATAACACACTCGCATCTTCCATGGC
SEQ ID NO: 1296	**334465**	AGAGTTTTAGCGTAGTGTGCGTCGT	TCTCAAAATCGCATCACACGCAGCA
SEQ ID NO: 1297	**334468**	CGCACGTCCAGCGTAGCTACAGCCA	GCGTGCAGGTCGCATCGATGTCGGT
SEQ ID NO: 1298	**334613**	AGGAACCAGCGTGTGTGGAACTGTC	TCCTTGGTCGCACACACCTTGACAG

SEQ ID NO: 1299	**335972**	CACGTCGCAGCGCCCATTGGGGGTC	GTGCAGCGTCGCGGGTAACCCCCAG
SEQ ID NO: 1300	**336078**	CGCCTGCCGCCGGGCCGCCAGCCCG	GCGGACGGCGGCCCGGCGGTCGGGC
SEQ ID NO: 1301	**336208**	ACGCCCGCCGCGGTCTTTGACGTTT	TGCGGGCGGCGCCAGAAACTGCAAA
SEQ ID NO: 1302	**336244**	TCGTGTCGGTGAGCGTCGAACTCCC	AGCACAGCCACTCGCAGCTTGAGGG
SEQ ID NO: 1303	**336341**	AAATCCCGCCGCTAACTTAACGTGG	TTTAGGGCGGCGATTGAATTGCACC
SEQ ID NO: 1304	**336346**	AAGTCATCCGCCGTTTCCGCCGGCT	TTCAGTAGGCGGCAAAGGCGGCCGA
SEQ ID NO: 1305	**336359**	CGCCCGCGCGCCGCCGGCTGCGCCC	GCGGGCGCGCGGCGGCCGACGCGGG
SEQ ID NO: 1306	**336674**	GGAGGCGCCGCCCGCCAGCTCGCCC	CCTCCGCGGCGGGCGGTCGAGCGGG
SEQ ID NO: 1307	**336773**	NA	NA
SEQ ID NO: 1308	**336902**	AGTTTCGCCGCCGACTCCAGTTTCT	TCAAAGCGGCGGCTGAGGTCAAAGA
SEQ ID NO: 1309	**336985**	TCCGCGCGCCGCACCATAGGGGTTT	AGGCGCGCGGCGTGGTATCCCCAAA
SEQ ID NO: 1310	**337109**	TTCCGCCGCGCCTTAGGGAAGAAGT	AAGGCGGCGCGGAATCCCTTCTTCA
SEQ ID NO: 1311	**337116**	CCCGCGCCGCCCGTCACGCCTTCGG	GGGCGCGGCGGGCAGTGCGGAAGCC
SEQ ID NO: 1312	**337190**	CGCCGGCCGCCAGCCGGGGGACTCG	GCGGCCGGCGGTCGGCCCCCTGAGC
SEQ ID NO: 1313	**337198**	ACGTTTCGCCGCCACCCAACAGGGT	TGCAAAGCGGCGGTGGGTTGTCCCA
SEQ ID NO: 1314	**337221**	AGCCACGCCGCCATGGTAAAAGAAG	TCGGTGCGGCGGTACCATTTTCTTC
SEQ ID NO: 1315	**337398**	TGTTCCGCCGCAGTCCGCAAGGAGT	ACAAGGCGGCGTCAGGCGTTCCTCA
SEQ ID NO: 1316	**337405**	GTGCTGGACCGCCACCAGAAGGTGA	CACGACCTGGCGGTGGTCTTCCACT
SEQ ID NO: 1317	**337443**	ACACCGGCCGCCGTCTTAAGTAGGA	TGTGGCCGGCGGCAGAATTCATCCT
SEQ ID NO: 1318	**337468**	CAGGGCCGCCGTCAGCACGATGGAC	GTCCCGGCGGCAGTCGTGCTACCTG
SEQ ID NO: 1319	**337528**	TTAGCCGCCGCCATAAAGAGACTGC	AATCGGCGGCGGTATTTCTCTGACG

SEQ ID NO: 1320	**337663**	GTTCCATCCGCCGTATCTCGACGAG	CAAGGTAGGCGGCATAGAGCTGCTC
SEQ ID NO: 1321	**338038**	CCTGAGCCGCCGCAGGACAACGGTT	GGACTCGGCGGCGTCCTGTTGCCAA
SEQ ID NO: 1322	**338084**	CCTCCCGCGCCACACCAGTAAAATT	GGAGGGCGCGGTGTGGTCATTTTAA
SEQ ID NO: 1323	**338085**	CGACCAACCGCAACCACAGAAATTT	GCTGGTTGGCGTTGGTGTCTTTAAA
SEQ ID NO: 1324	**338217**	TTCTTTCCGCCGACGAACTTCCTGT	AAGAAAGGCGGCTGCTTGAAGGACA
SEQ ID NO: 1325	**338357**	ATCCTCTACCGCATACATTTAGGGG	TAGGAGATGGCGTATGTAAATCCCC
SEQ ID NO: 1326	**338379**	AGCCGCCGCGCCAGCGCCGGCCCCC	TCGGCGGCGCGGTCGCGGCCGGGGG
SEQ ID NO: 1327	**338425**	CTCGTCCACCGCCACGGTAGAGGTG	GAGCAGGTGGCGGTGCCATCTCCAC
SEQ ID NO: 1328	**338724**	AGGTCCGCCGCAAAGTCCAAGAGTC	TCCAGGCGGCGTTTCAGGTTCTCAG
SEQ ID NO: 1329	**338908**	GGTCGTCCGCCGCAGACTCGGTCAT	CCAGCAGGCGGCGTCTGAGCCAGTA
SEQ ID NO: 1330	**339024**	CCCGCCGCGCAATGCTCCCTGTGTC	GGGCGGCGCGTTACGAGGGACACAG
SEQ ID NO: 1331	**339247**	TGTATCAGCCGCACGCACACCTTGG	ACATAGTCGGCGTGCGTGTGGAACC
SEQ ID NO: 1332	**339275**	TCATGTCCCGCACCGACGACAACCA	AGTACAGGGCGTGGCTGCTGTTGGT
SEQ ID NO: 1333	**339303**	GAAAGAATCGCCGACCGACGAGCCG	CTTTCTTAGCGGCTGGCTGCTCGGC
SEQ ID NO: 1334	**339379**	AGACAGTACGCCGCAGCTTCGCCTG	TCTGTCATGCGGCGTCGAAGCGGAC
SEQ ID NO: 1335	**339567**	TCGCCCGCCGCATGCCGGACCCCGG	AGCGGGCGGCGTACGGCCTGGGGCC
SEQ ID NO: 1336	**339817**	GCGCCCGCCGCAGCCGGCCGGCCCG	CGCGGGCGGCGTCGGCCGGCCGGGC
SEQ ID NO: 1337	**339820**	GGTCACCACCGCAGCTCCTTATAAT	CCAGTGGTGGCGTCGAGGAATATTA
SEQ ID NO: 1338	**339857**	TGTCACACTCCGCACACGTGGTGAC	ACAGTGTGAGGCGTGTGCACCACTG
SEQ ID NO: 1339	**340046**	TTTCACACTCGCACACATCGGGAGC	AAAGTGTGAGCGTGTGTAGCCCTCG
SEQ ID NO: 1340	**340127**	ACACAGAGCCGCACCAAAGGACGAG	TGTGTCTCGGCGTGGTTTCCTGCTC

SEQ ID NO: 1341	**340169**	GTGTCACACTCCGCACACGTGGTGA	CACAGTGTGAGGCGTGTGCACCACT
SEQ ID NO: 1342	**340463**	CTATCGTCCCGCACTCCTTGAAGTG	GATAGCAGGGCGTGAGGAACTTCAC
SEQ ID NO: 1343	**340507**	CGGCGTGTGCGCATATGACATATGT	GCCGCACACGCGTATACTGTATACA
SEQ ID NO: 1344	**340520**	CGTCAGCCTCGCCAACACCAGGGGC	GCAGTCGGAGCGGTTGTGGTCCCCG
SEQ ID NO: 1345	**340762**	GCGTCCGCCGCGCACCCGCGCCGCG	CGCAGGCGGCGCGTGGGCGCGGCGC
SEQ ID NO: 1346	**340768**	GACCCGCGGCGCACCGCCGCCGCGC	CTGGGCGCCGCGTGGCGGCGGCGCG
SEQ ID NO: 1347	**340794**	CTCTCCGTCTCGCACAAGTTGAGTC	GAGAGGCAGAGCGTGTTCAACTCAG
SEQ ID NO: 1348	**340862**	ACACCCGGCGCACATCATTTTAGAC	TGTGGGCCGCGTGTAGTAAAATCTG
SEQ ID NO: 1349	**341017**	ATCGTCCGCTCGCACCGATGAGGAT	TAGCAGGCGAGCGTGGCTACTCCTA
SEQ ID NO: 1350	**341020**	CTGTGCGTGCGCAAGAAGAACCTAC	GACACGCACGCGTTCTTCTTGGATG
SEQ ID NO: 1351	**341862**	GCGCGGCCTCGCACACACACACATG	CGCGCCGGAGCGTGTGTGTGTGTAC
SEQ ID NO: 1352	**342128**	CTTTCACTCGCACACGCGACGTCCT	GAAAGTGAGCGTGTGCGCTGCAGGA
SEQ ID NO: 1353	**342526**	AACCGGCTCGCACCCACAGAGGGGA	TTGGCCGAGCGTGGGTGTCTCCCCT
SEQ ID NO: 1354	**342851**	GCCGCCAGCGCTGCCCGCAGCCGGC	CGGCGGTCGCGACGGGCGTCGGCCG
SEQ ID NO: 1355	**343108**	CTACTCCACGCGCTGCTGCAAGAGT	GATGAGGTGCGCGACGACGTTCTCA
SEQ ID NO: 1356	**343263**	CGGCCGCCGCTCCTGAAGAAACAGA	GCCGGCGGCGAGGACTTCTTTGTCT
SEQ ID NO: 1357	**343321**	CACACACGTACTCGCACCTGGGCCT	GTGTGTGCATGAGCGTGGACCCGGA
SEQ ID NO: 1358	**344124**	GACCACTGCCGCTACTTGCCATGTA	CTGGTGACGGCGATGAACGGTACAT
SEQ ID NO: 1359	**344212**	AGAACTACGCCGCTCACCGACGGAA	TCTTGATGCGGCGAGTGGCTGCCTT
SEQ ID NO: 1360	**344326**	CCATTTCGCTAGGTGTGTGGACCCA	GGTAAAGCGATCCACACACCTGGGT
SEQ ID NO: 1361	**344401**	AATATATATCGCTGGTGTTGGCGGG	TTATATATAGCGACCACAACCGCCC

SEQ ID NO: 1362	**346035**	CATGTTAACGCACCATACACGGAGG	GTACAATTGCGTGGTATGTGCCTCC
SEQ ID NO: 1363	**346646**	CACACACACACGCAGGAGGAGAGAG	GTGTGTGTGTGCGTCCTCCTCTCTC
SEQ ID NO: 1364	**346689**	AGATCCCGACGCCTGATATTAGGGT	TCTAGGGCTGCGGACTATAATCCCA
SEQ ID NO: 1365	**346992**	ATCAGCCACGCACCACTGGACATGG	TAGTCGGTGCGTGGTGACCTGTACC
SEQ ID NO: 1366	**347220**	TCTACATTCACGCACACACTCTAAA	AGATGTAAGTGCGTGTGTGAGATTT
SEQ ID NO: 1367	**347524**	TTGGCATACGCACACGAAGACACGC	AACCGTATGCGTGTGCTTCTGTGCG
SEQ ID NO: 1368	**347607**	GACGCCGCGCACGCCAGGGCCGCCC	CTGCGGCGCGTGCGGTCCCGGCGGG
SEQ ID NO: 1369	**347640**	GGAGTCTACGACACGCAACCGGCTT	CCTCAGATGCTGTGCGTTGGCCGAA
SEQ ID NO: 1370	**347683**	CTGTTCACACGCCACACGGGAAACT	GACAAGTGTGCGGTGTGCCCTTTGA
SEQ ID NO: 1371	**347704**	ATTATTCACGCACACACTTCTAAGA	TAATAAGTGCGTGTGTGAAGATTCT
SEQ ID NO: 1372	**348010**	GTGGGGACACGCACCTACGAGTTCA	CACCCCTGTGCGTGGATGCTCAAGT
SEQ ID NO: 1373	**348017**	AGGTTGCACGCACCGACCGTGACCG	TCCAACGTGCGTGGCTGGCACTGGC
SEQ ID NO: 1374	**348236**	AGGTCCCGACGCAGGCCGACGACGT	TCCAGGGCTGCGTCCGGCTGCTGCA
SEQ ID NO: 1375	**348258**	GTAGCGACTGCACGCACACTACGTC	CATCGCTGACGTGCGTGTGATGCAG
SEQ ID NO: 1376	**348474**	AGGTTCTCACGCACACCAGGTACTC	TCCAAGAGTGCGTGTGGTCCATGAG
SEQ ID NO: 1377	**348540**	GTGCACACGTACACGCAGACATTCG	CACGTGTGCATGTGCGTCTGTAAGC
SEQ ID NO: 1378	**348801**	ATCAACCACGCGCACGGGACCAGGG	TAGTTGGTGCGCGTGCCCTGGTCCC
SEQ ID NO: 1379	**349110**	CACGACCACCGCGCCGTCCTGGGAG	GTGCTGGTGGCGCGGCAGGACCCTC
SEQ ID NO: 1380	**349425**	CTGACCCTACGCAGGGAATCTGACC	GACTGGGATGCGTCCCTTAGACTGG
SEQ ID NO: 1381	**349433**	GGTGGCTGAACCGACCTACTGCCGA	CCACCGACTTGGCTGGATGACGGCT
SEQ ID NO: 1382	**349983**	CCACAGACCGCGAGGACTGTAGTAC	GGTGTCTGGCGCTCCTGACATCATG

SEQ ID NO: 1383	**349989**	TCCCCGCCGCGCTACGTCTCCGCCG	AGGGGCGGCGCGATGCAGAGGCGGC
SEQ ID NO: 1384	**350124**	GTCGCCGCCCGCGCGGTGGCCCCCG	CAGCGGCGGGCGCGCCACCGGGGGC
SEQ ID NO: 1385	**350302**	CGGCCGCCGCGCCAGCGGGGCCGCG	GCCGGCGGCGCGGTCGCCCCGGCGC
SEQ ID NO: 1386	**350728**	AGCGGGTGCGCGTGATACAGCTACA	TCGCCCACGCGCACTATGTCGATGT
SEQ ID NO: 1387	**351094**	ACCTCCCGTCGCGTCCGAGTAACAA	TGGAGGGCAGCGCAGGCTCATTGTT
SEQ ID NO: 1388	**351143**	TGCGCCGCCGCGTAAACATAGGCAC	ACGCGGCGGCGCATTTGTATCCGTG
SEQ ID NO: 1389	**351223**	CACGCCAACGCGCCAGCCCGCGCGG	GTGCGGTTGCGCGGTCGGGCGCGCC
SEQ ID NO: 1390	**351719**	CGCACAGACCGCGACGCAAACGTGA	GCGTGTCTGGCGCTGCGTTTGCACT
SEQ ID NO: 1391	**351777**	TTGACGCACCGCGACGACTACCTGT	AACTGCGTGGCGCTGCTGATGGACA
SEQ ID NO: 1392	**351783**	TCCTACAGCCGCGTGTCGACCGAAG	AGGATGTCGGCGCACAGCTGGCTTC
SEQ ID NO: 1393	**351863**	ACACGTTCAGTAAATGGGGGTCGAT	TGTGCAAGTCATTTACCCCCAGCTA
SEQ ID NO: 1394	**352555**	AGACACACACGTACGCGGAACCCTG	TCTGTGTGTGCATGCGCCTTGGGAC
SEQ ID NO: 1395	**352671**	GGACCCAACGCGCACGCACTGAAGG	CCTGGGTTGCGCGTGCGTGACTTCC
SEQ ID NO: 1396	**355303**	NA	NA
SEQ ID NO: 1397	**356152**	AGTTGCGAAAATGTGAGTGTGTGTC	TCAACGCTTTTACACTCACACACAG
SEQ ID NO: 1398	**357646**	GAAACACAAAAGGTAGTCCCGGAGT	CTTTGTGTTTTCCATCAGGGCCTCA
SEQ ID NO: 1399	**359502**	ATCTACCTCAAATGGTGGGCGAAAC	TAGATGGAGTTTACCACCCGCTTTG
SEQ ID NO: 1400	**362727**	ACATCCTACAAATGTGTGTGATGTC	TGTAGGATGTTTACACACACTACAG
SEQ ID NO: 1401	**363474**	GTAAAACCAAGAGTCCCAAACAATA	CATTTTGGTTCTCAGGGTTTGTTAT
SEQ ID NO: 1402	**363607**	GAAGAGTCCAAAGCGCCGACCACGT	CTTCTCAGGTTTCGCGGCTGGTGCA
SEQ ID NO: 1403	**364087**	TCGTGCGTGACAAAGCCCAAGCCCT	AGCACGCACTGTTTCGGGTTCGGGA

SEQ ID NO: 1404	**365423**	AGATCCGCAAAGTGTGCGTCGTCGC	TCTAGGCGTTTCACACGCAGCAGCG
SEQ ID NO: 1405	**366896**	ACACACCAAAACAGACACACACGTA	TGTGTGGTTTTGTCTGTGTGTGCAT
SEQ ID NO: 1406	**371967**	GGTGTGTGTGAAAACATTAACTTTA	CCACACACACTTTTGTAATTGAAAT
SEQ ID NO: 1407	**375331**	CGGAAAGAAAGACCTCAGCCGTCTG	GCCTTTCTTTCTGGAGTCGGCAGAC
SEQ ID NO: 1408	**376284**	GTCTCCGCCGAAATAATCTTGATCT	CAGAGGCGGCTTTATTAGAACTAGA
SEQ ID NO: 1409	**377870**	CTCCACTCGAAAGTGAACGACAGGT	GAGGTGAGCTTTCACTTGCTGTCCA
SEQ ID NO: 1410	**378701**	TTCACCGGAAACAACACTAAAGAGG	AAGTGGCCTTTGTTGTGATTTCTCC
SEQ ID NO: 1411	**378768**	ACCGACCCGAAACTCCTAGTTAGTG	TGGCTGGGCTTTGAGGATCAATCAC
SEQ ID NO: 1412	**379035**	CTGAGAGGAAACTACCACCACTATC	GACTCTCCTTTGATGGTGGTGATAG
SEQ ID NO: 1413	**379071**	CGACCCGACGAAAGTAGTGCGCATT	GCTGGGCTGCTTTCATCACGCGTAA
SEQ ID NO: 1414	**379094**	NA	NA
SEQ ID NO: 1415	**379136**	ATTTTGAAACACGACACCGACTTCC	TAAAACTTTGTGCTGTGGCTGAAGG
SEQ ID NO: 1416	**380310**	GTTACCGAGGAAACGACGCACACCT	CAATGGCTCCTTTGCTGCGTGTGGA
SEQ ID NO: 1417	**383592**	CCTACTTTAAAGATTAGTGTGTGTG	GGATGAAATTTCTAATCACACACAC
SEQ ID NO: 1418	**383865**	CCTGTCATAAATAGTGTGTGTCCTG	GGACAGTATTTATCACACACAGGAC
SEQ ID NO: 1419	**388057**	CGTTGTGTGTAAAGGATCTCCCGTT	GCAACACACATTTCCTAGAGGGCAA
SEQ ID NO: 1420	**389368**	CTTTGTAGTAAATCCACGGGTCGTT	GAAACATCATTTAGGTGCCCAGCAA
SEQ ID NO: 1421	**392355**	TTAACGAAAATTACGTGTGTGTTTG	AATTGCTTTTAATGCACACACAAAC
SEQ ID NO: 1422	**392647**	TGGGATAAATTGTGTTGTGGGTAAT	ACCCTATTTAACACAACACCCATTA
SEQ ID NO: 1423	**394005**	ATCCTACAAATGTGTGTGATGTCGT	TAGGATGTTTACACACACTACAGCA
SEQ ID NO: 1424	**397445**	CAGCACAAATCTGTGTGTAGGGTGT	GTCGTGTTTAGACACACATCCCACA

SEQ ID NO: 1425	**401195**	TGTGTGTGGAATGTGTGTGCATAAT	ACACACACCTTACACACACGTATTA
SEQ ID NO: 1426	**401544**	NA	NA
SEQ ID NO: 1427	**402078**	AGAAGAACGAATGAATATGGGTCGG	TCTTCTTGCTTACTTATACCCAGCC
SEQ ID NO: 1428	**402881**	GGGAACGACGAATGCCGCGACCGTC	CCCTTGCTGCTTACGGCGCTGGCAG
SEQ ID NO: 1429	**409965**	TCTTGACCTAATTAGTGTAAGGAAC	AGAACTGGATTAATCACATTCCTTG
SEQ ID NO: 1430	**410674**	GGTGTGTGTATAATGAGTATCAAAT	CCACACACATATTACTCATAGTTTA
SEQ ID NO: 1431	**411895**	GTCCGTCCCGTAATTAAAGTAGAAG	CAGGCAGGGCATTAATTTCATCTTC
SEQ ID NO: 1432	**413858**	GTGGTGGTGTAATCGAATCTATACC	CACCACCACATTAGCTTAGATATGG
SEQ ID NO: 1433	**417164**	ATTTCTCAAGGAGGGATCAGGACCT	TAAAGAGTTCCTCCCTAGTCCTGGA
SEQ ID NO: 1434	**421111**	GTCCCGAGAAAGCAACAACCTGATG	CAGGGCTCTTTCGTTGTTGGACTAC
SEQ ID NO: 1435	**423647**	ACACCGACGCGAAGGCTACGGCCAA	TGTGGCTGCGCTTCCGATGCCGGTT
SEQ ID NO: 1436	**424623**	ACCCTGCGAAGGTGAACTACGGTAT	TGGGACGCTTCCACTTGATGCCATA
SEQ ID NO: 1437	**436546**	GCGACTACTACGACGAAGAATTTGG	CGCTGATGATGCTGCTTCTTAAACC
SEQ ID NO: 1438	**437364**	CCGACTACCGTAAGGTCATGACCCA	GGCTGATGGCATTCCAGTACTGGGT
SEQ ID NO: 1439	**444536**	ACAACGACGAAAGTGACCGGGGCAT	TGTTGCTGCTTTCACTGGCCCCGTA
SEQ ID NO: 1440	**447471**	TCGGCGTGAAAGTCGCGTGCGTCCT	AGCCGCACTTTCAGCGCACGCAGGA
SEQ ID NO: 1441	**448852**	AAAACCAAGTCGCACACACACACAT	TTTTGGTTCAGCGTGTGTGTGTGTA
SEQ ID NO: 1442	**452417**	GTGGAAGAAAGTACACACGCACACC	CACCTTCTTTCATGTGTGCGTGTGG
SEQ ID NO: 1443	**452822**	ACTCATCAAAGTAGGTGTGTGTCTG	TGAGTAGTTTCATCCACACACAGAC
SEQ ID NO: 1444	**454255**	GTCTGATTTAAGTGTGCGTGGTCCC	CAGACTAAATTCACACGCACCAGGG
SEQ ID NO: 1445	**454406**	ACCAAACTAAGTGCGTGTGTAAATA	TGGTTTGATTCACGCACACATTTAT

SEQ ID NO: 1446	**457672**	ATACGCACGCCAATGGTGCCGTTGT	TATGCGTGCGGTTACCACGGCAACA
SEQ ID NO: 1447	**462579**	ACAACTCACACAACTCACACCACAG	TGTTGAGTGTGTTGAGTGTGGTGTC
SEQ ID NO: 1448	**463044**	GGAATTACCAACCAACCAAGATGAT	CCTTAATGGTTGGTTGGTTCTACTA
SEQ ID NO: 1449	**463384**	GTGCGCCGCCAACACCTAGAGTAAT	CACGCGGCGGTTGTGGATCTCATTA
SEQ ID NO: 1450	**463910**	ACCACAGCCAACGAGGTCATGGTTG	TGGTGTCGGTTGCTCCAGTACCAAC
SEQ ID NO: 1451	**464449**	TCCAGAGACCACATGCCACCGTGTG	AGGTCTCTGGTGTACGGTGGCACAC
SEQ ID NO: 1452	**464475**	GTCCGTCGTCCCAACCGATAAATTT	CAGGCAGCAGGGTTGGCTATTTAAA
SEQ ID NO: 1453	**465922**	CTACATAGGCAACCGGCTCAACCGT	GATGTATCCGTTGGCCGAGTTGGCA
SEQ ID NO: 1454	**473007**	ACAATTTCAAGTGGTGTGTGTCACC	TGTTAAAGTTCACCACACACAGTGG
SEQ ID NO: 1455	**474127**	AGACCAGACTCAACCTCACCAGGAG	TCTGGTCTGAGTTGGAGTGGTCCTC
SEQ ID NO: 1456	**474343**	CCATACATACAACTCACACCACACA	GGTATGTATGTTGAGTGTGGTGTGT
SEQ ID NO: 1457	**475793**	CGACCACGACTCAACGGACGAGGGA	GCTGGTGCTGAGTTGCCTGCTCCCT
SEQ ID NO: 1458	**476538**	GTTTATTTCAACGACGACATCGTTC	CAAATAAAGTTGCTGCTGTAGCAAG
SEQ ID NO: 1459	**476685**	GTACGCTACACATCAACTGTCGGTG	CATGCGATGTGTAGTTGACAGCCAC
SEQ ID NO: 1460	**478744**	AGAGTGTGTGTCAAGCGGAGAAACT	TCTCACACACAGTTCGCCTCTTTGA
SEQ ID NO: 1461	**479041**	CTAAACGACGTCAACTGAGACTGGG	GATTTGCTGCAGTTGACTCTGACCC
SEQ ID NO: 1462	**479681**	CACTTGTGTCAAGTGGTGGTGGTAT	GTGAACACAGTTCACCACCACCATA
SEQ ID NO: 1463	**481037**	GTGTGTGTGCCATTGATCCATTCCT	CACACACACGGTAACTAGGTAAGGA
SEQ ID NO: 1464	**482470**	CTAGTGTGTCCATTGTGTGTGCACC	GATCACACAGGTAACACACACGTGG
SEQ ID NO: 1465	**482962**	GACGTCATCCCATGGTGTGTGTCGT	CTGCAGTAGGGTACCACACACAGCA
SEQ ID NO: 1466	**483733**	AAGGGCCATGACCACGTCGTCCAGT	TTCCCGGTACTGGTGCAGCAGGTCA

SEQ ID NO: 1467	**483789**	CCGTGAGCCATGACGACGTCCTCGA	GGCACTCGGTACTGCTGCAGGAGCT
SEQ ID NO: 1468	**483952**	GTGCCGCACCATGACGCATACGTCG	CACGGCGTGGTACTGCGTATGCAGC
SEQ ID NO: 1469	**484154**	CTCCGTCTCCATGTACGAACTTGGA	GAGGCAGAGGTACATGCTTGAACCT
SEQ ID NO: 1470	**485016**	CACTACCACCATCGCATAAAGAAGG	GTGATGGTGGTAGCGTATTTCTTCC
SEQ ID NO: 1471	**488375**	AGCTCGACGGCATCCTTTGTAAGCA	TCGAGCTGCCGTAGGAAACATTCGT
SEQ ID NO: 1472	**489528**	NA	NA
SEQ ID NO: 1473	**489529**	NA	NA
SEQ ID NO: 1474	**491076**	AGGAGAACCATACCGTCCGTGAACT	TCCTCTTGGTATGGCAGGCACTTGA
SEQ ID NO: 1475	**491120**	TCTCTCGACACCATATTATAATCCG	AGAGAGCTGTGGTATAATATTAGGC
SEQ ID NO: 1476	**492541**	ACGGTGTGTGCATAGTGTGTATACA	TGCCACACACGTATCACACATATGT
SEQ ID NO: 1477	**493658**	GGGACAATCATTGACACCGACGACA	CCCTGTTAGTAACTGTGGCTGCTGT
SEQ ID NO: 1478	**494355**	CCGTGCGTTCATGTGTCGGAGACAT	GGCACGCAAGTACACAGCCTCTGTA
SEQ ID NO: 1479	**496192**	AGAACTACTTCATCGAGTGGTCGGC	TCTTGATGAAGTAGCTCACCAGCCG
SEQ ID NO: 1480	**496588**	GTGTCATACCGTCATCCATCCCGAG	CACAGTATGGCAGTAGGTAGGGCTC
SEQ ID NO: 1481	**497163**	GCTGCTTGTCATTGTGTGTCTTTGT	CGACGAACAGTAACACACAGAAACA
SEQ ID NO: 1482	**497823**	AGAACTTAGTCATGTGTGTGCCTTA	TCTTGAATCAGTACACACACGGAAT
SEQ ID NO: 1483	**498510**	CACCCGTCGTCATTAGAGGAAGAAT	GTGGGCAGCAGTAATCTCCTTCTTA
SEQ ID NO: 1484	**500775**	TTCACACCACAAAAAGATATTGAGT	AAGTGTGGTGTTTTTCTATAACTCA
SEQ ID NO: 1485	**503824**	ACTGACACACACAAAGACAGACACA	TGACTGTGTGTGTTTCTGTCTGTGT
SEQ ID NO: 1486	**503826**	GCGCGCACACACAAAGAGCCGATGA	CGCGCGTGTGTGTTTCTCGGCTACT
SEQ ID NO: 1487	**504422**	GACCACACGCACAACTCGGGGCTTG	CTGGTGTGCGTGTTGAGCCCCGAAC

SEQ ID NO: 1488	**507149**	CGATCGGACGACAACCCGACGCAAA	GCTAGCCTGCTGTTGGGCTGCGTTT
SEQ ID NO: 1489	**507381**	GTCGGTGGTGACAAGTAAAATCAAG	CAGCCACCACTGTTCATTTTAGTTC
SEQ ID NO: 1490	**507447**	ATTACTCAGACAAATGTGTGTGGTT	TAATGAGTCTGTTTACACACACCAA
SEQ ID NO: 1491	**509574**	CTACGCGACCGACAACTAGAGGCAC	GATGCGCTGGCTGTTGATCTCCGTG
SEQ ID NO: 1492	**509652**	GTCTCGCCCGACAACGACCTCCTCT	CAGAGCGGGCTGTTGCTGGAGGAGA
SEQ ID NO: 1493	**509978**	TTGTGACGACGACAACTCCGCCGGT	AACACTGCTGCTGTTGAGGCGGCCA
SEQ ID NO: 1494	**511769**	AGTACGGCGACTACAACGACACGTC	TCATGCCGCTGATGTTGCTGTGCAG
SEQ ID NO: 1495	**513815**	CACACGTACACACATTTCTACTCTA	GTGTGCATGTGTGTAAAGATGAGAT
SEQ ID NO: 1496	**514143**	TCACACGTACACACATTTCTACTCT	AGTGTGCATGTGTGTAAAGATGAGA
SEQ ID NO: 1497	**514200**	GTACACACGTACTCACATGGTAATT	CATGTGTGCATGAGTGTACCATTAA
SEQ ID NO: 1498	**514802**	ACCACAAACATCACACACACATTAC	TGGTGTTTGTAGTGTGTGTGTAATG
SEQ ID NO: 1499	**515771**	CGTCTACCGACGACATTCCATGTAC	GCAGATGGCTGCTGTAAGGTACATG
SEQ ID NO: 1500	**516647**	GGTACTGTGTGACATGTGTGGTCCC	CCATGACACACTGTACACACCAGGG
SEQ ID NO: 1501	**516703**	ACGACTCCGACGACATTATTCCCGA	TGCTGAGGCTGCTGTAATAAGGGCT
SEQ ID NO: 1502	**516781**	TCTGTGTAAGACATGTGTGTCTGTG	AGACACATTCTGTACACACAGACAC
SEQ ID NO: 1503	**519951**	GTACTTAACGACGACATAGGGGAGC	CATGAATTGCTGCTGTATCCCCTCG
SEQ ID NO: 1504	**522163**	TCGAACTCCCAGGTGTGTGTGTTAA	AGCTTGAGGGTCCACACACACAATT
SEQ ID NO: 1505	**522856**	AGAGGCACCAGGCACCATTTCGTGT	TCTCCGTGGTCCGTGGTAAAGCACA
SEQ ID NO: 1506	**523277**	CTTCAGTCCAGCCTCCATCAGGGTT	GAAGTCAGGTCGGAGGTAGTCCCAA
SEQ ID NO: 1507	**523417**	ACCACTACTACCAGGGACTCTTTTT	TGGTGATGATGGTCCCTGAGAAAAA
SEQ ID NO: 1508	**523428**	GTCTACGACACCCAGCAAGAAAATG	CAGATGCTGTGGGTCGTTCTTTTAC

SEQ ID NO: 1509	**523820**	GGCCCGGCAGCCCACCGCCGCGCCG	CCGGGCCGTCGGGTGGCGGCGCGGC
SEQ ID NO: 1510	**524191**	GGTACACCGCCAGCTTCTGCACGTG	CCATGTGGCGGTCGAAGACGTGCAC
SEQ ID NO: 1511	**525402**	ACACTCCACGCAGGTCCACGTGGGT	TGTGAGGTGCGTCCAGGTGCACCCA
SEQ ID NO: 1512	**526597**	GCTTCGACACCAGAACCCTCAATAA	CGAAGCTGTGGTCTTGGGAGTTATT
SEQ ID NO: 1513	**526949**	ACAGCCGCGCAGCCTCCCAGGCCGT	TGTCGGCGCGTCGGAGGGTCCGGCA
SEQ ID NO: 1514	**528173**	TCCGTCGTCCCAGAGGTTCCTCCGA	AGGCAGCAGGGTCTCCAAGGAGGCT
SEQ ID NO: 1515	**532701**	CTTAGTTTCAGGACGTGTGTGTTAC	GAATCAAAGTCCTGCACACACAATG
SEQ ID NO: 1516	**535076**	AGCGTGTGCGTCAGCAACTCGTCGC	TCGCACACGCAGTCGTTGAGCAGCG
SEQ ID NO: 1517	**535144**	NA	NA
SEQ ID NO: 1518	**537291**	GAAGAACCGTCAGAATGTCGCCATG	CTTCTTGGCAGTCTTACAGCGGTAC
SEQ ID NO: 1519	**537986**	GTACCTACCTACTCAGACGTATGTG	CATGGATGGATGAGTCTGCATACAC
SEQ ID NO: 1520	**540251**	CCAAGTGCAGTGGTTGTTTCGCGCC	GGTTCACGTCACCAACAAAGCGCGG
SEQ ID NO: 1521	**541072**	AGACGTGCGTGCAGTGCTATAGACC	TCTGCACGCACGTCACGATATCTGG
SEQ ID NO: 1522	**541735**	GTGACCACACCAGTAGTGCCGAGAG	CACTGGTGTGGTCATCACGGCTCTC
SEQ ID NO: 1523	**541864**	ACGACCGACGCGCAGTTATCCTCTT	TGCTGGCTGCGCGTCAATAGGAGAA
SEQ ID NO: 1524	**542653**	GGTGTCCGCCAGTACGACGACCTCC	CCACAGGCGGTCATGCTGCTGGAGG
SEQ ID NO: 1525	**544631**	CGTTGTTGTCAGTCACCTCGTACCT	GCAACAACAGTCAGTGGAGCATGGA
SEQ ID NO: 1526	**544956**	CGTACTTGTGTCAGTGGGTGATGAT	GCATGAACACAGTCACCCACTACTA
SEQ ID NO: 1527	**545669**	GCACGCACAACAGCCTCAACGGTAT	CGTGCGTGTTGTCGGAGTTGCCATA
SEQ ID NO: 1528	**545708**	GGTGGGTGTCAGTGAGTACCCTCCT	CCACCCACAGTCACTCATGGGAGGA
SEQ ID NO: 1529	**546039**	GACCCGCCACAGGAGCAATAGCTAT	CTGGGCGGTGTCCTCGTTATCGATA

SEQ ID NO: 1530	**546073**	CTTGTGTGTCAGTAGTGAGCCCGAA	GAACACACAGTCATCACTCGGGCTT
SEQ ID NO: 1531	**546666**	NA	NA
SEQ ID NO: 1532	**547478**	AGGGAGCACAGCAACCACCGGTGTC	TCCCTCGTGTCGTTGGTGGCCACAG
SEQ ID NO: 1533	**548214**	GCACACGTACACACAGGAACCGGCT	CGTGTGCATGTGTGTCCTTGGCCGA
SEQ ID NO: 1534	**548361**	CTTACACACACAGCAGGAAGACGTC	GAATGTGTGTGTCGTCCTTCTGCAG
SEQ ID NO: 1535	**548517**	CAGAACGACGACAGGATGAATCTAC	GTCTTGCTGCTGTCCTACTTAGATG
SEQ ID NO: 1536	**548627**	GTCACACACCACAGCTAGGACGTAT	CAGTGTGTGGTGTCGATCCTGCATA
SEQ ID NO: 1537	**550286**	GTCTCCGTCCACAGATTCGGCCTGG	CAGAGGCAGGTGTCTAAGCCGGACC
SEQ ID NO: 1538	**550740**	TCGAACTCCACAGACCGGGACAACT	AGCTTGAGGTGTCTGGCCCTGTTGA
SEQ ID NO: 1539	**551066**	NA	NA
SEQ ID NO: 1540	**551372**	NA	NA
SEQ ID NO: 1541	**551838**	TTCAGGTGACAGACCACGCACACGT	AAGTCCACTGTCTGGTGCGTGTGCA
SEQ ID NO: 1542	**553302**	CTACTAGAGATACAGGGTCCGTCGT	GATGATCTCTATGTCCCAGGCAGCA
SEQ ID NO: 1543	**555027**	AAAACACACAGTCACACCACACATA	TTTTGTGTGTCAGTGTGGTGTGTAT
SEQ ID NO: 1544	**555461**	TCTAGTCGGCGACAGTGTGCGTGTC	AGATCAGCCGCTGTCACACGCACAG
SEQ ID NO: 1545	**557008**	GGTCCCGACGACAGTACATTAGATC	CCAGGGCTGCTGTCATGTAATCTAG
SEQ ID NO: 1546	**557173**	GGTCCCGAAACCTGGGCTACTAATT	CCAGGGCTTTGGACCCGATGATTAA
SEQ ID NO: 1547	**557821**	CGACCTACGAAACCGCCGCTTCCGC	GCTGGATGCTTTGGCGGCGAAGGCG
SEQ ID NO: 1548	**558199**	GACCGACCTAAACCCTTATGTCCGA	CTGGCTGGATTTGGGAATACAGGCT
SEQ ID NO: 1549	**559118**	AGTCTGTCGAAACCACGTGTGTGTG	TCAGACAGCTTTGGTGCACACACAC
SEQ ID NO: 1550	**559193**	CGAGACGACGTAAACCCGGACGTAG	GCTCTGCTGCATTTGGGCCTGCATC

SEQ ID NO: 1551	**559592**	ACAATTAAACCTCTGTCCGGTCCAC	TGTTAATTTGGAGACAGGCCAGGTG
SEQ ID NO: 1552	**561014**	GACATCGGCAACCACAGCAACCAGA	CTGTAGCCGTTGGTGTCGTTGGTCT
SEQ ID NO: 1553	**561197**	ACACGTCCGCAACCTCACGGAAAAG	TGTGCAGGCGTTGGAGTGCCTTTTC
SEQ ID NO: 1554	**561275**	GTTTCCCAACCGTGTGTGTAACGTC	CAAAGGGTTGGCACACACATTGCAG
SEQ ID NO: 1555	**561740**	ACGTCGTCCGCAACCTCTAGTAGTT	TGCAGCAGGCGTTGGAGATCATCAA
SEQ ID NO: 1556	**561992**	ATGGACACAACCCACGTCCACGGGT	TACCTGTGTTGGGTGCAGGTGCCCA
SEQ ID NO: 1557	**562254**	AACACCGGAACCAACAGGTCAGCCG	TTGTGGCCTTGGTTGTCCAGTCGGC
SEQ ID NO: 1558	**562318**	CAGGGGAACCCACCTCAGCAGGAGT	GTCCCCTTGGGTGGAGTCGTCCTCA
SEQ ID NO: 1559	**564873**	TCACTGTTGAACCGCCGACGACGGT	AGTGACAACTTGGCGGCTGCTGCCA
SEQ ID NO: 1560	**565130**	GTGTGTGACCGAACCTTAACCCGTA	CACACACTGGCTTGGAATTGGGCAT
SEQ ID NO: 1561	**565984**	GTGTGTGTGTCGAACCTTAACCATC	CACACACACAGCTTGGAATTGGTAG
SEQ ID NO: 1562	**567626**	ACGCCGCCAACAAGACACTAGATGA	TGCGGCGGTTGTTCTGTGATCTACT
SEQ ID NO: 1563	**570168**	AGAGCACAAACACACATACGAGTTG	TCTCGTGTTTGTGTGTATGCTCAAC
SEQ ID NO: 1564	**573762**	TGCACACCGAACACACGGAGGACGC	ACGTGTGGCTTGTGTGCCTCCTGCG
SEQ ID NO: 1565	**576538**	GGCACACTGTAACCGTCCGTCACGG	CCGTGTGACATTGGCAGGCAGTGCC
SEQ ID NO: 1566	**587891**	ATCGAAAAACGGGACAGAGGAGATC	TAGCTTTTTGCCCTGTCTCCTCTAG
SEQ ID NO: 1567	**590383**	CGTGTGTGTGAACGGTCCTCCCGTC	GCACACACACTTGCCAGGAGGGCAG
SEQ ID NO: 1568	**592486**	GACGTACCGCCAACGACGGGCCGAG	CTGCATGGCGGTTGCTGCCCGGCTC
SEQ ID NO: 1569	**594041**	GTGTGTGTGTAAACGTGTGGCCCCT	CACACACACATTTGCACACCGGGGA
SEQ ID NO: 1570	**594058**	AGAACGAACTAACGACTACCCTTTG	TCTTGCTTGATTGCTGATGGGAAAC
SEQ ID NO: 1571	**595090**	ACTTCCTAGAACGTGCGTGTGTCTC	TGAAGGATCTTGCACGCACACAGAG

SEQ ID NO: 1572	**595215**	CCACCGTGTAACGTGTGTGTACGCA	GGTGGCACATTGCACACACATGCGT
SEQ ID NO: 1573	**595235**	TTATATTCTAACGTGTGGTGGGACC	AATATAAGATTGCACACCACCCTGG
SEQ ID NO: 1574	**596093**	GCACCAACGCACCATTAGGGACCGT	CGTGGTTGCGTGGTAATCCCTGGCA
SEQ ID NO: 1575	**597195**	CAGACACTCCACACCGCGCCGCAGA	GTCTGTGAGGTGTGGCGCGGCGTCT
SEQ ID NO: 1576	**597268**	TCCGCTGCCACCATCGTGGTGAGTT	AGGCGACGGTGGTAGCACCACTCAA
SEQ ID NO: 1577	**597399**	CTATTGCTCACCTCCGTCCGATGGA	GATAACGAGTGGAGGCAGGCTACCT
SEQ ID NO: 1578	**597820**	CAACACCCACCAACAGGGAGCTGTT	GTTGTGGGTGGTTGTCCCTCGACAA
SEQ ID NO: 1579	**597883**	AGTTACTCACCACCGCCTATGGACG	TCAATGAGTGGTGGCGGATACCTGC
SEQ ID NO: 1580	**597903**	CACACACCCACCCACGCGTAAACAC	GTGTGTGGGTGGGTGCGCATTTGTG
SEQ ID NO: 1581	**598536**	AGCAACGACCACCTTGACGACGGTT	TCGTTGCTGGTGGAACTGCTGCCAA
SEQ ID NO: 1582	**598818**	NA	NA
SEQ ID NO: 1583	**598970**	GAGAGTCCTCCACCACACCGTCGCT	CTCTCAGGAGGTGGTGTGGCAGCGA
SEQ ID NO: 1584	**599365**	GCCGACGAGCCACCGGCGTTGATCA	CGGCTGCTCGGTGGCCGCAACTAGT
SEQ ID NO: 1585	**599836**	CGCGTGCGTGCACCCGTGATAAAAA	GCGCACGCACGTGGGCACTATTTTT
SEQ ID NO: 1586	**600442**	GTGTGCGTCGCCACCGACACTCATA	CACACGCAGCGGTGGCTGTGAGTAT
SEQ ID NO: 1587	**601075**	CGTTCCGCACACACATGATGATAGT	GCAAGGCGTGTGTGTACTACTATCA
SEQ ID NO: 1588	**601291**	TGAGTCCACGCACACATGATCCGGC	ACTCAGGTGCGTGTGTACTAGGCCG
SEQ ID NO: 1589	**601348**	GTTATGTCCGCACCGACTGACTCGC	CAATACAGGCGTGGCTGACTGAGCG
SEQ ID NO: 1590	**601390**	ACACATCACCACACATACACATCAC	TGTGTAGTGGTGTGTATGTGTAGTG
SEQ ID NO: 1591	**601565**	GTCCGGACCGCACATGGAACGAACC	CAGGCCTGGCGTGTACCTTGCTTGG
SEQ ID NO: 1592	**601912**	ACACACGTACTCGCACCTGGGCCTC	TGTGTGCATGAGCGTGGACCCGGAG

SEQ ID NO: 1593	**602002**	ACACACTCCCACACTCCACACTCAC	TGTGTGAGGGTGTGAGGTGTGAGTG
SEQ ID NO: 1594	**602032**	GGGTTCACCACAGGGCCTCTACGTC	CCCAAGTGGTGTCCCGGAGATGCAG
SEQ ID NO: 1595	**602601**	GGATAACCCACACAACATTTGTCTC	CCTATTGGGTGTGTTGTAAACAGAG
SEQ ID NO: 1596	**603099**	ACACACACCCACAGGTTACGGAGGG	TGTGTGTGGGTGTCCAATGCCTCCC
SEQ ID NO: 1597	**603465**	CGCCGCCCACAGTTAGACGTTCTGT	GCGGCGGGTGTCAATCTGCAAGACA
SEQ ID NO: 1598	**603470**	GCAGACACTCCACACCGCGCCGCAG	CGTCTGTGAGGTGTGGCGCGGCGTC
SEQ ID NO: 1599	**603583**	AAGGGCCACACACCGCACTGTACAA	TTCCCGGTGTGTGGCGTGACATGTT
SEQ ID NO: 1600	**603678**	GTACCTCCGGCACAATGGTACCGAG	CATGGAGGCCGTGTTACCATGGCTC
SEQ ID NO: 1601	**604108**	CTACTCAACCACACCCTCAGAGGGC	GATGAGTTGGTGTGGGAGTCTCCCG
SEQ ID NO: 1602	**604291**	GTGTACACCGACCACAGAGGATATG	CACATGTGGCTGGTGTCTCCTATAC
SEQ ID NO: 1603	**604358**	GTCTTACACGTCCACAGACGCCTAT	CAGAATGTGCAGGTGTCTGCGGATA
SEQ ID NO: 1604	**604639**	TTCTTATCCACACACGGGAGCCTCT	AAGAATAGGTGTGTGCCCTCGGAGA
SEQ ID NO: 1605	**604647**	CGACGCCGGCACAACTGTGTTTGAC	GCTGCGGCCGTGTTGACACAAACTG
SEQ ID NO: 1606	**604772**	GGCCGCCCACACACCAGGTGGAGGT	CCGGCGGGTGTGTGGTCCACCTCCA
SEQ ID NO: 1607	**604856**	CAGACACTCCACACCGTGCCGCAGA	GTCTGTGAGGTGTGGCACGGCGTCT
SEQ ID NO: 1608	**604863**	AAGACACCCACACGCCAAAGTCAAT	TTCTGTGGGTGTGCGGTTTCAGTTA
SEQ ID NO: 1609	**604864**	ATGAACTACCACACGCGCAACAGCG	TACTTGATGGTGTGCGCGTTGTCGC
SEQ ID NO: 1610	**604942**	GGTATCAGACCACACACACGTCTTT	CCATAGTCTGGTGTGTGTGCAGAAA
SEQ ID NO: 1611	**604996**	CTTCGACTCCACACCGACGTAAGGT	GAAGCTGAGGTGTGGCTGCATTCCA
SEQ ID NO: 1612	**605130**	NA	NA
SEQ ID NO: 1613	**605152**	TATACGTTCCGCACACACATGATGA	ATATGCAAGGCGTGTGTGTACTACT

SEQ ID NO: 1614	**605170**	ACACGGGACCACACCTTTTCGGAGG	TGTGCCCTGGTGTGGAAAAGCCTCC
SEQ ID NO: 1615	**605204**	TCTGCCGTCCACACGACCTGTGAGT	AGACGGCAGGTGTGCTGGACACTCA
SEQ ID NO: 1616	**605233**	GTGATCTTCGCACACCGCAACCGGG	CACTAGAAGCGTGTGGCGTTGGCCC
SEQ ID NO: 1617	**605366**	AGTCGCGCCGCACACTCAGGACTTG	TCAGCGCGGCGTGTGAGTCCTGAAC
SEQ ID NO: 1618	**605428**	NA	NA
SEQ ID NO: 1619	**605533**	TCACAACGACCACACGTACGAGGTG	AGTGTTGCTGGTGTGCATGCTCCAC
SEQ ID NO: 1620	**605539**	CGCCACCGCACAGCGACATTATGGT	GCGGTGGCGTGTCGCTGTAATACCA
SEQ ID NO: 1621	**605623**	CCGACGTCGGCACACTCGGGGCGTA	GGCTGCAGCCGTGTGAGCCCCGCAT
SEQ ID NO: 1622	**605745**	GTTCCGTCGCGCACACGTTCTTTCA	CAAGGCAGCGCGTGTGCAAGAAAGT
SEQ ID NO: 1623	**605849**	GTCCCTGTCTCACCATGGTTCCTTG	CAGGGACAGAGTGGTACCAAGGAAC
SEQ ID NO: 1624	**605882**	GTGGGACACGCACACGCTCTACATA	CACCCTGTGCGTGTGCGAGATGTAT
SEQ ID NO: 1625	**605883**	ACAGGTACACGCACACGCGCACGCG	TGTCCATGTGCGTGTGCGCGTGCGC
SEQ ID NO: 1626	**605916**	ACACACACGTGCACAGAGACACACG	TGTGTGTGCACGTGTCTCTGTGTGC
SEQ ID NO: 1627	**605962**	GCGCACACGCGCACAACACAAGGGT	CGCGTGTGCGCGTGTTGTGTTCCCA
SEQ ID NO: 1628	**605988**	AGTACTCCACGCACACGTCCGAGGT	TCATGAGGTGCGTGTGCAGGCTCCA
SEQ ID NO: 1629	**606144**	CGTCACCCGCACATCTTCCTTGTTT	GCAGTGGGCGTGTAGAAGGAACAAA
SEQ ID NO: 1630	**606162**	GTCACACTCCGCACACGTGGTGACG	CAGTGTGAGGCGTGTGCACCACTGC
SEQ ID NO: 1631	**606368**	GTCTTTCGAGCACACGTACACTCCA	CAGAAAGCTCGTGTGCATGTGAGGT
SEQ ID NO: 1632	**606379**	TACCGACCCTCACCACAGATGTGGA	ATGGCTGGGAGTGGTGTCTACACCT
SEQ ID NO: 1633	**606615**	TTTCACTCGCACACGCGACGTCCTC	AAAGTGAGCGTGTGCGCTGCAGGAG
SEQ ID NO: 1634	**606829**	GTAGAACACGGCACACACACCACAG	CATCTTGTGCCGTGTGTGTGGTGTC

SEQ ID NO: 1635	**606955**	ACGTACCACGTACGCACACATACAT	TGCATGGTGCATGCGTGTGTATGTA
SEQ ID NO: 1636	**606956**	AGTACACCCGCACACACTGATTGTC	TCATGTGGGCGTGTGTGACTAACAG
SEQ ID NO: 1637	**606988**	ACACACGGGCACACGTACACACAGG	TGTGTGCCCGTGTGCATGTGTGTCC
SEQ ID NO: 1638	**607080**	CGCCCGTTCACCGACGCAGAGGGGT	GCGGGCAAGTGGCTGCGTCTCCCCA
SEQ ID NO: 1639	**608168**	CTAGAGGGTCACCACACACGCACGA	GATCTCCCAGTGGTGTGTGCGTGCT
SEQ ID NO: 1640	**608681**	TTAAAATCACACACACGATGAGTTC	AATTTTAGTGTGTGTGCTACTCAAG
SEQ ID NO: 1641	**611733**	GGTCGACGGCGTCACACACGCACTT	CCAGCTGCCGCAGTGTGTGCGTGAA
SEQ ID NO: 1642	**612075**	ACAGTGTACACGTCACACCACACTG	TGTCACATGTGCAGTGTGGTGTGAC
SEQ ID NO: 1643	**612904**	GTGTCCCGACCACTCCGGTGGGAAA	CACAGGGCTGGTGAGGCCACCCTTT
SEQ ID NO: 1644	**613176**	GTGACTCGACCCACTGTTTAGGTGA	CACTGAGCTGGGTGACAAATCCACT
SEQ ID NO: 1645	**614283**	GTGCACACGCCACTCACACCGTCCG	CACGTGTGCGGTGAGTGTGGCAGGC
SEQ ID NO: 1646	**614960**	CTACGCCTACGCACTCCGACGTTCG	GATGCGGATGCGTGAGGCTGCAAGC
SEQ ID NO: 1647	**615028**	ACGTCCGACCGCACTCCTGAAATGG	TGCAGGCTGGCGTGAGGACTTTACC
SEQ ID NO: 1648	**615296**	GTTTATACAGCACTCCACACTCAAA	CAAATATGTCGTGAGGTGTGAGTTT
SEQ ID NO: 1649	**615359**	CACACACACCACTAATCGTACGGAA	GTGTGTGTGGTGATTAGCATGCCTT
SEQ ID NO: 1650	**615397**	GGTCCCGACCACTACCAAGGTAAGT	CCAGGGCTGGTGATGGTTCCATTCA
SEQ ID NO: 1651	**616006**	ATCCGACACCACTATCAGGACATAG	TAGGCTGTGGTGATAGTCCTGTATC
SEQ ID NO: 1652	**616047**	AGGAGTCCCACTATCGTGTGTGTGA	TCCTCAGGGTGATAGCACACACACT
SEQ ID NO: 1653	**616167**	ACGTGTGTGCCACTATAGAACGCCC	TGCACACACGGTGATATCTTGCGGG
SEQ ID NO: 1654	**616187**	AGACGACTCACGCACTTACTCGTCT	TCTGCTGAGTGCGTGAATGAGCAGA
SEQ ID NO: 1655	**616565**	AACTTTCCACTATTTACGTCTCTGA	TTGAAAGGTGATAAATGCAGAGACT

SEQ ID NO: 1656	**617244**	GGTACACCGCGCACTACCTGGTCAT	CCATGTGGCGCGTGATGGACCAGTA
SEQ ID NO: 1657	**617643**	GGGTCCACCACTACGCACACGAGGT	CCCAGGTGGTGATGCGTGTGCTCCA
SEQ ID NO: 1658	**617716**	CCAATTCACTGTGTGTGCCCGTTGA	GGTTAAGTGACACACACGGGCAACT
SEQ ID NO: 1659	**617760**	TGTTACTTTCACTCGCTCACTCACT	ACAATGAAAGTGAGCGAGTGAGTGA
SEQ ID NO: 1660	**618612**	CTACCGTCCTCACTAGTATTAAAGG	GATGGCAGGAGTGATCATAATTTCC
SEQ ID NO: 1661	**618767**	ACCACGGACACACATGCAACATACA	TGGTGCCTGTGTGTACGTTGTATGT
SEQ ID NO: 1662	**618980**	GGGAGCCTCACTCACACACGCGCCG	CCCTCGGAGTGAGTGTGTGCGCGGC
SEQ ID NO: 1663	**619727**	AACTGGAACACCACGGCCCGGAACG	TTGACCTTGTGGTGCCGGGCCTTGC
SEQ ID NO: 1664	**619740**	TTACAGGCACACTCCCAAGTTCCGG	AATGTCCGTGTGAGGGTTCAAGGCC
SEQ ID NO: 1665	**620009**	GTGGCCGTCACACCGCCGGAGAGAC	CACCGGCAGTGTGGCGGCCTCTCTG
SEQ ID NO: 1666	**620246**	GTGACCACCACACCGAAACTTGTTT	CACTGGTGGTGTGGCTTTGAACAAA
SEQ ID NO: 1667	**620478**	TCCTCACCACACCTGGTCGAAGGTG	AGGAGTGGTGTGGACCAGCTTCCAC
SEQ ID NO: 1668	**620987**	AGTGACCACACACCCAGAGGAATCG	TCACTGGTGTGTGGGTCTCCTTAGC
SEQ ID NO: 1669	**621297**	GCCTCGCTCACACCGTAGAGATGGT	CGGAGCGAGTGTGGCATCTCTACCA
SEQ ID NO: 1670	**621603**	GTTCCGCACACACATGATGATAGTA	CAAGGCGTGTGTGTACTACTATCAT
SEQ ID NO: 1671	**621635**	GGTGGAAGACACCATCCGACGACCG	CCACCTTCTGTGGTAGGCTGCTGGC
SEQ ID NO: 1672	**621851**	ACACATCACACACACGTAAACCGTA	TGTGTAGTGTGTGTGCATTTGGCAT
SEQ ID NO: 1673	**621915**	ACCACGGACACACATCAGGGGATGA	TGGTGCCTGTGTGTAGTCCCCTACT
SEQ ID NO: 1674	**621930**	GGAGACGGAACACCGGGACACACTC	CCTCTGCCTTGTGGCCCTGTGTGAG
SEQ ID NO: 1675	**621944**	GTTATCCTCACACCACACAGATGGG	CAATAGGAGTGTGGTGTGTCTACCC
SEQ ID NO: 1676	**621949**	GTCGCACCACACACCAGAGCAGAGA	CAGCGTGGTGTGTGGTCTCGTCTCT

SEQ ID NO: 1677	**622094**	CGGACACACACACCCACGTGTAAAC	GCCTGTGTGTGTGGGTGCACATTTG
SEQ ID NO: 1678	**622119**	ACAACACACACACCATATATCATAC	TGTTGTGTGTGTGGTATATAGTATG
SEQ ID NO: 1679	**622120**	GTCACTCCACACACCATACATACAA	CAGTGAGGTGTGTGGTATGTATGTT
SEQ ID NO: 1680	**622302**	TGTCTCACTGACACCGTATCTTAGG	ACAGAGTGACTGTGGCATAGAATCC
SEQ ID NO: 1681	**622369**	TGACACACACACACCCAGATGTATG	ACTGTGTGTGTGTGGGTCTACATAC
SEQ ID NO: 1682	**622462**	TTCGGACACACACCGGCTGCGTACG	AAGCCTGTGTGTGGCCGACGCATGC
SEQ ID NO: 1683	**622494**	CGAAGGACACACACACCTATAAATT	GCTTCCTGTGTGTGTGGATATTTAA
SEQ ID NO: 1684	**622589**	ACGGGACCACACACACCTGCATGGT	TGCCCTGGTGTGTGTGGACGTACCA
SEQ ID NO: 1685	**623025**	GTCCGACACCACACAGTACCTGAAA	CAGGCTGTGGTGTGTCATGGACTTT
SEQ ID NO: 1686	**623110**	ATCTCACCACACATGGTTCTGGTAG	TAGAGTGGTGTGTACCAAGACCATC
SEQ ID NO: 1687	**623373**	ACCTCACACACACACGGGTGGTCAC	TGGAGTGTGTGTGTGCCCACCAGTG
SEQ ID NO: 1688	**623374**	TAAGTACCACACACACTTTGAGTTT	ATTCATGGTGTGTGTGAAACTCAAA
SEQ ID NO: 1689	**623678**	AGGTCCCACACACGACAGGCGTCGG	TCCAGGGTGTGTGCTGTCCGCAGCC
SEQ ID NO: 1690	**623720**	GTACGTCTGCGACGACACCAGCTTT	CATGCAGACGCTGCTGTGGTCGAAA
SEQ ID NO: 1691	**623745**	GTAGACACCGAACACACCAACAGTT	CATCTGTGGCTTGTGTGGTTGTCAA
SEQ ID NO: 1692	**623795**	TACGTTCCGCACACACATGATGATA	ATGCAAGGCGTGTGTGTACTACTAT
SEQ ID NO: 1693	**623962**	TTCGGGACACACACGGAGCGACAGG	AAGCCCTGTGTGTGCCTCGCTGTCC
SEQ ID NO: 1694	**623982**	NA	NA
SEQ ID NO: 1695	**624173**	TTCTGGCACACACTCGCCGATCTGT	AAGACCGTGTGTGAGCGGCTAGACA
SEQ ID NO: 1696	**624175**	ATTACACCACACACTCGCTCGGAGT	TAATGTGGTGTGTGAGCGAGCCTCA
SEQ ID NO: 1697	**624187**	ACGCGAACGACACACACACGATCGA	TGCGCTTGCTGTGTGTGTGCTAGCT

SEQ ID NO: 1698	**624317**	GGGGATCACACACGCACAACCTGTC	CCCCTAGTGTGTGCGTGTTGGACAG
SEQ ID NO: 1699	**624324**	GACATACTGACACACACAAAGACAG	CTGTATGACTGTGTGTGTTTCTGTC
SEQ ID NO: 1700	**624340**	AACAGGCACACAGACAGGCGCGCGC	TTGTCCGTGTGTCTGTCCGCGCGCG
SEQ ID NO: 1701	**624365**	CCGACACTCACACAAGTACCCTCTT	GGCTGTGAGTGTGTTCATGGGAGAA
SEQ ID NO: 1702	**624451**	NA	NA
SEQ ID NO: 1703	**624474**	ACCAGGGACACACCCGGTAGAAACC	TGGTCCCTGTGTGGGCCATCTTTGG
SEQ ID NO: 1704	**624476**	CTACGACTGGACACACCGGATTCCT	GATGCTGACCTGTGTGGCCTAAGGA
SEQ ID NO: 1705	**624658**	ACACCACAGACACACATACTACAGT	TGTGGTGTCTGTGTGTATGATGTCA
SEQ ID NO: 1706	**624670**	GAGACAGATCACACACACACCAACT	CTCTGTCTAGTGTGTGTGTGGTTGA
SEQ ID NO: 1707	**624677**	TGAACACGCACACACGGAAGATCCC	ACTTGTGCGTGTGTGCCTTCTAGGG
SEQ ID NO: 1708	**624678**	CGATACTCACACACACGAGACAGAT	GCTATGAGTGTGTGTGCTCTGTCTA
SEQ ID NO: 1709	**624695**	AGGGACACACACATAGACATGGGAT	TCCCTGTGTGTGTATCTGTACCCTA
SEQ ID NO: 1710	**624705**	CCGTCCGACGACACAAGAAGTAGGT	GGCAGGCTGCTGTGTTCTTCATCCA
SEQ ID NO: 1711	**624768**	GTACACACTCTACACACACGTGTAC	CATGTGTGAGATGTGTGTGCACATG
SEQ ID NO: 1712	**624791**	TTCACACGCACACACGAAAAATCGC	AAGTGTGCGTGTGTGCTTTTTAGCG
SEQ ID NO: 1713	**624830**	AGTCACATCACACACGTACAGGTGG	TCAGTGTAGTGTGTGCATGTCCACC
SEQ ID NO: 1714	**624871**	AAGTCACGGACACACCCAGGTTATC	TTCAGTGCCTGTGTGGGTCCAATAG
SEQ ID NO: 1715	**624936**	AAAACTAACACACCCACGGGGTAAA	TTTTGATTGTGTGGGTGCCCCATTT
SEQ ID NO: 1716	**625030**	GTTTAACACACACACGAGAGGCGGT	CAAATTGTGTGTGTGCTCTCCGCCA
SEQ ID NO: 1717	**625040**	CTAGGGCACACACACGTTTCAGTTC	GATCCCGTGTGTGTGCAAAGTCAAG
SEQ ID NO: 1718	**625056**	GTATCAGACCACACACACGTCTTTA	CATAGTCTGGTGTGTGTGCAGAAAT

SEQ ID NO: 1719	**625118**	ACCGATACACACACACGATACACAA	TGGCTATGTGTGTGTGCTATGTGTT
SEQ ID NO: 1720	**625173**	AAAACTACACACACTCGCACTCAAA	TTTTGATGTGTGTGAGCGTGAGTTT
SEQ ID NO: 1721	**625193**	CTAGGCACACACACTCTGAAAGGGT	GATCCGTGTGTGTGAGACTTTCCCA
SEQ ID NO: 1722	**625234**	CACACGCGGACACACCCACGTGTAA	GTGTGCGCCTGTGTGGGTGCACATT
SEQ ID NO: 1723	**625238**	CTCGTCGCACGACACAAGTGGTCAC	GAGCAGCGTGCTGTGTTCACCAGTG
SEQ ID NO: 1724	**625378**	GCGAACGACACACACACACGATCGA	CGCTTGCTGTGTGTGTGTGCTAGCT
SEQ ID NO: 1725	**625383**	GTCCGTACATCACACACGACTCGTG	CAGGCATGTAGTGTGTGCTGAGCAC
SEQ ID NO: 1726	**625386**	TTGCAACACACACCCACGTTACGTG	AACGTTGTGTGTGGGTGCAATGCAC
SEQ ID NO: 1727	**625390**	CCACGTTACACACACGTTTCCGGGT	GGTGCAATGTGTGTGCAAAGGCCCA
SEQ ID NO: 1728	**625438**	GTGGTCCCACACACACCACAGGGGT	CACCAGGGTGTGTGTGGTGTCCCCA
SEQ ID NO: 1729	**625443**	CCGATACTCACACACACGAGACAGA	GGCTATGAGTGTGTGTGCTCTGTCT
SEQ ID NO: 1730	**625458**	CACGCGGACACACACACCCACGGAC	GTGCGCCTGTGTGTGTGGGTGCCTG
SEQ ID NO: 1731	**625497**	TCAGGTCGTACACACACACGGTCCT	AGTCCAGCATGTGTGTGTGCCAGGA
SEQ ID NO: 1732	**625527**	CAGGTGCACACACTCCTACTTGAGG	GTCCACGTGTGTGAGGATGAACTCC
SEQ ID NO: 1733	**625545**	ACTCACGTACTCACACACTGTAAAC	TGAGTGCATGAGTGTGTGACATTTG
SEQ ID NO: 1734	**625635**	CGTACACACTCTACACACACGTGTA	GCATGTGTGAGATGTGTGTGCACAT
SEQ ID NO: 1735	**625640**	GAACGACACACACACACGATCGACA	CTTGCTGTGTGTGTGTGCTAGCTGT
SEQ ID NO: 1736	**626061**	NA	NA
SEQ ID NO: 1737	**626109**	ACACACGGAGACACACGTGCATGTG	TGTGTGCCTCTGTGTGCACGTACAC
SEQ ID NO: 1738	**626180**	ACATACTGCGACACACACACAGAGA	TGTATGACGCTGTGTGTGTGTCTCT
SEQ ID NO: 1739	**626233**	ATTGGGACACACACAACAGTCCGGA	TAACCCTGTGTGTGTTGTCAGGCCT

SEQ ID NO: 1740	**626419**	AAATCACGTACACAACGGTTTCACT	TTTAGTGCATGTGTTGCCAAAGTGA
SEQ ID NO: 1741	**626421**	TGGTTCTACTACACACCTCACCTGT	ACCAAGATGATGTGTGGAGTGGACA
SEQ ID NO: 1742	**626760**	ATACACACAGTACACACAGTATACA	TATGTGTGTCATGTGTGTCATATGT
SEQ ID NO: 1743	**627167**	GTCCCGTCCGTACACATAACAAAGG	CAGGGCAGGCATGTGTATTGTTTCC
SEQ ID NO: 1744	**627269**	GGGCCCACACTCACGCTCACTCGCG	CCCGGGTGTGAGTGCGAGTGAGCGC
SEQ ID NO: 1745	**627487**	ACGTCACGGGACACTCCATAAGGGT	TGCAGTGCCCTGTGAGGTATTCCCA
SEQ ID NO: 1746	**627575**	TTCGTCCACACACTTTCTGCTAGGT	AAGCAGGTGTGTGAAAGACGATCCA
SEQ ID NO: 1747	**627809**	ACTCAACCACACTTAATACATACTC	TGAGTTGGTGTGAATTATGTATGAG
SEQ ID NO: 1748	**628118**	ACGTACACACTCTACACACACGTGT	TGCATGTGTGAGATGTGTGTGCACA
SEQ ID NO: 1749	**628394**	AGACGTCCACACACTTAACGTGGTA	TCTGCAGGTGTGTGAATTGCACCAT
SEQ ID NO: 1750	**628518**	GCAACTACGCACACTGGCTGTAACT	CGTTGATGCGTGTGACCGACATTGA
SEQ ID NO: 1751	**628955**	CCCGTACACACACTTCTAGTAGGGA	GGGCATGTGTGTGAAGATCATCCCT
SEQ ID NO: 1752	**629203**	CACACTCACACACTCATCCTCTCTC	GTGTGAGTGTGTGAGTAGGAGAGAG
SEQ ID NO: 1753	**629453**	GTCGTTAGCGTCACACTCCCACTGG	CAGCAATCGCAGTGTGAGGGTGACC
SEQ ID NO: 1754	**631277**	ACTCCGACCCACGAGTCCTTCCGGG	TGAGGCTGGGTGCTCAGGAAGGCCC
SEQ ID NO: 1755	**631481**	TTCACCGCCACGACGAAGAAGGACG	AAGTGGCGGTGCTGCTTCTTCCTGC
SEQ ID NO: 1756	**631600**	ACCTCTGGCACGCACGGTATGCCTT	TGGAGACCGTGCGTGCCATACGGAA
SEQ ID NO: 1757	**631676**	TTTACCGCCACGCTACCTCGTATGA	AAATGGCGGTGCGATGGAGCATACT
SEQ ID NO: 1758	**631706**	CGGTCGGCCACGCAGGAAATTAGGA	GCCAGCCGGTGCGTCCTTTAATCCT
SEQ ID NO: 1759	**631822**	ACTAGAAGTACCACGCACACGCCGT	TGATCTTCATGGTGCGTGTGCGGCA
SEQ ID NO: 1760	**631835**	AGTCAACGACCACGCTGTTCTAGGA	TCAGTTGCTGGTGCGACAAGATCCT

SEQ ID NO: 1761	**632206**	CGCCGACGAGCACGACCGACAAGGT	GCGGCTGCTCGTGCTGGCTGTTCCA
SEQ ID NO: 1762	**632280**	CCACCGACCACGAGCATAGATGTTT	GGTGGCTGGTGCTCGTATCTACAAA
SEQ ID NO: 1763	**632554**	ATGTAAGTACCACGGGCACACACAC	TACATTCATGGTGCCCGTGTGTGTG
SEQ ID NO: 1764	**632583**	GTGACACCTACGCACGCACGAGGTC	CACTGTGGATGCGTGCGTGCTCCAG
SEQ ID NO: 1765	**632850**	ACCTCCGTCCACGAAGATGACGACG	TGGAGGCAGGTGCTTCTACTGCTGC
SEQ ID NO: 1766	**633516**	ACGAGACTACGCCACGACGCAGAGG	TGCTCTGATGCGGTGCTGCGTCTCC
SEQ ID NO: 1767	**633521**	GTTGCTACGACCACGAGTCCCATGT	CAACGATGCTGGTGCTCAGGGTACA
SEQ ID NO: 1768	**633673**	TTCCCGACCACGAGAAACCATCTTT	AAGGGCTGGTGCTCTTTGGTAGAAA
SEQ ID NO: 1769	**635078**	TTTAACCACACGACCACACATGGGT	AAATTGGTGTGCTGGTGTGTACCCA
SEQ ID NO: 1770	**635230**	ATCCCAGACACGGTTATACGCTTAG	TAGGGTCTGTGCCAATATGCGAATC
SEQ ID NO: 1771	**635912**	AGCTCCGACCACGTTTGGACCGTAC	TCGAGGCTGGTGCAAACCTGGCATG
SEQ ID NO: 1772	**635945**	ACTACCGCACCACGTCTCTAGTTGA	TGATGGCGTGGTGCAGAGATCAACT
SEQ ID NO: 1773	**636150**	CCTCCAGACACGGTGCATACGGTAG	GGAGGTCTGTGCCACGTATGCCATC
SEQ ID NO: 1774	**636406**	TGCTCGCTCCACGTCCGAGGTACTT	ACGAGCGAGGTGCAGGCTCCATGAA
SEQ ID NO: 1775	**636587**	CTAGACAACTCACGTTAGTAGAGTG	GATCTGTTGAGTGCAATCATCTCAC
SEQ ID NO: 1776	**637017**	AGGGTCGCACACGTACAACAATGTC	TCCCAGCGTGTGCATGTTGTTACAG
SEQ ID NO: 1777	**637349**	GTGGGACACACACGTCCTCGATACG	CACCCTGTGTGTGCAGGAGCTATGC
SEQ ID NO: 1778	**637391**	GGATAACACACACGTCCTCCGGACA	CCTATTGTGTGTGCAGGAGGCCTGT
SEQ ID NO: 1779	**637486**	TGGGACACACACGTCCTCGATACGA	ACCCTGTGTGTGCAGGAGCTATGCT
SEQ ID NO: 1780	**637689**	GTCCGGACACACACGGAAAGGACCG	CAGGCCTGTGTGTGCCTTTCCTGGC
SEQ ID NO: 1781	**637698**	AGGTACACGCACACGCGCACGCGCG	TCCATGTGCGTGTGCGCGTGCGCGC

SEQ ID NO: 1782	**637765**	ACGTCTGCACACACGGTCTGACAGG	TGCAGACGTGTGTGCCAGACTGTCC
SEQ ID NO: 1783	**638195**	AACACACACACACGGGCACAGGTAC	TTGTGTGTGTGTGCCCGTGTCCATG
SEQ ID NO: 1784	**638285**	AGTGACACACTACACGCTACTCGGT	TCACTGTGTGATGTGCGATGAGCCA
SEQ ID NO: 1785	**638655**	AGATCTCCGACACGACCAGGGACAT	TCTAGAGGCTGTGCTGGTCCCTGTA
SEQ ID NO: 1786	**638669**	GACACCAGGACACGTTTACAGAATC	CTGTGGTCCTGTGCAAATGTCTTAG
SEQ ID NO: 1787	**638756**	ATACTCACACACACGAGACAGATCA	TATGAGTGTGTGTGCTCTGTCTAGT
SEQ ID NO: 1788	**639206**	ACACTTATCACACGTACACACAGCT	TGTGAATAGTGTGCATGTGTGTCGA
SEQ ID NO: 1789	**639233**	CTACACACCACACGAGACGGGTCGT	GATGTGTGGTGTGCTCTGCCCAGCA
SEQ ID NO: 1790	**639347**	GATACTCACACACACGAGACAGATC	CTATGAGTGTGTGTGCTCTGTCTAG
SEQ ID NO: 1791	**639384**	CACCCACACACGTACTCGCACCTGG	GTGGGTGTGTGCATGAGCGTGGACC
SEQ ID NO: 1792	**639385**	AGACCACGCACACGTACTCGAACAT	TCTGGTGCGTGTGCATGAGCTTGTA
SEQ ID NO: 1793	**639401**	TTGTGTCCACACGACCCGAGACTCG	AACACAGGTGTGCTGGGCTCTGAGC
SEQ ID NO: 1794	**639408**	GTCCGGGACACACGAACGACGGAGA	CAGGCCCTGTGTGCTTGCTGCCTCT
SEQ ID NO: 1795	**639521**	CGATTACTACACACGTACACGGTCT	GCTAATGATGTGTGCATGTGCCAGA
SEQ ID NO: 1796	**640320**	ACACGCACGCACACGTACGTATATA	TGTGCGTGCGTGTGCATGCATATAT
SEQ ID NO: 1797	**640594**	GTACGTATGCACACACGTATCTGGA	CATGCATACGTGTGTGCATAGACCT
SEQ ID NO: 1798	**641380**	NA	NA
SEQ ID NO: 1799	**644033**	GTCCGCCGAGGAAAGACACGGGTCA	CAGGCGGCTCCTTTCTGTGCCCAGT
SEQ ID NO: 1800	**644559**	ACGGGTTAGGAAACTAATCAGTTAC	TGCCCAATCCTTTGATTAGTCAATG
SEQ ID NO: 1801	**648334**	AGAAAGCGGAAAGAAAGACCTCAGC	TCTTTCGCCTTTCTTTCTGGAGTCG
SEQ ID NO: 1802	**649029**	NA	NA

SEQ ID NO: 1803	**652312**	ATCTCGAACGGAACGAATTACTCGT	TAGAGCTTGCCTTGCTTAATGAGCA
SEQ ID NO: 1804	**652881**	CGACTCGACTCGGAACGCTGGGCCA	GCTGAGCTGAGCCTTGCGACCCGGT
SEQ ID NO: 1805	**653568**	GGACGTCCACGGAACGACACCAGGG	CCTGCAGGTGCCTTGCTGTGGTCCC
SEQ ID NO: 1806	**660634**	NA	NA
SEQ ID NO: 1807	**661676**	NA	NA
SEQ ID NO: 1808	**661964**	AGTCTGCTGTGAACCAACTCGGGTC	TCAGACGACACTTGGTTGAGCCCAG
SEQ ID NO: 1809	**663565**	NA	NA
SEQ ID NO: 1810	**666177**	CAAGGTGGATGTCCTGTGTCTGAGT	GTTCCACCTACAGGACACAGACTCA
SEQ ID NO: 1811	**668501**	TTCGGGTGTGATGATAGGAGAAACA	AAGCCCACACTACTATCCTCTTTGT
SEQ ID NO: 1812	**669092**	GTGTGGTTGTGATTAAGCAAACCCT	CACACCAACACTAATTCGTTTGGGA
SEQ ID NO: 1813	**670862**	AATGTTTGATTCTGTGTTGGTGCGT	TTACAAACTAAGACACAACCACGCA
SEQ ID NO: 1814	**672756**	AATCGTGTGTGATTTGGATCAAATC	TTAGCACACACTAAACCTAGTTTAG
SEQ ID NO: 1815	**673171**	AAAGTCGTCGTGATTGTTACATCCC	TTTCAGCAGCACTAACAATGTAGGG
SEQ ID NO: 1816	**674203**	TAACTCGGTCGTGATCGTGGGTCTA	ATTGAGCCAGCACTAGCACCCAGAT
SEQ ID NO: 1817	**677247**	CTTGGAAGAAGCCTCTGGACGACGA	GAACCTTCTTCGGAGACCTGCTGCT
SEQ ID NO: 1818	**678749**	AGCCGTCGCAGAAACCTCGTTCCGT	TCGGCAGCGTCTTTGGAGCAAGGCA
SEQ ID NO: 1819	**681649**	ACACGTACACACAGAAGTCGGCTTA	TGTGCATGTGTGTCTTCAGCCGAAT
SEQ ID NO: 1820	**685679**	CTTGGGAGAAGACACACACGTTTCA	GAACCCTCTTCTGTGTGTGCAAAGT
SEQ ID NO: 1821	**687015**	ATTCTCCGAGAAGTGTGTGTTGTCC	TAAGAGGCTCTTCACACACAACAGG
SEQ ID NO: 1822	**687452**	TGCGTGAGCGAGAACCCTCTTCTCT	ACGCACTCGCTCTTGGGAGAAGAGA
SEQ ID NO: 1823	**688422**	NA	NA

SEQ ID NO: 1824	**689612**	NA	NA
SEQ ID NO: 1825	**691978**	NA	NA
SEQ ID NO: 1826	**697750**	CTCATCTTAGATGTGTGCGTTTCGT	GAGTAGAATCTACACACGCAAAGCA
SEQ ID NO: 1827	**698022**	GTGTCGGTCGGAGATACTCTTCAAT	CACAGCCAGCCTCTATGAGAAGTTA
SEQ ID NO: 1828	**699097**	NA	NA
SEQ ID NO: 1829	**699340**	TCTGCAGGGAGGGATAACGTGTACC	AGACGTCCCTCCCTATTGCACATGG
SEQ ID NO: 1830	**700276**	NA	NA
SEQ ID NO: 1831	**700530**	CCGTGGTGGAGGTGATAAGTCCTTC	GGCACCACCTCCACTATTCAGGAAG
SEQ ID NO: 1832	**704721**	NA	NA
SEQ ID NO: 1833	**705954**	GTGGTGTTGGAGACCTTTAGTTAAT	CACCACAACCTCTGGAAATCAATTA
SEQ ID NO: 1834	**707528**	AATACTTCTGAGGTGTGGTGAGTAT	TTATGAAGACTCCACACCACTCATA
SEQ ID NO: 1835	**708090**	TTGGAGTTGAGCCACCACGACGCCG	AACCTCAACTCGGTGGTGCTGCGGC
SEQ ID NO: 1836	**708322**	CCTTTTGAGGTGTGTGTTTCGTGGA	GGAAAACTCCACACACAAAGCACCT
SEQ ID NO: 1837	**708569**	NA	NA
SEQ ID NO: 1838	**709268**	AAGTCTATTGAGTGGTGGTGGAAAC	TTCAGATAACTCACCACCACCTTTG
SEQ ID NO: 1839	**711288**	TAAGTGTGTGTGAGGATATAACGGT	ATTCACACACACTCCTATATTGCCA
SEQ ID NO: 1840	**711399**	GTCTGTTGTGTGAGGTCCTTTGTCT	CAGACAACACACTCCAGGAAACAGA
SEQ ID NO: 1841	**711846**	CCAGTGTGTGAGCATTCGTTGTCTT	GGTCACACACTCGTAAGCAACAGAA
SEQ ID NO: 1842	**711989**	GTCGCGTGCGCGTGAGCTACGGAGA	CAGCGCACGCGCACTCGATGCCTCT
SEQ ID NO: 1843	**712228**	CGTTATAGTAGTGGTGTGCGTGAAT	GCAATATCATCACCACACGCACTTA
SEQ ID NO: 1844	**712386**	NA	NA

SEQ ID NO: 1845	**713383**	NA	NA
SEQ ID NO: 1846	**715209**	CTCTCAGGGAGTCCACACACCGTTG	GAGAGTCCCTCAGGTGTGTGGCAAC
SEQ ID NO: 1847	**717303**	AGTGTGTGTACGGAGTCCACCCGAC	TCACACACATGCCTCAGGTGGGCTG
SEQ ID NO: 1848	**718886**	TCGGTGGTGTGAGTCTGAATTCACA	AGCCACCACACTCAGACTTAAGTGT
SEQ ID NO: 1849	**719167**	ATAAGTGTGTGAGTTTCCCAGGTCC	TATTCACACACTCAAAGGGTCCAGG
SEQ ID NO: 1850	**719172**	GAGGTCTGTGTGAGTCTTAACTTAA	CTCCAGACACACTCAGAATTGAATT
SEQ ID NO: 1851	**719610**	GACTTTATCGTGAGTGTGGATCCAA	CTGAAATAGCACTCACACCTAGGTT
SEQ ID NO: 1852	**719635**	GTCCTCTGTGTGAGTGCCTCGGAGC	CAGGAGACACACTCACGGAGCCTCG
SEQ ID NO: 1853	**719734**	ACCGGGTGTGAGTGATCGTCACATT	TGGCCCACACTCACTAGCAGTGTAA
SEQ ID NO: 1854	**720383**	CAACTAGGTGAGTGTGTGAATCGAC	GTTGATCCACTCACACACTTAGCTG
SEQ ID NO: 1855	**720647**	ACTTAGTAGGTGAGTGTGTCTCCGA	TGAATCATCCACTCACACAGAGGCT
SEQ ID NO: 1856	**720955**	GTGTGTGTCGTATGAGTAGAAGAAA	CACACACAGCATACTCATCTTCTTT
SEQ ID NO: 1857	**721715**	GCGCCCAGCGCGGGAAGTACTTCTA	CGCGGGTCGCGCCCTTCATGAAGAT
SEQ ID NO: 1858	**725675**	ACACTCGTCCAGAGATTCGGAACCA	TGTGAGCAGGTCTCTAAGCCTTGGT
SEQ ID NO: 1859	**726816**	TCACACACACAGAGATGGGTCGAGA	AGTGTGTGTGTCTCTACCCAGCTCT
SEQ ID NO: 1860	**731943**	CGTCCCTCAGAGTCTTACCAAAGGT	GCAGGGAGTCTCAGAATGGTTTCCA
SEQ ID NO: 1861	**735985**	GTAACCACACCGAAACCCGTCCAAG	CATTGGTGTGGCTTTGGGCAGGTTC
SEQ ID NO: 1862	**736740**	CTCCGTCCCGAAGATTCGGAGACTC	GAGGCAGGGCTTCTAAGCCTCTGAG
SEQ ID NO: 1863	**738201**	GTGTCCGAGACCGAACTCCTCTAAA	CACAGGCTCTGGCTTGAGGAGATTT
SEQ ID NO: 1864	**738216**	ACAGCCGTCCGAACCGTTTCTACGA	TGTCGGCAGGCTTGGCAAAGATGCT
SEQ ID NO: 1865	**738425**	GTGGACACACCGAACACACACGGGG	CACCTGTGTGGCTTGTGTGTGCCCC

SEQ ID NO: 1866	**738540**	GGCGTGTGGCGAAGAGAATTACCTT	CCGCACACCGCTTCTCTTAATGGAA
SEQ ID NO: 1867	**738586**	GTGGTGTGGCGAACACTAAGAGTCC	CACCACACCGCTTGTGATTCTCAGG
SEQ ID NO: 1868	**738824**	TCACACACACGCGAACCAAGTCATT	AGTGTGTGTGCGCTTGGTTCAGTAA
SEQ ID NO: 1869	**738956**	GACACACATGCGAACACACACGCGA	CTGTGTGTACGCTTGTGTGTGCGCT
SEQ ID NO: 1870	**739377**	CCCGTATGCGAACTGTGTGTGCGTA	GGGCATACGCTTGACACACACGCAT
SEQ ID NO: 1871	**742851**	ACGGTGACTTCGATTGTGTGGATAC	TGCCACTGAAGCTAACACACCTATG
SEQ ID NO: 1872	**743971**	CACGTCCGACCGATTTAGGTTTTTC	GTGCAGGCTGGCTAAATCCAAAAAG
SEQ ID NO: 1873	**744248**	GTACTACAACGTCCGATGGGTCCAG	CATGATGTTGCAGGCTACCCAGGTC
SEQ ID NO: 1874	**744719**	GTGTGGGTGTCGATTCTGCGACCCT	CACACCCACAGCTAAGACGCTGGGA
SEQ ID NO: 1875	**744962**	CGAGTGTGTCCGATCGTCTGTCGTC	GCTCACACAGGCTAGCAGACAGCAG
SEQ ID NO: 1876	**747612**	ATTCTTCTACGAATTCAAGGTAACG	TAAGAAGATGCTTAAGTTCCATTGC
SEQ ID NO: 1877	**747946**	GCCTAAAACGAAAGCGACGGCGCTC	CGGATTTTGCTTTCGCTGCCGCGAG
SEQ ID NO: 1878	**749494**	AGACCACCACGAACAGACTCGTCGG	TCTGGTGGTGCTTGTCTGAGCAGCC
SEQ ID NO: 1879	**752216**	ACGACACCCGACGATCTTTGAAGTA	TGCTGTGGGCTGCTAGAAACTTCAT
SEQ ID NO: 1880	**752766**	GCGTTCCGACGACGATCTGGTCCGC	CGCAAGGCTGCTGCTAGACCAGGCG
SEQ ID NO: 1881	**753062**	ACACCGACCACGATCAAACTTGACG	TGTGGCTGGTGCTAGTTTGAACTGC
SEQ ID NO: 1882	**753369**	CGACTGTAGGCGAGGTTGTCCAAAG	GCTGACATCCGCTCCAACAGGTTTC
SEQ ID NO: 1883	**753609**	ACTGTCGGTCGTACGATGGGTCACA	TGACAGCCAGCATGCTACCCAGTGT
SEQ ID NO: 1884	**754623**	CTGACCGACCGAGCGGGTGCCTCTT	GACTGGCTGGCTCGCCCACGGAGAA
SEQ ID NO: 1885	**759120**	CTGTCGTCTGTCGAGGCCATACTCC	GACAGCAGACAGCTCCGGTATGAGG
SEQ ID NO: 1886	**759510**	CGTCTCCACTCGAGAGCGACCGGTA	GCAGAGGTGAGCTCTCGCTGGCCAT

SEQ ID NO: 1887	**759816**	TCACCGCGACCGAGTACTTATTAGT	AGTGGCGCTGGCTCATGAATAATCA
SEQ ID NO: 1888	**760463**	ATCTACCTACCGAGTGAATGACCGT	TAGATGGATGGCTCACTTACTGGCA
SEQ ID NO: 1889	**760544**	CCGGGTCCGAGTACTTCGGCGTCGT	GGCCCAGGCTCATGAAGCCGCAGCA
SEQ ID NO: 1890	**760837**	GTAGTATTGTTCGAGTGTGTACGCG	CATCATAACAAGCTCACACATGCGC
SEQ ID NO: 1891	**761738**	CGACGAGCCACGAGGTTCACTTCGC	GCTGCTCGGTGCTCCAAGTGAAGCG
SEQ ID NO: 1892	**762023**	AAGAGACGGTACGAGTGTGGCAACC	TTCTCTGCCATGCTCACACCGTTGG
SEQ ID NO: 1893	**762693**	ACCACCGACACGAGGTTCTCATTCG	TGGTGGCTGTGCTCCAAGAGTAAGC
SEQ ID NO: 1894	**762994**	CACCGACCACGAGCATAGATGTTTT	GTGGCTGGTGCTCGTATCTACAAAA
SEQ ID NO: 1895	**764257**	TACTCACACACACGAGACAGATCAC	ATGAGTGTGTGTGCTCTGTCTAGTG
SEQ ID NO: 1896	**764858**	CGTGGGTGACGAGTCTGTGCTCTCT	GCACCCACTGCTCAGACACGAGAGA
SEQ ID NO: 1897	**765399**	TTTCCGGGACCCGTTAATCGAGGAG	AAAGGCCCTGGGCAATTAGCTCCTC
SEQ ID NO: 1898	**767717**	ACACTGGGTGACCACGCGCACCGAG	TGTGACCCACTGGTGCGCGTGGCTC
SEQ ID NO: 1899	**767743**	GAGGTCCAGGACCACACACGGAGAA	CTCCAGGTCCTGGTGTGTGCCTCTT
SEQ ID NO: 1900	**767854**	AGATGACGGGACAACACCTTAAAAT	TCTACTGCCCTGTTGTGGAATTTTA
SEQ ID NO: 1901	**771218**	TCACCTCGCGGACACCTAAATCGGC	AGTGGAGCGCCTGTGGATTTAGCCG
SEQ ID NO: 1902	**771424**	AGTGAAAGGACACGCACCGACACCG	TCACTTTCCTGTGCGTGGCTGTGGC
SEQ ID NO: 1903	**771849**	CTGAACGGGACACGCGACACCATGT	GACTTGCCCTGTGCGCTGTGGTACA
SEQ ID NO: 1904	**771861**	AAGTACAAGGACACTGGACACACCA	TTCATGTTCCTGTGACCTGTGTGGT
SEQ ID NO: 1905	**771970**	CACACACGCGGACACACCCACGTGT	GTGTGTGCGCCTGTGTGGGTGCACA
SEQ ID NO: 1906	**772336**	TTCCACCTGACCTCGAGGGAGACTT	AAGGTGGACTGGAGCTCCCTCTGAA
SEQ ID NO: 1907	**772366**	NA	NA

SEQ ID NO: 1908	**772373**	ACAGTACATGGACACCGACGAGTTA	TGTCATGTACCTGTGGCTGCTCAAT
SEQ ID NO: 1909	**773223**	CTCGCCGCGTGACCAGGTCCATCTC	GAGCGGCGCACTGGTCCAGGTAGAG
SEQ ID NO: 1910	**774047**	ACGTGCGTGCTGACCTACCGTCCGA	TGCACGCACGACTGGATGGCAGGCT
SEQ ID NO: 1911	**775092**	CGTAGTACCACTGACCTCCACGGAG	GCATCATGGTGACTGGAGGTGCCTC
SEQ ID NO: 1912	**775919**	GCTTCATTGACACCGACCACGACAG	CGAAGTAACTGTGGCTGGTGCTGTC
SEQ ID NO: 1913	**780397**	AGACTACGTCGTGGACTGTTCCCGG	TCTGATGCAGCACCTGACAAGGGCC
SEQ ID NO: 1914	**781284**	GTGTCCTTGGACTCGAGGTGTCCTG	CACAGGAACCTGAGCTCCACAGGAC
SEQ ID NO: 1915	**781818**	GTTGTTATGGACTATGCTACTTTTT	CAACAATACCTGATACGATGAAAAA
SEQ ID NO: 1916	**784431**	GTGACCCATGACTACCGAACCGACA	CACTGGGTACTGATGGCTTGGCTGT
SEQ ID NO: 1917	**784643**	GTAGTGGTGGTGACTGTTCCACTCC	CATCACCACCACTGACAAGGTGAGG
SEQ ID NO: 1918	**787058**	GAAGGTATCAGACCACACACACGTC	CTTCCATAGTCTGGTGTGTGTGCAG
SEQ ID NO: 1919	**787311**	AAGGTATCAGACCACACACACGTCT	TTCCATAGTCTGGTGTGTGTGCAGA
SEQ ID NO: 1920	**788419**	CGACGCACGCAGACACACCAATGAT	GCTGCGTGCGTCTGTGTGGTTACTA
SEQ ID NO: 1921	**789371**	GTGTCTGTGTAAGACATGTGTGTCT	CACAGACACATTCTGTACACACAGA
SEQ ID NO: 1922	**789633**	ATATCGACGACAGACAGATCGGGTC	TATAGCTGCTGTCTGTCTAGCCCAG
SEQ ID NO: 1923	**790429**	GAACCCACAGACACACTTAAATAGT	CTTGGGTGTCTGTGTGAATTTATCA
SEQ ID NO: 1924	**790989**	AGCTGTCGAGTAGACAATCCGATTC	TCGACAGCTCATCTGTTAGGCTAAG
SEQ ID NO: 1925	**793882**	ACAAAACTAGACTGCGTCCGAATAC	TGTTTTGATCTGACGCAGGCTTATG
SEQ ID NO: 1926	**797012**	CCAGAGGGACGCGTGTGCCGACTGA	GGTCTCCCTGCGCACACGGCTGACT
SEQ ID NO: 1927	**797080**	NA	NA
SEQ ID NO: 1928	**798633**	AGCACACTCTGACGACACACACTGT	TCGTGTGAGACTGCTGTGTGTGACA

SEQ ID NO: 1929	**801722**	CAGTACATGTGACGTGCGAGCGATC	GTCATGTACACTGCACGCTCGCTAG
SEQ ID NO: 1930	**801890**	ACTCCCGATGACGTAGAGGTAAGAG	TGAGGGCTACTGCATCTCCATTCTC
SEQ ID NO: 1931	**803396**	ATACACACACAGACGCGTTCACTCT	TATGTGTGTGTCTGCGCAAGTGAGA
SEQ ID NO: 1932	**803564**	GTACCGACCCAGACGATGTAATGTT	CATGGCTGGGTCTGCTACATTACAA
SEQ ID NO: 1933	**803954**	GGACACACACAGACGCGTCCAGACA	CCTGTGTGTGTCTGCGCAGGTCTGT
SEQ ID NO: 1934	**803962**	CGTACGCCCAGACGAGTGTGTATAC	GCATGCGGGTCTGCTCACACATATG
SEQ ID NO: 1935	**804903**	AGGAAACCGACGACCATCCGAATGT	TCCTTTGGCTGCTGGTAGGCTTACA
SEQ ID NO: 1936	**805891**	GAAAGAACCGACCTGCCTCCGAACG	CTTTCTTGGCTGGACGGAGGCTTGC
SEQ ID NO: 1937	**806531**	GTTCATTCCGACCATCACCTTGTAT	CAAGTAAGGCTGGTAGTGGAACATA
SEQ ID NO: 1938	**806698**	GACCTCCACCGACAGACCCTTTGTG	CTGGAGGTGGCTGTCTGGGAAACAC
SEQ ID NO: 1939	**807382**	ACCACGACTCCGACAGAAGTAACTC	TGGTGCTGAGGCTGTCTTCATTGAG
SEQ ID NO: 1940	**807541**	AGAACACCCGACACTTAATGTGACT	TCTTGTGGGCTGTGAATTACACTGA
SEQ ID NO: 1941	**807682**	CTGTCCTCCGACCTTTTCTACTGGA	GACAGGAGGCTGGAAAAGATGACCT
SEQ ID NO: 1942	**808265**	NA	NA
SEQ ID NO: 1943	**808448**	AGTCCGTCTCGCGACCGCTCTAAAG	TCAGGCAGAGCGCTGGCGAGATTTC
SEQ ID NO: 1944	**809170**	CGCGCGCCTCGACCGCCGCAGCGGC	GCGCGCGGAGCTGGCGGCGTCGCCG
SEQ ID NO: 1945	**809854**	GCACCGACACGCGACAAGTAGATTA	CGTGGCTGTGCGCTGTTCATCTAAT
SEQ ID NO: 1946	**810298**	GCCTCTGACTCGACTTGCCTTTCAA	CGGAGACTGAGCTGAACGGAAAGTT
SEQ ID NO: 1947	**811475**	TTTGTCACCGACTGACTTAACCCGG	AAACAGTGGCTGACTGAATTGGGCC
SEQ ID NO: 1948	**811962**	ACGACACACGATCGACACACATGCG	TGCTGTGTGCTAGCTGTGTGTACGC
SEQ ID NO: 1949	**812138**	CCTCGCGTGCGACTGTGTAAATTGC	GGAGCGCACGCTGACACATTTAACG

SEQ ID NO: 1950	**813903**	CATGTAGAACGACCTTTTACGACGG	GTACATCTTGCTGGAAAATGCTGCC
SEQ ID NO: 1951	**814284**	ATGTCGCACCGACTACGACGAGGAC	TACAGCGTGGCTGATGCTGCTCCTG
SEQ ID NO: 1952	**814687**	GTTTAACCGACGACATAGGGCATCT	CAAATTGGCTGCTGTATCCCGTAGA
SEQ ID NO: 1953	**814732**	GGGTCACACACGACACCCTGTCTTA	CCCAGTGTGTGCTGTGGGACAGAAT
SEQ ID NO: 1954	**815645**	GGTGTGTGTCACGACCCTGTGAATG	CCACACACAGTGCTGGGACACTTAC
SEQ ID NO: 1955	**816046**	GACCTACACCGACGACCGAAGTAAG	CTGGATGTGGCTGCTGGCTTCATTC
SEQ ID NO: 1956	**816226**	AGACGCTCCGACGACCAACCGCAGA	TCTGCGAGGCTGCTGGTTGGCGTCT
SEQ ID NO: 1957	**816274**	AGCCGACGAACGACACTCTACTGTG	TCGGCTGCTTGCTGTGAGATGACAC
SEQ ID NO: 1958	**816362**	TTCCGACCACGACTCTCTCAATCGT	AAGGCTGGTGCTGAGAGAGTTAGCA
SEQ ID NO: 1959	**816522**	GCTAGCTACCACGACACGGTGTATT	CGATCGATGGTGCTGTGCCACATAA
SEQ ID NO: 1960	**817059**	CGTTGCACCGACGAACCACAGGAGT	GCAACGTGGCTGCTTGGTGTCCTCA
SEQ ID NO: 1961	**817636**	TCACGAGCCCGACGCACACGGTCTT	AGTGCTCGGGCTGCGTGTGCCAGAA
SEQ ID NO: 1962	**818797**	CGTATCTACGACACGACGAAGGGAG	GCATAGATGCTGTGCTGCTTCCCTC
SEQ ID NO: 1963	**819989**	CTACTCCCGACGACGTTACAAGTCG	GATGAGGGCTGCTGCAATGTTCAGC
SEQ ID NO: 1964	**820109**	TTACGTCACCTCGACGCCTCTGAGG	AATGCAGTGGAGCTGCGGAGACTCC
SEQ ID NO: 1965	**821178**	GTTCGTGACACCGACGTATAAGGTT	CAAGCACTGTGGCTGCATATTCCAA
SEQ ID NO: 1966	**821389**	CGTGTAGTGTGTCGACGTGTACTTG	GCACATCACACAGCTGCACATGAAC
SEQ ID NO: 1967	**822524**	AGATCAGTTTTTTCGTGGGTGTGCC	TCTAGTCAAAAAAGCACCCACACGG
SEQ ID NO: 1968	**824641**	CTGGGATTTTCGTGTGTGTTCAGAC	GACCCTAAAAGCACACACAAGTCTG
SEQ ID NO: 1969	**824900**	AAAAATTTTAGTACGGACGGTCGGG	TTTTTAAAATCATGCCTGCCAGCCC
SEQ ID NO: 1970	**825716**	CTACTAGTGTATTTTGTCTAAACGT	GATGATCACATAAAACAGATTTGCA

SEQ ID NO: 1971	**825911**	GTGTGTGTTTTTGGTCTACTGTTGT	CACACACAAAAACCAGATGACAACA
SEQ ID NO: 1972	**826297**	ATTACTCTTTTGGTCGGTCGGTCCT	TAATGAGAAAACCAGCCAGCCAGGA
SEQ ID NO: 1973	**826441**	ACTCGTGGTTTTGGTCGGTTAGACT	TGAGCACCAAAACCAGCCAATCTGA
SEQ ID NO: 1974	**826598**	ACGTGAGTTTTTGTGCGTGCCCGAC	TGCACTCAAAAACACGCACGGGCTG
SEQ ID NO: 1975	**827313**	CAAGATTTTGTGTGGGAAGTCACCG	GTTCTAAAACACACCCTTCAGTGGC
SEQ ID NO: 1976	**827599**	GAAAGTGTTTTGTGTTTCACGAAGA	CTTTCACAAAACACAAAGTGCTTCT
SEQ ID NO: 1977	**827612**	CATTCTTTTGTGTGTACCGGTCCAC	GTAAGAAAACACACATGGCCAGGTG
SEQ ID NO: 1978	**827624**	TGAAACATTTGGTGGTGGTGTAATC	ACTTTGTAAACCACCACCACATTAG
SEQ ID NO: 1979	**827698**	AGTCGGGTTTTGTTCGTCACTGCCA	TCAGCCCAAAACAAGCAGTGACGGT
SEQ ID NO: 1980	**827939**	ACCCAATTTGTGTCCGTGATGTCGG	TGGGTTAAACACAGGCACTACAGCC
SEQ ID NO: 1981	**828971**	CCTTCTATTTGTGCGTCGTGCGGAA	GGAAGATAAACACGCAGCACGCCTT
SEQ ID NO: 1982	**830066**	TTTTGCTTTTGGTGTGCGTCGGCAC	AAAACGAAAACCACACGCAGCCGTG
SEQ ID NO: 1983	**830364**	CAAGTCACTTTGTCTCCCTTACTTC	GTTCAGTGAAACAGAGGGAATGAAG
SEQ ID NO: 1984	**832421**	AGGTCTCGTCTTTGGTTTGTGAGTA	TCCAGAGCAGAAACCAAACACTCAT
SEQ ID NO: 1985	**837494**	CTACTAAATTTCTGTGTGTGACCAC	GATGATTTAAAGACACACACTGGTG
SEQ ID NO: 1986	**839374**	AAATCCTTTCAGAGTCCGGTCCGCT	TTTAGGAAAGTCTCAGGCCAGGCGA
SEQ ID NO: 1987	**840973**	TACATGGGTTTTCGCGGTTAGGACA	ATGTACCCAAAAGCGCCAATCCTGT
SEQ ID NO: 1988	**841165**	TACGGTCGGGTTTTTGGTCAGCAGT	ATGCCAGCCCAAAAACCAGTCGTCA
SEQ ID NO: 1989	**841462**	GTTGTCGTGGTTTTCCTGGTTCCTT	CAACAGCACCAAAAGGACCAAGGAA
SEQ ID NO: 1990	**841909**	ACTTTCGTGTTTGTGTCAGGAAGCG	TGAAAGCACAAACACAGTCCTTCGC
SEQ ID NO: 1991	**842277**	GTAAATGGTTTGTGTCTGGTCCGTG	CATTTACCAAACACAGACCAGGCAC

SEQ ID NO: 1992	**842529**	ATTAGGGTTTGTCGTCCGTTATATT	TAATCCCAAACAGCAGGCAATATAA
SEQ ID NO: 1993	**842815**	ATGTCATGTTTGTTCCGACTCCCAG	TACAGTACAAACAAGGCTGAGGGTC
SEQ ID NO: 1994	**842967**	GATGGCGTCGTTTGTCTGCGGTTTT	CTACCGCAGCAAACAGACGCCAAAA
SEQ ID NO: 1995	**843347**	GTCGGTGGTGTTTTCTTCGGCACAT	CAGCCACCACAAAAGAAGCCGTGTA
SEQ ID NO: 1996	**843625**	ATGGTGGTTTGTGCCTCCCTGTAGG	TACCACCAAACACGGAGGGACATCC
SEQ ID NO: 1997	**843655**	AATCCGTGTTTGTGGTTTAGTACGA	TTAGGCACAAACACCAAATCATGCT
SEQ ID NO: 1998	**844208**	AATTACTGTTTGTGGCGTTAATGAA	TTAATGACAAACACCGCAATTACTT
SEQ ID NO: 1999	**844286**	AGGTCCTGTTTGTGTGCTTAGAATC	TCCAGGACAAACACACGAATCTTAG
SEQ ID NO: 2000	**844301**	CAAACAGTTTGTGTGTCCGATGGAC	GTTTGTCAAACACACAGGCTACCTG
SEQ ID NO: 2001	**844635**	GTCGTCGTGGTGTTTGTGCTCATTA	CAGCAGCACCACAAACACGAGTAAT
SEQ ID NO: 2002	**844710**	NA	NA
SEQ ID NO: 2003	**845163**	AGGCAGTGTTTGTGTGTGCCGTAAA	TCCGTCACAAACACACACGGCATTT
SEQ ID NO: 2004	**845312**	CGTGTGAGTGTTTGTCGACTAGACC	GCACACTCACAAACAGCTGATCTGG
SEQ ID NO: 2005	**846432**	GCTAGTGGCGTTTGTAGTCGTACCT	CGATCACCGCAAACATCAGCATGGA
SEQ ID NO: 2006	**846847**	TGGTCGGTGTTTCTCGGTATAAACA	ACCAGCCACAAAGAGCCATATTTGT
SEQ ID NO: 2007	**847033**	TTTACTATACGTTTGCTGTGTGTTT	AAATGATATGCAAACGACACACAAA
SEQ ID NO: 2008	**848780**	AAAGAAGTTTCGTCGTGTGTAGTGG	TTTCTTCAAAGCAGCACACATCACC
SEQ ID NO: 2009	**851570**	GTTATTCTTTTAAGTGTGTGTGAGG	CAATAAGAAAATTCACACACACTCC
SEQ ID NO: 2010	**856648**	ACGGTCGGTCGTTTAGGGATCTCAA	TGCCAGCCAGCAAATCCCTAGAGTT
SEQ ID NO: 2011	**857999**	CGTGTGGCGTTTATACTACTGGACT	GCACACCGCAAATATGATGACCTGA
SEQ ID NO: 2012	**858936**	CGTTCAACATTTGTGGTGGTGTGAG	GCAAGTTGTAAACACCACCACACTC

SEQ ID NO: 2013	**859034**	TGTGAACACGTTTAGTGTGGTGTGT	ACACTTGTGCAAATCACACCACACA
SEQ ID NO: 2014	**862315**	AACCAACATTTGTGGTGGCGTAGTG	TTGGTTGTAAACACCACCGCATCAC
SEQ ID NO: 2015	**862396**	ATGAAACATTTGGTGGTGGTGTAAT	TACTTTGTAAACCACCACCACATTA
SEQ ID NO: 2016	**865667**	ACGGACACGACATTGTTCCAACCTC	TGCCTGTGCTGTAACAAGGTTGGAG
SEQ ID NO: 2017	**868067**	NA	NA
SEQ ID NO: 2018	**869110**	CCTGGGATTTTGTGGTGTGGACTAC	GGACCCTAAAACACCACACCTGATG
SEQ ID NO: 2019	**869507**	ATCAAGGATTTTGAGTTCCCGTGCG	TAGTTCCTAAAACTCAAGGGCACGC
SEQ ID NO: 2020	**872292**	CACCCTACGATTTGGGACCGACCGG	GTGGGATGCTAAACCCTGGCTGGCC
SEQ ID NO: 2021	**875728**	GTCACCGCTACATTACTTTCACCAG	CAGTGGCGATGTAATGAAAGTGGTC
SEQ ID NO: 2022	**875841**	CGTTACGTCAGATTACCCTTTCGGT	GCAATGCAGTCTAATGGGAAAGCCA
SEQ ID NO: 2023	**876885**	AAGTGTGTGATTAGATGGGTAAGTA	TTCACACACTAATCTACCCATTCAT
SEQ ID NO: 2024	**879420**	GCTCCCATATTTTCGTGTGTCGTGT	CGAGGGTATAAAAGCACACAGCACA
SEQ ID NO: 2025	**879754**	CGAACGTCCTATTGTGTGTGAGATC	GCTTGCAGGATAACACACACTCTAG
SEQ ID NO: 2026	**880362**	ATTCGACACTATTGGGTGGTGGTAA	TAAGCTGTGATAACCCACCACCATT
SEQ ID NO: 2027	**881218**	CGATGTAGTTATTCGTGTGTGGTCA	GCTACATCAATAAGCACACACCAGT
SEQ ID NO: 2028	**882966**	ACACACACGGTATTGACTCGAGCCA	TGTGTGTGCCATAACTGAGCTCGGT
SEQ ID NO: 2029	**883159**	GCCTTTGTTGGTCCTCGTGATAAGG	CGGAAACAACCAGGAGCACTATTCC
SEQ ID NO: 2030	**883837**	CTTTATGTTGCGTGGTTTTGAGCGC	GAAATACAACGCACCAAAACTCGCG
SEQ ID NO: 2031	**884171**	CCCTAGTCTTGGGTGTGTGGCAATT	GGGATCAGAACCCACACACCGTTAA
SEQ ID NO: 2032	**884682**	AGGGGAGTTGTCGTGAGAAAGGTTA	TCCCCTCAACAGCACTCTTTCCAAT
SEQ ID NO: 2033	**884706**	GTTTGGTTTGGTTGTGACTTACTTG	CAAACCAAACCAACACTGAATGAAC

SEQ ID NO: 2034	**885407**	ACGTGTGTATTTGGAGGTAGGTATC	TGCACACATAAACCTCCATCCATAG
SEQ ID NO: 2035	**885449**	TAAGACATTTGGGTTGGTGTGGACC	ATTCTGTAAACCCAACCACACCTGG
SEQ ID NO: 2036	**886143**	ATTTGTTTGGCTCCACACTCGTACG	TAAACAAACCGAGGTGTGAGCATGC
SEQ ID NO: 2037	**886330**	CCGAAATTGGTGGTGTTCGTGGACT	GGCTTTAACCACCACAAGCACCTGA
SEQ ID NO: 2038	**886377**	CTATTCATTGGTCGGTGTCCTGCCT	GATAAGTAACCAGCCACAGGACGGA
SEQ ID NO: 2039	**886659**	CTACACTGTTTGGTCTGTTGCTTCT	GATGTGACAAACCAGACAACGAAGA
SEQ ID NO: 2040	**886753**	CTCAACGGTTGGTTGGCCAGCAGTC	GAGTTGCCAACCAACCGGTCGTCAG
SEQ ID NO: 2041	**887025**	CCTCGGTTTGGTGTGTCCTTTCAGA	GGAGCCAAACCACACAGGAAAGTCT
SEQ ID NO: 2042	**887074**	CCGAAGCTTGGCACCGACGGTACAC	GGCTTCGAACCGTGGCTGCCATGTG
SEQ ID NO: 2043	**887082**	GTAGTGACGTCTTTGGTGTGAGTTA	CATCACTGCAGAAACCACACTCAAT
SEQ ID NO: 2044	**888358**	TCCGACGCCTTGGAGAGGACTGGTC	AGGCTGCGGAACCTCTCCTGACCAG
SEQ ID NO: 2045	**888828**	GTAAGACCTCTTGGCTTCGAGTCGA	CATTCTGGAGAACCGAAGCTCAGCT
SEQ ID NO: 2046	**888931**	ATAGTATCACTTGGTTTTGGTGTCG	TATCATAGTGAACCAAAACCACAGC
SEQ ID NO: 2047	**889194**	GGGGTCTCTTGGTGTGGTGACAGAC	CCCCAGAGAACCACACCACTGTCTG
SEQ ID NO: 2048	**889977**	AGGTAACTTTGCATGTGTGTGGGTC	TCCATTGAAACGTACACACACCCAG
SEQ ID NO: 2049	**890231**	GACAACTCCGTTGCTTGGTGAAGTC	CTGTTGAGGCAACGAACCACTTCAG
SEQ ID NO: 2050	**890606**	CAATTTTGCAGTGTTTCCACGACGA	GTTAAAACGTCACAAAGGTGCTGCT
SEQ ID NO: 2051	**891380**	CAAATTTGCGTGCTGTGGGTAACTT	GTTTAAACGCACGACACCCATTGAA
SEQ ID NO: 2052	**891684**	AGTCAACTACTTGCTCGATGAGAAA	TCAGTTGATGAACGAGCTACTCTTT
SEQ ID NO: 2053	**891717**	TTGCCGTCTTGCGTGCGAACCGCAT	AACGGCAGAACGCACGCTTGGCGTA
SEQ ID NO: 2054	**891936**	AGGTCTGGTTGGTAAAGAATATCAG	TCCAGACCAACCATTTCTTATAGTC

SEQ ID NO: 2055	**892102**	GGAGGAGACTTGCACACGCACACGC	CCTCCTCTGAACGTGTGCGTGTGCG
SEQ ID NO: 2056	**892319**	ATCTCGTGGTTGGTGAAGTTCTTTG	TAGAGCACCAACCACTTCAAGAAAC
SEQ ID NO: 2057	**892590**	AAACCCGTTGGTGTGTCAGTAGCTG	TTTGGGCAACCACACAGTCATCGAC
SEQ ID NO: 2058	**892592**	TTCTACGGTGTTGGTGTGGATCCCT	AAGATGCCACAACCACACCTAGGGA
SEQ ID NO: 2059	**892698**	CTATCGGTCGTTGGTGTGAAGTTCT	GATAGCCAGCAACCACACTTCAAGA
SEQ ID NO: 2060	**892838**	GTTCTACGGTGTTGGTGTGGATCCC	CAAGATGCCACAACCACACCTAGGG
SEQ ID NO: 2061	**892839**	GTTGGTTGTTGGTTGTGCTCACACC	CAACCAACAACCAACACGAGTGTGG
SEQ ID NO: 2062	**892936**	GTCGTTGAAGTTGGTGGGATATATT	CAGCAACTTCAACCACCCTATATAA
SEQ ID NO: 2063	**893152**	ACGGACGTGGTTGGTGTAAATCCGA	TGCCTGCACCAACCACATTTAGGCT
SEQ ID NO: 2064	**893265**	ATTCTGCGTTGGTGTCCTCCTTTGA	TAAGACGCAACCACAGGAGGAAACT
SEQ ID NO: 2065	**893514**	CATTGTGTTGGTGGTGGAGACCCTC	GTAACACAACCACCACCTCTGGGAG
SEQ ID NO: 2066	**893867**	ACGTCCTGTGTTGGTAGTAACCCTT	TGCAGGACACAACCATCATTGGGAA
SEQ ID NO: 2067	**893993**	CAATCAGTTGGGTGTGTGAGTAACC	GTTAGTCAACCCACACACTCATTGG
SEQ ID NO: 2068	**894001**	ACCTGTGTCGTTGGTGGTTCCGTAA	TGGACACAGCAACCACCAAGGCATT
SEQ ID NO: 2069	**894520**	GTCCATTGTTGCGTGTGTCTCCATT	CAGGTAACAACGCACACAGAGGTAA
SEQ ID NO: 2070	**896386**	ATGTGTGTTTGAGGTTTCGTGATTC	TACACACAAACTCCAAAGCACTAAG
SEQ ID NO: 2071	**897023**	TTAAGTCTATTGAGTGGTGGTGGAA	AATTCAGATAACTCACCACCACCTT
SEQ ID NO: 2072	**897212**	CACAGGGTTGAAAAAAGGTACACGA	GTGTCCCAACTTTTTTCCATGTGCT
SEQ ID NO: 2073	**899603**	TTGTTTTTGACATAGGTGGTGGTGA	AACAAAAACTGTATCCACCACCACT
SEQ ID NO: 2074	**901240**	ACTTCAACTTGACCACACACACGGT	TGAAGTTGAACTGGTGTGTGTGCCA
SEQ ID NO: 2075	**901539**	CATCACTGTTGAACCGCCGACGACG	GTAGTGACAACTTGGCGGCTGCTGC

SEQ ID NO: 2076	**902026**	TCCTTGTCTTGTGGGTGGAATCGAG	AGGAACAGAACACCCACCTTAGCTC
SEQ ID NO: 2077	**902041**	ATGTTATGTTGATGTCACGTTTAGT	TACAATACAACTACAGTGCAAATCA
SEQ ID NO: 2078	**904159**	GTAACGTGCGTTTGTTGCTCAACCC	CATTGCACGCAAACAACGAGTTGGG
SEQ ID NO: 2079	**904783**	AATAAATTGTTTGTGGGTGTGTCGT	TTATTTAACAAACACCCACACAGCA
SEQ ID NO: 2080	**904785**	ATTATCATTGTCAGGTGTGTGTGTT	TAATAGTAACAGTCCACACACACAA
SEQ ID NO: 2081	**904929**	AGATCTCGATTGTGTGTATCCTTCC	TCTAGAGCTAACACACATAGGAAGG
SEQ ID NO: 2082	**904969**	AAGAGTGTTTGTGGGCTCGAACCGA	TTCTCACAAACACCCGAGCTTGGCT
SEQ ID NO: 2083	**905655**	CATCATTTGTGGTGGCGTGAGTCTC	GTAGTAAACACCACCGCACTCAGAG
SEQ ID NO: 2084	**906397**	AAGAGTGTTTGTGTCGTCCATCCCA	TTCTCACAAACACAGCAGGTAGGGT
SEQ ID NO: 2085	**906485**	ACCAGTCGTTTGTGTGGTGTCCCAG	TGGTCAGCAAACACACCACAGGGTC
SEQ ID NO: 2086	**906647**	CTAATTATTGTGCTTGTGCGGTCCC	GATTAATAACACGAACACGCCAGGG
SEQ ID NO: 2087	**907329**	ACCTGAGCTTGTGGTGATGGTCTAC	TGGACTCGAACACCACTACCAGATG
SEQ ID NO: 2088	**907445**	AGTGGGACGTTGTGTAAGTCATTCG	TCACCCTGCAACACATTCAGTAAGC
SEQ ID NO: 2089	**907675**	TCATTGTTTGTCTGTGTGCCCTACC	AGTAACAAACAGACACACGGGATGG
SEQ ID NO: 2090	**907734**	GTGTGCGAGTACTTGTTGTTTACCT	CACACGCTCATGAACAACAAATGGA
SEQ ID NO: 2091	**907851**	AAGTCACTTTGTCTCCCTTACTTCT	TTCAGTGAAACAGAGGGAATGAAGA
SEQ ID NO: 2092	**907983**	CTGAATTTGTCGTGTTGTCCGAGGA	GACTTAAACAGCACAACAGGCTCCT
SEQ ID NO: 2093	**908793**	CTTGTCCTTGTCGTTGTGTGCCCGT	GAACAGGAACAGCAACACACGGGCA
SEQ ID NO: 2094	**909175**	ATAATGTCGTTGTGTTCTGTGCCGC	TATTACAGCAACACAAGACACGGCG
SEQ ID NO: 2095	**909336**	GTCAAAGGTTGTTGTGGCTAGAAGC	CAGTTTCCAACAACACCGATCTTCG
SEQ ID NO: 2096	**909819**	AACTCGTGTCGTTGTTTTGTTATCA	TTGAGCACAGCAACAAAACAATAGT

SEQ ID NO: 2097	**910111**	AGACTTGGTTGTGTGAACACTTTGT	TCTGAACCAACACACTTGTGAAACA
SEQ ID NO: 2098	**910380**	CCACTTGTTGTTGTCGTTCTGTCTC	GGTGAACAACAACAGCAAGACAGAG
SEQ ID NO: 2099	**910399**	AGTTCCGTGTTGTGAGGTTGGACAC	TCAAGGCACAACACTCCAACCTGTG
SEQ ID NO: 2100	**910636**	CCAGTGGTTGTGAGTCCGTCCCTTT	GGTCACCAACACTCAGGCAGGGAAA
SEQ ID NO: 2101	**910884**	GCCTGAGGTTGTGGCACCGGTACTT	CGGACTCCAACACCGTGGCCATGAA
SEQ ID NO: 2102	**910887**	CGAGGACCGTTGTGTGTACGTCATT	GCTCCTGGCAACACACATGCAGTAA
SEQ ID NO: 2103	**910936**	AGGTGTGGTTGTCCTTACCGTCCCG	TCCACACCAACAGGAATGGCAGGGC
SEQ ID NO: 2104	**911002**	TTCCAGGTTGTGTGTTGGCCTCACC	AAGGTCCAACACACAACCGGAGTGG
SEQ ID NO: 2105	**911552**	CGTAATGTCGTTGTTGGCTCACTCT	GCATTACAGCAACAACCGAGTGAGA
SEQ ID NO: 2106	**911554**	ACTCCGGGTTGTGTTGGTCAACGTC	TGAGGCCCAACACAACCAGTTGCAG
SEQ ID NO: 2107	**912309**	GTATGTGTGTTTGTAAGGTATGTGT	CATACACACAAACATTCCATACACA
SEQ ID NO: 2108	**916325**	TCTATACTAAATGGTGGTGGTGGGA	AGATATGATTTACCACCACCACCCT
SEQ ID NO: 2109	**916781**	CCACAGACATGGGTGGTGGTAGTAC	GGTGTCTGTACCCACCACCATCATG
SEQ ID NO: 2110	**917126**	ACTGTGGTCATGGTGGTGTACTATC	TGACACCAGTACCACCACATGATAG
SEQ ID NO: 2111	**917260**	GGTCAGTGCATGGTGTGTCGATACA	CCAGTCACGTACCACACAGCTATGT
SEQ ID NO: 2112	**918316**	AGAGGCAGATGGTGGTGAAACTTTT	TCTCCGTCTACCACCACTTTGAAAA
SEQ ID NO: 2113	**918908**	ATCGACACACATGCGAACACACACG	TAGCTGTGTGTACGCTTGTGTGTGC
SEQ ID NO: 2114	**919232**	ATTATGAGATGCGATCCGTACCACG	TAATACTCTACGCTAGGCATGGTGC
SEQ ID NO: 2115	**919334**	GTCACGACATGATGGTGGTGGAAAT	CAGTGCTGTACTACCACCACCTTTA
SEQ ID NO: 2116	**919684**	TAAAGCAGATGGTGTGTGACACTGG	ATTTCGTCTACCACACACTGTGACC
SEQ ID NO: 2117	**919707**	ACATCTCTAGATGGAACGTGTGTGG	TGTAGAGATCTACCTTGCACACACC

SEQ ID NO: 2118	**923552**	ATTTCGAATGACTCGTGTGTGGTAC	TAAAGCTTACTGAGCACACACCATG
SEQ ID NO: 2119	**923601**	CAGTGGTGATGATGGTGACGTCCCA	GTCACCACTACTACCACTGCAGGGT
SEQ ID NO: 2120	**924047**	CCATGGTATGCGTGTGAAGTATACT	GGTACCATACGCACACTTCATATGA
SEQ ID NO: 2121	**924611**	CGGGTCGTTATGTGGTGGTGCCGAA	GCCCAGCAATACACCACCACGGCTT
SEQ ID NO: 2122	**925503**	GTAGTGGTGTGTATGGATGTTTCAT	CATCACCACACATACCTACAAAGTA
SEQ ID NO: 2123	**925554**	CTCGTCCCTATGGTGGTGGACAAGT	GAGCAGGGATACCACCACCTGTTCA
SEQ ID NO: 2124	**925840**	CTGCAGTAGTATGCGCTGTTGTGGC	GACGTCATCATACGCGACAACACCG
SEQ ID NO: 2125	**926188**	GAGGGCCTATGCGACCGACACGACC	CTCCCGGATACGCTGGCTGTGCTGG
SEQ ID NO: 2126	**926233**	AGACTGTCCTATGCTACCCTGCGAA	TCTGACAGGATACGATGGGACGCTT
SEQ ID NO: 2127	**926360**	TTCTGTGTGTATGGAATGTGTGTAC	AAGACACACATACCTTACACACATG
SEQ ID NO: 2128	**926726**	NA	NA
SEQ ID NO: 2129	**927044**	ATGTGTGTGTATGCGACTTTTGCCC	TACACACACATACGCTGAAAACGGG
SEQ ID NO: 2130	**927045**	GTTTGTGTGTATGCCATTCGAGTCA	CAAACACACATACGGTAAGCTCAGT
SEQ ID NO: 2131	**927256**	GTGTGTATACATATGCGTGTGTTCA	CACACATATGTATACGCACACAAGT
SEQ ID NO: 2132	**928213**	NA	NA
SEQ ID NO: 2133	**929157**	ATGTTGAATGTGTGTGTGATGTCGT	TACAACTTACACACACACTACAGCA
SEQ ID NO: 2134	**929382**	GTGCGTGTTCATGTGTTTCTGTGTC	CACGCACAAGTACACAAAGACACAG
SEQ ID NO: 2135	**929417**	TCTTGATCATGTGTCGGTGGTTCCG	AGAACTAGTACACAGCCACCAAGGC
SEQ ID NO: 2136	**930320**	TCCCATCATGTGGAGTGTGTACGTG	AGGGTAGTACACCTCACACATGCAC
SEQ ID NO: 2137	**930701**	ATTGGTAATGTGTGTGTCGTGACTC	TAACCATTACACACACAGCACTGAG
SEQ ID NO: 2138	**931819**	GTAGTAGTAAGACATGTGTGTGTTC	CATCATCATTCTGTACACACACAAG

SEQ ID NO: 2139	**932145**	CGGACTGAGATGTTGTGTGGATATA	GCCTGACTCTACAACACACCTATAT
SEQ ID NO: 2140	**932455**	GTACACACACGTCATGTCCCGACAG	CATGTGTGTGCAGTACAGGGCTGTC
SEQ ID NO: 2141	**933456**	ACACACACAGATGTATGACACACAC	TGTGTGTGTCTACATACTGTGTGTG
SEQ ID NO: 2142	**933787**	CTATAGGGTATGTCCTTCGGCGGAT	GATATCCCATACAGGAAGCCGCCTA
SEQ ID NO: 2143	**934756**	ATCTGGTTATGTTGTGTGGGTTTAA	TAGACCAATACAACACACCCAAATT
SEQ ID NO: 2144	**934836**	CACACACACATGTATCGTAAGGATA	GTGTGTGTGTACATAGCATTCCTAT
SEQ ID NO: 2145	**935480**	ATTCTTCTATGTGTGGGTGTTACAG	TAAGAAGATACACACCCACAATGTC
SEQ ID NO: 2146	**935657**	NA	NA
SEQ ID NO: 2147	**935961**	CCACCATATGTGTCGTGTCTTGATA	GGTGGTATACACAGCACAGAACTAT
SEQ ID NO: 2148	**935996**	TGTATAAGGTATGTGTGTGTAAGGT	ACATATTCCATACACACACATTCCA
SEQ ID NO: 2149	**936130**	ATTGTCCGTATGTGTTTTGGGTGGT	TAACAGGCATACACAAAACCCACCA
SEQ ID NO: 2150	**936133**	CTGTGTGGTATGTAGTAGCGACTTC	GACACACCATACATCATCGCTGAAG
SEQ ID NO: 2151	**936442**	GTAGAGACCCTATGTGTCCCGTGGT	CATCTCTGGGATACACAGGGCACCA
SEQ ID NO: 2152	**936600**	ACAGTGCCGTATGTGGTTTGTCCTA	TGTCACGGCATACACCAAACAGGAT
SEQ ID NO: 2153	**936934**	ACGTCCACCTCTTCTATAAAAAATC	TGCAGGTGGAGAAGATATTTTTTAG
SEQ ID NO: 2154	**937615**	GGTGATACCCTTTTAGACGGTGACA	CCACTATGGGAAAATCTGCCACTGT
SEQ ID NO: 2155	**939108**	TTACCAACCTTTGTTGTGTCTGTCC	AATGGTTGGAAACAACACAGACAGG
SEQ ID NO: 2156	**939926**	ATGAGTCGTACCTTTGTTCTACTTT	TACTCAGCATGGAAACAAGATGAAA
SEQ ID NO: 2157	**941061**	TTAATCCCTTGAGACATCTTGTCCG	AATTAGGGAACTCTGTAGAACAGGC
SEQ ID NO: 2158	**941312**	CTACGACTACTACCTTTGTGTACCT	GATGCTGATGATGGAAACACATGGA
SEQ ID NO: 2159	**947242**	CGGTCACACCTTCGTGTGTGTCGTT	GCCAGTGTGGAAGCACACACAGCAA

SEQ ID NO: 2160	**947263**	AAAACTGCTTGTGGGTCGTTCGTCA	TTTTGACGAACACCCAGCAAGCAGT
SEQ ID NO: 2161	**947597**	CCATCGTGCTTGTGGTGGCGTCTGT	GGTAGCACGAACACCACCGCAGACA
SEQ ID NO: 2162	**948218**	TCGTGTGCGGCTTGCCCTTCTGCGC	AGCACACGCCGAACGGGAAGACGCG
SEQ ID NO: 2163	**948454**	CCTTGTGCTTGGTGTGTAGGCACAC	GGAACACGAACCACACATCCGTGTG
SEQ ID NO: 2164	**948455**	TCTCTACTCGGCTTGTGTGTGTCAG	AGAGATGAGCCGAACACACACAGTC
SEQ ID NO: 2165	**948567**	AGTGAGGTACGCTTGTGTAGGATCT	TCACTCCATGCGAACACATCCTAGA
SEQ ID NO: 2166	**948877**	TAAGTGTGTGCTTGAGTGAGTAAGT	ATTCACACACGAACTCACTCATTCA
SEQ ID NO: 2167	**951822**	AAAACTACCTTATCCTCGGCGGTGA	TTTTGATGGAATAGGAGCCGCCACT
SEQ ID NO: 2168	**952512**	ACCGCTCGCCTTACCTTATGTGTAG	TGGCGAGCGGAATGGAATACACATC
SEQ ID NO: 2169	**953367**	AGTCCGTATCCTTACTTCCCGTGGG	TCAGGCATAGGAATGAAGGGCACCC
SEQ ID NO: 2170	**954539**	CTAGTGGTTCTTGTGGTTCTTGTCC	GATCACCAAGAACACCAAGAACAGG
SEQ ID NO: 2171	**954763**	CAAATTCTTTGTGGGTCGGTGTCGA	GTTTAAGAAACACCCAGCCACAGCT
SEQ ID NO: 2172	**956520**	GAAAACCTCTTGTGTGTGGGGACTG	CTTTTGGAGAACACACACCCCTGAC
SEQ ID NO: 2173	**956633**	GATTACCGTTCTTGTTGTTGATGAA	CTAATGGCAAGAACAACAACTACTT
SEQ ID NO: 2174	**957025**	ACGAGTCTCTTCTTGTGTGTGCCGA	TGCTCAGAGAAGAACACACACGGCT
SEQ ID NO: 2175	**959894**	AACACAAGTCTTTGGGTCCGGGTTG	TTGTGTTCAGAAACCCAGGCCCAAC
SEQ ID NO: 2176	**960545**	CTGACCGATCTTCGTTTGACAATAG	GACTGGCTAGAAGCAAACTGTTATC
SEQ ID NO: 2177	**960785**	GTCTCGCCCTCTTCTGGAGTCCATG	CAGAGCGGGAGAAGACCTCAGGTAC
SEQ ID NO: 2178	**961615**	AAAACTCTCTTCGTGTGGAGTGAGT	TTTTGAGAGAAGCACACCTCACTCA
SEQ ID NO: 2179	**963732**	CCTTTGTCTTGTCGGGTATGGTTCT	GGAAACAGAACAGCCCATACCAAGA
SEQ ID NO: 2180	**963939**	GTGTGTGTCTAGTCTTGTTCCGCCC	CACACACAGATCAGAACAAGGCGGG

SEQ ID NO: 2181	**966684**	CTACCTTTCTTAGGTGTTGTGCGGA	GATGGAAAGAATCCACAACACGCCT
SEQ ID NO: 2182	**968624**	TAAAAAACTTGTGGTGCTTAGACAC	ATTTTTTGAACACCACGAATCTGTG
SEQ ID NO: 2183	**969088**	TACCACACACACTTTGAGTTTAAAT	ATGGTGTGTGTGAAACTCAAATTTA
SEQ ID NO: 2184	**973211**	NA	NA
SEQ ID NO: 2185	**973283**	CGTCACCACGACTTCGATATCGGTT	GCAGTGGTGCTGAAGCTATAGCCAA
SEQ ID NO: 2186	**973862**	GGTCGTGCGTGACTTGAGTTAAAAC	CCAGCACGCACTGAACTCAATTTTG
SEQ ID NO: 2187	**976020**	CTGTTATGACTTCTGTGTGTTTGGA	GACAATACTGAAGACACACAAACCT
SEQ ID NO: 2188	**976643**	GTCGAACCGAACTTAGCGAAGGTCT	CAGCTTGGCTTGAATCGCTTCCAGA
SEQ ID NO: 2189	**979517**	TAGTCGTGCGTATACTTGATACTTT	ATCAGCACGCATATGAACTATGAAA
SEQ ID NO: 2190	**980990**	ACCGAATCCTGGTGGGTCGGCACCC	TGGCTTAGGACCACCCAGCCGTGGG
SEQ ID NO: 2191	**981427**	GCCGGCGCCTGCCTCTAATGCAGTG	CGGCCGCGGACGGAGATTACGTCAC
SEQ ID NO: 2192	**981528**	CTCACTTCGCTGGTGCGTGGACGAA	GAGTGAAGCGACCACGCACCTGCTT
SEQ ID NO: 2193	**982059**	TTTGTGCCTGGTGTCTCGCATTAGA	AAACACGGACCACAGAGCGTAATCT
SEQ ID NO: 2194	**982847**	CAAAGGCTGGTCTGTGTCAGTGACT	GTTTCCGACCAGACACAGTCACTGA
SEQ ID NO: 2195	**984036**	AACGGGTCGCTGGTTGACACTGGTA	TTGCCCAGCGACCAACTGTGACCAT
SEQ ID NO: 2196	**984134**	CCTCCAGCTGGGTGCGGTGTGCAGC	GGAGGTCGACCCACGCCACACGTCG
SEQ ID NO: 2197	**984283**	TCTGAGTGTGCTGGTGGAGTCTACT	AGACTCACACGACCACCTCAGATGA
SEQ ID NO: 2198	**984572**	CACTCTGTGCTGGTGTGTTGTCCGT	GTGAGACACGACCACACAACAGGCA
SEQ ID NO: 2199	**984957**	CGTGTGGCGCTGGTCGTGCGCCAGC	GCACACCGCGACCAGCACGCGGTCG
SEQ ID NO: 2200	**985025**	CGCGTGTGACCTGCGTGTGCCCTGC	GCGCACACTGGACGCACACGGGACG
SEQ ID NO: 2201	**987433**	ATATATTGCTGATGCCGTGTGTGCG	TATATAACGACTACGGCACACACGC

SEQ ID NO: 2202	**988040**	NA	NA
SEQ ID NO: 2203	**989431**	TTCACCCTCTGCAAACCGATCGTGG	AAGTGGGAGACGTTTGGCTAGCACC
SEQ ID NO: 2204	**990585**	CTTTAGTTCTGGTTTGGTGTGCCAC	GAAATCAAGACCAAACCACACGGTG
SEQ ID NO: 2205	**990814**	TCCAACTTCTGCGTGTGTCGACTCC	AGGTTGAAGACGCACACAGCTGAGG
SEQ ID NO: 2206	**991258**	CTGCTACGTTCTGCCACCTGGACGA	GACGATGCAAGACGGTGGACCTGCT
SEQ ID NO: 2207	**991896**	TCGTGTGGCTCTGCGAGGTAGTCCC	AGCACACCGAGACGCTCCATCAGGG
SEQ ID NO: 2208	**992332**	GTAGCCTGTGTCTGCGGAATCCCTA	CATCGGACACAGACGCCTTAGGGAT
SEQ ID NO: 2209	**992834**	ACAGAGGTGTCTGGTGGTACCGTAT	TGTCTCCACAGACCACCATGGCATA
SEQ ID NO: 2210	**993469**	TCGCCTAGGTCTGCGCGTGTGGTCC	AGCGGATCCAGACGCGCACACCAGG
SEQ ID NO: 2211	**993665**	GGAGACCCTCTGACCCTGAAACAGA	CCTCTGGGAGACTGGGACTTTGTCT
SEQ ID NO: 2212	**995239**	NA	NA
SEQ ID NO: 2213	**995323**	CTCAGGTCCTGTGGCGGAACCTACC	GAGTCCAGGACACCGCCTTGGATGG
SEQ ID NO: 2214	**995516**	CTTCGGCCTGTGTGTGAATAACGTC	GAAGCCGGACACACACTTATTGCAG
SEQ ID NO: 2215	**995954**	AAGTTCTGCTGTGGTGGTTTACACC	TTCAAGACGACACCACCAAATGTGG
SEQ ID NO: 2216	**995955**	ACTGTTTCCTGTGGTGGTTCTCCTC	TGACAAAGGACACCACCAAGAGGAG
SEQ ID NO: 2217	**996090**	GTGTGTGCCCTGTTTCGAGAAGGTC	CACACACGGGACAAAGCTCTTCCAG
SEQ ID NO: 2218	**996107**	AGGTGTGCCTGTGCATCTACTACTG	TCCACACGGACACGTAGATGATGAC
SEQ ID NO: 2219	**996306**	ATCGTGTGCCTGTGCTATACCTGCC	TAGCACACGGACACGATATGGACGG
SEQ ID NO: 2220	**996684**	AGTCCCGACCTGTGTGTGTCGAAGG	TCAGGGCTGGACACACACAGCTTCC
SEQ ID NO: 2221	**996711**	AGGTACTAGTCCTGTGAGTGTGCGT	TCCATGATCAGGACACTCACACGCA
SEQ ID NO: 2222	**997134**	TCGTGTGTCCCTGTGTCGTTGATCT	AGCACACAGGGACACAGCAACTAGA

SEQ ID NO: 2223	**997226**	CCTTTCCTGTGTGTCAGGGTCCCGT	GGAAAGGACACACAGTCCCAGGGCA
SEQ ID NO: 2224	**997282**	GTCTTGGCCTGTGTTGGTCGACACT	CAGAACCGGACACAACCAGCTGTGA
SEQ ID NO: 2225	**998209**	GTGGTGGTGTCTGTGCTCCCTCCAG	CACCACCACAGACACGAGGGAGGTC
SEQ ID NO: 2226	**998744**	ATTGTATATCTGTTTGCGTGTGGCC	TAACATATAGACAAACGCACACCGG
SEQ ID NO: 2227	**998766**	GCCCTGGCTGTGTCTGCGCCTGTCG	CGGGACCGACACAGACGCGGACAGC
SEQ ID NO: 2228	**999771**	TTTCATCGTCTGTTGTGTGAGGTCC	AAAGTAGCAGACAACACACTCCAGG
SEQ ID NO: 2229	**1000128**	ACATTCAGTCTGTGTGGTGAATCCC	TGTAAGTCAGACACACCACTTAGGG
SEQ ID NO: 2230	**1000411**	AGCAGATTCTGTGCTGTGTGACCGA	TCGTCTAAGACACGACACACTGGCT
SEQ ID NO: 2231	**1000486**	AGACCCTACTCTGTGTGTGCCCAAC	TCTGGGATGAGACACACACGGGTTG
SEQ ID NO: 2232	**1000948**	CATTGTCTCTGTGGTGTATCGTCAC	GTAACAGAGACACCACATAGCAGTG
SEQ ID NO: 2233	**1001147**	CTCAGTGTGTCTGTTCTGGTTCCTC	GAGTCACACAGACAAGACCAAGGAG
SEQ ID NO: 2234	**1001408**	ACGAGCGGTGTCTGTGTTAAGTTCA	TGCTCGCCACAGACACAATTCAAGT
SEQ ID NO: 2235	**1001586**	GTCGCGCGTCCTCTGTGTGAGTGCC	CAGCGCGCAGGAGACACACTCACGG
SEQ ID NO: 2236	**1001922**	AGTGTCGACTATCTGTCGCTTCGGA	TCACAGCTGATAGACAGCGAAGCCT
SEQ ID NO: 2237	**1001992**	AACAGCTTCTGTCGGTGTCGTGTCA	TTGTCGAAGACAGCCACAGCACAGT
SEQ ID NO: 2238	**1002061**	ATAAATGTCTGTGCGGGTGACACCC	TATTTACAGACACGCCCACTGTGGG
SEQ ID NO: 2239	**1002278**	CGTCACCGGTCTGTGTGGACAACCC	GCAGTGGCCAGACACACCTGTTGGG
SEQ ID NO: 2240	**1002374**	ATGGGTGTCTGTGTGCCGCTCACCA	TACCCACAGACACACGGCGAGTGGT
SEQ ID NO: 2241	**1002375**	ACAAGTCGTGTCTGTGGTGCCTCAG	TGTTCAGCACAGACACCACGGAGTC
SEQ ID NO: 2242	**1003343**	GTCCTAGATAACTGGTGTGTGAATT	CAGGATCTATTGACCACACACTTAA
SEQ ID NO: 2243	**1005170**	CTTCATAACTGTGTGGTTGGGGCAC	GAAGTATTGACACACCAACCCCGTG

SEQ ID NO: 2244	**1005584**	ATGTACGTTCACTGTGGTGTGAATG	TACATGCAAGTGACACCACACTTAC
SEQ ID NO: 2245	**1009270**	CGGTTGTGACTGTGGTTTAAAAACT	GCCAACACTGACACCAAATTTTTGA
SEQ ID NO: 2246	**1010851**	GAACATTGACTGTGTGTGTAGTTCC	CTTGTAACTGACACACACATCAAGG
SEQ ID NO: 2247	**1010993**	AGTTTGTGCGTGCACTTGTGGGTCA	TCAAACACGCACGTGAACACCCAGT
SEQ ID NO: 2248	**1012186**	ACTTTCATTCCCGTTTTTAGCGTTA	TGAAAGTAAGGGCAAAAATCGCAAT
SEQ ID NO: 2249	**1013507**	AGGTGAGTTTCCTGCGTGTGTCCAC	TCCACTCAAAGGACGCACACAGGTG
SEQ ID NO: 2250	**1014363**	TTAATATTTCCTTCGGTGGTGGTCC	AATTATAAAGGAAGCCACCACCAGG
SEQ ID NO: 2251	**1017120**	ACTTTTTTCCGAAGAGTGTGGGTGC	TGAAAAAAGGCTTCTCACACCCACG
SEQ ID NO: 2252	**1018510**	TCCTCTGCTTCCTCGGTACTACTGA	AGGAGACGAAGGAGCCATGATGACT
SEQ ID NO: 2253	**1018596**	CGAAGTCCTTCCTGTGTGTGTCTCA	GCTTCAGGAAGGACACACACAGAGT
SEQ ID NO: 2254	**1018626**	GGTCCTACCGTTCCCGAGAGGACTT	CCAGGATGGCAAGGGCTCTCCTGAA
SEQ ID NO: 2255	**1022090**	ACTAGTGTGTGTTCCTCAAGAAAGG	TGATCACACACAAGGAGTTCTTTCC
SEQ ID NO: 2256	**1023649**	TCCGACCTCGTTCCTCGTCCAGCAG	AGGCTGGAGCAAGGAGCAGGTCGTC
SEQ ID NO: 2257	**1027307**	CCCTTATTCAGGTGTGTGTTGCCAC	GGGAATAAGTCCACACACAACGGTG
SEQ ID NO: 2258	**1031172**	NA	NA
SEQ ID NO: 2259	**1031193**	ACCACAGGTTCAAGGCAGTTTCTAG	TGGTGTCCAAGTTCCGTCAAAGATC
SEQ ID NO: 2260	**1035045**	CCTTTTTCTGTCTGCGTGTCGACCC	GGAAAAAGACAGACGCACAGCTGGG
SEQ ID NO: 2261	**1036397**	ACGACAACCTTCTGTGTGTAGTACT	TGCTGTTGGAAGACACACATCATGA
SEQ ID NO: 2262	**1036613**	ACTCGCGTCATTCTGTTGTTGTTTT	TGAGCGCAGTAAGACAACAACAAAA
SEQ ID NO: 2263	**1037343**	ACCAAGTCTTCTGTTTTTGAGGAAG	TGGTTCAGAAGACAAAAACTCCTTC
SEQ ID NO: 2264	**1039149**	CTGACTTTTCTCGTCCGTGTGTACC	GACTGAAAAGAGCAGGCACACATGG

SEQ ID NO: 2265	**1039673**	GACGCCGACCTTCTCTCTCCCGCAG	CTGCGGCTGGAAGAGAGAGGGCGTC
SEQ ID NO: 2266	**1040846**	AGTGCGTGTCGTTCTGCGTTTTGCA	TCACGCACAGCAAGACGCAAAACGT
SEQ ID NO: 2267	**1041991**	TCCCTCTGTTCTGTGCGTGCCTCGG	AGGGAGACAAGACACGCACGGAGCC
SEQ ID NO: 2268	**1043629**	TTCGACACGACTTCTATTTTGATCT	AAGCTGTGCTGAAGATAAAACTAGA
SEQ ID NO: 2269	**1045681**	CGAGTAGACAATCCGATTCAGGGTC	GCTCATCTGTTAGGCTAAGTCCCAG
SEQ ID NO: 2270	**1047199**	ACGCCGCCTTATGCAAGGTTTAATC	TGCGGCGGAATACGTTCCAAATTAG
SEQ ID NO: 2271	**1048814**	CTAAAACATCCACGCACACGACGGT	GATTTTGTAGGTGCGTGTGCTGCCA
SEQ ID NO: 2272	**1050765**	CTGGTTAATCGACGTTTGTGGTGGC	GACCAATTAGCTGCAAACACCACCG
SEQ ID NO: 2273	**1051112**	CTATGACGACGATCCGAAGTTTCCT	GATACTGCTGCTAGGCTTCAAAGGA
SEQ ID NO: 2274	**1054070**	CCGACGACCATCAGGACGAGAGTCC	GGCTGCTGGTAGTCCTGCTCTCAGG
SEQ ID NO: 2275	**1056674**	ATGAATTATCCTCTCTGTCCGGACG	TACTTAATAGGAGAGACAGGCCTGC
SEQ ID NO: 2276	**1059856**	CGACGGGAATCTTTCGTGTGTGAGT	GCTGCCCTTAGAAAGCACACACTCA
SEQ ID NO: 2277	**1061155**	GGAATATCATCTGTGTGCCGTGGAG	CCTTATAGTAGACACACGGCACCTC
SEQ ID NO: 2278	**1061298**	ATGTAAACATCTAAAAAAGGGGTCT	TACATTTGTAGATTTTTTCCCCAGA
SEQ ID NO: 2279	**1061526**	GTGTGTCCGTCATCTTTCCGTGAGA	CACACAGGCAGTAGAAAGGCACTCT
SEQ ID NO: 2280	**1062746**	ACGGTCCAGATCTTTGTGTGTGCAC	TGCCAGGTCTAGAAACACACACGTG
SEQ ID NO: 2281	**1065904**	GTTCCCACTATCTACTCCCAGTAGT	CAAGGGTGATAGATGAGGGTCATCA
SEQ ID NO: 2282	**1066242**	TTGTGACTCGTATCTGTATCGGAGA	AACACTGAGCATAGACATAGCCTCT
SEQ ID NO: 2283	**1067063**	GTATTTATTTCGCTTGTGTGGTTCC	CATAAATAAAGCGAACACACCAAGG
SEQ ID NO: 2284	**1067209**	CTGTACGTCGAGTATCTGCGTGCGT	GACATGCAGCTCATAGACGCACGCA
SEQ ID NO: 2285	**1067374**	TCAGTGTCGTGTTCGGTGGTGGCTT	AGTCACAGCACAAGCCACCACCGAA

SEQ ID NO: 2286	**1067872**	GGTTTCGATTCGACCGACCCATGGT	CCAAAGCTAAGCTGGCTGGGTACCA
SEQ ID NO: 2287	**1068399**	CAATCTTTCGGTTGCGTGTGTCCCT	GTTAGAAAGCCAACGCACACAGGGA
SEQ ID NO: 2288	**1068520**	TATTTATTTCGCTTGTGTGGTTCCT	ATAAATAAAGCGAACACACCAAGGA
SEQ ID NO: 2289	**1073284**	CTCACATTTCGTTGTGTGGGTCCCG	GAGTGTAAAGCAACACACCCAGGGC
SEQ ID NO: 2290	**1073537**	GAGTGTGGATTCGTATTTTTGGATT	CTCACACCTAAGCATAAAAACCTAA
SEQ ID NO: 2291	**1076388**	ATTATAGAGTTCGTGTTCGTGTCGT	TAATATCTCAAGCACAAGCACAGCA
SEQ ID NO: 2292	**1076575**	TACGTGTATATACGTTCGTGTGTGT	ATGCACATATATGCAAGCACACACA
SEQ ID NO: 2293	**1076936**	GTTTTCACATCGAACCGAACCGTCG	CAAAAGTGTAGCTTGGCTTGGCAGC
SEQ ID NO: 2294	**1079159**	CTTAACATATCGGTCTGTGTCGGTG	GAATTGTATAGCCAGACACAGCCAC
SEQ ID NO: 2295	**1079743**	ATAATGCTATCGGTGAGTGTGCCGC	TATTACGATAGCCACTCACACGGCG
SEQ ID NO: 2296	**1080423**	TAGAGGTTCATCGTGGTGTGCCATC	ATCTCCAAGTAGCACCACACGGTAG
SEQ ID NO: 2297	**1080441**	GTAAAAAATCGTTCGTCTGCCGGTG	CATTTTTTAGCAAGCAGACGGCCAC
SEQ ID NO: 2298	**1081506**	CGTTTCGTCGTATCGTTGTTAGCAC	GCAAAGCAGCATAGCAACAATCGTG
SEQ ID NO: 2299	**1082030**	TGTCGTCGGGATCGTATGTCTATGC	ACAGCAGCCCTAGCATACAGATACG
SEQ ID NO: 2300	**1082083**	CTTCTCGGATCGTGTGTGTCAGTCA	GAAGAGCCTAGCACACACAGTCAGT
SEQ ID NO: 2301	**1084207**	TTCCCTCCTCCTCGTTTAATAACTA	AAGGGAGGAGGAGCAAATTATTGAT
SEQ ID NO: 2302	**1084419**	CTCACGACTCCTCCTTGAAAGGGGA	GAGTGCTGAGGAGGAACTTTCCCCT
SEQ ID NO: 2303	**1084677**	GATATATCGTCCTCCCGACGACGCA	CTATATAGCAGGAGGGCTGCTGCGT
SEQ ID NO: 2304	**1085379**	GGGATCCCTCCTACCTACGTGACGG	CCCTAGGGAGGATGGATGCACTGCC
SEQ ID NO: 2305	**1085921**	NA	NA
SEQ ID NO: 2306	**1089017**	GGTTGTTAGCTCAGAGGTTGTCGTT	CCAACAATCGAGTCTCCAACAGCAA

SEQ ID NO: 2307	**1089365**	GACGCTGCCGTCTCCCTGCAGTGGT	CTGCGACGGCAGAGGGACGTCACCA
SEQ ID NO: 2308	**1090079**	CCGGCACCTCACAGGGGAAGGTCGT	GGCCGTGGAGTGTCCCCTTCCAGCA
SEQ ID NO: 2309	**1090306**	ACCTCCTCCTCACTCGTCCAGGGTT	TGGAGGAGGAGTGAGCAGGTCCCAA
SEQ ID NO: 2310	**1092316**	ATTTGTTCTCCGATTAGACTGTTTT	TAAACAAGAGGCTAATCTGACAAAA
SEQ ID NO: 2311	**1093533**	CTTCTCCTCTCCCTGTGTGTGTGTG	GAAGAGGAGAGGGACACACACACAC
SEQ ID NO: 2312	**1093888**	ATCCCGGTCTCCAGACAGACGGTCT	TAGGGCCAGAGGTCTGTCTGCCAGA
SEQ ID NO: 2313	**1094512**	ATCATACTTCTCACACGCACGGGTT	TAGTATGAAGAGTGTGCGTGCCCAA
SEQ ID NO: 2314	**1094711**	CGTGCGTGTGTCTCCTGACCGTAGA	GCACGCACACAGAGGACTGGCATCT
SEQ ID NO: 2315	**1097398**	CGGTCCTCGTCTCATTGTCAGTTTT	GCCAGGAGCAGAGTAACAGTCAAAA
SEQ ID NO: 2316	**1097608**	AGAGGGCCTCTTCGGCCTCAACAGT	TCTCCCGGAGAAGCCGGAGTTGTCA
SEQ ID NO: 2317	**1097767**	GGAAAACCTCTTGTGTGTGGGGACT	CCTTTTGGAGAACACACACCCCTGA
SEQ ID NO: 2318	**1098039**	GACCGCCTCCTCTTAGTCAGTAGGG	CTGGCGGAGGAGAATCAGTCATCCC
SEQ ID NO: 2319	**1098234**	CTTACCTCCTCTCATCCTTTAAGGG	GAATGGAGGAGAGTAGGAAATTCCC
SEQ ID NO: 2320	**1098403**	GTGTGGTGTCGTCTCACATTGATTT	CACACCACAGCAGAGTGTAACTAAA
SEQ ID NO: 2321	**1099498**	ACGACTCGTCACCTCTTTGTGTTGA	TGCTGAGCAGTGGAGAAACACAACT
SEQ ID NO: 2322	**1099633**	CTTCCTCCTCTCCATGTTAAGAGAC	GAAGGAGGAGAGGTACAATTCTCTG
SEQ ID NO: 2323	**1100267**	AAAGGACCTCTGGTTAGTCGTCGGA	TTTCCTGGAGACCAATCAGCAGCCT
SEQ ID NO: 2324	**1100282**	GATCACCTCCTCTCCTCCGTACCCG	CTAGTGGAGGAGAGGAGGCATGGGC
SEQ ID NO: 2325	**1101444**	ATAACGACACCTCTCTATTTCTGCT	TATTGCTGTGGAGAGATAAAGACGA
SEQ ID NO: 2326	**1104707**	ACACCGTCCTCTCTGAAGGAGGGTC	TGTGGCAGGAGAGACTTCCTCCCAG
SEQ ID NO: 2327	**1104769**	TTTCCTCGTCTCTTCGAAACCTAGG	AAAGGAGCAGAGAAGCTTTGGATCC

SEQ ID NO: 2328	**1104818**	ACATAATATCTCTGTGTGTGCGGAA	TGTATTATAGAGACACACACGCCTT
SEQ ID NO: 2329	**1105284**	NA	NA
SEQ ID NO: 2330	**1106623**	GTAGTGTGCGTGTCTCTCGAACCTT	CATCACACGCACAGAGAGCTTGGAA
SEQ ID NO: 2331	**1106976**	ATCCGACACACTCCCAGAGGTCAGG	TAGGCTGTGTGAGGGTCTCCAGTCC
SEQ ID NO: 2332	**1109019**	AGAATGTGTACTCCACTTTGGGGTT	TCTTACACATGAGGTGAAACCCCAA
SEQ ID NO: 2333	**1109073**	NA	NA
SEQ ID NO: 2334	**1109316**	GTGTGTGTGTAGACTCCCGGAACCA	CACACACACATCTGAGGGCCTTGGT
SEQ ID NO: 2335	**1109714**	ATCACACACACTCACAAAAGGGTCC	TAGTGTGTGTGAGTGTTTTCCCAGG
SEQ ID NO: 2336	**1109975**	GGAAGTGTCACTCACGATGTCAAGT	CCTTCACAGTGAGTGCTACAGTTCA
SEQ ID NO: 2337	**1110045**	TGGTCCCGACTCCTTCTGGTGCAAG	ACCAGGGCTGAGGAAGACCACGTTC
SEQ ID NO: 2338	**1111206**	GGTGTACACCACTCACGGCCCATGT	CCACATGTGGTGAGTGCCGGGTACA
SEQ ID NO: 2339	**1111749**	CTTATGTACACTCACTCACGTCGTG	GAATACATGTGAGTGAGTGCAGCAC
SEQ ID NO: 2340	**1112727**	AGAACCCGACTCTCTGCGATATCAC	TCTTGGGCTGAGAGACGCTATAGTG
SEQ ID NO: 2341	**1112932**	AGACGTCCCGACTCTTCCACTTGGG	TCTGCAGGGCTGAGAAGGTGAACCC
SEQ ID NO: 2342	**1114124**	TTTTCGTGACTCTTTCGGTTTGTAT	AAAAGCACTGAGAAAGCCAAACATA
SEQ ID NO: 2343	**1114715**	ATTTTCACTCTTGTGTGTTGTGTCG	TAAAAGTGAGAACACACAACACAGC
SEQ ID NO: 2344	**1115358**	GTCCGCACGACACTCTCGAGAAAAG	CAGGCGTGCTGTGAGAGCTCTTTTC
SEQ ID NO: 2345	**1115989**	ACTCCTTCCTCGTATAAGGTTTGAG	TGAGGAAGGAGCATATTCCAAACTC
SEQ ID NO: 2346	**1118120**	CCGGTCTGCTCGTGTGTGTCAACAA	GGCCAGACGAGCACACACAGTTGTT
SEQ ID NO: 2347	**1118166**	CGTCATCGTCCTCGCGAGTCAGATG	GCAGTAGCAGGAGCGCTCAGTCTAC
SEQ ID NO: 2348	**1119908**	ATGACGACGTCCTCGACAACGACCT	TACTGCTGCAGGAGCTGTTGCTGGA

SEQ ID NO: 2349	**1120238**	GTCTGGTTCGTCTCGAGAGTCCCTC	CAGACCAAGCAGAGCTCTCAGGGAG
SEQ ID NO: 2350	**1120962**	CGCCTCTGCTCGTGCGAGTGCGTGC	GCGGAGACGAGCACGCTCACGCACG
SEQ ID NO: 2351	**1121171**	CTCGCCGCCTCGTAAGTGTCACTTT	GAGCGGCGGAGCATTCACAGTGAAA
SEQ ID NO: 2352	**1121211**	CTAGTGTTCGTCTCGGTTCCAAGTA	GATCACAAGCAGAGCCAAGGTTCAT
SEQ ID NO: 2353	**1121745**	ACTCGCCGCCTCGTAAGTGTCACTT	TGAGCGGCGGAGCATTCACAGTGAA
SEQ ID NO: 2354	**1121748**	TCCACCGTCCTCGTAGAAGACTCTT	AGGTGGCAGGAGCATCTTCTGAGAA
SEQ ID NO: 2355	**1121892**	CACACGCCCTCGTGCATGTGTGTGT	GTGTGCGGGAGCACGTACACACACA
SEQ ID NO: 2356	**1122944**	GTCCCATCCTCGTGTACTACGTAGG	CAGGGTAGGAGCACATGATGCATCC
SEQ ID NO: 2357	**1123017**	GTCGACTCGTCCCTCGTCCGAGGGT	CAGCTGAGCAGGGAGCAGGCTCCCA
SEQ ID NO: 2358	**1123072**	TTACACCACACTCGTATAGGGGATG	AATGTGGTGTGAGCATATCCCCTAC
SEQ ID NO: 2359	**1123625**	GTGTGTGTGCTCTCGTACTTCGTGT	CACACACACGAGAGCATGAAGCACA
SEQ ID NO: 2360	**1123918**	CCACACACGTACTCGCACCTGGGCC	GGTGTGTGCATGAGCGTGGACCCGG
SEQ ID NO: 2361	**1124662**	CTTTGTGTCTCGTGTGACTCTCGAA	GAAACACAGAGCACACTGAGAGCTT
SEQ ID NO: 2362	**1125622**	TGCGGCGCTGTGCTCGTGTAGCCCA	ACGCCGCGACACGAGCACATCGGGT
SEQ ID NO: 2363	**1125711**	GACCATCAACTCGTGTGTGTAGTGT	CTGGTAGTTGAGCACACACATCACA
SEQ ID NO: 2364	**1126160**	GGACCTGCCGTCATTCCTCAGTGAG	CCTGGACGGCAGTAAGGAGTCACTC
SEQ ID NO: 2365	**1126194**	GTGGTGGTGGTTCCCTAACGTTTCC	CACCACCACCAAGGGATTGCAAAGG
SEQ ID NO: 2366	**1126260**	CCTTATAACTCGTGGGTGTGTCTCC	GGAATATTGAGCACCCACACAGAGG
SEQ ID NO: 2367	**1127027**	NA	NA
SEQ ID NO: 2368	**1127028**	AGAGTGTTGGTTTGAATGGAGTATA	TCTCACAACCAAACTTACCTCATAT
SEQ ID NO: 2369	**1127076**	ACGTTTGTGGTTGTTTGCCCGAATC	TGCAAACACCAACAAACGGGCTTAG

SEQ ID NO: 2370	**1128817**	ACATGGTGGTTTGTGCCTCCCTGTA	TGTACCACCAAACACGGAGGGACAT
SEQ ID NO: 2371	**1128918**	AAGAGTCTGGTTGGTCTGAAGAAAA	TTCTCAGACCAACCAGACTTCTTTT
SEQ ID NO: 2372	**1129197**	ATTGTTGGTTGGTGCTTACCCTCCG	TAACAACCAACCACGAATGGGAGGC
SEQ ID NO: 2373	**1129283**	CAGTTATGGTTTAAGTGTGTGGAAA	GTCAATACCAAATTCACACACCTTT
SEQ ID NO: 2374	**1129412**	TCGTGTATGTGGTTTCGTCCGTTAC	AGCACATACACCAAAGCAGGCAATG
SEQ ID NO: 2375	**1129943**	ACGTAGTGGTGGTTGGCCTACCTCC	TGCATCACCACCAACCGGATGGAGG
SEQ ID NO: 2376	**1130571**	AACCGTTGGTTGTGCGGGCGTCACA	TTGGCAACCAACACGCCCGCAGTGT
SEQ ID NO: 2377	**1130677**	GTTAGGGTCGGTTTGTTCGTTAAAA	CAATCCCAGCCAAACAAGCAATTTT
SEQ ID NO: 2378	**1131170**	ACGGTTGTGGTTGTACTTAGTCCTC	TGCCAACACCAACATGAATCAGGAG
SEQ ID NO: 2379	**1132801**	AGGGTTGTGTTCGTGCCGTCCTTCA	TCCCAACACAAGCACGGCAGGAAGT
SEQ ID NO: 2380	**1134438**	AGTGTGTGGGTTCGTCCATTCGTGC	TCACACACCCAAGCAGGTAAGCACG
SEQ ID NO: 2381	**1134619**	CCGGTGTGGTTCTCGAAGCCTTTGC	GGCCACACCAAGAGCTTCGGAAACG
SEQ ID NO: 2382	**1134856**	AGACCGCTGGTTCGTGTTTGACTGA	TCTGGCGACCAAGCACAAACTGACT
SEQ ID NO: 2383	**1135913**	ACCACTCGTGGTTCGTGTTCCGTAG	TGGTGAGCACCAAGCACAAGGCATC
SEQ ID NO: 2384	**1136388**	AAGTGTAGTGGTTCGTGTTTCGACC	TTCACATCACCAAGCACAAAGCTGG
SEQ ID NO: 2385	**1137042**	TTGTGTCGGGTTATGGATTACTATG	AACACAGCCCAATACCTAATGATAC
SEQ ID NO: 2386	**1137118**	ATACATGTCGGTTCGGTTGAGTCAG	TATGTACAGCCAAGCCAACTCAGTC
SEQ ID NO: 2387	**1138309**	ATATCTTATGTTGTGGTTGCAGCGT	TATAGAATACAACACCAACGTCGCA
SEQ ID NO: 2388	**1138501**	GGTCTTTGTGTTCGATTTATAAAAT	CCAGAAACACAAGCTAAATATTTTA
SEQ ID NO: 2389	**1139086**	ACACTCAGTTGTTTGTTGTTGGAGA	TGTGAGTCAACAAACAACAACCTCT
SEQ ID NO: 2390	**1139108**	CTACGAGGTTGTTGGTGTAAGTGTC	GATGCTCCAACAACCACATTCACAG

SEQ ID NO: 2391	**1139197**	TCTCAGTCGTTGTTGTTAAGCCATC	AGAGTCAGCAACAACAATTCGGTAG
SEQ ID NO: 2392	**1139429**	CATCGAGTTGTTTTTGTGTGCTTGC	GTAGCTCAACAAAAACACACGAACG
SEQ ID NO: 2393	**1139799**	TTTCAGTTGTTTCGGTGGTCGTTTT	AAAGTCAACAAAGCCACCAGCAAAA
SEQ ID NO: 2394	**1140226**	CGTTGTTTGTTGAGTGCTTAGTCCG	GCAACAAACAACTCACGAATCAGGC
SEQ ID NO: 2395	**1140289**	AGTAGGTACGTTGTTTGTCGATAAC	TCATCCATGCAACAAACAGCTATTG
SEQ ID NO: 2396	**1140878**	CACATCGTTGTTGTCGGGTTTGGGA	GTGTAGCAACAACAGCCCAAACCCT
SEQ ID NO: 2397	**1141098**	GTGACCGGTGTGTTGACTCAGCCTT	CACTGGCCACACAACTGAGTCGGAA
SEQ ID NO: 2398	**1141169**	AGTTCCATGTTGGTGTGTTTCTCCC	TCAAGGTACAACCACACAAAGAGGG
SEQ ID NO: 2399	**1141232**	AGGTCTGCTGTTGTCTGGATCGATT	TCCAGACGACAACAGACCTAGCTAA
SEQ ID NO: 2400	**1141327**	CGGATGTTGTTGTCGTAGTTCGCAC	GCCTACAACAACAGCATCAAGCGTG
SEQ ID NO: 2401	**1141516**	CAGGGTCTGTTGTTAGGGTTCTTTC	GTCCCAGACAACAATCCCAAGAAAG
SEQ ID NO: 2402	**1141566**	TTCGGTGTACTGTTTGGATATTTCT	AAGCCACATGACAAACCTATAAAGA
SEQ ID NO: 2403	**1141631**	CATGTATCTGTTGTGGTGATTAAAC	GTACATAGACAACACCACTAATTTG
SEQ ID NO: 2404	**1142176**	CCTACCGCTGTTTGTGTGTGACTTG	GGATGGCGACAAACACACACTGAAC
SEQ ID NO: 2405	**1142462**	TTCATCGTCTGTTGTGTGAGGTCCT	AAGTAGCAGACAACACACTCCAGGA
SEQ ID NO: 2406	**1142463**	AATTTCTGTTGTGGTGGTCCAACTT	TTAAAGACAACACCACCAGGTTGAA
SEQ ID NO: 2407	**1142797**	CTGACTGTGTGTTTCCCTGAACCGG	GACTGACACACAAAGGGACTTGGCC
SEQ ID NO: 2408	**1142988**	TCAGGTTGTGTTTGTTCTTGAAGTC	AGTCCAACACAAACAAGAACTTCAG
SEQ ID NO: 2409	**1143551**	NA	NA
SEQ ID NO: 2410	**1143552**	NA	NA
SEQ ID NO: 2411	**1144094**	ACGTCGGTCGATGTTCCTTTCTCCA	TGCAGCCAGCTACAAGGAAAGAGGT

SEQ ID NO: 2412	**1144700**	TTCGACTGGTGTTGTCGGTGATGCT	AAGCTGACCACAACAGCCACTACGA
SEQ ID NO: 2413	**1144746**	AGGTGTCGGTGTTAGTTTCGGTTCC	TCCACAGCCACAATCAAAGCCAAGG
SEQ ID NO: 2414	**1144825**	TTGTGGTGTGTTGGATGTACGACCT	AACACCACACAACCTACATGCTGGA
SEQ ID NO: 2415	**1144905**	AGCTCTGGTGTTGGGTCTTAGGACC	TCGAGACCACAACCCAGAATCCTGG
SEQ ID NO: 2416	**1145067**	GTCTGACTGTGTGTTTCCCTGAACC	CAGACTGACACACAAAGGGACTTGG
SEQ ID NO: 2417	**1145100**	TTATAAGGTGTTTACGGTGTTTCTT	AATATTCCACAAATGCCACAAAGAA
SEQ ID NO: 2418	**1145112**	AGAGTGAGTGTGTTCTTACTCTTTT	TCTCACTCACACAAGAATGAGAAAA
SEQ ID NO: 2419	**1145742**	AGGGGTCTGTTCGTGGTGTACACCC	TCCCCAGACAAGCACCACATGTGGG
SEQ ID NO: 2420	**1145836**	CTTTGTGTGTTTCGAGCCCGTCTCT	GAAACACACAAAGCTCGGGCAGAGA
SEQ ID NO: 2421	**1145838**	AGCAGTGTGTGTTTGTGCCACGCCC	TCGTCACACACAAACACGGTGCGGG
SEQ ID NO: 2422	**1145936**	TCCTCGCGTGTGTTGGTCTGCCACC	AGGAGCGCACACAACCAGACGGTGG
SEQ ID NO: 2423	**1146226**	GTTGTGTCAGTGTTTACGGAAGTAA	CAACACAGTCACAAATGCCTTCATT
SEQ ID NO: 2424	**1146400**	GACCTGTCGTGTGTTGGATAGGACT	CTGGACAGCACACAACCTATCCTGA
SEQ ID NO: 2425	**1146464**	CTTTTGTGTTGTGTCTGTCTGCGTT	GAAAACACAACACAGACAGACGCAA
SEQ ID NO: 2426	**1146471**	CACTGAGTGTGTTGGGTCGTGAACC	GTGACTCACACAACCCAGCACTTGG
SEQ ID NO: 2427	**1146472**	CTGTAATGTGTTGGTGTCGTGAACG	GACATTACACAACCACAGCACTTGC
SEQ ID NO: 2428	**1146516**	TCCATTGTGTTCGTGCTGCGCTAGT	AGGTAACACAAGCACGACGCGATCA
SEQ ID NO: 2429	**1146704**	TCTTCCTGTGTTCTTGTGCCTCGTG	AGAAGGACACAAGAACACGGAGCAC
SEQ ID NO: 2430	**1146730**	CCGTGAGTGTGTTGGTGTACAATCT	GGCACTCACACAACCACATGTTAGA
SEQ ID NO: 2431	**1147054**	AAATTGTGTTCCGTGTGTGCTCCCA	TTTAACACAAGGCACACACGAGGGT
SEQ ID NO: 2432	**1147600**	GAGCGGTCTGTGTTAGGGTCCTCTA	CTCGCCAGACACAATCCCAGGAGAT

SEQ ID NO: 2433	**1147907**	TTGAGTAAGTGTGTTGGGTTGAATA	AACTCATTCACACAACCCAACTTAT
SEQ ID NO: 2434	**1148196**	CGGCACACTGTTAGGTCATGTTCCC	GCCGTGTGACAATCCAGTACAAGGG
SEQ ID NO: 2435	**1149562**	CTTTCAAGTTTGTGTTTGCGTGACG	GAAAGTTCAAACACAAACGCACTGC
SEQ ID NO: 2436	**1151590**	AATGTCTCAGTTGGTCGGGTAACCC	TTACAGAGTCAACCAGCCCATTGGG
SEQ ID NO: 2437	**1153141**	CTGTGTGGAGTTTGTTCACACTTTC	GACACACCTCAAACAAGTGTGAAAG
SEQ ID NO: 2438	**1154222**	GCTGAACCGAGTTGTTTGACGTAAT	CGACTTGGCTCAACAAACTGCATTA
SEQ ID NO: 2439	**1156487**	GTCGACAACGTTAGTTCCGGTACCG	CAGCTGTTGCAATCAAGGCCATGGC
SEQ ID NO: 2440	**1157982**	CAATTTAGTTGGTGGTGATGGTGAC	GTTAAATCAACCACCACTACCACTG
SEQ ID NO: 2441	**1158414**	CTAGTAGAGGAGTTACGATCACCCA	GATCATCTCCTCAATGCTAGTGGGT
SEQ ID NO: 2442	**1158516**	CCTACTCCGTAGTTGTGTGGGGTAG	GGATGAGGCATCAACACACCCCATC
SEQ ID NO: 2443	**1158866**	AGGTGTTTAGTTCGTGTGTTCGTCC	TCCACAAATCAAGCACACAAGCAGG
SEQ ID NO: 2444	**1159545**	TTCGACCGGGTGGTTACTGGGCCCA	AAGCTGGCCCACCAATGACCCGGGT
SEQ ID NO: 2445	**1159569**	GTGTTCGGTGGTGGCTTTCAAGACT	CACAAGCCACCACCGAAAGTTCTGA
SEQ ID NO: 2446	**1159612**	NA	NA
SEQ ID NO: 2447	**1159613**	AGTCTTGGGTGGTGGTTACATTCTA	TCAGAACCCACCACCAATGTAAGAT
SEQ ID NO: 2448	**1159971**	ACCGGTTGGTGGGTCTACTTCGTTT	TGGCCAACCACCCAGATGAAGCAAA
SEQ ID NO: 2449	**1160037**	NA	NA
SEQ ID NO: 2450	**1160209**	GTTATTCGTGTGTGGTCAAAAAAGG	CAATAAGCACACACCAGTTTTTTCC
SEQ ID NO: 2451	**1160307**	AGCTCCTGGTGGTGTGCTTACCCTT	TCGAGGACCACCACACGAATGGGAA
SEQ ID NO: 2452	**1160338**	CGGCCGTGGTGGTCTTCAGTCCTTT	GCCGGCACCACCAGAAGTCAGGAAA
SEQ ID NO: 2453	**1160341**	AGGGTTGGTGGACTTTGACTTCTTA	TCCCAACCACCTGAAACTGAAGAAT

SEQ ID NO: 2454	**1160362**	ATTTGTGGTGGCGTGATACTAATCG	TAAACACCACCGCACTATGATTAGC
SEQ ID NO: 2455	**1160472**	GTAAATGGGTGTGGTGCCTTCCACC	CATTTACCCACACCACGGAAGGTGG
SEQ ID NO: 2456	**1160488**	ACCATTGGTGGTGTGCTCACGTCGT	TGGTAACCACCACACGAGTGCAGCA
SEQ ID NO: 2457	**1160577**	ATGGTAGTGGTGGACTTTATAGGAA	TACCATCACCACCTGAAATATCCTT
SEQ ID NO: 2458	**1160578**	GTACTTGGTGGTGGCTTTTGAAGAA	CATGAACCACCACCGAAAACTTCTT
SEQ ID NO: 2459	**1160651**	ATCTTCGAGGTGGTGTTTGTACAGC	TAGAAGCTCCACCACAAACATGTCG
SEQ ID NO: 2460	**1160739**	CTAGTGGTGGTGGAATTTCCCGTTC	GATCACCACCACCTTAAAGGGCAAG
SEQ ID NO: 2461	**1160923**	ATATATAGTGGTGGTGCGTAGTATC	TATATATCACCACCACGCATCATAG
SEQ ID NO: 2462	**1160983**	ATCCGGTGGTGGTATCAGTCCCTTC	TAGGCCACCACCATAGTCAGGGAAG
SEQ ID NO: 2463	**1161139**	ACTTCAGTGGTGGTGACTCTGGACA	TGAAGTCACCACCACTGAGACCTGT
SEQ ID NO: 2464	**1161239**	CTTTTACGGTGGTAGTGGTATGAAG	GAAAATGCCACCATCACCATACTTC
SEQ ID NO: 2465	**1161361**	TGTTGGTGGTGCCAGTGAGTCTCGT	ACAACCACCACGGTCACTCAGAGCA
SEQ ID NO: 2466	**1161375**	AGTTGGTGGTGGTAATCCTACACTC	TCAACCACCACCATTAGGATGTGAG
SEQ ID NO: 2467	**1161386**	ACTATTACGTGGTGGTAGTCTGGTC	TGATAATGCACCACCATCAGACCAG
SEQ ID NO: 2468	**1161552**	ACATTGTGGTGGTGAGGACGTCAAC	TGTAACACCACCACTCCTGCAGTTG
SEQ ID NO: 2469	**1161681**	CACGGTGTGGTGGTCGACAAGACAA	GTGCCACACCACCAGCTGTTCTGTT
SEQ ID NO: 2470	**1161682**	ACCTGTGCGGTGGTCGGACAGACTT	TGGACACGCCACCAGCCTGTCTGAA
SEQ ID NO: 2471	**1161707**	ACGTATAGGTGGTGGTATCTCGAGT	TGCATATCCACCACCATAGAGCTCA
SEQ ID NO: 2472	**1161855**	TACCGAGAGTCGGTGGTGTTTTACC	ATGGCTCTCAGCCACCACAAAATGG
SEQ ID NO: 2473	**1162461**	CACTCTTCGGTGGTGCCGTCTGTTA	GTGAGAAGCCACCACGGCAGACAAT
SEQ ID NO: 2474	**1162487**	TTTATAGACGGTGCGGTGCGCAAGT	AAATATCTGCCACGCCACGCGTTCA

SEQ ID NO: 2475	**1162502**	ATCGTGGTGGTGCCCGTCTCGGTCC	TAGCACCACCACGGGCAGAGCCAGG
SEQ ID NO: 2476	**1162573**	CTATCTGTCGGTGGTTCGTGACTTC	GATAGACAGCCACCAAGCACTGAAG
SEQ ID NO: 2477	**1162668**	GGTGTGTTGGTGCACTAGTAGTTAA	CCACACAACCACGTGATCATCAATT
SEQ ID NO: 2478	**1164422**	AGTAGGGTCGGTGCGTGATACTCTT	TCATCCCAGCCACGCACTATGAGAA
SEQ ID NO: 2479	**1165039**	GAAACGCGTCTGTGGAATGATTAGA	CTTTGCGCAGACACCTTACTAATCT
SEQ ID NO: 2480	**1165255**	CAGTGTGTGGTGATCCAGGCGTCCC	GTCACACACCACTAGGTCCGCAGGG
SEQ ID NO: 2481	**1165498**	ATGTGGTGGTGAGGACACATCTCTT	TACACCACCACTCCTGTGTAGAGAA
SEQ ID NO: 2482	**1165920**	GAGAGGAGTGTGTGGTCTGTCGAGT	CTCTCCTCACACACCAGACAGCTCA
SEQ ID NO: 2483	**1166117**	ATCCACTGGTGACATCTTCGGACCT	TAGGTGACCACTGTAGAAGCCTGGA
SEQ ID NO: 2484	**1166388**	ACATCGTCCTGTGGTTTTGGCATAA	TGTAGCAGGACACCAAAACCGTATT
SEQ ID NO: 2485	**1166407**	CTGTGGTCCGTGCAGGTACCATTAT	GACACCAGGCACGTCCATGGTAATA
SEQ ID NO: 2486	**1166619**	TTCCGTTATGTGTGGTTGGTTACTT	AAGGCAATACACACCAACCAATGAA
SEQ ID NO: 2487	**1166767**	TCAATATCTGTGGTCGTGTGAACCT	AGTTATAGACACCAGCACACTTGGA
SEQ ID NO: 2488	**1166849**	CGTGTAGGTCTGTGGTTAATGAGTT	GCACATCCAGACACCAATTACTCAA
SEQ ID NO: 2489	**1167187**	ACTTTGTCTGTGTGCCGCAGACGGG	TGAAACAGACACACGGCGTCTGCCC
SEQ ID NO: 2490	**1167204**	AGTAGCTTGTGTGGGGTTGCCTCCA	TCATCGAACACACCCCAACGGAGGT
SEQ ID NO: 2491	**1167258**	TTATGGATGTGGTGTTTCGTGACTC	AATACCTACACCACAAAGCACTGAG
SEQ ID NO: 2492	**1167362**	AACGTGTGATGTGGTGTGTCTGCCA	TTGCACACTACACCACACAGACGGT
SEQ ID NO: 2493	**1167496**	GAGGTGGTTGTGGTTAACACGTCAC	CTCCACCAACACCAATTGTGCAGTG
SEQ ID NO: 2494	**1167632**	ATAATATTGTGGTGGTGTCTTCAGA	TATTATAACACCACCACAGAAGTCT
SEQ ID NO: 2495	**1167699**	GTCGGTTCGTTGTGGTTCCCAACCG	CAGCCAAGCAACACCAAGGGTTGGC

SEQ ID NO: 2496	**1167708**	TCACAGGTGTGTGGAATAAGGAGAA	AGTGTCCACACACCTTATTCCTCTT
SEQ ID NO: 2497	**1168036**	GAGGTTTTGTGGTCTTAGGTGTTCC	CTCCAAAACACCAGAATCCACAAGG
SEQ ID NO: 2498	**1168064**	CAACACTTGTGGTGAAGTGAGTGTG	GTTGTGAACACCACTTCACTCACAC
SEQ ID NO: 2499	**1168079**	GGTCCTGTTGTGGTGGTCCTTTCAC	CCAGGACAACACCACCAGGAAAGTG
SEQ ID NO: 2500	**1168370**	GTGAGGTCTGTGTGCATGCCGAACC	CACTCCAGACACACGTACGGCTTGG
SEQ ID NO: 2501	**1168423**	GCTCATACTGTGTGGTGTCGTCAAT	CGAGTATGACACACCACAGCAGTTA
SEQ ID NO: 2502	**1168447**	ATACGCATGTGTGGGTCTATGTGTG	TATGCGTACACACCCAGATACACAC
SEQ ID NO: 2503	**1168737**	CTATATCCTGTGGTGTGTTTTACCC	GATATAGGACACCACACAAAATGGG
SEQ ID NO: 2504	**1168982**	TCTTGTATCGTGTGGGTGACATCTC	AGAACATAGCACACCCACTGTAGAG
SEQ ID NO: 2505	**1169053**	GTCCTGCGCGTGTGCTTGTCGGACA	CAGGACGCGCACACGAACAGCCTGT
SEQ ID NO: 2506	**1169137**	TTACCTGGTGTGGTGTCACCTCTGA	AATGGACCACACCACAGTGGAGACT
SEQ ID NO: 2507	**1169417**	CCTCGGGTGTGGTGTACACAGGTCC	GGAGCCCACACCACATGTGTCCAGG
SEQ ID NO: 2508	**1169638**	GTTACCTGGTGTGGTGTCACCTCTG	CAATGGACCACACCACAGTGGAGAC
SEQ ID NO: 2509	**1169817**	TAGGGTGCGTGTGGCTTCCCGACCA	ATCCCACGCACACCGAAGGGCTGGT
SEQ ID NO: 2510	**1169819**	NA	NA
SEQ ID NO: 2511	**1169842**	ATCATGTGTGTGCTTACTGGTGACA	TAGTACACACACGAATGACCACTGT
SEQ ID NO: 2512	**1169844**	CCACAGGTGTGGGTGTTTGTCCCTA	GGTGTCCACACCCACAAACAGGGAT
SEQ ID NO: 2513	**1170015**	TTCGTGTCGTAGTGTGCAGGGTCCT	AAGCACAGCATCACACGTCCCAGGA
SEQ ID NO: 2514	**1170142**	AATGTTGTGTGGGTTGTCCTTCGAC	TTACAACACACCCAACAGGAAGCTG
SEQ ID NO: 2515	**1170342**	CCACAAGTGTGGTGTTGTCTGTGCA	GGTGTTCACACCACAACAGACACGT
SEQ ID NO: 2516	**1170387**	GTATAGAATGTGTGGTGTCATCCGT	CATATCTTACACACCACAGTAGGCA

SEQ ID NO: 2517	**1170418**	ATTTGTGTGTGCCAACCGGTCACTA	TAAACACACACGGTTGGCCAGTGAT
SEQ ID NO: 2518	**1170706**	GCACCGAGTGTGTGGTCTTCCATAA	CGTGGCTCACACACCAGAAGGTATT
SEQ ID NO: 2519	**1170825**	CCACTCTACGTGTGGTGTAAGCACA	GGTGAGATGCACACCACATTCGTGT
SEQ ID NO: 2520	**1170980**	CTTGATGTGTGAGTGGTGTCTGTAC	GAACTACACACTCACCACAGACATG
SEQ ID NO: 2521	**1171004**	GTACTCTCAGTGTGTGCTCCAAGGT	CATGAGAGTCACACACGAGGTTCCA
SEQ ID NO: 2522	**1171033**	ACTACATGTGTGTGCGATCTGGGAC	TGATGTACACACACGCTAGACCCTG
SEQ ID NO: 2523	**1171168**	CAGGTGGTGTGACGTGACCGTCACC	GTCCACCACACTGCACTGGCAGTGG
SEQ ID NO: 2524	**1171251**	NA	NA
SEQ ID NO: 2525	**1171983**	ACAGTGGTGGTGTTCAGGTAAAGAA	TGTCACCACCACAAGTCCATTTCTT
SEQ ID NO: 2526	**1172003**	NA	NA
SEQ ID NO: 2527	**1172202**	CGGGGAGGTGTGGATGTCGAAAGGT	GCCCCTCCACACCTACAGCTTTCCA
SEQ ID NO: 2528	**1172229**	CACCTGTGGTGTGGGTAGTGGGTAA	GTGGACACCACACCCATCACCCATT
SEQ ID NO: 2529	**1172264**	CGAAGTGTGTGTGACCTGGTAAGCA	GCTTCACACACACTGGACCATTCGT
SEQ ID NO: 2530	**1172379**	CACGTGTTGTGTGAGACGATGTGTC	GTGCACAACACACTCTGCTACACAG
SEQ ID NO: 2531	**1172412**	ACCTAGTTCGTGTGAGCGAGTCATC	TGGATCAAGCACACTCGCTCAGTAG
SEQ ID NO: 2532	**1172569**	NA	NA
SEQ ID NO: 2533	**1172619**	ACGTATTGTGTGTGATAGGTGCATT	TGCATAACACACACTATCCACGTAA
SEQ ID NO: 2534	**1172651**	TCCTGGTGGTGTGACCTCATCGTGA	AGGACCACCACACTGGAGTAGCACT
SEQ ID NO: 2535	**1172654**	AGGTCCTGGTGTGGCAACCGTCCAC	TCCAGGACCACACCGTTGGCAGGTG
SEQ ID NO: 2536	**1172689**	AATTCCGGTGTGTGCTATAAGTGCC	TTAAGGCCACACACGATATTCACGG
SEQ ID NO: 2537	**1172714**	CCAAAGGTGTGTGGGATCTTGTGAC	GGTTTCCACACACCCTAGAACACTG

SEQ ID NO: 2538	**1172741**	ACACGGGTGTGTGAGACCAGGTTCT	TGTGCCCACACACTCTGGTCCAAGA
SEQ ID NO: 2539	**1172761**	ACGTTCCGGGTGTGGCTCGTGCATC	TGCAAGGCCCACACCGAGCACGTAG
SEQ ID NO: 2540	**1172799**	CTACTCGAGTGTGTGAAAGACCTAG	GATGAGCTCACACACTTTCTGGATC
SEQ ID NO: 2541	**1172909**	CCCTGTGTGTGATCACGCGACCGAA	GGGACACACACTAGTGCGCTGGCTT
SEQ ID NO: 2542	**1173069**	NA	NA
SEQ ID NO: 2543	**1173135**	CGGTGTTGGTGTGGATCCCTACGAA	GCCACAACCACACCTAGGGATGCTT
SEQ ID NO: 2544	**1173285**	TATCGTTTGGTGTGAGCCGTGTCCT	ATAGCAAACCACACTCGGCACAGGA
SEQ ID NO: 2545	**1173341**	TCGTTTGGTGTGAGCCGTGTCCTTC	AGCAAACCACACTCGGCACAGGAAG
SEQ ID NO: 2546	**1173420**	TATTTTGGTGTTCGTTTGGTCGGAC	ATAAAACCACAAGCAAACCAGCCTG
SEQ ID NO: 2547	**1173535**	TCTCAAGGTGTGTGCATAGTAGGTA	AGAGTTCCACACACGTATCATCCAT
SEQ ID NO: 2548	**1173570**	AGTGCGTTGGTGTGAGATTGGACCC	TCACGCAACCACACTCTAACCTGGG
SEQ ID NO: 2549	**1173737**	CCTACGGTGGTGTTGTGTTTCTCCT	GGATGCCACCACAACACAAAGAGGA
SEQ ID NO: 2550	**1173822**	TCTCAAAGGTGTGGTGTCTGTCTCC	AGAGTTTCCACACCACAGACAGAGG
SEQ ID NO: 2551	**1174211**	GAGGCATAGGTGTGTGTGCACTTCC	CTCCGTATCCACACACACGTGAAGG
SEQ ID NO: 2552	**1174225**	AGCAGAGTGGTGTGATCTCTGACGC	TCGTCTCACCACACTAGAGACTGCG
SEQ ID NO: 2553	**1174322**	ACAGTTGTGGTGTTGGTCGTCATAC	TGTCAACACCACAACCAGCAGTATG
SEQ ID NO: 2554	**1174422**	TGTAAGTGTGGTGTGCTACGTCGGA	ACATTCACACCACACGATGCAGCCT
SEQ ID NO: 2555	**1174436**	AAGACTCCGGTGTGTAGAGCTCCGT	TTCTGAGGCCACACATCTCGAGGCA
SEQ ID NO: 2556	**1174455**	AGAAAAGGTGTGTGTGTCGTCCGAC	TCTTTTCCACACACACAGCAGGCTG
SEQ ID NO: 2557	**1174462**	TGGCGTCGGGTGTCAAAGATACACT	ACCGCAGCCCACAGTTTCTATGTGA
SEQ ID NO: 2558	**1174463**	GTGGTCGTGGGTGTCCAACCGACTC	CACCAGCACCCACAGGTTGGCTGAG

SEQ ID NO: 2559	**1174487**	GTTTTGTGGTGTGTGCCGTCAACTC	CAAAACACCACACACGGCAGTTGAG
SEQ ID NO: 2560	**1174551**	ACCTTTGGTGTGTTTCGTGAGCCAC	TGGAAACCACACAAAGCACTCGGTG
SEQ ID NO: 2561	**1174699**	CGTCAGGTTGTGTTTGTTCTTGAAG	GCAGTCCAACACAAACAAGAACTTC
SEQ ID NO: 2562	**1174709**	AATCCTAGGTGTGGTTGTGTCTCCG	TTAGGATCCACACCAACACAGAGGC
SEQ ID NO: 2563	**1174730**	CGAGCTATGGTGTGTGGTTCCAGAC	GCTCGATACCACACACCAAGGTCTG
SEQ ID NO: 2564	**1174791**	ACTGGGTCGGTGTGAGTACCTCTAC	TGACCCAGCCACACTCATGGAGATG
SEQ ID NO: 2565	**1174793**	TACGGTGTTGGTGTGGATCCCTACG	ATGCCACAACCACACCTAGGGATGC
SEQ ID NO: 2566	**1174807**	ACAATACGTGGTGTGTTGTGTCACG	TGTTATGCACCACACAACACAGTGC
SEQ ID NO: 2567	**1175375**	ATGGTTCGGTGTGTGTTCACCATCC	TACCAAGCCACACACAAGTGGTAGG
SEQ ID NO: 2568	**1175378**	TCGTGTGTCTCGGTGTTGTCCTCAA	AGCACACAGAGCCACAACAGGAGTT
SEQ ID NO: 2569	**1175474**	TACCTTGTCGGTGTCCTCGGTGCAA	ATGGAACAGCCACAGGAGCCACGTT
SEQ ID NO: 2570	**1175642**	NA	NA
SEQ ID NO: 2571	**1175651**	GTGTGGGTCGGTGTCTAATCTAAAA	CACACCCAGCCACAGATTAGATTTT
SEQ ID NO: 2572	**1175722**	AAGTATCCGTGTGTGCAGGACGCCA	TTCATAGGCACACACGTCCTGCGGT
SEQ ID NO: 2573	**1176035**	ACGGTAATTGTGTGTCTGAGGTCAT	TGCCATTAACACACAGACTCCAGTA
SEQ ID NO: 2574	**1176358**	GTCCTTGTTGTGTGAAGTCAACCCG	CAGGAACAACACACTTCAGTTGGGC
SEQ ID NO: 2575	**1176393**	GTGTTGTTGGTGTATACTTCATATA	CACAACAACCACATATGAAGTATAT
SEQ ID NO: 2576	**1176557**	CTTATGGTGTGTGACACTGTGTCCG	GAATACCACACACTGTGACACAGGC
SEQ ID NO: 2577	**1176601**	AAGGTATGTGTGTTTGTAAGGTATG	TTCCATACACACAAACATTCCATAC
SEQ ID NO: 2578	**1176690**	ATTCATCGTGTGTCCTGGGTTAGAC	TAAGTAGCACACAGGACCCAATCTG
SEQ ID NO: 2579	**1176724**	TATTTCTTGTGTGTGAGGGGTAACG	ATAAAGAACACACACTCCCCATTGC

SEQ ID NO: 2580	**1176768**	TTCACCGTCGGTGTCGCACTCCGTA	AAGTGGCAGCCACAGCGTGAGGCAT
SEQ ID NO: 2581	**1176774**	ATCATCGTTGTGTTCGTGCGTTTGG	TAGTAGCAACACAAGCACGCAAACC
SEQ ID NO: 2582	**1176776**	GAAATCTCGTGTGTTGTTTGTAAAG	CTTTAGAGCACACAACAAACATTTC
SEQ ID NO: 2583	**1176930**	GCTGAACGTTGTGTGGTTCTGTTTA	CGACTTGCAACACACCAAGACAAAT
SEQ ID NO: 2584	**1177172**	ATCAGGTTGTGTGATCACTCCTCTC	TAGTCCAACACACTAGTGAGGAGAG
SEQ ID NO: 2585	**1177187**	AAGTGTTTGTGTTGCTGAGTGTAAG	TTCACAAACACAACGACTCACATTC
SEQ ID NO: 2586	**1177189**	GTAAGGTATGTGTGTTTGTAAGGTA	CATTCCATACACACAAACATTCCAT
SEQ ID NO: 2587	**1177215**	TTTATACCTGTGTGTGATTTGTGTG	AAATATGGACACACACTAAACACAC
SEQ ID NO: 2588	**1177220**	AGGAGTCGGTGTGTCTCTGAACCTA	TCCTCAGCCACACAGAGACTTGGAT
SEQ ID NO: 2589	**1177234**	ACAGCTGAGTGTGTTCGTGCCTCCT	TGTCGACTCACACAAGCACGGAGGA
SEQ ID NO: 2590	**1177237**	GTGACTAAAGTGTGTGGGGCCTCTC	CACTGATTTCACACACCCCGGAGAG
SEQ ID NO: 2591	**1177291**	ACCGTCGGTGGTGTACCGTACTTCT	TGGCAGCCACCACATGGCATGAAGA
SEQ ID NO: 2592	**1177317**	CTGAACGTTGTGTGGTTCTGTTTAC	GACTTGCAACACACCAAGACAAATG
SEQ ID NO: 2593	**1177319**	GGCCGGTTGTGTGTAGGTACACTAC	CCGGCCAACACACATCCATGTGATG
SEQ ID NO: 2594	**1177419**	ATATGGGTGTGTCTGGTAATACTCC	TATACCCACACAGACCATTATGAGG
SEQ ID NO: 2595	**1177420**	NA	NA
SEQ ID NO: 2596	**1177474**	GTCTTGACCTGTGTGGTCTGTCAAT	CAGAACTGGACACACCAGACAGTTA
SEQ ID NO: 2597	**1177524**	CTATCGTGTAGTGTGTCCGAAAGCC	GATAGCACATCACACAGGCTTTCGG
SEQ ID NO: 2598	**1177570**	AGAGACCTCGTGTGTGCACTTGCGG	TCTCTGGAGCACACACGTGAACGCC
SEQ ID NO: 2599	**1177697**	NA	NA
SEQ ID NO: 2600	**1177738**	GCGTTTTTGTGTGATAAAGTGCATC	CGCAAAAACACACTATTTCACGTAG

SEQ ID NO: 2601	**1177754**	TTTCCGATGTGTGGTATGCTTAGGT	AAAGGCTACACACCATACGAATCCA
SEQ ID NO: 2602	**1177883**	AGAATTGTGTGTGCTCTACGGAACA	TCTTAACACACACGAGATGCCTTGT
SEQ ID NO: 2603	**1178009**	GCGTGAGCCGTGTGTGTATCCCAAA	CGCACTCGGCACACACATAGGGTTT
SEQ ID NO: 2604	**1178047**	ACAATTTGTGTGGTGTCTGTTCTAC	TGTTAAACACACCACAGACAAGATG
SEQ ID NO: 2605	**1178118**	NA	NA
SEQ ID NO: 2606	**1178274**	CCAATTGTGTGTGGTTCGTCAGCGA	GGTTAACACACACCAAGCAGTCGCT
SEQ ID NO: 2607	**1178337**	CGTTTCCTGTGTCTGTGACTACTGT	GCAAAGGACACAGACACTGATGACA
SEQ ID NO: 2608	**1178425**	CATCGTGAGTGTGTAGGTGCACTTA	GTAGCACTCACACATCCACGTGAAT
SEQ ID NO: 2609	**1178427**	ATAAACGAGTGTGTGAGCCCTTGGT	TATTTGCTCACACACTCGGGAACCA
SEQ ID NO: 2610	**1178502**	NA	NA
SEQ ID NO: 2611	**1178504**	ATTTCATGTGTGTGTCGACTGCCAC	TAAAGTACACACACAGCTGACGGTG
SEQ ID NO: 2612	**1178505**	GTCAGTCTGATGTGTGGTCGACCCT	CAGTCAGACTACACACCAGCTGGGA
SEQ ID NO: 2613	**1178604**	CAAAGTCTGTGTGTCGCTGTGTCTC	GTTTCAGACACACAGCGACACAGAG
SEQ ID NO: 2614	**1178630**	ACTTCTTGTGTGTTGGGTCCTACTA	TGAAGAACACACAACCCAGGATGAT
SEQ ID NO: 2615	**1178633**	CCGGGTGTGTGTTAACTCACAAGTA	GGCCCACACACAATTGAGTGTTCAT
SEQ ID NO: 2616	**1178642**	ACCGGTCGTGTGTGTGCTATTCCCT	TGGCCAGCACACACACGATAAGGGA
SEQ ID NO: 2617	**1178819**	CGTAGAGTCGTCTGTGTGGACAAAC	GCATCTCAGCAGACACACCTGTTTG
SEQ ID NO: 2618	**1178887**	CCTGGTGTGTGTAGTAGTCTTGTCC	GGACCACACACATCATCAGAACAGG
SEQ ID NO: 2619	**1178946**	TCAAGTGTTGTGTCGTCGTGTGTGT	AGTTCACAACACAGCAGCACACACA
SEQ ID NO: 2620	**1178963**	CAAAGACTGTGTGTGTCGAGTCGTC	GTTTCTGACACACACAGCTCAGCAG
SEQ ID NO: 2621	**1178964**	AAAACTACTGTGTGTAGGAGGTCAT	TTTTGATGACACACATCCTCCAGTA

SEQ ID NO: 2622	**1179093**	NA	NA
SEQ ID NO: 2623	**1179097**	ACGTCTGGTGTGTGTTTCAATTTAT	TGCAGACCACACACAAAGTTAAATA
SEQ ID NO: 2624	**1179098**	CGTCGTGTAGTGTGTGTATTCGTAC	GCAGCACATCACACACATAAGCATG
SEQ ID NO: 2625	**1179104**	CTTTCCGTGTGTGCGACCTTTCCGA	GAAAGGCACACACGCTGGAAAGGCT
SEQ ID NO: 2626	**1179157**	GGCACATAGTGTGTGGTTATTTTTA	CCGTGTATCACACACCAATAAAAAT
SEQ ID NO: 2627	**1179196**	ATTCACTGTGTGTGCCCGTTGACCT	TAAGTGACACACACGGGCAACTGGA
SEQ ID NO: 2628	**1179222**	GTGCGTCTGTTGTGTCGAGAGTCTT	CACGCAGACAACACAGCTCTCAGAA
SEQ ID NO: 2629	**1179295**	ACTGAACGAGTGTGTGACCGTGAGC	TGACTTGCTCACACACTGGCACTCG
SEQ ID NO: 2630	**1179308**	ACGACTATGAGTGTGTGCCTTGCTT	TGCTGATACTCACACACGGAACGAA
SEQ ID NO: 2631	**1179309**	GCTTATGGTGTGTGACACTGTGTCC	CGAATACCACACACTGTGACACAGG
SEQ ID NO: 2632	**1179343**	ACAAAGAGTGTGTGGATGCTTAGAA	TGTTTCTCACACACCTACGAATCTT
SEQ ID NO: 2633	**1179404**	ATTTCAGTGTGTCGTGTCATGGTCG	TAAAGTCACACAGCACAGTACCAGC
SEQ ID NO: 2634	**1179495**	GTAAAACTCGTGTGTGAGTGTCCAC	CATTTTGAGCACACACTCACAGGTG
SEQ ID NO: 2635	**1179557**	AAGTTGGTGTGTGAGGAGACCCTTC	TTCAACCACACACTCCTCTGGGAAG
SEQ ID NO: 2636	**1179564**	GTGTCTTAAGTGTGTGTTTGCCAAA	CACAGAATTCACACACAAACGGTTT
SEQ ID NO: 2637	**1179575**	CTCTATCGGTGTGTGACAGGAGACA	GAGATAGCCACACACTGTCCTCTGT
SEQ ID NO: 2638	**1179681**	TGTCCACTGTGTGTGAGGTCCCGTA	ACAGGTGACACACACTCCAGGGCAT
SEQ ID NO: 2639	**1179698**	ACTACCTCAGTGTGTGGTCCTTTCA	TGATGGAGTCACACACCAGGAAAGT
SEQ ID NO: 2640	**1179720**	CTACCTCGTGAGTGTGTCAGCCCAA	GATGGAGCACTCACACAGTCGGGTT
SEQ ID NO: 2641	**1179796**	CGGCCTCGTGTGTGCAGGCTTCTCA	GCCGGAGCACACACGTCCGAAGAGT
SEQ ID NO: 2642	**1179808**	CGTCACCCGTGTGTGTGAGAGACAC	GCAGTGGGCACACACACTCTCTGTG

SEQ ID NO: 2643	**1179818**	GACGACCGCGTGTGTGTCTCCGGCC	CTGCTGGCGCACACACAGAGGCCGG
SEQ ID NO: 2644	**1179820**	ATTTGGTGTGTTGGAGTCGCTCTAC	TAAACCACACAACCTCAGCGAGATG
SEQ ID NO: 2645	**1179843**	ACCGTATGCGTGTGTATTTCTTCCC	TGGCATACGCACACATAAAGAAGGG
SEQ ID NO: 2646	**1179893**	GTATGTACTCGTGTGTGTGTAAATG	CATACATGAGCACACACACATTTAC
SEQ ID NO: 2647	**1179951**	CGCATCAGTGTGTGTGTACGGTAGA	GCGTAGTCACACACACATGCCATCT
SEQ ID NO: 2648	**1180022**	CTCATATCGTGTGTGGTACTCGGGA	GAGTATAGCACACACCATGAGCCCT
SEQ ID NO: 2649	**1180149**	ATATGTCTCGTGTGTGGAGTACCCG	TATACAGAGCACACACCTCATGGGC
SEQ ID NO: 2650	**1180159**	TGTATGTACTCGTGTGTGTGTAAAT	ACATACATGAGCACACACACATTTA
SEQ ID NO: 2651	**1180284**	CGTCCCTGTGTGTAGTTCGTCGCTC	GCAGGGACACACATCAAGCAGCGAG
SEQ ID NO: 2652	**1180322**	GCGTCTTCGTGTGTGTCGTCCAGAC	CGCAGAAGCACACACAGCAGGTCTG
SEQ ID NO: 2653	**1180473**	ACTCCCACTGTGTAGAGTGTGTGCG	TGAGGGTGACACATCTCACACACGC
SEQ ID NO: 2654	**1180595**	CGCTTTCAGTGGTGTCCGGGGCCCT	GCGAAAGTCACCACAGGCCCCGGGA
SEQ ID NO: 2655	**1181702**	ATAACATAAGTGGTGTGTGCATCCG	TATTGTATTCACCACACACGTAGGC
SEQ ID NO: 2656	**1183527**	TTCGTGGCGAGTGGACACTCTAGTG	AAGCACCGCTCACCTGTGAGATCAC
SEQ ID NO: 2657	**1183534**	GTAAGTGGTCGAGTGGTCTGTACAC	CATTCACCAGCTCACCAGACATGTG
SEQ ID NO: 2658	**1184217**	AACTGCCTAGTGGTGGTGGACCCTG	TTGACGGATCACCACCACCTGGGAC
SEQ ID NO: 2659	**1186083**	ACCGACACGACGAGTGAGTTCCCTC	TGGCTGTGCTGCTCACTCAAGGGAG
SEQ ID NO: 2660	**1186543**	ACCTTAAAGTGTGTGGGTCACTTAC	TGGAATTTCACACACCCAGTGAATG
SEQ ID NO: 2661	**1186622**	CCACATTAGTGTGTGCCGTGTCATC	GGTGTAATCACACACGGCACAGTAG
SEQ ID NO: 2662	**1186682**	ACTTCTGTAGTAGTGGGTCCTCCCT	TGAAGACATCATCACCCAGGAGGGA
SEQ ID NO: 2663	**1186990**	CTTATGTGTAGTGGTGGAGGCACTC	GAATACACATCACCACCTCCGTGAG

SEQ ID NO: 2664	**1187921**	ACTACCTCGTGAGTGTGTCAGCCCA	TGATGGAGCACTCACACAGTCGGGT
SEQ ID NO: 2665	**1188221**	ATGAGTCAAGTGTGTGTCTGTCGTT	TACTCAGTTCACACACAGACAGCAA
SEQ ID NO: 2666	**1188700**	TGTCGAGAGTGAGTGTTTGCCTACT	ACAGCTCTCACTCACAAACGGATGA
SEQ ID NO: 2667	**1188715**	CTCCGGTAGAGTGTGTACGGACACT	GAGGCCATCTCACACATGCCTGTGA
SEQ ID NO: 2668	**1188741**	AAGAGACGTGAGTGTGCCCTCTCCT	TTCTCTGCACTCACACGGGAGAGGA
SEQ ID NO: 2669	**1188755**	CCCACGCAGTGTGTGTGTCCTACGA	GGGTGCGTCACACACACAGGATGCT
SEQ ID NO: 2670	**1188769**	ACCGGTGTCAGTGTGTGGCGTGGTG	TGGCCACAGTCACACACCGCACCAC
SEQ ID NO: 2671	**1188770**	TCAGTGTGTCAGTGTGTGCCTTCGT	AGTCACACAGTCACACACGGAAGCA
SEQ ID NO: 2672	**1189265**	CCGTGTGTCAGTGTAGGTGATGTCC	GGCACACAGTCACATCCACTACAGG
SEQ ID NO: 2673	**1189660**	GTATTGTTCGAGTGTGTACGCGCAC	CATAACAAGCTCACACATGCGCGTG
SEQ ID NO: 2674	**1189687**	GCCTTCCGAGTGTTACATGTCGTAC	CGGAAGGCTCACAATGTACAGCATG
SEQ ID NO: 2675	**1189702**	CTAACTTCTAGTGTGTGTGTTAACA	GATTGAAGATCACACACACAATTGT
SEQ ID NO: 2676	**1189754**	CCCAACGAGTGTGTCGTCACTGAGT	GGGTTGCTCACACAGCAGTGACTCA
SEQ ID NO: 2677	**1189771**	ATTGTTCGAGTGTGTACGCGCACTT	TAACAAGCTCACACATGCGCGTGAA
SEQ ID NO: 2678	**1189907**	CCAGGCGAGTGTGTATACGTCTTGC	GGTCCGCTCACACATATGCAGAACG
SEQ ID NO: 2679	**1190447**	ACACGCGTGTACGAGTGTAGCCGAC	TGTGCGCACATGCTCACATCGGCTG
SEQ ID NO: 2680	**1190554**	GAAAATCCGTTTGTGTTGGACGAAG	CTTTTAGGCAAACACAACCTGCTTC
SEQ ID NO: 2681	**1190604**	CTCAACGCTAGTGTGTGGAGACGTG	GAGTTGCGATCACACACCTCTGCAC
SEQ ID NO: 2682	**1191559**	ATTATTCCGTTGGTGTGTGAAGTGT	TAATAAGGCAACCACACACTTCACA
SEQ ID NO: 2683	**1192772**	AAGTACGAGTCCGTTGTTGTGACTC	TTCATGCTCAGGCAACAACACTGAG
SEQ ID NO: 2684	**1193213**	ACCACCGACCGTTGAACACAGGGAA	TGGTGGCTGGCAACTTGTGTCCCTT

SEQ ID NO: 2685	**1193397**	CCCGTAGACCGTTGTAGGCCGTATT	GGGCATCTGGCAACATCCGGCATAA
SEQ ID NO: 2686	**1193440**	AGGTTCCCGTTATTTCGTCGAGGTG	TCCAAGGGCAATAAAGCAGCTCCAC
SEQ ID NO: 2687	**1193650**	GGACGACACCGCGTTTTCAACCTGG	CCTGCTGTGGCGCAAAAGTTGGACC
SEQ ID NO: 2688	**1194246**	GAAGATTACCGTTCTTGTTGTTGAT	CTTCTAATGGCAAGAACAACAACTA
SEQ ID NO: 2689	**1196959**	GGTAAATGTCGTTCTTCTCGGTCGT	CCATTTACAGCAAGAAGAGCCAGCA
SEQ ID NO: 2690	**1196970**	AGAGACGATCTCGTTGTTCCACTCG	TCTCTGCTAGAGCAACAAGGTGAGC
SEQ ID NO: 2691	**1196995**	AGTGGTGGTCGTTTTTGTATCGGTT	TCACCACCAGCAAAAACATAGCCAA
SEQ ID NO: 2692	**1197434**	ATAATCCGTCGTTGTGCTTCCCAGA	TATTAGGCAGCAACACGAAGGGTCT
SEQ ID NO: 2693	**1198180**	GTCTGCGTCGTGTCGTTTGTAAAAA	CAGACGCAGCACAGCAAACATTTTT
SEQ ID NO: 2694	**1198195**	AACCTCTCGTCGTTTGGTCGGTTTC	TTGGAGAGCAGCAAACCAGCCAAAG
SEQ ID NO: 2695	**1198285**	TTGTGAACACGTTTAGTGTGGTGTG	AACACTTGTGCAAATCACACCACAC
SEQ ID NO: 2696	**1199737**	TGGCTGAACGTTGTGTGGTTCTGTT	ACCGACTTGCAACACACCAAGACAA
SEQ ID NO: 2697	**1201644**	CGTTGCGAGCGTGCAGGCTGTCGTG	GCAACGCTCGCACGTCCGACAGCAC
SEQ ID NO: 2698	**1201693**	CTTTGTGCGTGACTATTCGATGTGG	GAAACACGCACTGATAAGCTACACC
SEQ ID NO: 2699	**1202006**	CCTGGTGCGTGCATAGAGAACTCTT	GGACCACGCACGTATCTCTTGAGAA
SEQ ID NO: 2700	**1202418**	ACTCTGAAGCGTGCGTACCGAACCT	TGAGACTTCGCACGCATGGCTTGGA
SEQ ID NO: 2701	**1202420**	ATCTACTTGCGTGCGACTGTGCATC	TAGATGAACGCACGCTGACACGTAG
SEQ ID NO: 2702	**1202641**	NA	NA
SEQ ID NO: 2703	**1202817**	CTGGGTAGCGTGGGTCACGTTCATC	GACCCATCGCACCCAGTGCAAGTAG
SEQ ID NO: 2704	**1202852**	AGCATACGGCGTGCGTACAGCGTCT	TCGTATGCCGCACGCATGTCGCAGA
SEQ ID NO: 2705	**1203161**	TCGTCCTGTGCGTGAACGGCCAGGA	AGCAGGACACGCACTTGCCGGTCCT

SEQ ID NO: 2706	**1203246**	AATTTGCGTGCTGTGGGTAACTTGT	TTAAACGCACGACACCCATTGAACA
SEQ ID NO: 2707	**1203248**	ACAGCTCGGCGTGCGTGACGCACAG	TGTCGAGCCGCACGCACTGCGTGTC
SEQ ID NO: 2708	**1203249**	CGAACCGTGCGTGCTACGGGAAGAA	GCTTGGCACGCACGATGCCCTTCTT
SEQ ID NO: 2709	**1203268**	AGGTGCGTCCGTGGAGTCCCACTAC	TCCACGCAGGCACCTCAGGGTGATG
SEQ ID NO: 2710	**1204067**	CGTAGACGAGTGCGTGCGACGACTA	GCATCTGCTCACGCACGCTGCTGAT
SEQ ID NO: 2711	**1204215**	TGTACGTGTACGTGCGTGCGCGCGT	ACATGCACATGCACGCACGCGCGCA
SEQ ID NO: 2712	**1204304**	AGTGGTGGCGTGACTGATTCGTCCA	TCACCACCGCACTGACTAAGCAGGT
SEQ ID NO: 2713	**1204536**	GCGGTGCGTCTCGTGATCCCGCTAC	CGCCACGCAGAGCACTAGGGCGATG
SEQ ID NO: 2714	**1204879**	CGCGAGGTGCGTGAAAACAAATAAG	GCGCTCCACGCACTTTTGTTTATTC
SEQ ID NO: 2715	**1204883**	CGTTGTGTTCGTGCGTTTGGTTTCC	GCAACACAAGCACGCAAACCAAAGG
SEQ ID NO: 2716	**1205406**	ACTCATGGTCGTGCTGGTAGTCATT	TGAGTACCAGCACGACCATCAGTAA
SEQ ID NO: 2717	**1205516**	CTTCTATTCGTGGTGTGTCTATACC	GAAGATAAGCACCACACAGATATGG
SEQ ID NO: 2718	**1205921**	GTGAACTGTGCGTGTATTACCTCCT	CACTTGACACGCACATAATGGAGGA
SEQ ID NO: 2719	**1206125**	AACTCTCTGCGTGTGGTGGCAGACC	TTGAGAGACGCACACCACCGTCTGG
SEQ ID NO: 2720	**1206414**	AAGTTGGCGTGTTTGCGTCCGTGCC	TTCAACCGCACAAACGCAGGCACGG
SEQ ID NO: 2721	**1206490**	ACGTGTCTTGCGTGTGTCACGTGCC	TGCACAGAACGCACACAGTGCACGG
SEQ ID NO: 2722	**1206790**	CTCTTTAGTCGTGAGTGTGGGTCAA	GAGAAATCAGCACTCACACCCAGTT
SEQ ID NO: 2723	**1207154**	GTGTGAATCCGTGTTTGTGGTTTAG	CACACTTAGGCACAAACACCAAATC
SEQ ID NO: 2724	**1207669**	TTCCGTGTGCGTGTCTCTCCCTCTA	AAGGCACACGCACAGAGAGGGAGAT
SEQ ID NO: 2725	**1207803**	CGTCGTCTGTCCGTGTGTCGTCGGC	GCAGCAGACAGGCACACAGCAGCCG
SEQ ID NO: 2726	**1207859**	CCTAAACGCGTGTGTCTGTTGAAAA	GGATTTGCGCACACAGACAACTTTT

SEQ ID NO: 2727	**1208184**	GCACCGGGTCGTGTGTCTTGAGACC	CGTGGCCCAGCACACAGAACTCTGG
SEQ ID NO: 2728	**1208211**	GTTTTACTTCGTGTGTGGTCTCAGG	CAAAATGAAGCACACACCAGAGTCC
SEQ ID NO: 2729	**1208292**	GGTCCACACGCGTGTGTGTCAGTAG	CCAGGTGTGCGCACACACAGTCATC
SEQ ID NO: 2730	**1208484**	ACGAATGATCGTGTGTGTTACTCCT	TGCTTACTAGCACACACAATGAGGA
SEQ ID NO: 2731	**1208507**	CACCATGCGTGTGGTCGTCGTAGTC	GTGGTACGCACACCAGCAGCATCAG
SEQ ID NO: 2732	**1208509**	AAATAAGTCGTGTGTGTCTCATCCC	TTTATTCAGCACACACAGAGTAGGG
SEQ ID NO: 2733	**1208969**	ATGTGTGTTCGTGTACACGTGTGTA	TACACACAAGCACATGTGCACACAT
SEQ ID NO: 2734	**1208970**	TAAGATTTCGTGTGGTCGTGTCGCC	ATTCTAAAGCACACCAGCACAGCGG
SEQ ID NO: 2735	**1208973**	TGGCCTATCGTGTCGGGTGTACAAT	ACCGGATAGCACAGCCCACATGTTA
SEQ ID NO: 2736	**1209201**	TAAACACACACGTGGCGCAGAGGTC	ATTTGTGTGTGCACCGCGTCTCCAG
SEQ ID NO: 2737	**1209795**	TTTGGGTCGTGTGTAGTGTATGTGT	AAACCCAGCACACATCACATACACA
SEQ ID NO: 2738	**1209914**	GACACTTGACGTCGTGTGTGTGGTA	CTGTGAACTGCAGCACACACACCAT
SEQ ID NO: 2739	**1210142**	ACGTTGGTGTCGTGTCTACTAGACC	TGCAACCACAGCACAGATGATCTGG
SEQ ID NO: 2740	**1210284**	CACGTTCTAACGTGGGTGTTGACCC	GTGCAAGATTGCACCCACAACTGGG
SEQ ID NO: 2741	**1211982**	CACGTGTACGTGTACGTGCGTGCGC	GTGCACATGCACATGCACGCACGCG
SEQ ID NO: 2742	**1217805**	GTGCTTTCGGTCAGGGTGTTACTAC	CACGAAAGCCAGTCCCACAATGATG
SEQ ID NO: 2743	**1217975**	TATGTGGTGGTCAGTAGTAGTAACC	ATACACCACCAGTCATCATCATTGG
SEQ ID NO: 2744	**1218435**	TTCGGTGTCGGTCAACATTATGTAA	AAGCCACAGCCAGTTGTAATACATT
SEQ ID NO: 2745	**1218594**	GTGTGCTGTGGTCATCAGTTGTGAC	CACACGACACCAGTAGTCAACACTG
SEQ ID NO: 2746	**1219562**	AGTGGGTCGGTCTAGCTTACTTAGT	TCACCCAGCCAGATCGAATGAATCA
SEQ ID NO: 2747	**1222273**	CACTCGTGCTGTCCTGTGGACTCGG	GTGAGCACGACAGGACACCTGAGCC

SEQ ID NO: 2748	**1223264**	GTCAGTGTGGTGTCCTGTTTTCGTT	CAGTCACACCACAGGACAAAAGCAA
SEQ ID NO: 2749	**1224366**	GACCAGTGTGTGTCCTCGTGTCTGT	CTGGTCACACACAGGAGCACAGACA
SEQ ID NO: 2750	**1224464**	CGTTTGGTGTCCGATGTTTTTAAAT	GCAAACCACAGGCTACAAAAATTTA
SEQ ID NO: 2751	**1224481**	TTTATAACGTGTCCTGTGTGTGATT	AAATATTGCACAGGACACACACTAA
SEQ ID NO: 2752	**1225594**	AGGTGGGTGTCAGTGAGTACCCTCC	TCCACCCACAGTCACTCATGGGAGG
SEQ ID NO: 2753	**1226950**	GTGGGTGGGTCTCTTTAGAGATTAA	CACCCACCCAGAGAAATCTCTAATT
SEQ ID NO: 2754	**1227075**	TGTGTGGTGTGTCACGTGTACACGT	ACACACCACACAGTGCACATGTGCA
SEQ ID NO: 2755	**1228448**	CTTGGTGGTCTGAAGGTATGTAAAC	GAACCACCAGACTTCCATACATTTG
SEQ ID NO: 2756	**1229623**	TTACCGTTGGTCTGTTGGCTGTACA	AATGGCAACCAGACAACCGACATGT
SEQ ID NO: 2757	**1230313**	ATAGTGTGTCGGTCTGTATGTGAGA	TATCACACAGCCAGACATACACTCT
SEQ ID NO: 2758	**1231737**	AAATTGTGTCTTGGGGTATCGGTCT	TTTAACACAGAACCCCATAGCCAGA
SEQ ID NO: 2759	**1231906**	ACACCGTCTTGTCTAACTTCTTCAA	TGTGGCAGAACAGATTGAAGAAGTT
SEQ ID NO: 2760	**1231907**	ACACCGGTTGTCTTTTGTGTCTGAA	TGTGGCCAACAGAAAACACAGACTT
SEQ ID NO: 2761	**1231918**	GGTGGCGGTGTCTATGCTCCCTCCA	CCACCGCCACAGATACGAGGGAGGT
SEQ ID NO: 2762	**1232002**	CGTCCGAGTGTGTCTTGATAATCGT	GCAGGCTCACACAGAACTATTAGCA
SEQ ID NO: 2763	**1232739**	ACTAAACTGTGTCTGTCGCCCTGAC	TGATTTGACACAGACAGCGGGACTG
SEQ ID NO: 2764	**1233069**	GACATACTGTGTGTCTGCTCTTCAC	CTGTATGACACACAGACGAGAAGTG
SEQ ID NO: 2765	**1233106**	GGTGGCGGTGTCTGTGCTCCCGCCA	CCACCGCCACAGACACGAGGGCGGT
SEQ ID NO: 2766	**1233108**	GGTGGTGGTGTCTGTGCTCCCTCCA	CCACCACCACAGACACGAGGGAGGT
SEQ ID NO: 2767	**1233309**	ACGAGCCGTGTGTCTGTCTAAAAGT	TGCTCGGCACACAGACAGATTTTCA
SEQ ID NO: 2768	**1233316**	TTTATAGTCTGTCTGGGTCGTCCCT	AAATATCAGACAGACCCAGCAGGGA

SEQ ID NO: 2769	**1233376**	ACCTGTGTGTGTCTAAAGCATCTCC	TGGACACACACAGATTTCGTAGAGG
SEQ ID NO: 2770	**1233757**	AGTTCAGATGTCTGTTGTGGTGTCT	TCAAGTCTACAGACAACACCACAGA
SEQ ID NO: 2771	**1234587**	AGGCTACTATGTCTATATAATGTCC	TCCGATGATACAGATATATTACAGG
SEQ ID NO: 2772	**1234830**	TACGCCCTCCGTCCAAGGGCTCCTC	ATGCGGGAGGCAGGTTCCCGAGGAG
SEQ ID NO: 2773	**1234938**	ACTACTCGTCGTGTGTCTGCCGTAA	TGATGAGCAGCACACAGACGGCATT
SEQ ID NO: 2774	**1235508**	AACGTTTGTGTCTCGGGGTCTCTAG	TTGCAAACACAGAGCCCCAGAGATC
SEQ ID NO: 2775	**1235639**	TTGCGGCGTGTCTAAATAGTAGAGC	AACGCCGCACAGATTTATCATCTCG
SEQ ID NO: 2776	**1236291**	AGAACCGAAGTCAACCGCTCGAACC	TCTTGGCTTCAGTTGGCGAGCTTGG
SEQ ID NO: 2777	**1237314**	ACTTCACCAGTCCAAGTTGGTCATG	TGAAGTGGTCAGGTTCAACCAGTAC
SEQ ID NO: 2778	**1237895**	GTTCTTACAAGTCCGTGTGTGCGCA	CAAGAATGTTCAGGCACACACGCGT
SEQ ID NO: 2779	**1238371**	AAATAATAGTCGAGAGGGTGGTAGA	TTTATTATCAGCTCTCCCACCATCT
SEQ ID NO: 2780	**1239651**	CTAATCAAGTCAGTGTCGTGTGTCG	GATTAGTTCAGTCACAGCACACAGC
SEQ ID NO: 2781	**1243253**	TTGAACCGTAGTCCGTGTGAGTGCT	AACTTGGCATCAGGCACACTCACGA
SEQ ID NO: 2782	**1243442**	AGTCGTTTGAGTCTTGTTTTCAGTC	TCAGCAAACTCAGAACAAAAGTCAG
SEQ ID NO: 2783	**1245668**	CGCGCCTCGAGTCTGTGTGCAGGTA	GCGCGGAGCTCAGACACACGTCCAT
SEQ ID NO: 2784	**1245798**	ATTTATTAGTCTGTGTGTGATGTGA	TAAATAATCAGACACACACTACACT
SEQ ID NO: 2785	**1246141**	GACCCGGTGTAGTCTGTGTGTCATT	CTGGGCCACATCAGACACACAGTAA
SEQ ID NO: 2786	**1247294**	CGGACCGGGTCGGTTGGACCGTGTC	GCCTGGCCCAGCCAACCTGGCACAG
SEQ ID NO: 2787	**1247398**	TTTGTTTGTCGCGAGCGGCTTCCCA	AAACAAACAGCGCTCGCCGAAGGGT
SEQ ID NO: 2788	**1247632**	GTCTATGTTGGTCGGAACATAACTG	CAGATACAACCAGCCTTGTATTGAC
SEQ ID NO: 2789	**1247675**	CCGTGGGGTCGGTACCTCGTGAAAC	GGCACCCCAGCCATGGAGCACTTTG

SEQ ID NO: 2790	**1248241**	TCTCTAGGTCGGTCGGTGTTTAAGG	AGAGATCCAGCCAGCCACAAATTCC
SEQ ID NO: 2791	**1248585**	CTTTGTGTGTCGTTATGAAATTTGC	GAAACACACAGCAATACTTTAAACG
SEQ ID NO: 2792	**1248849**	TTGAAATGTCGAAGTGTGTGGGTCC	AACTTTACAGCTTCACACACCCAGG
SEQ ID NO: 2793	**1249908**	GTACAAAGTTGTCGGTTTTGTGAAA	CATGTTTCAACAGCCAAAACACTTT
SEQ ID NO: 2794	**1249923**	AGACCTGGGTCGACGTATCTTCTGT	TCTGGACCCAGCTGCATAGAAGACA
SEQ ID NO: 2795	**1250152**	GTGTTTGGGTCGTGTGTAGTGTATG	CACAAACCCAGCACACATCACATAC
SEQ ID NO: 2796	**1250528**	GTCTATCGGTGTGTCGCCAGTTTAC	CAGATAGCCACACAGCGGTCAAATG
SEQ ID NO: 2797	**1250912**	ACAAGTGTGTGTCGGTGCAACCTCC	TGTTCACACACAGCCACGTTGGAGG
SEQ ID NO: 2798	**1250919**	TGGCTCGTGTGTCGAAGTCCTCCCT	ACCGAGCACACAGCTTCAGGAGGGA
SEQ ID NO: 2799	**1251246**	AACCTGTGGTCGTGTGCCTGTTTGA	TTGGACACCAGCACACGGACAAACT
SEQ ID NO: 2800	**1251329**	AAATCGTGTGTCGTTTTGTACTTCA	TTTAGCACACAGCAAAACATGAAGT
SEQ ID NO: 2801	**1251821**	ACCAATGGTCGTTCCGTCGTGTCTA	TGGTTACCAGCAAGGCAGCACAGAT
SEQ ID NO: 2802	**1251947**	CCTTCTCGGTCGTTGGTGCACATAG	GGAAGAGCCAGCAACCACGTGTATC
SEQ ID NO: 2803	**1251953**	CCGTGTAGTGTGTCGACGTGTACTT	GGCACATCACACAGCTGCACATGAA
SEQ ID NO: 2804	**1252042**	ATTATGATGTCGTGTGGTTCCCAAT	TAATACTACAGCACACCAAGGGTTA
SEQ ID NO: 2805	**1252361**	GTCCTAGTGGGTCGTGTCGACGTAC	CAGGATCACCCAGCACAGCTGCATG
SEQ ID NO: 2806	**1252654**	ACTATTTTGTCGTGGTGTATTGCGT	TGATAAAACAGCACCACATAACGCA
SEQ ID NO: 2807	**1252825**	TTGTCCTTGTCGTTGTGTGCCCGTG	AACAGGAACAGCAACACACGGGCAC
SEQ ID NO: 2808	**1253312**	ATGAGGTTGTCGTGTTTGGTACTAG	TACTCCAACAGCACAAACCATGATC
SEQ ID NO: 2809	**1253389**	TCCTGGTGTGTCGTCTCGTGGACCA	AGGACCACACAGCAGAGCACCTGGT
SEQ ID NO: 2810	**1256856**	AGGGTAGACCGTCCATTGCCGCTTA	TCCCATCTGGCAGGTAACGGCGAAT

SEQ ID NO: 2811	**1257243**	CGCGCCCCGTCACCCGCCGCGTAGG	GCGCGGGGCAGTGGGCGGCGCATCC
SEQ ID NO: 2812	**1257521**	GGGACCTCCGTCCTACAGACTTTTG	CCCTGGAGGCAGGATGTCTGAAAAC
SEQ ID NO: 2813	**1258550**	GTTTGTGTCCGTCCTAATAAGAGTG	CAAACACAGGCAGGATTATTCTCAC
SEQ ID NO: 2814	**1261761**	GACCTCTGGCGTCTGTTGTGTCTGC	CTGGAGACCGCAGACAACACAGACG
SEQ ID NO: 2815	**1262041**	GGATATCATCGTCAGAAGTGATTAA	CCTATAGTAGCAGTCTTCACTAATT
SEQ ID NO: 2816	**1262626**	CTTCCGCCGTCTTTTTCTGATGGTC	GAAGGCGGCAGAAAAAGACTACCAG
SEQ ID NO: 2817	**1263985**	NA	NA
SEQ ID NO: 2818	**1267886**	TGAAGCGTGCGTCGTGGTCTCCGAC	ACTTCGCACGCAGCACCAGAGGCTG
SEQ ID NO: 2819	**1268146**	CGACCCACGACGTCACATATAGAAA	GCTGGGTGCTGCAGTGTATATCTTT
SEQ ID NO: 2820	**1268465**	TCCTACACACACGTCTTAAGTGAGT	AGGATGTGTGTGCAGAATTCACTCA
SEQ ID NO: 2821	**1269887**	ACGACCTCGACCGTCGATCGCGGAG	TGCTGGAGCTGGCAGCTAGCGCCTC
SEQ ID NO: 2822	**1274262**	NA	NA
SEQ ID NO: 2823	**1275219**	ATTCGGTTTAAGTTTGTGGTGAGAC	TAAGCCAAATTCAAACACCACTCTG
SEQ ID NO: 2824	**1277004**	GTGGTGGTGTTAATACGTCAACTCA	CACCACCACAATTATGCAGTTGAGT
SEQ ID NO: 2825	**1277331**	GTCCCGACGACGTTAACATTATCCA	CAGGGCTGCTGCAATTGTAATAGGT
SEQ ID NO: 2826	**1278087**	CACCGTTTTATAGGATCTGAAAGTC	GTGGCAAAATATCCTAGACTTTCAG
SEQ ID NO: 2827	**1278662**	CTATACTTGTTAAGGTGGTGGTCGG	GATATGAACAATTCCACCACCAGCC
SEQ ID NO: 2828	**1281562**	ACCGATGTAGTTATTCGTGTGTGGT	TGGCTACATCAATAAGCACACACCA
SEQ ID NO: 2829	**1281656**	ACCGGGATTATGTGTGTGACGACTC	TGGCCCTAATACACACACTGCTGAG
SEQ ID NO: 2830	**1281851**	AGATTCTACTTATGGTGTGTGAGGT	TCTAAGATGAATACCACACACTCCA
SEQ ID NO: 2831	**1282648**	TCACGTTGCTTATTCGGTGTGTGTC	AGTGCAACGAATAAGCCACACACAG

SEQ ID NO: 2832	**1284113**	ATATTCTGTTATGTGTGTTCCCT	TATAAGACAATACACACACAAGGGA
SEQ ID NO: 2833	**1285072**	CGGTCAGAATAAACGAATAAAAAGG	GCCAGTCTTATTTGCTTATTTTTCC
SEQ ID NO: 2834	**1286161**	ACGTAGTGTGGTTATAGGTGTGTCA	TGCATCACACCAATATCCACACAGT
SEQ ID NO: 2835	**1295218**	GTGTCGGACCGATATGTCACGTAGG	CACAGCCTGGCTATACAGTGCATCC
SEQ ID NO: 2836	**1296139**	NA	NA
SEQ ID NO: 2837	**1298175**	TCCAATTTAGGAGGGCTGTGTGGTC	AGGTTAAATCCTCCCGACACACCAG
SEQ ID NO: 2838	**1298545**	AGTGGTTGTTAGCTCAGAGGTTGTC	TCACCAACAATCGAGTCTCCAACAG
SEQ ID NO: 2839	**1301093**	TCGATTAAGTTAGGTCGTCGGTCTC	AGCTAATTCAATCCAGCAGCCAGAG
SEQ ID NO: 2840	**1305159**	GTGAACACGTTTAGTGTGGTGTGTC	CACTTGTGCAAATCACACCACACAG
SEQ ID NO: 2841	**1306013**	ATGTGCGTGTTAGTCTTGTGGTGTA	TACACGCACAATCAGAACACCACAT
SEQ ID NO: 2842	**1307352**	CTTACGACTAATAGGTGTGTGCGCG	GAATGCTGATTATCCACACACGCGC
SEQ ID NO: 2843	**1308170**	CCCTGTGATAGGGTCGTGTGTACCC	GGGACACTATCCCAGCACACATGGG
SEQ ID NO: 2844	**1309641**	GTCCGTCGACCATAGACAAGCGTCC	CAGGCAGCTGGTATCTGTTCGCAGG
SEQ ID NO: 2845	**1313122**	ACGTGGGACCTAAACGTATGTAAGA	TGCACCCTGGATTTGCATACATTCT
SEQ ID NO: 2846	**1319634**	CACCTCTCTCTATGTGGTGTGACGG	GTGGAGAGAGATACACCACACTGCC
SEQ ID NO: 2847	**1320898**	CTGTGTCCTCTATGTGTGTGTGACA	GACACAGGAGATACACACACACTGT
SEQ ID NO: 2848	**1321811**	AATTAAGTCTATTGAGTGGTGGTGG	TTAATTCAGATAACTCACCACCACC
SEQ ID NO: 2849	**1323930**	GTTCTCCAGTACTAACGTCTTCTCC	CAAGAGGTCATGATTGCAGAAGAGG
SEQ ID NO: 2850	**1325304**	CGTTCACACACTATCTTACTAAATT	GCAAGTGTGTGATAGAATGATTTAA
SEQ ID NO: 2851	**1325880**	CATCACACACGTATCACCACACACA	GTAGTGTGTGCATAGTGGTGTGTGT
SEQ ID NO: 2852	**1326560**	CTGTTCATCTAGAGGTGTGGTGTTA	GACAAGTAGATCTCCACACCACAAT

SEQ ID NO: 2853	**1330968**	CTACCCCCTAGTTGTGTGTGGAAGT	GATGGGGGATCAACACACACCTTCA
SEQ ID NO: 2854	**1341399**	GTCGGGTCTGTTACTCTACGTTCTC	CAGCCCAGACAATGAGATGCAAGAG
SEQ ID NO: 2855	**1347638**	ACTATGTGCATACGTGTCGTGTGTC	TGATACACGTATGCACAGCACACAG
SEQ ID NO: 2856	**1350977**	AGACAAACCTACACACACACGGGAG	TCTGTTTGGATGTGTGTGTGCCCTC
SEQ ID NO: 2857	**1352467**	ATGTACCTACCTACAAGTCTCGGAC	TACATGGATGGATGTTCAGAGCCTG
SEQ ID NO: 2858	**1357955**	AGACGAAACACTACGACGCCGTCCG	TCTGCTTTGTGATGCTGCGGCAGGC
SEQ ID NO: 2859	**1358132**	TCGTGCGTGAACTACGGGTCGAGAC	AGCACGCACTTGATGCCCAGCTCTG
SEQ ID NO: 2860	**1358670**	CTACCGGACTCTACGAGTTTGTCTA	GATGGCCTGAGATGCTCAAACAGAT
SEQ ID NO: 2861	**1360071**	GGACCGTTTGTAATCTTATATGTTC	CCTGGCAAACATTAGAATATACAAG
SEQ ID NO: 2862	**1360185**	CTATTGTTGTAATCCGTGTTTGAAG	GATAACAACATTAGGCACAAACTTC
SEQ ID NO: 2863	**1363791**	GGTGGTGGTGTAATCGAATCTATAC	CCACCACCACATTAGCTTAGATATG
SEQ ID NO: 2864	**1365006**	GTTTGTGTGTGTAAATATTGAACTA	CAAACACACACATTTATAACTTGAT
SEQ ID NO: 2865	**1365912**	TGTGATGTGTGTATGTTGAATGTGT	ACACTACACACATACAACTTACACA
SEQ ID NO: 2866	**1368598**	TGGTCTGTTGTATCAGTCTGTGCCC	ACCAGACAACATAGTCAGACACGGG
SEQ ID NO: 2867	**1371278**	AGTGTGGCGTGTATCTCTACCCATC	TCACACCGCACATAGAGATGGGTAG
SEQ ID NO: 2868	**1371280**	CGTGTAGTGTGTGTATTCGTACTTT	GCACATCACACACATAAGCATGAAA
SEQ ID NO: 2869	**1372477**	TGTTTAAAGTATTCGAGGTGGAGCT	ACAAATTTCATAAGCTCCACCTCGA
SEQ ID NO: 2870	**1374002**	CTTGTAACGAGTAATCCGGTCGTTG	GAACATTGCTCATTAGGCCAGCAAC
SEQ ID NO: 2871	**1376182**	NA	NA
SEQ ID NO: 2872	**1377163**	CTAGGTCGGTGTAGTGTGGTCCTAA	GATCCAGCCACATCACACCAGGATT
SEQ ID NO: 2873	**1379134**	TAGTACCTCCGGTAGTGGTGGGCTA	ATCATGGAGGCCATCACCACCCGAT

SEQ ID NO: 2874	**1380122**	TTTCCTTGTAGAGCGTGTGTTCACA	AAAGGAACATCTCGCACACAAGTGT
SEQ ID NO: 2875	**1381172**	CCCACTGTGTAGAGTGTGTGCGTAC	GGGTGACACATCTCACACACGCATG
SEQ ID NO: 2876	**1382161**	ACTAGGTCGGTGTAGTGTGGTCCTA	TGATCCAGCCACATCACACCAGGAT
SEQ ID NO: 2877	**1388558**	CTCCTATCCGTAGTCGACGTGTTTG	GAGGATAGGCATCAGCTGCACAAAC
SEQ ID NO: 2878	**1389853**	GTGTTTCACACGTAACCCACACACG	CACAAAGTGTGCATTGGGTGTGTGC
SEQ ID NO: 2879	**1390462**	AGTCGTTCCGCGTAGTGTGTTTTCC	TCAGCAAGGCGCATCACACAAAAGG
SEQ ID NO: 2880	**1391453**	ACCCACACACGTACTCGCACCTGGG	TGGGTGTGTGCATGAGCGTGGACCC
SEQ ID NO: 2881	**1391951**	AGAGAACGGGTACGTATGAGACTTC	TCTCTTGCCCATGCATACTCTGAAG
SEQ ID NO: 2882	**1394033**	TACGTCAGGGGTACTGTTGTTTACT	ATGCAGTCCCCATGACAACAAATGA
SEQ ID NO: 2883	**1397286**	NA	NA
SEQ ID NO: 2884	**1399309**	ACCCGATCAGTACATTGGAGGTCCT	TGGGCTAGTCATGTAACCTCCAGGA
SEQ ID NO: 2885	**1399579**	GACCTACCTACGGTACTACCAGGAC	CTGGATGGATGCCATGATGGTCCTG
SEQ ID NO: 2886	**1400495**	TGTCGAGTGTGTACGTACACTTGTG	ACAGCTCACACATGCATGTGAACAC
SEQ ID NO: 2887	**1401565**	GTGTCGAGTGTGTACGTACACTTGT	CACAGCTCACACATGCATGTGAACA
SEQ ID NO: 2888	**1401979**	CCCACACACGTACTCGCACCTGGGC	GGGTGTGTGCATGAGCGTGGACCCG
SEQ ID NO: 2889	**1403450**	TGTTCGAGTGTGTACGCGCACTTTT	ACAAGCTCACACATGCGCGTGAAAA
SEQ ID NO: 2890	**2706**	CCGAATATCCGCCATCAAAGGAGTC	GGCTTATAGGCGGTAGTTTCCTCAG
SEQ ID NO: 2891	**3823**	CTCCACGCCCGGCCGCGCCAGCCCG	GAGGTGCGGGCCGGCGCGGTCGGGC
SEQ ID NO: 2892	**6196**	CTACGAGAGGCCCAGACACGGCTCC	GATGCTCTCCGGGTCTGTGCCGAGG
SEQ ID NO: 2893	**8081**	ATTTTGCCCGCCGTCCTATGCCGCG	TAAAACGGGCGGCAGGATACGGCGC
SEQ ID NO: 2894	**9167**	GTTTGGGCCCGACACGTTGTTCACA	CAAACCCGGGCTGTGCAACAAGTGT

SEQ ID NO: 2895	**9831**	GCCGCGCCGCCCGATATATCGTCCT	CGGCGCGGCGGGCTATATAGCAGGA
SEQ ID NO: 2896	**10605**	AGCCGACGCCCATATAAGGTTAAGG	TCGGCTGCGGGTATATTCCAATTCC
SEQ ID NO: 2897	**12374**	CTCCACGTCCCAAGTCCAGAAATTA	GAGGTGCAGGGTTCAGGTCTTTAAT
SEQ ID NO: 2898	**13635**	GGACCCGACCCAAGGGCCTCTACAG	CCTGGGCTGGGTTCCCGGAGATGTC
SEQ ID NO: 2899	**13958**	AGACACAGACCCATCGTCACGGGGT	TCTGTGTCTGGGTAGCAGTGCCCCA
SEQ ID NO: 2900	**14035**	GTTCTTATCCCAGACCGACCTAAGG	CAAGAATAGGGTCTGGCTGGATTCC
SEQ ID NO: 2901	**14491**	CAATTACCCAAAAACACGGACTTCT	GTTAATGGGTTTTTGTGCCTGAAGA
SEQ ID NO: 2902	**15200**	TGGTACGGCCCAGACCCAGACACGG	ACCATGCCGGGTCTGGGTCTGTGCC
SEQ ID NO: 2903	**15767**	ACCTCTTCCCACTGCTGATTCCGCT	TGGAGAAGGGTGACGACTAAGGCGA
SEQ ID NO: 2904	**16856**	ACACACACACCCAGATGTATGTGTA	TGTGTGTGTGGGTCTACATACACAT
SEQ ID NO: 2905	**17273**	TGGACGGCCCACCACCGCGACATGT	ACCTGCCGGGTGGTGGCGCTGTACA
SEQ ID NO: 2906	**17909**	ACGCACACACCCACCCACGCGTAAA	TGCGTGTGTGGGTGGGTGCGCATTT
SEQ ID NO: 2907	**18140**	AAACGGTCCCACACGCGCAGAAGGG	TTTGCCAGGGTGTGCGCGTCTTCCC
SEQ ID NO: 2908	**18289**	GCGGACACACCCACGTGTAAACACA	CGCCTGTGTGGGTGCACATTTGTGT
SEQ ID NO: 2909	**18297**	GTGTCCTCGCCCACTGGAAGTACGA	CACAGGAGCGGGTGACCTTCATGCT
SEQ ID NO: 2910	**19105**	CTTCCGACCCACACATAAGGTGATT	GAAGGCTGGGTGTGTATTCCACTAA
SEQ ID NO: 2911	**19229**	AGTGGACACCCACGCACAGACTGTC	TCACCTGTGGGTGCGTGTCTGACAG
SEQ ID NO: 2912	**20299**	GGACAGACCGCCAGTAGCAACAGGA	CCTGTCTGGCGGTCATCGTTGTCCT
SEQ ID NO: 2913	**20700**	GGTCTCCTGCCAGCCGCTTCGCGGT	CCAGAGGACGGTCGGCGAAGCGCCA
SEQ ID NO: 2914	**20863**	CATCGCCGCCAATAGCGCTTTGATT	GTAGCGGCGGTTATCGCGAAACTAA
SEQ ID NO: 2915	**21375**	GCGCCGCCGCCAGGCCGCCCGCCGG	CGCGGCGGCGGTCCGGCGGGCGGCC

SEQ ID NO: 2916	**21541**	ACACACACGGCCAGGACCTGTCAGT	TGTGTGTGCCGGTCCTGGACAGTCA
SEQ ID NO: 2917	**21726**	GACAGCCAGCCAGACACGTAGGACC	CTGTCGGTCGGTCTGTGCATCCTGG
SEQ ID NO: 2918	**21770**	TTGGACCGCCAACACACGTACCTAG	AACCTGGCGGTTGTGTGCATGGATC
SEQ ID NO: 2919	**21925**	TTCTCAACGCCACCGCCGACTCGGG	AAGAGTTGCGGTGGCGGCTGAGCCC
SEQ ID NO: 2920	**21946**	CCCGCCGCCACGCAGCAATAGTACG	GGGCGGCGGTGCGTCGTTATCATGC
SEQ ID NO: 2921	**22123**	AACGTCCTCGCCACGGCGGAAGAGA	TTGCAGGAGCGGTGCCGCCTTCTCT
SEQ ID NO: 2922	**22223**	AGGCCACGCCAGGTAGCGCCCGTTG	TCCGGTGCGGTCCATCGCGGGCAAC
SEQ ID NO: 2923	**22288**	GTGTGTGGCGCCAGTTCCTCTCGGT	CACACACCGCGGTCAAGGAGAGCCA
SEQ ID NO: 2924	**22364**	CTGTGCCGCCAGAACTGTCGTATCT	GACACGGCGGTCTTGACAGCATAGA
SEQ ID NO: 2925	**22723**	TGTCTCGTCCGCCATAACTGTGTCG	ACAGAGCAGGCGGTATTGACACAGC
SEQ ID NO: 2926	**23053**	ATCGAAGGCCACCACCGACCGGTAA	TAGCTTCCGGTGGTGGCTGGCCATT
SEQ ID NO: 2927	**23088**	GTGACACCCGCCAGCACCGATGGTA	CACTGTGGGCGGTCGTGGCTACCAT
SEQ ID NO: 2928	**23366**	AAAGGGCCACACACCGCACTGTACA	TTTCCCGGTGTGTGGCGTGACATGT
SEQ ID NO: 2929	**23531**	ACACTCCGGCCACGACCCACGTCTG	TGTGAGGCCGGTGCTGGGTGCAGAC
SEQ ID NO: 2930	**23992**	GAGGCGAGACGCCACGACTCCGACG	CTCCGCTCTGCGGTGCTGAGGCTGC
SEQ ID NO: 2931	**24092**	TACCGGACCGCCACCGACTCGAGGT	ATGGCCTGGCGGTGGCTGAGCTCCA
SEQ ID NO: 2932	**24142**	GTGCAACTCGCCACACCACAGGGAG	CACGTTGAGCGGTGTGGTGTCCCTC
SEQ ID NO: 2933	**24296**	ATTGTCCGCCACACACGACGGTCTA	TAACAGGCGGTGTGTGCTGCCAGAT
SEQ ID NO: 2934	**26646**	CAGACGTCATCCCATGGTGTGTGTC	GTCTGCAGTAGGGTACCACACACAG
SEQ ID NO: 2935	**29925**	CGCGGCGACTCCCAGGTAGAAAAAT	GCGCCGCTGAGGGTCCATCTTTTTA
SEQ ID NO: 2936	**31050**	TACCCACGGTCCCAGGGTCGGTGTC	ATGGGTGCCAGGGTCCCAGCCACAG

SEQ ID NO: 2937	**31188**	GACTTACACGGTCCCACTCACTCGT	CTGAATGTGCCAGGGTGAGTGAGCA
SEQ ID NO: 2938	**31535**	NA	NA
SEQ ID NO: 2939	**32240**	GGACCCGAGTCCCAAGTCGTCGAGG	CCTGGGCTCAGGGTTCAGCAGCTCC
SEQ ID NO: 2940	**33413**	CGTGCCCGTCCCACTACGCCTTATG	GCACGGGCAGGGTGATGCGGAATAC
SEQ ID NO: 2941	**38325**	CTTACGCCGTCCAGCAGAAACGTCA	GAATGCGGCAGGTCGTCTTTGCAGT
SEQ ID NO: 2942	**40637**	GAGACCCGTCTCCACGTGCCGAGTC	CTCTGGGCAGAGGTGCACGGCTCAG
SEQ ID NO: 2943	**40674**	GTCTCGACCCTCCACACACCACGGT	CAGAGCTGGGAGGTGTGTGGTGCCA
SEQ ID NO: 2944	**41094**	GTAGGAGGATCCACGACACGAGTCC	CATCCTCCTAGGTGCTGTGCTCAGG
SEQ ID NO: 2945	**41696**	CCACCGGTCCACAGTACGAATCGAG	GGTGGCCAGGTGTCATGCTTAGCTC
SEQ ID NO: 2946	**42916**	TTTGTGTGTCCATGTGACCGCCCGT	AAACACACAGGTACACTGGCGGGCA
SEQ ID NO: 2947	**43358**	ACTCCTCCGTCCAAAAGTTGTAAGG	TGAGGAGGCAGGTTTTCAACATTCC
SEQ ID NO: 2948	**43399**	CGTTGTGTGTCCATTGTACTTGTCC	GCAACACACAGGTAACATGAACAGG
SEQ ID NO: 2949	**44442**	TACGCCACCGTCCACAGTGTCGGTT	ATGCGGTGGCAGGTGTCACAGCCAA
SEQ ID NO: 2950	**45129**	GTGGTCACCGTCCACCTCATGGGCT	CACCAGTGGCAGGTGGAGTACCCGA
SEQ ID NO: 2951	**45267**	ATCGTCGTCCGTCCATGACCATGGT	TAGCAGCAGGCAGGTACTGGTACCA
SEQ ID NO: 2952	**45293**	TCGGTGCCGTCCATACCGCAGACGT	AGCCACGGCAGGTATGGCGTCTGCA
SEQ ID NO: 2953	**45434**	AGTACTCCGTCGTCCATGTGATAAA	TCATGAGGCAGCAGGTACACTATTT
SEQ ID NO: 2954	**45539**	ACACACACACGTCCATGTATATGTG	TGTGTGTGTGCAGGTACATATACAC
SEQ ID NO: 2955	**45749**	ACGTTCCGACCCTTCCGAAGGTCTT	TGCAAGGCTGGGAAGGCTTCCAGAA
SEQ ID NO: 2956	**45867**	GTCCACCGGTCCACAGTACGAATCG	CAGGTGGCCAGGTGTCATGCTTAGC
SEQ ID NO: 2957	**47880**	TTAGACTCGTCCCTTCGCCACGGCT	AATCTGAGCAGGGAAGCGGTGCCGA

SEQ ID NO: 2958	**50705**	ACCACGCACCCTGGGAGGGACGTCT	TGGTGCGTGGGACCCTCCCTGCAGA
SEQ ID NO: 2959	**51238**	GACACCGACTCCCTGTCAGTACTGA	CTGTGGCTGAGGGACAGTCATGACT
SEQ ID NO: 2960	**53762**	CGTCCGGTCCCTCGTTCTGAACTAA	GCAGGCCAGGGAGCAAGACTTGATT
SEQ ID NO: 2961	**54702**	ACCATAGGCCTTTTCGGTGTGCGTT	TGGTATCCGGAAAAGCCACACGCAA
SEQ ID NO: 2962	**55951**	GCTCAAGCGCCTGTGCGTGCTCTGC	CGAGTTCGCGGACACGCACGAGACG
SEQ ID NO: 2963	**56454**	TGAAGGGCCTGTGTCTGTGTCTACG	ACTTCCCGGACACAGACACAGATGC
SEQ ID NO: 2964	**56725**	AGCCCGTGCCTGTCGCGTTACCGTA	TCGGGCACGGACAGCGCAATGGCAT
SEQ ID NO: 2965	**57020**	GTGTGTGGTGCCTCTTCTAAACCTA	CACACACCACGGAGAAGATTTGGAT
SEQ ID NO: 2966	**57235**	GTGGTTAACGCCTGTGTTCGAGTAA	CACCAATTGCGGACACAAGCTCATT
SEQ ID NO: 2967	**57548**	CGAAGGGCCTCTCGACACCGACGTA	GCTTCCCGGAGAGCTGTGGCTGCAT
SEQ ID NO: 2968	**58413**	CGGACCTCGCCTCTTGCCGCAAAGG	GCCTGGAGCGGAGAACGGCGTTTCC
SEQ ID NO: 2969	**59324**	AACTCGCCGCCTCGTAAGTGTCACT	TTGAGCGGCGGAGCATTCACAGTGA
SEQ ID NO: 2970	**59765**	ATCAGGGCCTACACGAACTGGTGCA	TAGTCCCGGATGTGCTTGACCACGT
SEQ ID NO: 2971	**60815**	CGACACACGACCCTAGTGAAGTCTC	GCTGTGTGCTGGGATCACTTCAGAG
SEQ ID NO: 2972	**61831**	AGCACCGACGCCTACTATATCAGGT	TCGTGGCTGCGGATGATATAGTCCA
SEQ ID NO: 2973	**62043**	ACGTCGTGTAGAGCCTACCCAGGGT	TGCAGCACATCTCGGATGGGTCCCA
SEQ ID NO: 2974	**62768**	ACTCTTCTTCCTGGCCTGTATGGGT	TGAGAAGAAGGACCGGACATACCCA
SEQ ID NO: 2975	**65471**	TCCCGTCCTCCTGTGTGGAATCCTG	AGGGCAGGAGGACACACCTTAGGAC
SEQ ID NO: 2976	**66722**	CCTCTCCTCCTCCGCTGTTCTCTGT	GGAGAGGAGGAGGCGACAAGAGACA
SEQ ID NO: 2977	**68006**	AGTGAGGTTCCTCCGACGCATACCG	TCACTCCAAGGAGGCTGCGTATGGC
SEQ ID NO: 2978	**69229**	CTGCTGCTCCTCCTCGTCAAGTAGG	GACGACGAGGAGGAGCAGTTCATCC

SEQ ID NO: 2979	**69280**	ACCTCCGGTCCTTTAGGTTCTAACT	TGGAGGCCAGGAAATCCAAGATTGA
SEQ ID NO: 2980	**70263**	ACCGCAGGTCCTGTGTGTGCAACTT	TGGCGTCCAGGACACACACGTTGAA
SEQ ID NO: 2981	**72494**	GACACTCCGCGTCCTGAACGTCTGA	CTGTGAGGCGCAGGACTTGCAGACT
SEQ ID NO: 2982	**73252**	AGACCTACTACGTCCTGATCTCCGT	TCTGGATGATGCAGGACTAGAGGCA
SEQ ID NO: 2983	**74399**	CAGTGTGCGTCCTCGTGTCTGTGCA	GTCACACGCAGGAGCACAGACACGT
SEQ ID NO: 2984	**75835**	TCCACACACGTCCTAGTTAAGAAAG	AGGTGTGTGCAGGATCAATTCTTTC
SEQ ID NO: 2985	**77189**	GTGTACGCGAGGTCCTAGCTCAAGT	CACATGCGCTCCAGGATCGAGTTCA
SEQ ID NO: 2986	**77510**	AGAATTCACCTCACCAGATTGGAAG	TCTTAAGTGGAGTGGTCTAACCTTC
SEQ ID NO: 2987	**77537**	GTGGTCCAACCCAAGCAGTAGGAGG	CACCAGGTTGGGTTCGTCATCCTCC
SEQ ID NO: 2988	**77640**	CTCACACAACCCAGCCGGTCAGGTC	GAGTGTGTTGGGTCGGCCAGTCCAG
SEQ ID NO: 2989	**79898**	AGGGACACACCCGACTCAAGGCCGA	TCCCTGTGTGGGCTGAGTTCCGGCT
SEQ ID NO: 2990	**80049**	ACCTTCCACCCAGTCGCCGGACCAA	TGGAAGGTGGGTCAGCGGCCTGGTT
SEQ ID NO: 2991	**80214**	AAGCGACACACCCACTCCTGTATAG	TTCGCTGTGTGGGTGAGGACATATC
SEQ ID NO: 2992	**80266**	GAACGAACGCACCCACATATGTACG	CTTGCTTGCGTGGGTGTATACATGC
SEQ ID NO: 2993	**81374**	AGCGTTCACACCCACACTACTGTGA	TCGCAAGTGTGGGTGTGATGACACT
SEQ ID NO: 2994	**81425**	AGTACTCACACACCCACGTCTGTGG	TCATGAGTGTGTGGGTGCAGACACC
SEQ ID NO: 2995	**81440**	AAAGGGACCCATCGACGCCACTCAA	TTTCCCTGGGTAGCTGCGGTGAGTT
SEQ ID NO: 2996	**81679**	GCGTCGTCACCACCCGATTGAGAAG	CGCAGCAGTGGTGGGCTAACTCTTC
SEQ ID NO: 2997	**81752**	GACCCACGGACCCTGGAGGACTGAC	CTGGGTGCCTGGGACCTCCTGACTG
SEQ ID NO: 2998	**84223**	ACGCGACTCACGACCCGTGCAGTGG	TGCGCTGAGTGCTGGGCACGTCACC
SEQ ID NO: 2999	**84426**	TTGACCCGACCCAACGCTGACATGG	AACTGGGCTGGGTTGCGACTGTACC

SEQ ID NO: 3000	**84690**	GAAGCTGAACCAACGTTACCCAAGG	CTTCGACTTGGTTGCAATGGGTTCC
SEQ ID NO: 3001	**84696**	CGATCACCGACCCTCGTTCAGTAAG	GCTAGTGGCTGGGAGCAAGTCATTC
SEQ ID NO: 3002	**85138**	GCGGCCGAACCAAAACTGGAAGCAC	CGCCGGCTTGGTTTTGACCTTCGTG
SEQ ID NO: 3003	**85400**	TCGGCGACCACCAGGCACATGTGGT	AGCCGCTGGTGGTCCGTGTACACCA
SEQ ID NO: 3004	**85717**	TGGTCACACACCAGGACAATTTGGT	ACCAGTGTGTGGTCCTGTTAAACCA
SEQ ID NO: 3005	**85923**	GTCTGACCCACCACCGACCCATCTC	CAGACTGGGTGGTGGCTGGGTAGAG
SEQ ID NO: 3006	**85948**	CGTTCGTCCACCAGTTCCTTTTATT	GCAAGCAGGTGGTCAAGGAAAATAA
SEQ ID NO: 3007	**87709**	GGAGAGACGCACCAACGACTACGAC	CCTCTCTGCGTGGTTGCTGATGCTG
SEQ ID NO: 3008	**88129**	CGACCACACACCAGGACACTTTAAA	GCTGGTGTGTGGTCCTGTGAAATTT
SEQ ID NO: 3009	**88477**	ACCGCGCACACCACGATTTGAGATG	TGGCGCGTGTGGTGCTAAACTCTAC
SEQ ID NO: 3010	**88610**	AGAACGTCCACCACGTGGTACTCGC	TCTTGCAGGTGGTGCACCATGAGCG
SEQ ID NO: 3011	**89807**	GTGAAGCGTCACCACTGTCCGTTGG	CACTTCGCAGTGGTGACAGGCAACC
SEQ ID NO: 3012	**90484**	GTACATACACGCACCACACATATAC	CATGTATGTGCGTGGTGTGTATATG
SEQ ID NO: 3013	**90513**	TGTCCACGCACCACGACGCCCACGG	ACAGGTGCGTGGTGCTGCGGGTGCC
SEQ ID NO: 3014	**91844**	NA	NA
SEQ ID NO: 3015	**93110**	AGGACCGACGACCATCATACGGGGT	TCCTGGCTGCTGGTAGTATGCCCCA
SEQ ID NO: 3016	**93144**	CTACCGTCCGTACCCGCAACCCAGT	GATGGCAGGCATGGGCGTTGGGTCA
SEQ ID NO: 3017	**93202**	CGATGTGACGACCACGACTGCCCTT	GCTACACTGCTGGTGCTGACGGGAA
SEQ ID NO: 3018	**93601**	GTATTCACACGACCACCCTCGAGAG	CATAAGTGTGCTGGTGGGAGCTCTC
SEQ ID NO: 3019	**93652**	AGACGAGGGACCACACCCACGAGAC	TCTGCTCCCTGGTGTGGGTGCTCTG
SEQ ID NO: 3020	**94122**	ACGGAGCCGACCACACGTCTTTTCG	TGCCTCGGCTGGTGTGCAGAAAAGC

SEQ ID NO: 3021	**94429**	AGTACCAATACCCACCGACCAGGGG	TCATGGTTATGGGTGGCTGGTCCCC
SEQ ID NO: 3022	**94538**	TTAAGCACGACCACGATCCCGAATG	AATTCGTGCTGGTGCTAGGGCTTAC
SEQ ID NO: 3023	**94616**	TTGTAGCTGACCACGACCACCCGGT	AACATCGACTGGTGCTGGTGGGCCA
SEQ ID NO: 3024	**95086**	ATTTCCGACCACGAAGGTCCTCGCA	TAAAGGCTGGTGCTTCCAGGAGCGT
SEQ ID NO: 3025	**95433**	TACATATATATACCCACACGTACAC	ATGTATATATATGGGTGTGCATGTG
SEQ ID NO: 3026	**96064**	GGAGTACTTGTACCCACCGACGACA	CCTCATGAACATGGGTGGCTGCTGT
SEQ ID NO: 3027	**96515**	CTAGCTGCTACCACGGAGGATCAAC	GATCGACGATGGTGCCTCCTAGTTG
SEQ ID NO: 3028	**97884**	GGTCGAACACTACCACCACTACAGT	CCAGCTTGTGATGGTGGTGATGTCA
SEQ ID NO: 3029	**100679**	CGTGCGTGAACCTGACCTAAGTGTC	GCACGCACTTGGACTGGATTCACAG
SEQ ID NO: 3030	**101121**	NA	NA
SEQ ID NO: 3031	**101583**	CCGAGACCACCTGATCGCGGAGGCG	GGCTCTGGTGGACTAGCGCCTCCGC
SEQ ID NO: 3032	**102273**	ACCACAACACCTCTGTATTGGAACG	TGGTGTTGTGGAGACATAACCTTGC
SEQ ID NO: 3033	**102612**	AGACCGCCACCTCTTCAGTTTCTAG	TCTGGCGGTGGAGAAGTCAAAGATC
SEQ ID NO: 3034	**102638**	TTACGTCCTCACCTCACTAGGTGGC	AATGCAGGAGTGGAGTGATCCACCG
SEQ ID NO: 3035	**103028**	ACCGTCGTCAACCTCGGTGTCGAGA	TGGCAGCAGTTGGAGCCACAGCTCT
SEQ ID NO: 3036	**103518**	TCTTATGAACCTCGCTGTGTGTGTC	AGAATACTTGGAGCGACACACACAG
SEQ ID NO: 3037	**103770**	GGGAGGCACCTCTCGCCGACGCTGA	CCCTCCGTGGAGAGCGGCTGCGACT
SEQ ID NO: 3038	**104113**	GTCCGACCCGACCTTGCTTTAAACT	CAGGCTGGGCTGGAACGAAATTTGA
SEQ ID NO: 3039	**104891**	CTTTATGACCTTCCGGAACCTGAAG	GAAATACTGGAAGGCCTTGGACTTC
SEQ ID NO: 3040	**105763**	ATCGTGTGTCGACCTTGGCTTTAAG	TAGCACACAGCTGGAACCGAAATTC
SEQ ID NO: 3041	**106037**	CCGACACGGACCTGGAGTTCTCAGT	GGCTGTGCCTGGACCTCAAGAGTCA

SEQ ID NO: 3042	**106774**	GTCGACGCACCGACCTGTCAATTCT	CAGCTGCGTGGCTGGACAGTTAAGA
SEQ ID NO: 3043	**106931**	ATATTTAGACCTCAACCGGACGGGA	TATAAATCTGGAGTTGGCCTGCCCT
SEQ ID NO: 3044	**107188**	ACTTTGTCGACCTCGTCGCCACTGA	TGAAACAGCTGGAGCAGCGGTGACT
SEQ ID NO: 3045	**107322**	TAGGTCCACGACCTGCCCGAGAAGG	ATCCAGGTGCTGGACGGGCTCTTCC
SEQ ID NO: 3046	**107347**	CGCACCCACCTACCGTAAGGTATAA	GCGTGGGTGGATGGCATTCCATATT
SEQ ID NO: 3047	**107419**	TTTCGCCGACCTCCCAGGGTTTCAC	AAAGCGGCTGGAGGGTCCCAAAGTG
SEQ ID NO: 3048	**107981**	TGGGGCACCTATACCTCGTCAGCGG	ACCCCGTGGATATGGAGCAGTCGCC
SEQ ID NO: 3049	**111002**	ACCGCTGCTACCTCTTCGGAAGGAG	TGGCGACGATGGAGAAGCCTTCCTC
SEQ ID NO: 3050	**111584**	GTGTCCTACCTACCTTTGAAAGGTG	CACAGGATGGATGGAAACTTTCCAC
SEQ ID NO: 3051	**112775**	GTACCTCACCTACCTCGTTCGAAGA	CATGGAGTGGATGGAGCAAGCTTCT
SEQ ID NO: 3052	**112787**	CGTCACCCGCCGCGTAGGGAGTGTC	GCAGTGGGCGGCGCATCCCTCACAG
SEQ ID NO: 3053	**113201**	ACGCCCGGCCGCGCCAGCCCGGGCT	TGCGGGCCGGCGCGGTCGGGCCCGA
SEQ ID NO: 3054	**113213**	TTGTACTGGTACCTCCGTCGTCCGA	AACATGACCATGGAGGCAGCAGGCT
SEQ ID NO: 3055	**113251**	AGAATGCCCGGCCGACCAACTTGGT	TCTTACGGGCCGGCTGGTTGAACCA
SEQ ID NO: 3056	**113262**	CTCACACCACCGCGGTAGTATCAAG	GAGTGTGGTGGCGCCATCATAGTTC
SEQ ID NO: 3057	**113907**	GAGTCCTTCCCGGATCCAAGGTCAT	CTCAGGAAGGGCCTAGGTTCCAGTA
SEQ ID NO: 3058	**113925**	ACTAAAACCCGGGTCCGTCCCTGGG	TGATTTTGGGCCCAGGCAGGGACCC
SEQ ID NO: 3059	**114062**	CGGTTTCCCGGTCGCCATAAGGTAT	GCCAAAGGGCCAGCGGTATTCCATA
SEQ ID NO: 3060	**114639**	ACTCCCGTCCCGGTAGAAAGGCACG	TGAGGGCAGGGCCATCTTTCCGTGC
SEQ ID NO: 3061	**115702**	CGAACCGACCCGGACCGTCTAGACC	GCTTGGCTGGGCCTGGCAGATCTGG
SEQ ID NO: 3062	**116367**	NA	NA

SEQ ID NO: 3063	**116424**	CCTTGGCCGGCACGTGTGTGACGTC	GGAACCGGCCGTGCACACACTGCAG
SEQ ID NO: 3064	**116744**	TTCGCGCCGCCGATCTACATCCCTT	AAGCGCGGCGGCTAGATGTAGGGAA
SEQ ID NO: 3065	**116769**	GCCGCGCACGCCGCGGCGCCTGGCC	CGGCGCGTGCGGCGCCGCGGACCGG
SEQ ID NO: 3066	**116854**	TGTTCGCCGCCGCACATCCGGAGGA	ACAAGCGGCGGCGTGTAGGCCTCCT
SEQ ID NO: 3067	**116886**	ATTCCTGCCGCCGCGGAAATATACC	TAAGGACGGCGGCGCCTTTATATGG
SEQ ID NO: 3068	**117084**	TGGTCCCGCCGCAGGTCTACCAAGA	ACCAGGGCGGCGTCCAGATGGTTCT
SEQ ID NO: 3069	**117094**	GCCGCCGGCCGCTGTGACTCAAGTA	CGGCGGCCGGCGACACTGAGTTCAT
SEQ ID NO: 3070	**117577**	CCGCCCGCCGGGGCAGCGCCGCCGC	GGCGGGCGGCCCCGTCGCGGCGGCG
SEQ ID NO: 3071	**117829**	CTCCCCGCCGGCCAGCGCCGCCCGC	GAGGGGCGGCCGGTCGCGGCGGGCG
SEQ ID NO: 3072	**118069**	TCCTGGTCCCGAACATGTCAGGACC	AGGACCAGGGCTTGTACAGTCCTGG
SEQ ID NO: 3073	**118197**	CACTACCGTCCCGATGCGAGGGAGA	GTGATGGCAGGGCTACGCTCCCTCT
SEQ ID NO: 3074	**118249**	TCCTGGACCCGACTCAACATATGCC	AGGACCTGGGCTGAGTTGTATACGG
SEQ ID NO: 3075	**118310**	ACACTGACACCCGATGGATGTAGTC	TGTGACTGTGGGCTACCTACATCAG
SEQ ID NO: 3076	**118355**	AGCCCGACCCGAGACGATTAATAGA	TCGGGCTGGGCTCTGCTAATTATCT
SEQ ID NO: 3077	**118708**	CTCCGTGTCCCGATTAACAGAGAAA	GAGGCACAGGGCTAATTGTCTCTTT
SEQ ID NO: 3078	**118936**	GTGTCCCGACCCGAAGCAACGTGCA	CACAGGGCTGGGCTTCGTTGCACGT
SEQ ID NO: 3079	**119168**	GGGTCAGCCCGAGCGCGAACTCGTC	CCCAGTCGGGCTCGCGCTTGAGCAG
SEQ ID NO: 3080	**119215**	ATCCGACGCCCGACAAGAGGAATCG	TAGGCTGCGGGCTGTTCTCCTTAGC
SEQ ID NO: 3081	**119217**	GGGGACACCCGACACCGTAGGCACT	CCCCTGTGGGCTGTGGCATCCGTGA
SEQ ID NO: 3082	**119263**	GAAACCGTCCCGACTTTTAAACTAG	CTTTGGCAGGGCTGAAAATTTGATC
SEQ ID NO: 3083	**119628**	TGCTCCGACCCGATCTACTTATAGG	ACGAGGCTGGGCTAGATGAATATCC

SEQ ID NO: 3084	**119913**	ACCTGGACCCGACCTAGGAATCCGA	TGGACCTGGGCTGGATCCTTAGGCT
SEQ ID NO: 3085	**120366**	CTGGTGACCCGAGTTCTAAGAGAAG	GACCACTGGGCTCAAGATTCTCTTC
SEQ ID NO: 3086	**120406**	CGGAGTCCGCCGACAAAGGTTTCCA	GCCTCAGGCGGCTGTTTCCAAAGGT
SEQ ID NO: 3087	**120436**	GACACACAGCCCGACACACGTTTTG	CTGTGTGTCGGGCTGTGTGCAAAAC
SEQ ID NO: 3088	**120663**	CACCACCGCCGAAGGTTCAGAGGTC	GTGGTGGCGGCTTCCAAGTCTCCAG
SEQ ID NO: 3089	**121407**	NA	NA
SEQ ID NO: 3090	**121408**	NA	NA
SEQ ID NO: 3091	**121491**	CCCACGACGCCGACGAGCAGGTGAA	GGGTGCTGCGGCTGCTCGTCCACTT
SEQ ID NO: 3092	**121743**	CTTGCTACGCCGACAACCATGCTGT	GAACGATGCGGCTGTTGGTACGACA
SEQ ID NO: 3093	**121767**	TTTCCACGCCGAGACACGGTTGAGT	AAAGGTGCGGCTCTGTGCCAACTCA
SEQ ID NO: 3094	**122455**	CAGTAAGAGCCGACGACACGCAAAC	GTCATTCTCGGCTGCTGTGCGTTTG
SEQ ID NO: 3095	**122503**	ATAAACGTTCCGGTGGTTTGTTCCA	TATTTGCAAGGCCACCAAACAAGGT
SEQ ID NO: 3096	**122626**	CGGAACAGCCGACGACGATTCCTGT	GCCTTGTCGGCTGCTGCTAAGGACA
SEQ ID NO: 3097	**122681**	NA	NA
SEQ ID NO: 3098	**122682**	ACTATCTGCGCCGACGCCATGAGTC	TGATAGACGCGGCTGCGGTACTCAG
SEQ ID NO: 3099	**123350**	GTCCCTTCTCCGGTGCTCTATCAGT	CAGGGAAGAGGCCACGAGATAGTCA
SEQ ID NO: 3100	**123401**	CCCGCGATCCGGTGCCTCGGGTAAA	GGGCGCTAGGCCACGGAGCCCATTT
SEQ ID NO: 3101	**125056**	TCTTCATTCCGACGCGGGTACGTTC	AGAAGTAAGGCTGCGCCCATGCAAG
SEQ ID NO: 3102	**125821**	GTTCACTACGACGTCCGGACCAGGA	CAAGTGATGCTGCAGGCCTGGTCCT
SEQ ID NO: 3103	**125941**	CGTCCTCGCTCCGATCAGTGGAATT	GCAGGAGCGAGGCTAGTCACCTTAA
SEQ ID NO: 3104	**126568**	CCAACGACTCCGAGGTTCTATAGGA	GGTTGCTGAGGCTCCAAGATATCCT

SEQ ID NO: 3105	**126664**	ATTACTCCTCCGATAAAGGGTCCTC	TAATGAGGAGGCTATTTCCCAGGAG
SEQ ID NO: 3106	**129477**	TCCGCTCTCCCGTCCCTTCGCAGAC	AGGCGAGAGGGCAGGGAAGCGTCTG
SEQ ID NO: 3107	**129780**	NA	NA
SEQ ID NO: 3108	**130073**	AGACACCACCCGTACCGATGGGGAC	TCTGTGGTGGGCATGGCTACCCCTG
SEQ ID NO: 3109	**130161**	CTGACTCACCCGTGTTTTACCACAG	GACTGAGTGGGCACAAAATGGTGTC
SEQ ID NO: 3110	**130736**	CGGTGTTGCCGTTGTGGTTCGTTCT	GCCACAACGGCAACACCAAGCAAGA
SEQ ID NO: 3111	**131358**	ATATCTCGTCCCGTCTATCTAGGTC	TATAGAGCAGGGCAGATAGATCCAG
SEQ ID NO: 3112	**132255**	GCCGGCCGCCGTCTTAAGTAGGACA	CGGCCGGCGGCAGAATTCATCCTGT
SEQ ID NO: 3113	**132256**	ACCGGCCGCCGTCTTAAGTAGGACA	TGGCCGGCGGCAGAATTCATCCTGT
SEQ ID NO: 3114	**132418**	CCAGCCGCCGTAAGGGTGGTCCTGA	GGTCGGCGGCATTCCCACCAGGACT
SEQ ID NO: 3115	**132638**	GACACAAGACCCGTAGGGGTTCCCT	CTGTGTTCTGGGCATCCCCAAGGGA
SEQ ID NO: 3116	**133072**	GGTCCGTCTCCCGTATTTCCCTGGA	CCAGGCAGAGGGCATAAAGGGACCT
SEQ ID NO: 3117	**133144**	TAGTGTGAATCCGTGTTTGTGGTTT	ATCACACTTAGGCACAAACACCAAA
SEQ ID NO: 3118	**133650**	GTTTCCACTCCGTCCACAACGTAGT	CAAAGGTGAGGCAGGTGTTGCATCA
SEQ ID NO: 3119	**134176**	NA	NA
SEQ ID NO: 3120	**134494**	CCCGTCCTCCGTGTCTATAATAGGA	GGGCAGGAGGCACAGATATTATCCT
SEQ ID NO: 3121	**134645**	AGGACTCTCTCCGTTGAGCCAGGTC	TCCTGAGAGAGGCAACTCGGTCCAG
SEQ ID NO: 3122	**134918**	ATGGAACTCCGTCACACCGGTGGAC	TACCTTGAGGCAGTGTGGCCACCTG
SEQ ID NO: 3123	**136077**	CTTGGTGTCCGTGGCACTCAAGAGA	GAACCACAGGCACCGTGAGTTCTCT
SEQ ID NO: 3124	**136274**	TGGGCGGTACCGGGGTTGGTGTGTG	ACCCGCCATGGCCCCAACCACACAC
SEQ ID NO: 3125	**136306**	TTGATGGTCCGTATGTTTAGTCGTC	AACTACCAGGCATACAAATCAGCAG

SEQ ID NO: 3126	**136518**	CCAGTACGGTCCGTGTGTGACGACG	GGTCATGCCAGGCACACACTGCTGC
SEQ ID NO: 3127	**136658**	GCGAGTGTCCGTCCGTGTGCACTCG	CGCTCACAGGCAGGCACACGTGAGC
SEQ ID NO: 3128	**137587**	AGGCAGCACCGGACCGCACCTAAGG	TCCGTCGTGGCCTGGCGTGGATTCC
SEQ ID NO: 3129	**138066**	GCAAAACACCGGTGTGGGTGTCGTT	CGTTTTGTGGCCACACCCACAGCAA
SEQ ID NO: 3130	**138811**	CTGGAAACCGAACCGAACAGTCCCG	GACCTTTGGCTTGGCTTGTCAGGGC
SEQ ID NO: 3131	**138926**	AATTCACACCGGCAAGGCGAGACAG	TTAAGTGTGGCCGTTCCGCTCTGTC
SEQ ID NO: 3132	**139335**	GACCCACCACCGACCCATCTCTACG	CTGGGTGGTGGCTGGGTAGAGATGC
SEQ ID NO: 3133	**139343**	CGACGACGTCCACCGCTGTGAGTCA	GCTGCTGCAGGTGGCGACACTCAGT
SEQ ID NO: 3134	**139395**	NA	NA
SEQ ID NO: 3135	**139527**	ACCACGGCACCGATTTCTCTTTCTT	TGGTGCCGTGGCTAAAGAGAAAGAA
SEQ ID NO: 3136	**139860**	AGTCAGGCACCGACCTCATCTCTGT	TCAGTCCGTGGCTGGAGTAGAGACA
SEQ ID NO: 3137	**140232**	TTTTGAACCGAACCGCAAGAACTCC	AAAACTTGGCTTGGCGTTCTTGAGG
SEQ ID NO: 3138	**140772**	TCCGACCGAACCGACGACGCTTAGG	AGGCTGGCTTGGCTGCTGCGAATCC
SEQ ID NO: 3139	**140988**	TGTCCACCACCGATAATAATAATCG	ACAGGTGGTGGCTATTATTATTAGC
SEQ ID NO: 3140	**141089**	GTACCGGACCTACCGCCAGACGCGC	CATGGCCTGGATGGCGGTCTGCGCG
SEQ ID NO: 3141	**141102**	GTCCGTCCCACCGATTCTCGGAAGG	CAGGCAGGGTGGCTAAGAGCCTTCC
SEQ ID NO: 3142	**141108**	GCGCCGACGTCACCGACAAGCGGTT	CGCGGCTGCAGTGGCTGTTCGCCAA
SEQ ID NO: 3143	**141349**	CTACACCGACGACCGAAGTAAGACA	GATGTGGCTGCTGGCTTCATTCTGT
SEQ ID NO: 3144	**141452**	CTCCGCCACCGAGGTTATACTAGGT	GAGGCGGTGGCTCCAATATGATCCA
SEQ ID NO: 3145	**141675**	ATTGACGAACCGACCACTACGGTCT	TAACTGCTTGGCTGGTGATGCCAGA
SEQ ID NO: 3146	**141778**	AGGTAAACACCGACGCAACAGGGGT	TCCATTTGTGGCTGCGTTGTCCCCA

SEQ ID NO: 3147	**141975**	AGTGAACGCACCGACGACCTACACG	TCACTTGCGTGGCTGCTGGATGTGC
SEQ ID NO: 3148	**142070**	ATTTGACACCGACGACCGATTGGAT	TAAACTGTGGCTGCTGGCTAACCTA
SEQ ID NO: 3149	**142111**	CGGTCAACACCGACGCTCCGGTAGT	GCCAGTTGTGGCTGCGAGGCCATCA
SEQ ID NO: 3150	**142228**	TATTTTAGACCGAGTGTGTGTGTTG	ATAAAATCTGGCTCACACACACAAC
SEQ ID NO: 3151	**142231**	CGTTTCCACCGACGAGAGTTGTCGA	GCAAAGGTGGCTGCTCTCAACAGCT
SEQ ID NO: 3152	**143628**	CGGGGTTACCGTTTGTGTCTTCCTT	GCCCCAATGGCAAACACAGAAGGAA
SEQ ID NO: 3153	**143866**	AGCCGCCACCGTTTACCGCCGAGGA	TCGGCGGTGGCAAATGGCGGCTCCT
SEQ ID NO: 3154	**144587**	CCCAGGTACCGACTCACGTAATATC	GGGTCCATGGCTGAGTGCATTATAG
SEQ ID NO: 3155	**144910**	CAGAGCCACCGTCACGTCGGTATCG	GTCTCGGTGGCAGTGCAGCCATAGC
SEQ ID NO: 3156	**144918**	ACCGACGAGACACCGTGGTTGTAGA	TGGCTGCTCTGTGGCACCAACATCT
SEQ ID NO: 3157	**145355**	AGATACGCCACCGTGCTCCGACGGA	TCTATGCGGTGGCACGAGGCTGCCT
SEQ ID NO: 3158	**145628**	GTAACCACCGACCGTTCTGGAAACT	CATTGGTGGCTGGCAAGACCTTTGA
SEQ ID NO: 3159	**146161**	ACCCTCACGACCGTAAAGGATCCTG	TGGGAGTGCTGGCATTTCCTAGGAC
SEQ ID NO: 3160	**146444**	NA	NA
SEQ ID NO: 3161	**147323**	CTTCCTGGGGTGTCGGTTTGACTTT	GAAGGACCCCACAGCCAAACTGAAA
SEQ ID NO: 3162	**148793**	CACCACTGGGGCACCACCGTCGCAC	GTGGTGACCCCGTGGTGGCAGCGTG
SEQ ID NO: 3163	**149735**	GTAAGGGTAGGGGAACTCCTTCACC	CATTCCCATCCCCTTGAGGAAGTGG
SEQ ID NO: 3164	**152577**	TCGTAGACGTAGTCGGGGCTGTACT	AGCATCTGCATCAGCCCCGACATGA
SEQ ID NO: 3165	**152625**	CCGGATGGGCCGACGACCTTTAATC	GGCCTACCCGGCTGCTGGAAATTAG
SEQ ID NO: 3166	**152702**	CGGTGTGTCGGGGACGTCTAACTTC	GCCACACAGCCCCTGCAGATTGAAG
SEQ ID NO: 3167	**153175**	CATAAAGGGCCACACACCGCACTGT	GTATTTCCCGGTGTGTGGCGTGACA

SEQ ID NO: 3168	**153572**	NA	NA
SEQ ID NO: 3169	**153918**	TGAGTGTGCGGGCGTGGGTGCGTCC	ACTCACACGCCCGCACCCACGCAGG
SEQ ID NO: 3170	**157465**	ACGTGGTGTGGGAAGGTACCATCCA	TGCACCACACCCTTCCATGGTAGGT
SEQ ID NO: 3171	**159098**	TTGTGTGTGGGAAGTCTTACTGAGT	AACACACACCCTTCAGAATGACTCA
SEQ ID NO: 3172	**160390**	CCACTACGGGGAGGGATTACTTGTT	GGTGATGCCCCTCCCTAATGAACAA
SEQ ID NO: 3173	**161489**	ACCGTGCAGGGTCATAAATGCCTGG	TGGCACGTCCCAGTATTTACGGACC
SEQ ID NO: 3174	**162199**	CCCAGAGGGAGTATTTCACGCACAC	GGGTCTCCCTCATAAAGTGCGTGTG
SEQ ID NO: 3175	**162233**	ACGTGGGACGGGACACGCCAACCTA	TGCACCCTGCCCTGTGCGGTTGGAT
SEQ ID NO: 3176	**164428**	ATTGCACGGGACACAAAAGACCTGT	TAACGTGCCCTGTGTTTTCTGGACA
SEQ ID NO: 3177	**165895**	CTAAAGTGGGACGTTGTGTAAGTCA	GATTTCACCCTGCAACACATTCAGT
SEQ ID NO: 3178	**166770**	ATTTTCGGGACACACCTACACCATT	TAAAAGCCCTGTGTGGATGTGGTAA
SEQ ID NO: 3179	**167084**	TGTGTGATTGGGTGGGTAAGTGATT	ACACACTAACCCACCCATTCACTAA
SEQ ID NO: 3180	**167785**	GCCTCGGTTGGGTCGGTTCTTCTTC	CGGAGCCAACCCAGCCAAGAAGAAG
SEQ ID NO: 3181	**167948**	GGTGTCTTTGGGTGTGTCATCACAG	CCACAGAAACCCACACAGTAGTGTC
SEQ ID NO: 3182	**168240**	ACGTGCGTTTGGGATTGTGCCTCCT	TGCACGCAAACCCTAACACGGAGGA
SEQ ID NO: 3183	**168275**	AGGCAGATGGTGGTGAAACTTTTCT	TCCGTCTACCACCACTTTGAAAAGA
SEQ ID NO: 3184	**168832**	GTCTTCTCTTGGGTGGTGGACCTTC	CAGAAGAGAACCCACCACCTGGAAG
SEQ ID NO: 3185	**169453**	CACCCACTGGGTAAGGTGGTCTCCA	GTGGGTGACCCATTCCACCAGAGGT
SEQ ID NO: 3186	**170166**	TGGGGTCTGGGTCATTCAGTCTTAG	ACCCCAGACCCAGTAAGTCAGAATC
SEQ ID NO: 3187	**172401**	CTAAGGTGTGGGTTCGGCTATTTCT	GATTCCACACCCAAGCCGATAAAGA
SEQ ID NO: 3188	**172469**	NA	NA

SEQ ID NO: 3189	**173045**	CGGTTGTGTGGGTCTCACGTTACCT	GCCAACACACCCAGAGTGCAATGGA
SEQ ID NO: 3190	**173533**	CCTACTTGTGGGGTGTGTAATCCCG	GGATGAACACCCCACACATTAGGGC
SEQ ID NO: 3191	**173568**	TGTGAGTGTGTTGCCCGACTATTCT	ACACTCACACAACGGGCTGATAAGA
SEQ ID NO: 3192	**173653**	ATTTTGTGGGTCGTGCGTTGTACCA	TAAAACACCCAGCACGCAACATGGT
SEQ ID NO: 3193	**173846**	ATTCGTTGTGGGCTTTTCCGTCGCC	TAAGCAACACCCGAAAAGGCAGCGG
SEQ ID NO: 3194	**173925**	AAGTTCGGTGGGTATATTTGACGCA	TTCAAGCCACCCATATAAACTGCGT
SEQ ID NO: 3195	**173976**	NA	NA
SEQ ID NO: 3196	**173984**	ATCTGGCGTGGGTCGTATCTCTACC	TAGACCGCACCCAGCATAGAGATGG
SEQ ID NO: 3197	**174197**	GTTCGGTGGTGGCTTTCAAGACTCG	CAAGCCACCACCGAAAGTTCTGAGC
SEQ ID NO: 3198	**174199**	GTGTGCGTTCGTGGCCTACTCAGCC	CACACGCAAGCACCGGATGAGTCGG
SEQ ID NO: 3199	**174214**	CTTTCTGTGGGTCCTATCCTGCTGT	GAAAGACACCCAGGATAGGACGACA
SEQ ID NO: 3200	**174370**	CTTGTGTGTGGGGACTGAAAACAAC	GAACACACACCCCTGACTTTTGTTG
SEQ ID NO: 3201	**174386**	CCGGTGTGTGGGACGCAAAGTCTTC	GGCCACACACCCTGCGTTTCAGAAG
SEQ ID NO: 3202	**174601**	ATGTCTGTGTGGGTCTGACTGCATC	TACAGACACACCCAGACTGACGTAG
SEQ ID NO: 3203	**174765**	TGTGGACGTTGGATCGATGATCCCT	ACACCTGCAACCTAGCTACTAGGGA
SEQ ID NO: 3204	**174925**	AGAGTAGTGTGTGGCCATCGAGTCC	TCTCATCACACACCGGTAGCTCAGG
SEQ ID NO: 3205	**175138**	GTGTTGGTGTGGATCCCTACGAAAA	CACAACCACACCTAGGGATGCTTTT
SEQ ID NO: 3206	**175849**	CTCCTTTGGATGGTCGGTTGTCCGT	GAGGAAACCTACCAGCCAACAGGCA
SEQ ID NO: 3207	**180118**	ACGGTGTGGTGGAACCCTTCTTCGG	TGCCACACCACCTTGGGAAGAAGCC
SEQ ID NO: 3208	**180731**	ATGGTGGTGGAAATAGTCTACAGTT	TACCACCACCTTTATCAGATGTCAA
SEQ ID NO: 3209	**181269**	CGTGTGCGCGTGGATGCATTGCTTG	GCACACGCGCACCTACGTAACGAAC

SEQ ID NO: 3210	**181624**	ATCGTGAGTGTGGATCCAAGGTTCC	TAGCACTCACACCTAGGTTCCAAGG
SEQ ID NO: 3211	**181964**	NA	NA
SEQ ID NO: 3212	**182411**	GGGTGTGGTGGATCTTCAACGATAC	CCCACACCACCTAGAAGTTGCTATG
SEQ ID NO: 3213	**182569**	CGACAGTGGTGGAGTCCCAACATGT	GCTGTCACCACCTCAGGGTTGTACA
SEQ ID NO: 3214	**182745**	CGTCACGAGTGTGGAGATCATACTA	GCAGTGCTCACACCTCTAGTATGAT
SEQ ID NO: 3215	**182794**	TTTGTGTGTGGACGTTCTAAATGAC	AAACACACACCTGCAAGATTTACTG
SEQ ID NO: 3216	**183435**	CGACGACACCGTGGAAGAACAAGGT	GCTGCTGTGGCACCTTCTTGTTCCA
SEQ ID NO: 3217	**184321**	CGTGGTGGGGTTCGTGTCACCTCAT	GCACCACCCCAAGCACAGTGGAGTA
SEQ ID NO: 3218	**184563**	CTCTTGGGGTTGGTGCGTACCTAAC	GAGAACCCCAACCACGCATGGATTG
SEQ ID NO: 3219	**185445**	ACACTATTGGGTGGTGGTAACCTGG	TGTGATAACCCACCACCATTGGACC
SEQ ID NO: 3220	**185540**	TACTCTTGGGGTGCGTGGTCTTACT	ATGAGAACCCCACGCACCAGAATGA
SEQ ID NO: 3221	**185558**	GACACTATTGGGTGGTGGTAACCTG	CTGTGATAACCCACCACCATTGGAC
SEQ ID NO: 3222	**185563**	AGTCCGGTGGGTGATACGTCATTTA	TCAGGCCACCCACTATGCAGTAAAT
SEQ ID NO: 3223	**185711**	ACCTGTGTGGGTTGTGTCTTCCTCC	TGGACACACCCAACACAGAAGGAGG
SEQ ID NO: 3224	**186003**	CTCGGAAGGGTTCGTACTTTTATTT	GAGCCTTCCCAAGCATGAAAATAAA
SEQ ID NO: 3225	**186201**	NA	NA
SEQ ID NO: 3226	**186629**	NA	NA
SEQ ID NO: 3227	**186735**	CATTGGGGTGTCTGTGCAGTCAGTT	GTAACCCCACAGACACGTCAGTCAA
SEQ ID NO: 3228	**187137**	CACCTAAGGGTGTGGTTGTACCCGT	GTGGATTCCCACACCAACATGGGCA
SEQ ID NO: 3229	**187146**	ACACACACACGGGTGGTCACCTCTG	TGTGTGTGTGCCCACCAGTGGAGAC
SEQ ID NO: 3230	**187163**	TTTATCGTGGGTGTGACTTTATTTC	AAATAGCACCCACACTGAAATAAAG

SEQ ID NO: 3231	**187320**	CAATCACGGGTGTTGGTGTCTGAAC	GTTAGTGCCCACAACCACAGACTTG
SEQ ID NO: 3232	**187349**	TCCATGCGGGTGTTTGTAATGTCCC	AGGTACGCCCACAAACATTACAGGG
SEQ ID NO: 3233	**187521**	NA	NA
SEQ ID NO: 3234	**187822**	ACGTGTCTGCGGGTGGACAAAACCG	TGCACAGACGCCCACCTGTTTTGGC
SEQ ID NO: 3235	**188224**	GTTTATCCGGGTTTGTGCATTACCC	CAAATAGGCCCAAACACGTAATGGG
SEQ ID NO: 3236	**188377**	CCTACCTCGGGTTGTGGTCTTTCTA	GGATGGAGCCCAACACCAGAAAGAT
SEQ ID NO: 3237	**190416**	ATTCGGTGGGTCATATATCAGTAAA	TAAGCCACCCAGTATATAGTCATTT
SEQ ID NO: 3238	**192174**	TATCCGTGGGGTCGGTACCTCGTGA	ATAGGCACCCCAGCCATGGAGCACT
SEQ ID NO: 3239	**192571**	CCAGACACGGGTCTTTCCTCTGAGT	GGTCTGTGCCCAGAAAGGAGACTCA
SEQ ID NO: 3240	**193303**	CTTCTGGCGGTATTGGTGCCTCTTC	GAAGACCGCCATAACCACGGAGAAG
SEQ ID NO: 3241	**194088**	GTCTCGGTACGTGGGTAAATAGACG	CAGAGCCATGCACCCATTTATCTGC
SEQ ID NO: 3242	**195200**	TGTGTGTGGGGTAGTAGACCACTCT	ACACACACCCCATCATCTGGTGAGA
SEQ ID NO: 3243	**195573**	CCGACGACCGGGTAACGACGTACTA	GGCTGCTGGCCCATTGCTGCATGAT
SEQ ID NO: 3244	**196101**	AAGTCCGTTGGTGGGTCTTTGTGTA	TTCAGGCAACCACCCAGAAACACAT
SEQ ID NO: 3245	**196387**	TGGTGTGTTGGTGCACTAGTAGTTA	ACCACACAACCACGTGATCATCAAT
SEQ ID NO: 3246	**196661**	AACATTTGGTGGTGGTGTAATCGAA	TTGTAAACCACCACCACATTAGCTT
SEQ ID NO: 3247	**196709**	AACTGTTTGGTTGGTCTTGACACCT	TTGACAAACCAACCAGAACTGTGGA
SEQ ID NO: 3248	**197145**	ATACACCGTTGGTTTGTGTTGGTCC	TATGTGGCAACCAAACACAACCAGG
SEQ ID NO: 3249	**197337**	GTTCTTCGTTGGTTTTGTCAGTCAC	CAAGAAGCAACCAAAACAGTCAGTG
SEQ ID NO: 3250	**197934**	ATTCGTCGTTGGTGTGTGACCCTTT	TAAGCAGCAACCACACACTGGGAAA
SEQ ID NO: 3251	**198111**	CGGCTTATGGTGTGTGACACTGTGT	GCCGAATACCACACACTGTGACACA

SEQ ID NO: 3252	**198284**	ATGTTTTGGTGTAGTGTTGGCGATC	TACAAAACCACATCACAACCGCTAG
SEQ ID NO: 3253	**199303**	ATCCCACTGGTTGGTCGGCTCAAAG	TAGGGTGACCAACCAGCCGAGTTTC
SEQ ID NO: 3254	**199871**	GTTACTTTTGGTCGGTTGGAACGAC	CAATGAAAACCAGCCAACCTTGCTG
SEQ ID NO: 3255	**200199**	TTTACGGTGTGGTTGGTGATGTCTC	AAATGCCACACCAACCACTACAGAG
SEQ ID NO: 3256	**200264**	TGCCGGTTGGTCAGGTGTTTCTCGA	ACGGCCAACCAGTCCACAAAGAGCT
SEQ ID NO: 3257	**200561**	TTGGTGGTGGTGTAATCGAATCTAT	AACCACCACCACATTAGCTTAGATA
SEQ ID NO: 3258	**200880**	CACTGTGTCTGGTCTGCGTCCGAAA	GTGACACAGACCAGACGCAGGCTTT
SEQ ID NO: 3259	**201173**	CTACGGAGGTGGTGGTAATTCCTTC	GATGCCTCCACCACCATTAAGGAAG
SEQ ID NO: 3260	**201697**	CAACGTTGTGGTGGTGCTCCTTCAA	GTTGCAACACCACCACGAGGAAGTT
SEQ ID NO: 3261	**201730**	GTCTGGTGGTGGTGATATAACATCC	CAGACCACCACCACTATATTGTAGG
SEQ ID NO: 3262	**201918**	ACATGTCTCTGGTCTCTGGTTGCAA	TGTACAGAGACCAGAGACCAACGTT
SEQ ID NO: 3263	**201923**	ACAAGAGCGTGGTTTGAGGGACCCA	TGTTCTCGCACCAAACTCCCTGGGT
SEQ ID NO: 3264	**202084**	GTGTTGGGTGGTGGTACCCTCAGAC	CACAACCCACCACCATGGGAGTCTG
SEQ ID NO: 3265	**202088**	GTGGGTGGTGGTTGTCTACTCATAC	CACCCACCACCAACAGATGAGTATG
SEQ ID NO: 3266	**202090**	ACAGTCGGTGTGGTTTCTTCCTTAT	TGTCAGCCACACCAAAGAAGGAATA
SEQ ID NO: 3267	**202141**	ATACGGTGTGTGGTCCCTTTCATCA	TATGCCACACACCAGGGAAAGTAGT
SEQ ID NO: 3268	**202317**	AGTGGGTGTGGTCTGTCAACTCCAA	TCACCCACACCAGACAGTTGAGGTT
SEQ ID NO: 3269	**202511**	AAGACTCTGTGGTGTGTCAGAACCA	TTCTGAGACACCACACAGTCTTGGT
SEQ ID NO: 3270	**202541**	TTTCGGTGTGGTGATGCCTTCTCCT	AAAGCCACACCACTACGGAAGAGGA
SEQ ID NO: 3271	**202758**	CTCGCCGGTGGTGTTGAGACCTTAC	GAGCGGCCACCACAACTCTGGAATG
SEQ ID NO: 3272	**202804**	GTTGGTGGTGGTGGAACCTCTCAAA	CAACCACCACCACCTTGGAGAGTTT

SEQ ID NO: 3273	**202887**	GTCCTTATGTGGTGTGGTCCCTCCA	CAGGAATACACCACACCAGGGAGGT
SEQ ID NO: 3274	**203055**	TCGCTTGTGTGGTTCCTATTAAAGA	AGCGAACACACCAAGGATAATTTCT
SEQ ID NO: 3275	**203138**	GTTGGAGTGTGGTCCTTCGAAACTA	CAACCTCACACCAGGAAGCTTTGAT
SEQ ID NO: 3276	**203500**	TCGTGCTTGTGGTGGCGTCTGTTCC	AGCACGAACACCACCGCAGACAAGG
SEQ ID NO: 3277	**203521**	CCTTCCGTGGTTGTGAGTCTTTCTA	GGAAGGCACCAACACTCAGAAAGAT
SEQ ID NO: 3278	**203586**	CTCCACTGTGGTGTTGGTAGAGCCA	GAGGTGACACCACAACCATCTCGGT
SEQ ID NO: 3279	**203624**	GTACGACCTGGTGGTGTGACCCAAC	CATGCTGGACCACCACACTGGGTTG
SEQ ID NO: 3280	**203654**	TAGTATACTGTAGTGGTGGTCATCC	ATCATATGACATCACCACCAGTAGG
SEQ ID NO: 3281	**203718**	ATTCTACGTGTGGTGTAGGAGACAC	TAAGATGCACACCACATCCTCTGTG
SEQ ID NO: 3282	**203724**	ATCCGTCGTGTGGTGTCGTCTCACA	TAGGCAGCACACCACAGCAGAGTGT
SEQ ID NO: 3283	**203777**	GTCTCTCAAGTGGTGTGGCGCTTCA	CAGAGAGTTCACCACACCGCGAAGT
SEQ ID NO: 3284	**203848**	GTCTGTGACGCGTGGTTCTATTTCT	CAGACACTGCGCACCAAGATAAAGA
SEQ ID NO: 3285	**204343**	CTGTTCTCGTGGTGGTAACCTGACC	GACAAGAGCACCACCATTGGACTGG
SEQ ID NO: 3286	**204708**	TGGGTGTCGTGGTACCCTCTCTCCG	ACCCACAGCACCATGGGAGAGAGGC
SEQ ID NO: 3287	**204890**	AATTACAGTGGTCGGTTCCTACTCC	TTAATGTCACCAGCCAAGGATGAGG
SEQ ID NO: 3288	**205043**	GTGTCGTGTTACGTGGTCCTAGAAG	CACAGCACAATGCACCAGGATCTTC
SEQ ID NO: 3289	**205129**	AGGAGTGGTGGTCGTCACTACCGCA	TCCTCACCACCAGCAGTGATGGCGT
SEQ ID NO: 3290	**205428**	GCACCACGACTGGTATACCTGCAAC	CGTGGTGCTGACCATATGGACGTTG
SEQ ID NO: 3291	**205735**	CGATGGGTGGTAGCGGTCTGCGTCT	GCTACCCACCATCGCCAGACGCAGA
SEQ ID NO: 3292	**208733**	CTACCGTCAAGGGAGTGTGTGACTA	GATGGCAGTTCCCTCACACACTGAT
SEQ ID NO: 3293	**209563**	GTGGTCCCAGGGCACCACGACGACA	CACCAGGGTCCCGTGGTGCTGCTGT

SEQ ID NO: 3294	**210429**	AGTTATCCAGGGTACCACCTCAGGG	TCAATAGGTCCCATGGTGGAGTCCC
SEQ ID NO: 3295	**211006**	CCACACGCAGGGAACGAAATCTTCT	GGTGTGCGTCCCTTGCTTTAGAAGA
SEQ ID NO: 3296	**211802**	CTTCGAAAGGCCTTCGTGGAACATG	GAAGCTTTCCGGAAGCACCTTGTAC
SEQ ID NO: 3297	**212363**	TTAGCCGAAGGCCACCACGACCGAG	AATCGGCTTCCGGTGGTGCTGGCTC
SEQ ID NO: 3298	**213409**	GCACACGTCGAAGGCACTACGTCAA	CGTGTGCAGCTTCCGTGATGCAGTT
SEQ ID NO: 3299	**214907**	ACTCGTGCGTGAGGGGACACTTCTA	TGAGCACGCACTCCCCTGTGAAGAT
SEQ ID NO: 3300	**215020**	ACCGCAAGAGGGTCCGCACTGCGCA	TGGCGTTCTCCCAGGCGTGACGCGT
SEQ ID NO: 3301	**215556**	NA	NA
SEQ ID NO: 3302	**216014**	TGTAGAACCCGGCCCTCCAGAACAA	ACATCTTGGGCCGGGAGGTCTTGTT
SEQ ID NO: 3303	**216088**	CCCAAGAGGGAGAAGTCGACTCGTA	GGGTTCTCCCTCTTCAGCTGAGCAT
SEQ ID NO: 3304	**216358**	TAGACGCGCCGAGGCACCGGCTTTC	ATCTGCGCGGCTCCGTGGCCGAAAG
SEQ ID NO: 3305	**220613**	ACACCCGCAGGAGGTTCTAGAACGC	TGTGGGCGTCCTCCAAGATCTTGCG
SEQ ID NO: 3306	**221765**	TACGACTACGGCAGGATCTTAGGTA	ATGCTGATGCCGTCCTAGAATCCAT
SEQ ID NO: 3307	**222663**	GCATGAACAGGAGACGACGACTGTC	CGTACTTGTCCTCTGCTGCTGACAG
SEQ ID NO: 3308	**223128**	AGTTTCCAGGACCTTGAACAGTCAC	TCAAAGGTCCTGGAACTTGTCAGTG
SEQ ID NO: 3309	**224238**	GGACTTGCAGGACCGCTTCCATTGC	CCTGAACGTCCTGGCGAAGGTAACG
SEQ ID NO: 3310	**224261**	GGTTTGAAGGACGTTCACGAACGAT	CCAAACTTCCTGCAAGTGCTTGCTA
SEQ ID NO: 3311	**226127**	CCTCTCTGAGGATTGTGTTGTGTCT	GGAGAGACTCCTAACACAACACAGA
SEQ ID NO: 3312	**227344**	CAGACACACGAGGACTTTGTTCGTG	GTCTGTGTGCTCCTGAAACAAGCAC
SEQ ID NO: 3313	**227962**	TCGCCGCCGAGGAGTTGTACCGTCG	AGCGGCGGCTCCTCAACATGGCAGC
SEQ ID NO: 3314	**233282**	TGTGTGTGTGTAGGACGACACCTGA	ACACACACACATCCTGCTGTGGACT

SEQ ID NO: 3315	**233767**	CTTTCACTAGGACAGAGCCGTCGTC	GAAAGTGATCCTGTCTCGGCAGCAG
SEQ ID NO: 3316	**236385**	GAACCACACAGGTTAAAACATAAGT	CTTGGTGTGTCCAATTTTGTATTCA
SEQ ID NO: 3317	**236472**	CACGACCGAAGGTGCTACATCAGGT	GTGCTGGCTTCCACGATGTAGTCCA
SEQ ID NO: 3318	**237755**	GACTCCGACGACAGGTTACGACTCG	CTGAGGCTGCTGTCCAATGCTGAGC
SEQ ID NO: 3319	**239175**	AGTACTGTGCGAGGTGGTGATTAAA	TCATGACACGCTCCACCACTAATTT
SEQ ID NO: 3320	**240433**	CCTGACGGAGGTTTTGTTGTGTTCC	GGACTGCCTCCAAAACAACACAAGG
SEQ ID NO: 3321	**240816**	ACCGCACCAGGTCGAGGTGCAACCG	TGGCGTGGTCCAGCTCCACGTTGGC
SEQ ID NO: 3322	**241546**	CATAGGTCGAGGTTTCGTGTGTGTC	GTATCCAGCTCCAAAGCACACACAG
SEQ ID NO: 3323	**241768**	TCCGACCGACGAGGTTTGTCCGACG	AGGCTGGCTGCTCCAAACAGGCTGC
SEQ ID NO: 3324	**242178**	TCCAGTTCGAGGTGGTGCGTCTACT	AGGTCAAGCTCCACCACGCAGATGA
SEQ ID NO: 3325	**242999**	CTCCGCCAGGTAAGACGTATTTTAT	GAGGCGGTCCATTCTGCATAAAATA
SEQ ID NO: 3326	**243951**	GTCATCTCAGAGGTCCGAGACCAGT	CAGTAGAGTCTCCAGGCTCTGGTCA
SEQ ID NO: 3327	**247150**	CAGAACTTAGGTTTCGTGCGTGAGA	GTCTTGAATCCAAAGCACGCACTCT
SEQ ID NO: 3328	**247487**	GTCAACGACACGAGGTACTCCCGGT	CAGTTGCTGTGCTCCATGAGGGCCA
SEQ ID NO: 3329	**247567**	ACAGAAGTTAGGTGTGGTGCCTCCC	TGTCTTCAATCCACACCACGGAGGG
SEQ ID NO: 3330	**248868**	GGTCTAGTGTAGTAGGTTGGTTCCC	CCAGATCACATCATCCAACCAAGGG
SEQ ID NO: 3331	**249420**	TCGTGAGTGTGTAGGTGCACTTACG	AGCACTCACACATCCACGTGAATGC
SEQ ID NO: 3332	**249930**	AAGTTGCCGGGTCTGTCCGTGTACA	TTCAACGGCCCAGACAGGCACATGT
SEQ ID NO: 3333	**250091**	NA	NA
SEQ ID NO: 3334	**250647**	ACCGACCGCCGGGAAGGCCTACTTA	TGGCTGGCGGCCCTTCCGGATGAAT
SEQ ID NO: 3335	**250655**	TCCGGCCCGGGCCACGCGCCGCCGC	AGGCCGGGCCCGGTGCGCGGCGGCG

SEQ ID NO: 3336	**251124**	ACCGCCGCCGGGCTGGCATGTGTGG	TGGCGGCGGCCCGACCGTACACACC
SEQ ID NO: 3337	**251205**	CCGAAACCGGGTCTCGTGCCAAGAC	GGCTTTGGCCCAGAGCACGGTTCTG
SEQ ID NO: 3338	**251246**	AGCTGTGGCGGGTAAACCTCCCTTT	TCGACACCGCCCATTTGGAGGGAAA
SEQ ID NO: 3339	**251338**	TGAAGAACCGGCCTCCGTAGCGGCG	ACTTCTTGGCCGGAGGCATCGCCGC
SEQ ID NO: 3340	**251673**	CACCGCTCCGGGATCCTCTGGAGGG	GTGGCGAGGCCCTAGGAGACCTCCC
SEQ ID NO: 3341	**252296**	CTTCGCTCCGGGTACAACGACGACA	GAAGCGAGGCCCATGTTGCTGCTGT
SEQ ID NO: 3342	**252348**	AGAAGGACCGGGAGCCCAAGTTCGT	TCTTCCTGGCCCTCGGGTTCAAGCA
SEQ ID NO: 3343	**253198**	GCGCCCGCCGGCAGCGCGCGCCGCG	CGCGGGCGGCCGTCGCGCGCGGCGC
SEQ ID NO: 3344	**253880**	CTCTCGATGCGGCGTGCTATGTCCG	GAGAGCTACGCCGCACGATACAGGC
SEQ ID NO: 3345	**253922**	NA	NA
SEQ ID NO: 3346	**255202**	TCGACATGCCGGACCGAACCGTTCG	AGCTGTACGGCCTGGCTTGGCAAGC
SEQ ID NO: 3347	**255235**	ACCCTACGACCGGAACTGCCTGGTG	TGGGATGCTGGCCTTGACGGACCAC
SEQ ID NO: 3348	**255755**	GTGCTACCGCCGGAACCCGTCGGGA	CACGATGGCGGCCTTGGGCAGCCCT
SEQ ID NO: 3349	**256299**	TCTCACGCCCGGAGTGTGTGGTCTA	AGAGTGCGGGCCTCACACACCAGAT
SEQ ID NO: 3350	**256548**	ACCTGATCGCGGAGGCGTCCGGACC	TGGACTAGCGCCTCCGCAGGCCTGG
SEQ ID NO: 3351	**256564**	CCGACGACACCGGATGTGTGGACCC	GGCTGCTGTGGCCTACACACCTGGG
SEQ ID NO: 3352	**257147**	GACCTCAGACCGGAGAGTCTCGGCT	CTGGAGTCTGGCCTCTCAGAGCCGA
SEQ ID NO: 3353	**257230**	AGAACGCACCGGAGAACCGCAGCAG	TCTTGCGTGGCCTCTTGGCGTCGTC
SEQ ID NO: 3354	**257391**	TTTTTCGCGGACCTGTTCGACCTCG	AAAAAGCGCCTGGACAAGCTGGAGC
SEQ ID NO: 3355	**257495**	ACACTACTGCCGGACTCGGGAACCT	TGTGATGACGGCCTGAGCCCTTGGA
SEQ ID NO: 3356	**258562**	AGGACCACCGGACATGTCAAGATCG	TCCTGGTGGCCTGTACAGTTCTAGC

SEQ ID NO: 3357	**258570**	CCGACCACCGGACGAAGAACAACTA	GGCTGGTGGCCTGCTTCTTGTTGAT
SEQ ID NO: 3358	**258803**	TCAAGGTTCGGGTGTGGACTTCTAT	AGTTCCAAGCCCACACCTGAAGATA
SEQ ID NO: 3359	**259316**	NA	NA
SEQ ID NO: 3360	**259589**	CCTAATCGCGGACGACGACCTATTT	GGATTAGCGCCTGCTGCTGGATAAA
SEQ ID NO: 3361	**260326**	CGTTGTTTCGGGTGTAGAAATGCCC	GCAACAAAGCCCACATCTTTACGGG
SEQ ID NO: 3362	**260547**	ACCCATTCGGGTGTGTCGAGAAATC	TGGGTAAGCCCACACAGCTCTTTAG
SEQ ID NO: 3363	**260953**	TCTTGTCAGTCGGCACACTCAGAGG	AGAACAGTCAGCCGTGTGAGTCTCC
SEQ ID NO: 3364	**261855**	CTTGTGGTCGGGATAGACGTATTAC	GAACACCAGCCCTATCTGCATAATG
SEQ ID NO: 3365	**263128**	ACCTGTGGTCGGAGGCTTACACTCG	TGGACACCAGCCTCCGAATGTGAGC
SEQ ID NO: 3366	**264600**	TTTGTCTTCGGTGGTAAAGTCTCGT	AAACAGAAGCCACCATTTCAGAGCA
SEQ ID NO: 3367	**265707**	GCCAGAGCCGGTTTGACCTTACCTT	CGGTCTCGGCCAAACTGGAATGGAA
SEQ ID NO: 3368	**266034**	ACACACGGCCGGTTCCACCAGTCCA	TGTGTGCCGGCCAAGGTGGTCAGGT
SEQ ID NO: 3369	**266695**	ACTCCACGCCGGTGTCCTCTTACAC	TGAGGTGCGGCCACAGGAGAATGTG
SEQ ID NO: 3370	**267016**	GCAACCACCGGTCCTCGAAGAACAG	CGTTGGTGGCCAGGAGCTTCTTGTC
SEQ ID NO: 3371	**267410**	AATGGCCGGTGTGTGAACCACGGTC	TTACCGGCCACACACTTGGTGCCAG
SEQ ID NO: 3372	**268562**	GGTTCCCGCGGTGGTAGTTCGCGTA	CCAAGGGCGCCACCATCAAGCGCAT
SEQ ID NO: 3373	**269003**	AAGGAGGTCGGTCGGTTGAGTGTCA	TTCCTCCAGCCAGCCAACTCACAGT
SEQ ID NO: 3374	**269113**	CGACGACAAGCGGTCCACGACGACT	GCTGCTGTTCGCCAGGTGCTGCTGA
SEQ ID NO: 3375	**269186**	CCAGTGGCGGTGTCGGCCACGCTCC	GGTCACCGCCACAGCCGGTGCGAGG
SEQ ID NO: 3376	**269240**	CACAAACGCGGTGTGTGGACCTTTC	GTGTTTGCGCCACACACCTGGAAAG
SEQ ID NO: 3377	**269273**	CTCCGTCCCGGTACGAACCGAAGGG	GAGGCAGGGCCATGCTTGGCTTCCC

SEQ ID NO: 3378	**269676**	CCAACATCGGTTAAAAGAATTACAT	GGTTGTAGCCAATTTTCTTAATGTA
SEQ ID NO: 3379	**270218**	CTGACCGACCGGTACTACCAGTGAT	GACTGGCTGGCCATGATGGTCACTA
SEQ ID NO: 3380	**270504**	AGACGCCACCGGTACCACTTGTAGA	TCTGCGGTGGCCATGGTGAACATCT
SEQ ID NO: 3381	**270593**	ACTGGTTTCGGTGAACGTTTCTTTG	TGACCAAAGCCACTTGCAAAGAAAC
SEQ ID NO: 3382	**271229**	ATTGACTTCGGTTCAGTGTTTGTCC	TAACTGAAGCCAAGTCACAAACAGG
SEQ ID NO: 3383	**271315**	GTACGTGAGTGTGCGGTAGACACCT	CATGCACTCACACGCCATCTGTGGA
SEQ ID NO: 3384	**272032**	CGAACATTCGGTGTCTGTGGACGTC	GCTTGTAAGCCACAGACACCTGCAG
SEQ ID NO: 3385	**273076**	CTACCGGTGTCGGTGAGGTAAACTC	GATGGCCACAGCCACTCCATTTGAG
SEQ ID NO: 3386	**273264**	ATGGTCGGTCGGTTATCCTACGTGT	TACCAGCCAGCCAATAGGATGCACA
SEQ ID NO: 3387	**273756**	TCAAAGGACGGAGCAGCCCGCGTCG	AGTTTCCTGCCTCGTCGGGCGCAGC
SEQ ID NO: 3388	**273818**	CCACTCCGTCGGTTTAGGTACCACG	GGTGAGGCAGCCAAATCCATGGTGC
SEQ ID NO: 3389	**273871**	ATTGAGTGTCGGTGAGTAGCCCTTG	TAACTCACAGCCACTCATCGGGAAC
SEQ ID NO: 3390	**274013**	AGGACGAGGACGGGGAGGACGGGGA	TCCTGCTCCTGCCCCTCCTGCCCCT
SEQ ID NO: 3391	**274097**	TATTATGGTCGGTAGTGTGTGTTTT	ATAATACCAGCCATCACACACAAAA
SEQ ID NO: 3392	**274446**	CACACCCACGGGGTAAAGAACAGGA	GTGTGGGTGCCCCATTTCTTGTCCT
SEQ ID NO: 3393	**275489**	GTCTCACACGCACGGGGTAGAAGTG	CAGAGTGTGCGTGCCCCATCTTCAC
SEQ ID NO: 3394	**276840**	ACGACTTACTGACGGGACACACTGT	TGCTGAATGACTGCCCTGTGTGACA
SEQ ID NO: 3395	**276893**	ACACCGACCACGGAATGTTTCGTGT	TGTGGCTGGTGCCTTACAAAGCACA
SEQ ID NO: 3396	**277191**	CTCCGACCACGGAGAACAGTCGACG	GAGGCTGGTGCCTCTTGTCAGCTGC
SEQ ID NO: 3397	**277706**	AGGACCCGACGGACTCGAAAGGTCA	TCCTGGGCTGCCTGAGCTTTCCAGT
SEQ ID NO: 3398	**277837**	CTCACCTCACGGACAATATTTCTTT	GAGTGGAGTGCCTGTTATAAAGAAA

SEQ ID NO: 3399	**277886**	ATGATTCACGGATGACGACACGACC	TACTAAGTGCCTACTGCTGTGCTGG
SEQ ID NO: 3400	**277963**	CTTGTCCACGGAGGCACCTACACGT	GAACAGGTGCCTCCGTGGATGTGCA
SEQ ID NO: 3401	**279058**	ACACACACGGTACGGGTCTAACTTC	TGTGTGTGCCATGCCCAGATTGAAG
SEQ ID NO: 3402	**279153**	ATTGCACACGGACGGCTCAACCAGC	TAACGTGTGCCTGCCGAGTTGGTCG
SEQ ID NO: 3403	**279354**	AGCCCAGACGGAACGGGCTGACGTC	TCGGGTCTGCCTTGCCCGACTGCAG
SEQ ID NO: 3404	**279735**	ACACACACGTCTACGGCGGTAAAGA	TGTGTGTGCAGATGCCGCCATTTCT
SEQ ID NO: 3405	**280160**	ACGACAGTAGCTACGGCACGACCTG	TGCTGTCATCGATGCCGTGCTGGAC
SEQ ID NO: 3406	**280186**	AATAGGAACGGTGTGTGTTGACGCC	TTATCCTTGCCACACACAACTGCGG
SEQ ID NO: 3407	**280545**	CACGAACGAACGGTAAGTCGGTTCC	GTGCTTGCTTGCCATTCAGCCAAGG
SEQ ID NO: 3408	**280707**	ATTTTCACGGTGTGTCTGGATTACA	TAAAAGTGCCACACAGACCTAATGT
SEQ ID NO: 3409	**281090**	TGTCTACACACACGGTAACCGGGCG	ACAGATGTGTGTGCCATTGGCCCGC
SEQ ID NO: 3410	**281687**	ACGTATCATACACGGTGGTGGTCAT	TGCATAGTATGTGCCACCACCAGTA
SEQ ID NO: 3411	**281726**	CCACACTCACGGTTGGACGTCTCGG	GGTGTGAGTGCCAACCTGCAGAGCC
SEQ ID NO: 3412	**282721**	TTCCACGGACGGTGACAGCGACATG	AAGGTGCCTGCCACTGTCGCTGTAC
SEQ ID NO: 3413	**282916**	TCACACACACGACGGTCTCGTTCGT	AGTGTGTGTGCTGCCAGAGCAAGCA
SEQ ID NO: 3414	**283457**	CTACCCGAGGCCCGCGCCTCTTTGA	GATGGGCTCCGGGCGCGGAGAAACT
SEQ ID NO: 3415	**284476**	AGCCTCTGGCCCAGGTCTCGGGAGT	TCGGAGACCGGGTCCAGAGCCCTCA
SEQ ID NO: 3416	**285649**	GGACACTATGGCCACTACTCGCGGT	CCTGTGATACCGGTGATGAGCGCCA
SEQ ID NO: 3417	**286089**	CCACTGGGCCTACTTCCTAATTGTC	GGTGACCCGGATGAAGGATTAACAG
SEQ ID NO: 3418	**287027**	TGTCCCAGGCCACCGACGACTGAGG	ACAGGGTCCGGTGGCTGCTGACTCC
SEQ ID NO: 3419	**287755**	NA	NA

SEQ ID NO: 3420	**288103**	CCGTCCGGGCCGAGTCACAAGGCAA	GGCAGGCCCGGCTCAGTGTTCCGTT
SEQ ID NO: 3421	**288668**	AGGCAAGGCCGTACCGCCGACCGTA	TCCGTTCCGGCATGGCGGCTGGCAT
SEQ ID NO: 3422	**288794**	AAACGTCCGGCCTCCTGTCATCGAG	TTTGCAGGCCGGAGGACAGTAGCTC
SEQ ID NO: 3423	**289022**	GCTAGTCTATGGCAGCAACAAGGCT	CGATCAGATACCGTCGTTGTTCCGA
SEQ ID NO: 3424	**291667**	CTCGTGTGGGCAGATACATCGTTTT	GAGCACACCCGTCTATGTAGCAAAA
SEQ ID NO: 3425	**292366**	AGTCGGACGGGCACCACCTTCATTC	TCAGCCTGCCCGTGGTGGAAGTAAG
SEQ ID NO: 3426	**293317**	AGTCCTTCGGCACGCCGTCCAGGAG	TCAGGAAGCCGTGCGGCAGGTCCTC
SEQ ID NO: 3427	**293320**	TCCCGACCTGCCGATCCCACGACTG	AGGGCTGGACGGCTAGGGTGCTGAC
SEQ ID NO: 3428	**293402**	CTGAACAGGCACACAGACAGGCGCG	GACTTGTCCGTGTGTCTGTCCGCGC
SEQ ID NO: 3429	**293440**	ACAGTCACCGGCACACCGCTGAAGG	TGTCAGTGGCCGTGTGGCGACTTCC
SEQ ID NO: 3430	**293938**	CTCCACCGGCACAACGACTAGGTGT	GAGGTGGCCGTGTTGCTGATCCACA
SEQ ID NO: 3431	**293991**	AGACACCAGGCACACACCGTCGTAG	TCTGTGGTCCGTGTGTGGCAGCATC
SEQ ID NO: 3432	**294415**	AAACAGTTGCCGGAAAGGACGGAGA	TTTGTCAACGGCCTTTCCTGCCTCT
SEQ ID NO: 3433	**294498**	CCACACAGGCACGTACTACGTACAT	GGTGTGTCCGTGCATGATGCATGTA
SEQ ID NO: 3434	**294673**	ATTTGTTGCCACACCGACGAAGAGT	TAAACAACGGTGTGGCTGCTTCTCA
SEQ ID NO: 3435	**294865**	AGCGGTCATGCCGCCCAGCGCCGCC	TCGCCAGTACGGCGGGTCGCGGCGG
SEQ ID NO: 3436	**295067**	GGTCCTACCTGCCTTGTACCTGACA	CCAGGATGGACGGAACATGGACTGT
SEQ ID NO: 3437	**295360**	CTTTGATGCCCAGATTCGTGTGTGC	GAAACTACGGGTCTAAGCACACACG
SEQ ID NO: 3438	**295679**	AACAGGCTGCCGACGACGTTGACGC	TTGTCCGACGGCTGCTGCAACTGCG
SEQ ID NO: 3439	**295830**	CCACTCGCTGCCAGGTTACGGAAGT	GGTGAGCGACGGTCCAATGCCTTCA
SEQ ID NO: 3440	**297120**	AGTGACACTACTGCCGGCACCGACA	TCACTGTGATGACGGCCGTGGCTGT

SEQ ID NO: 3441	**297163**	CTTGTGTGTGCCTTAATACTCCACC	GAACACACACGGAATTATGAGGTGG
SEQ ID NO: 3442	**299580**	CTTCCGCTGCACCACAGGTTGGTAG	GAAGGCGACGTGGTGTCCAACCATC
SEQ ID NO: 3443	**299626**	TCCTGTCCTGCAATGGTTCGGGTCA	AGGACAGGACGTTACCAAGCCCAGT
SEQ ID NO: 3444	**299978**	ACTCCAGCTGCACCAGAGGTCACTG	TGAGGTCGACGTGGTCTCCAGTGAC
SEQ ID NO: 3445	**300538**	ACGTGTCTCGACTGCACCTGGAAAA	TGCACAGAGCTGACGTGGACCTTTT
SEQ ID NO: 3446	**300761**	ACAGTAGGTTGCACGCACCGACCGT	TGTCATCCAACGTGCGTGGCTGGCA
SEQ ID NO: 3447	**300823**	CGTCCACAGTGCACCCACACCGGAG	GCAGGTGTCACGTGGGTGTGGCCTC
SEQ ID NO: 3448	**301087**	CCAGCGGTGCAGACTAGACTCCAGC	GGTCGCCACGTCTGATCTGAGGTCG
SEQ ID NO: 3449	**301156**	ACGTGTGAGTCTGCACTTGTGTGTC	TGCACACTCAGACGTGAACACACAG
SEQ ID NO: 3450	**301363**	ACGGTGGTGGCTACTCTTTTTTTCC	TGCCACCACCGATGAGAAAAAAAGG
SEQ ID NO: 3451	**301443**	GACCCGTGTGTGCACCCGTATCCGT	CTGGGCACACACGTGGGCATAGGCA
SEQ ID NO: 3452	**301453**	CTACTCGCGGTGCAAGGACCCGAAC	GATGAGCGCCACGTTCCTGGGCTTG
SEQ ID NO: 3453	**301906**	TCTACGGTGTGTGCATAGTGTGTAT	AGATGCCACACACGTATCACACATA
SEQ ID NO: 3454	**302321**	ACGGTCGGTGTGCACGAGTCCTTCC	TGCCAGCCACACGTGCTCAGGAAGG
SEQ ID NO: 3455	**302418**	TCCTAGGTGTGCAGTGGGTCTCACT	AGGATCCACACGTCACCCAGAGTGA
SEQ ID NO: 3456	**302502**	TCCACACACGTGCAGAGTCTTGAGT	AGGTGTGTGCACGTCTCAGAACTCA
SEQ ID NO: 3457	**302507**	TGTAGCGTACGTGTGCAGTGGCACT	ACATCGCATGCACACGTCACCGTGA
SEQ ID NO: 3458	**302720**	GTTCGTGTGTGTGCACAACAGTACC	CAAGCACACACACGTGTTGTCATGG
SEQ ID NO: 3459	**303523**	AGTCACTAAGGCTTCGGACCGAGGC	TCAGTGATTCCGAAGCCTGGCTCCG
SEQ ID NO: 3460	**303607**	CTTTTGGCTTGGTGGTATGAATACT	GAAAACCGAACCACCATACTTATGA
SEQ ID NO: 3461	**303845**	ACACACGTAAGGCTTGTCCCGACGG	TGTGTGCATTCCGAACAGGGCTGCC

SEQ ID NO: 3462	**304800**	GTATACGGTTGGCTGTGTTTACCTT	CATATGCCAACCGACACAAATGGAA
SEQ ID NO: 3463	**305213**	AATCGACGCGGCTTGGGTCGGTTAC	TTAGCTGCGCCGAACCCAGCCAATG
SEQ ID NO: 3464	**306288**	GTCCGTGTGGGCTAAGGACCTCGCA	CAGGCACACCCGATTCCTGGAGCGT
SEQ ID NO: 3465	**306675**	GGCACGCACGGCTCACGACACGTTT	CCGTGCGTGCCGAGTGCTGTGCAAA
SEQ ID NO: 3466	**307025**	ACCGTCACACGGCTCTGACTCGGTA	TGGCAGTGTGCCGAGACTGAGCCAT
SEQ ID NO: 3467	**307326**	TGAGGGTGTGCTCGGTTCACGTCAT	ACTCCCACACGAGCCAAGTGCAGTA
SEQ ID NO: 3468	**309629**	TGGTGTCTGTGCTCCCTCCAGGGAG	ACCACAGACACGAGGGAGGTCCCTC
SEQ ID NO: 3469	**310020**	NA	NA
SEQ ID NO: 3470	**310227**	GAGTAGGTGTGTGCTCACCAGGTTA	CTCATCCACACACGAGTGGTCCAAT
SEQ ID NO: 3471	**310373**	ACTGTAGTGCGTGCTGTAGCTCCGC	TGACATCACGCACGACATCGAGGCG
SEQ ID NO: 3472	**310432**	GTCACTTGTCTGCTCACCTGCGTCA	CAGTGAACAGACGAGTGGACGCAGT
SEQ ID NO: 3473	**310996**	CCCATCGTGCTTGTGGTGGCGTCTG	GGGTAGCACGAACACCACCGCAGAC
SEQ ID NO: 3474	**311055**	ACTAGTGTGTGTGCTCGTCCCAAGA	TGATCACACACACGAGCAGGGTTCT
SEQ ID NO: 3475	**311200**	CCTTCACGTGCTGCGTGGTGGAGAA	GGAAGTGCACGACGCACCACCTCTT
SEQ ID NO: 3476	**311262**	TCGTGGTGCGTGCTACCGACAAAGA	AGCACCACGCACGATGGCTGTTTCT
SEQ ID NO: 3477	**311380**	CGAGTGGTCGTGCTACCTTGTGTAA	GCTCACCAGCACGATGGAACACATT
SEQ ID NO: 3478	**311445**	ACGTGCTCGTGTGCTCAAGTCTCCG	TGCACGAGCACACGAGTTCAGAGGC
SEQ ID NO: 3479	**311925**	CGTCTCGCCAGCCGCATGGTAGGCG	GCAGAGCGGTCGGCGTACCATCCGC
SEQ ID NO: 3480	**312173**	GTCGTGGTGCGTGCTACCGACAAAG	CAGCACCACGCACGATGGCTGTTTC
SEQ ID NO: 3481	**312175**	CGGAAGACGTGCTACACGACACGAA	GCCTTCTGCACGATGTGCTGTGCTT
SEQ ID NO: 3482	**312210**	CTGACGTCGTGTGCTACTGTAGTTT	GACTGCAGCACACGATGACATCAAA

SEQ ID NO: 3483	**313030**	GGCCGCCAGCCGGAGTTACTTCTAC	CCGGCGGTCGGCCTCAATGAAGATG
SEQ ID NO: 3484	**313417**	CTTCCAACGCCGAAGAAGGTCAAGA	GAAGGTTGCGGCTTCTTCCAGTTCT
SEQ ID NO: 3485	**314579**	AAGGCACGAGCCCACGAAGCCGGTC	TTCCGTGCTCGGGTGCTTCGGCCAG
SEQ ID NO: 3486	**314930**	ACAGGTGACAGCAGGTGAAGGAATC	TGTCCACTGTCGTCCACTTCCTTAG
SEQ ID NO: 3487	**315771**	GCGCGGACCGAGCCGCCCGGCCGGG	CGCGCCTGGCTCGGCGGGCCGGCCC
SEQ ID NO: 3488	**315863**	CTCAAAAGCAGAAGACTAGGCCGAA	GAGTTTTCGTCTTCTGATCCGGCTT
SEQ ID NO: 3489	**316097**	GACACCACCGAGCAACCAGAAACAG	CTGTGGTGGCTCGTTGGTCTTTGTC
SEQ ID NO: 3490	**318469**	TTTAGGAGAGCAACACGTATCGGTG	AAATCCTCTCGTTGTGCATAGCCAC
SEQ ID NO: 3491	**319062**	CCGACCACGAGCATAGATGTTTTTA	GGCTGGTGCTCGTATCTACAAAAAT
SEQ ID NO: 3492	**320311**	GCACAAAGTAGCACCGACGACAGAC	CGTGTTTCATCGTGGCTGCTGTCTG
SEQ ID NO: 3493	**321070**	GGGCGCTAGTAGCACCGACACCGAG	CCCGCGATCATCGTGGCTGTGGCTC
SEQ ID NO: 3494	**324272**	AGTGTGCGGGCGTGGGTGCGTCCAG	TCACACGCCCGCACCCACGCAGGTC
SEQ ID NO: 3495	**325199**	CCCCGGGCGGATGCGATGCGGCGAG	GGGGCCCGCCTACGCTACGCCGCTC
SEQ ID NO: 3496	**325343**	ACAGCAGCGGCGGAGAACCCAACCT	TGTCGTCGCCGCCTCTTGGGTTGGA
SEQ ID NO: 3497	**325432**	CTTGCCGGCGAAACCACGACCTGAG	GAACGGCCGCTTTGGTGCTGGACTC
SEQ ID NO: 3498	**327107**	NA	NA
SEQ ID NO: 3499	**327173**	AGGGTAATGCGACCGACCTATATTC	TCCCATTACGCTGGCTGGATATAAG
SEQ ID NO: 3500	**327797**	AGGACTACGGGCGACCTCCAGTCTC	TCCTGATGCCCGCTGGAGGTCAGAG
SEQ ID NO: 3501	**329140**	CTTACGGTATGCGCGCCGCCCCGGC	GAATGCCATACGCGCGGCGGGGCCG
SEQ ID NO: 3502	**329193**	ACTTTTGTGCGGTTCGTGTGTGACC	TGAAAACACGCCAAGCACACACTGG
SEQ ID NO: 3503	**329564**	CTCGTGCATGCGTGCCTGGCTGCAG	GAGCACGTACGCACGGACCGACGTC

SEQ ID NO: 3504	**329881**	TTTGGGGCGTCGCATCAAAGACCGA	AAACCCCGCAGCGTAGTTTCTGGCT
SEQ ID NO: 3505	**329937**	CTTGTGAGTGCGACATGAGCCTACC	GAACACTCACGCTGTACTCGGATGG
SEQ ID NO: 3506	**330048**	GCCGTTGTGTGCGATGGTATTTCCC	CGGCAACACACGCTACCATAAAGGG
SEQ ID NO: 3507	**330164**	CTTGTTGTGCGTTGACGTTACGTGG	GAACAACACGCAACTGCAATGCACC
SEQ ID NO: 3508	**330533**	ACGGGTCCTGCGTGTGTTTGTACTT	TGCCCAGGACGCACACAAACATGAA
SEQ ID NO: 3509	**330924**	TGTCTGGGTGCGTGCGACCTCCGAA	ACAGACCCACGCACGCTGGAGGCTT
SEQ ID NO: 3510	**331002**	ACTGTGGCGTGCGACTCGAGACACT	TGACACCGCACGCTGAGCTCTGTGA
SEQ ID NO: 3511	**331284**	CACAGCGTGTGCGTGCCTTATCATA	GTGTCGCACACGCACGGAATAGTAT
SEQ ID NO: 3512	**331316**	CTGTTTGTGCGTCAGTCCCTCACCT	GACAAACACGCAGTCAGGGAGTGGA
SEQ ID NO: 3513	**331630**	GGCGTTGCGGCGTGTCTAAATAGTA	CCGCAACGCCGCACAGATTTATCAT
SEQ ID NO: 3514	**332057**	GGCTCCACGGCGTGTCGACAGACGT	CCGAGGTGCCGCACAGCTGTCTGCA
SEQ ID NO: 3515	**332213**	GGCCGATAAGCGAGGTCCCATAGAT	CCGGCTATTCGCTCCAGGGTATCTA
SEQ ID NO: 3516	**332371**	CTCCTGGTGCGTGCATAGAGAACTC	GAGGACCACGCACGTATCTCTTGAG
SEQ ID NO: 3517	**332437**	AGTGCCCGTGCGTGTGCCTCCTGAC	TCACGGGCACGCACACGGAGGACTG
SEQ ID NO: 3518	**332500**	CTTCGGGTGCGTGCTGTACTACTTC	GAAGCCCACGCACGACATGATGAAG
SEQ ID NO: 3519	**332820**	AGACTTGTGTGCGTGTCGAAACCGA	TCTGAACACACGCACAGCTTTGGCT
SEQ ID NO: 3520	**332921**	ACTCTTTGTGCGTGTGTTTCGACGC	TGAGAAACACGCACACAAAGCTGCG
SEQ ID NO: 3521	**333248**	CGTGCCACAGCGTGTGCGGGACCTC	GCACGGTGTCGCACACGCCCTGGAG
SEQ ID NO: 3522	**333434**	NA	NA
SEQ ID NO: 3523	**333750**	CGCGTAGACGAGTGCGTGCGACGAC	GCGCATCTGCTCACGCACGCTGCTG
SEQ ID NO: 3524	**334168**	GTGTGCCTGTGCGTACTTTAAACCA	CACACGGACACGCATGAAATTTGGT

SEQ ID NO: 3525	**334183**	TCGTGCCACAGCGTGTGCGGGACCT	AGCACGGTGTCGCACACGCCCTGGA
SEQ ID NO: 3526	**334439**	TGCCGCACAGCGCAGCCAGGCGAGA	ACGGCGTGTCGCGTCGGTCCGCTCT
SEQ ID NO: 3527	**334907**	AAACTCATAGCGTAGTGTGTGGAGG	TTTGAGTATCGCATCACACACCTCC
SEQ ID NO: 3528	**335675**	ACTGACCCAGCGACACCAGTTGTGA	TGACTGGGTCGCTGTGGTCAACACT
SEQ ID NO: 3529	**335926**	CGCCGCGCCGCACCCAGCCCTCGCC	GCGGCGCGGCGTGGGTCGGGAGCGG
SEQ ID NO: 3530	**336222**	NA	NA
SEQ ID NO: 3531	**336603**	ACATAAGCCGCACACCGAAGGTTCA	TGTATTCGGCGTGTGGCTTCCAAGT
SEQ ID NO: 3532	**336608**	TTGGACCGCGCCGAAAACCGTGTTT	AACCTGGCGCGGCTTTTGGCACAAA
SEQ ID NO: 3533	**336646**	GCACCCGCCGCCATGCGTACCTGCT	CGTGGGCGGCGGTACGCATGGACGA
SEQ ID NO: 3534	**336849**	TGAGTCCGTCCGCCTCAACCGGAAG	ACTCAGGCAGGCGGAGTTGGCCTTC
SEQ ID NO: 3535	**336921**	GACCCGCGCCGCCCGGCCGTCCGGT	CTGGGCGCGGCGGGCCGGCAGGCCA
SEQ ID NO: 3536	**336988**	GGCCGCGCCGCCGTTTCTGAGATAA	CCGGCGCGGCGGCAAAGACTCTATT
SEQ ID NO: 3537	**337318**	AGTCACCACCGCCAAGATCAGTAGT	TCAGTGGTGGCGGTTCTAGTCATCA
SEQ ID NO: 3538	**337323**	CCCACTCCGCCGACGAGAGTATAAA	GGGTGAGGCGGCTGCTCTCATATTT
SEQ ID NO: 3539	**337533**	GGGCCGCCGCCAATAGTTTAGTGTC	CCCGGCGGCGGTTATCAAATCACAG
SEQ ID NO: 3540	**337546**	CCCGCCCGCCGCATGGCGCGCCTCC	GGGCGGGCGGCGTACCGCGCGGAGG
SEQ ID NO: 3541	**337592**	CCCGCCGCGCCCGGCCATCGCGTGG	GGGCGGCGCGGGCCGGTAGCGCACC
SEQ ID NO: 3542	**338224**	ATGCGCGCCGCCTACCAAAGGTGAA	TACGCGCGGCGGATGGTTTCCACTT
SEQ ID NO: 3543	**338271**	AAGGACACCGCCACACCGATGGAGT	TTCCTGTGGCGGTGTGGCTACCTCA
SEQ ID NO: 3544	**338343**	CACGCCGCCGCAGGCAATGCGAGGT	GTGCGGCGGCGTCCGTTACGCTCCA
SEQ ID NO: 3545	**338518**	GCGCCAGCGCGCCCGCTGCGGCCGC	CGCGGTCGCGCGGGCGACGCCGGCG

SEQ ID NO: 3546	**338633**	ATCTTCGCCGCCGTCCAGACGAGCG	TAGAAGCGGCGGCAGGTCTGCTCGC
SEQ ID NO: 3547	**338700**	TGCTTAGGCGCCACCGACAGACGCG	ACGAATCCGCGGTGGCTGTCTGCGC
SEQ ID NO: 3548	**338834**	AGTACGATGGCGCCGTGCGTGTACC	TCATGCTACCGCGGCACGCACATGG
SEQ ID NO: 3549	**339099**	ACCACGGACCGCAAGACACTTGTAG	TGGTGCCTGGCGTTCTGTGAACATC
SEQ ID NO: 3550	**339162**	AAGTGTGTGCGCATACCTCTGAACT	TTCACACACGCGTATGGAGACTTGA
SEQ ID NO: 3551	**339410**	CTCCTCAGTCGCACCACATCTTTTG	GAGGAGTCAGCGTGGTGTAGAAAAC
SEQ ID NO: 3552	**340150**	TTCCGCGCCGCAGTCCACCGCCGAC	AAGGCGCGGCGTCAGGTGGCGGCTG
SEQ ID NO: 3553	**340596**	CGTCCCTCTCGCCTATTTCGTGTTT	GCAGGGAGAGCGGATAAAGCACAAA
SEQ ID NO: 3554	**340760**	CGCGCGGCCGCACGCCGGCCGGGCG	GCGCGCCGGCGTGCGGCCGGCCCGC
SEQ ID NO: 3555	**340790**	AAGTCCCGTCGCCTTAAGGCCGAGG	TTCAGGGCAGCGGAATTCCGGCTCC
SEQ ID NO: 3556	**341995**	CGTGTCCACTCGCACACCTAGGGTA	GCACAGGTGAGCGTGTGGATCCCAT
SEQ ID NO: 3557	**342366**	GTGGACCGCCGCTATCATCTACCTA	CACCTGGCGGCGATAGTAGATGGAT
SEQ ID NO: 3558	**342506**	CGCCGGATCGCAACGACGGACGAAA	GCGGCCTAGCGTTGCTGCCTGCTTT
SEQ ID NO: 3559	**342544**	CCGAGACTTCGCACACACCGGTGTA	GGCTCTGAAGCGTGTGTGGCCACAT
SEQ ID NO: 3560	**342999**	CTCTCGGTCCGCTTCAGGAACAGTC	GAGAGCCAGGCGAAGTCCTTGTCAG
SEQ ID NO: 3561	**343168**	AGGTCCGCCGCTCTCACCAAGAGGT	TCCAGGCGGCGAGAGTGGTTCTCCA
SEQ ID NO: 3562	**344125**	ACCACTGCCGCTACTTGCCATGTAA	TGGTGACGGCGATGAACGGTACATT
SEQ ID NO: 3563	**344809**	CGAGTGTAGCACGCCGGCACGGGAT	GCTCACATCGTGCGGCCGTGCCCTA
SEQ ID NO: 3564	**345571**	TTGCCACCGCGACTACAATTTCTAG	AACGGTGGCGCTGATGTTAAAGATC
SEQ ID NO: 3565	**346381**	GCATCCACACGCACTGTAACACGAG	CGTAGGTGTGCGTGACATTGTGCTC
SEQ ID NO: 3566	**346547**	AAAGAGACACGCCATGCCGACTAGC	TTTCTCTGTGCGGTACGGCTGATCG

SEQ ID NO: 3567	**346902**	CACCGCCGACGCACCAGTTCTACGA	GTGGCGGCTGCGTGGTCAAGATGCT
SEQ ID NO: 3568	**346924**	TATACCCACACGCTCACATACATAT	ATATGGGTGTGCGAGTGTATGTATA
SEQ ID NO: 3569	**346925**	CTTCAACACGCACCACACTAAAGGT	GAAGTTGTGCGTGGTGTGATTTCCA
SEQ ID NO: 3570	**347057**	TCTGTCACCGTCGCTTTCGCCGAGG	AGACAGTGGCAGCGAAAGCGGCTCC
SEQ ID NO: 3571	**347167**	ACACACACACGTCGCTCATGGAGGA	TGTGTGTGTGCAGCGAGTACCTCCT
SEQ ID NO: 3572	**347675**	GGTAGTCTCTACACGCACGGGTTAA	CCATCAGAGATGTGCGTGCCCAATT
SEQ ID NO: 3573	**347810**	CAGGGCACGCACACACAGTCCGAGA	GTCCCGTGCGTGTGTGTCAGGCTCT
SEQ ID NO: 3574	**347921**	TTTGTCACCGCGCACAGTCTTCAGG	AAACAGTGGCGCGTGTCAGAAGTCC
SEQ ID NO: 3575	**348036**	ACCGACCTCACGCAAAAGTGGTCCT	TGGCTGGAGTGCGTTTTCACCAGGA
SEQ ID NO: 3576	**348125**	GTAATCGACACGACGCCGAACCGAC	CATTAGCTGTGCTGCGGCTTGGCTG
SEQ ID NO: 3577	**348435**	GACGCCGACGACACGCACGGTGACT	CTGCGGCTGCTGTGCGTGCCACTGA
SEQ ID NO: 3578	**348436**	GTGGGCGCACGCACAGGAACTCCGC	CACCCGCGTGCGTGTCCTTGAGGCG
SEQ ID NO: 3579	**349035**	TGTGCCGCCGCGACTTTATGGAGTA	ACACGGCGGCGCTGAAATACCTCAT
SEQ ID NO: 3580	**349672**	TACCCCGTCGCGCGCCACTCGACTC	ATGGGGCAGCGCGCGGTGAGCTGAG
SEQ ID NO: 3581	**350129**	GCCGCCGCCGCGGAAAGGTTATACC	CGGCGGCGGCGCCTTTCCAATATGG
SEQ ID NO: 3582	**350148**	TATTCACCACGCGTCCTCGCAGGAG	ATAAGTGGTGCGCAGGAGCGTCCTC
SEQ ID NO: 3583	**351251**	TCTAAAAGCAAGTAAAACCAAGAGT	AGATTTTCGTTCATTTTGGTTCTCA
SEQ ID NO: 3584	**351641**	GTCCGACTGTCACGCGTGCAACATC	CAGGCTGACAGTGCGCACGTTGTAG
SEQ ID NO: 3585	**353308**	NA	NA
SEQ ID NO: 3586	**353548**	GATCGACACACACGCGAACGACACA	CTAGCTGTGTGTGCGCTTGCTGTGT
SEQ ID NO: 3587	**354108**	CAGGAAAAATCCAACCCAGAGACGT	GTCCTTTTTAGGTTGGGTCTCTGCA

SEQ ID NO: 3588	**356107**	ACACCTCGAAAATCCTGCAAGACTT	TGTGGAGCTTTTAGGACGTTCTGAA
SEQ ID NO: 3589	**358771**	CTCTCCAAAAGACAGGCCGACGTTT	GAGAGGTTTTCTGTCCGGCTGCAAA
SEQ ID NO: 3590	**359283**	TTCCGACGTCAAATGAGACCGTTAC	AAGGCTGCAGTTTACTCTGGCAATG
SEQ ID NO: 3591	**359552**	GTAAGTGCCAAAACCAACCTCGCTA	CATTCACGGTTTTGGTTGGAGCGAT
SEQ ID NO: 3592	**361285**	AGCGCAACAAAACACACTCGAGCAC	TCGCGTTGTTTTGTGTGAGCTCGTG
SEQ ID NO: 3593	**363135**	GTCAAGTCACAAAACTAGACTGCGT	CAGTTCAGTGTTTTGATCTGACGCA
SEQ ID NO: 3594	**364054**	ACCGCCGCAAAGGGGCCGCCGCGAT	TGGCGGCGTTTCCCCGGCGGCGCTA
SEQ ID NO: 3595	**364422**	ACGTCACCCAAAGAACAAAAGTAAC	TGCAGTGGGTTTCTTGTTTTCATTG
SEQ ID NO: 3596	**364868**	TTACGGCTACAAAGTCCAAAGACTC	AATGCCGATGTTTCAGGTTTCTGAG
SEQ ID NO: 3597	**371315**	GTTCAGGGAAAACCGACCACCGTCC	CAAGTCCCTTTTGGCTGGTGGCAGG
SEQ ID NO: 3598	**372245**	GTTGAACTGAAAAGAACGAGACTCC	CAACTTGACTTTTCTTGCTCTGAGG
SEQ ID NO: 3599	**372869**	CTGTGTGTGAAATGTCATGGCTTCT	GACACACACTTTACAGTACCGAAGA
SEQ ID NO: 3600	**373495**	CCGATAAGAAAAGGTGTGTGGTTAC	GGCTATTCTTTTCCACACACCAATG
SEQ ID NO: 3601	**375449**	ACCTCCGTGAAAGACAGGGTCCTTC	TGGAGGCACTTTCTGTCCCAGGAAG
SEQ ID NO: 3602	**375738**	GAAAGGGAAAGTATACGATACACTT	CTTTCCCTTTCATATGCTATGTGAA
SEQ ID NO: 3603	**376103**	GTCGCCGTCCGAAAACATCCAAAAC	CAGCGGCAGGCTTTTGTAGGTTTTG
SEQ ID NO: 3604	**376963**	CCAGCCGAAAGAAAGGTACGTTACA	GGTCGGCTTTCTTTCCATGCAATGT
SEQ ID NO: 3605	**378308**	CGGTATCGACGAAAGGCCTCTGAGT	GCCATAGCTGCTTTCCGGAGACTCA
SEQ ID NO: 3606	**378874**	AAAAAGAAACCGTCTAGCAAGGTGT	TTTTTCTTTGGCAGATCGTTCCACA
SEQ ID NO: 3607	**380337**	ACGCCGCCGAAACTCACGCTCCGGT	TGCGGCGGCTTTGAGTGCGAGGCCA
SEQ ID NO: 3608	**380970**	ACCACACTCGAAACGGGAGGTCGTC	TGGTGTGAGCTTTGCCCTCCAGCAG

SEQ ID NO: 3609	**382627**	GTGTGTGTCTTAAAAACATCAGCAT	CACACACAGAATTTTTGTAGTCGTA
SEQ ID NO: 3610	**386844**	GTCGTGTCCCTAAACCGGTTCAGTT	CAGCACAGGGATTTGGCCAAGTCAA
SEQ ID NO: 3611	**387224**	TGTGTGTGTATAAACATTCGTCGAC	ACACACACATATTTGTAAGCAGCTG
SEQ ID NO: 3612	**395825**	ACATCCCAATCATCCTGACGAGAAC	TGTAGGGTTAGTAGGACTGCTCTTG
SEQ ID NO: 3613	**399360**	CACACACACAATCTCGACAATCGTA	GTGTGTGTGTTAGAGCTGTTAGCAT
SEQ ID NO: 3614	**400571**	CCTTAGGAATTGTGTCGTGTTCAAC	GGAATCCTTAACACAGCACAAGTTG
SEQ ID NO: 3615	**401221**	AAAGAAGAATGTCCGTCTCCGGACC	TTTCTTCTTACAGGCAGAGGCCTGG
SEQ ID NO: 3616	**403178**	AGACGACAACGAATGGGAACCGAGG	TCTGCTGTTGCTTACCCTTGGCTCC
SEQ ID NO: 3617	**404882**	GGAAGAACGAATCCATGACCGACGT	CCTTCTTGCTTAGGTACTGGCTGCA
SEQ ID NO: 3618	**408531**	CCTTCAGAATAGTTGTTGTGGGGCG	GGAAGTCTTATCAACAACACCCCGC
SEQ ID NO: 3619	**409823**	CGACACCGACTAATTATAGGTGGGT	GCTGTGGCTGATTAATATCCACCCA
SEQ ID NO: 3620	**411446**	CTTACCGTCTAATGTGTGTGAGATC	GAATGGCAGATTACACACACTCTAG
SEQ ID NO: 3621	**411808**	CTGAGTCCATTCAACGTTCCTAATT	GACTCAGGTAAGTTGCAAGGATTAA
SEQ ID NO: 3622	**413511**	TGGTGGTGTAATCGAATCTATACCA	ACCACCACATTAGCTTAGATATGGT
SEQ ID NO: 3623	**414748**	GCCAACAAAGGGACGCCACCGACAC	CGGTTGTTTCCCTGCGGTGGCTGTG
SEQ ID NO: 3624	**415678**	CCAGACAAAGGGTGTGTGACCGTAA	GGTCTGTTTCCCACACACTGGCATT
SEQ ID NO: 3625	**416383**	ACCGCCAAAGGTACAAGTCCAAAGA	TGGCGGTTTCCATGTTCAGGTTTCT
SEQ ID NO: 3626	**417708**	TACCGCCGCAAGGTTTTCCGTGGGC	ATGGCGGCGTTCCAAAAGGCACCCG
SEQ ID NO: 3627	**418509**	ACATCCCAAGGAACCGTCAGACGCG	TGTAGGGTTCCTTGGCAGTCTGCGC
SEQ ID NO: 3628	**419032**	CGTAGACTTCAAGGTTGTGTTGTGG	GCATCTGAAGTTCCAACACAACACC
SEQ ID NO: 3629	**419419**	AGTCTTGTCAAGGAGTGTGTGTTTC	TCAGAACAGTTCCTCACACACAAAG

SEQ ID NO: 3630	**420232**	GGTGTCCAAAGCGTACATTTACCGT	CCACAGGTTTCGCATGTAAATGGCA
SEQ ID NO: 3631	**420646**	NA	NA
SEQ ID NO: 3632	**421452**	CCGGTGACAAGCGTGTGTGGACCAC	GGCCACTGTTCGCACACACCTGGTG
SEQ ID NO: 3633	**421752**	ATACGAACGTAAAGCGAAAGAACTC	TATGCTTGCATTTCGCTTTCTTGAG
SEQ ID NO: 3634	**423348**	AGCCACCGAAGGTCCCGAACGGAAG	TCGGTGGCTTCCAGGGCTTGCCTTC
SEQ ID NO: 3635	**423899**	AGAAGGAGAAGGTGACTACAAAGAA	TCTTCCTCTTCCACTGATGTTTCTT
SEQ ID NO: 3636	**424361**	TCGGACCCAAGACCAAAGTGAACTC	AGCCTGGGTTCTGGTTTCACTTGAG
SEQ ID NO: 3637	**424362**	GTCGGACCTCGAAGGAGAAATAAGT	CAGCCTGGAGCTTCCTCTTTATTCA
SEQ ID NO: 3638	**426637**	NA	NA
SEQ ID NO: 3639	**430604**	ATCACACACAAGACGGTTTCGTTCA	TAGTGTGTGTTCTGCCAAAGCAAGT
SEQ ID NO: 3640	**432915**	GTTGTTCGCAAGACCGACGACGAGC	CAACAAGCGTTCTGGCTGCTGCTCG
SEQ ID NO: 3641	**440993**	GTGTCTGTGTGTAAGGTATGTGTCT	CACAGACACACATTCCATACACAGA
SEQ ID NO: 3642	**441077**	CTCGGTAAGTAAGGTCGTCCATCTC	GAGCCATTCATTCCAGCAGGTAGAG
SEQ ID NO: 3643	**442017**	CGTCGCTAATAAGAAACGTGCGTGT	GCAGCGATTATTCTTTGCACGCACA
SEQ ID NO: 3644	**442954**	GTCAAAAAAGTGCTTACGGGTTAAG	CAGTTTTTTCACGAATGCCCAATTC
SEQ ID NO: 3645	**443451**	ACAGAACGAAAGTTGATCTGTAGTC	TGTCTTGCTTTCAACTAGACATCAG
SEQ ID NO: 3646	**443484**	ATATTCCTAAGACCAGTAGGGGTTT	TATAAGGATTCTGGTCATCCCCAAA
SEQ ID NO: 3647	**444093**	ACTTGTGTCAAGTGGTGGTGGTATT	TGAACACAGTTCACCACCACCATAA
SEQ ID NO: 3648	**445464**	GACTTCCGCAAGTGTGGTGTCGTGC	CTGAAGGCGTTCACACCACAGCACG
SEQ ID NO: 3649	**447050**	GTAAGTGTCACAAGTGTGTGGAGTC	CATTCACAGTGTTCACACACCTCAG
SEQ ID NO: 3650	**449409**	CCGTGTCGGAAGTGTGAAAGCTACC	GGCACAGCCTTCACACTTTCGATGG

SEQ ID NO: 3651	**449456**	GTATGAATCGAAGTTCCCTACGACC	CATACTTAGCTTCAAGGGATGCTGG
SEQ ID NO: 3652	**452007**	AGAAAGAAAGTAGACGAGAAGCACG	TCTTTCTTTCATCTGCTCTTCGTGC
SEQ ID NO: 3653	**453647**	GAACACCGACGAAGTAGCAGTACCT	CTTGTGGCTGCTTCATCGTCATGGA
SEQ ID NO: 3654	**453750**	GTAGTGTGGTGAAGTAACGAGAACC	CATCACACCACTTCATTGCTCTTGG
SEQ ID NO: 3655	**456526**	ACCTCAGTCCAAAAGTGTGTGTCGT	TGGAGTCAGGTTTTCACACACAGCA
SEQ ID NO: 3656	**457369**	GTCCGACGCGCCAAAGGGCTTTGGT	CAGGCTGCGCGGTTTCCCGAAACCA
SEQ ID NO: 3657	**458019**	CAAATCCAAAGCGTGTGTGAGCCGG	GTTTAGGTTTCGCACACACTCGGCC
SEQ ID NO: 3658	**459685**	GTCTCTCCGACCAAACGCCTGTTAA	CAGAGAGGCTGGTTTGCGGACAATT
SEQ ID NO: 3659	**459996**	NA	NA
SEQ ID NO: 3660	**461557**	ACCTCGACCCAAGAACTTTGTGACG	TGGAGCTGGGTTCTTGAAACACTGC
SEQ ID NO: 3661	**463601**	CTTAATACCAACCTGAAGCACGAAC	GAATTATGGTTGGACTTCGTGCTTG
SEQ ID NO: 3662	**464716**	ACGTCCGTCTCCAACATATTGTCCC	TGCAGGCAGAGGTTGTATAACAGGG
SEQ ID NO: 3663	**466048**	AGTGATCGGCAAGTTTTTCCCTGTG	TCACTAGCCGTTCAAAAAGGGACAC
SEQ ID NO: 3664	**466653**	CTCGAGGGCAAACCTGCGGTCCCTT	GAGCTCCCGTTTGGACGCCAGGGAA
SEQ ID NO: 3665	**468517**	CGTCCGTCACGCAACGCAGATATTT	GCAGGCAGTGCGTTGCGTCTATAAA
SEQ ID NO: 3666	**469466**	CGCCGTCACGCAAACAACTAAAGTA	GCGGCAGTGCGTTTGTTGATTTCAT
SEQ ID NO: 3667	**470165**	CGCGACCTTCAACAGACACGGGTGT	GCGCTGGAAGTTGTCTGTGCCCACA
SEQ ID NO: 3668	**472736**	ACGCACGCACTCAAGGGGTCTCATA	TGCGTGCGTGAGTTCCCCAGAGTAT
SEQ ID NO: 3669	**476311**	CTCCGCCTCAACACGAGTCAGTGGG	GAGGCGGAGTTGTGCTCAGTCACCC
SEQ ID NO: 3670	**478507**	TGAAACGTGTCAAACCGGGTCGCCC	ACTTTGCACAGTTTGGCCCAGCGGG
SEQ ID NO: 3671	**478543**	CCGGGGTCAATATGTGTGTGTGTCA	GGCCCCAGTTATACACACACACAGT

SEQ ID NO: 3672	**479256**	TCACTTGTGTCAAGTGGTGGTGGTA	AGTGAACACAGTTCACCACCACCAT
SEQ ID NO: 3673	**481386**	CGTCATCCCATGGTGTGTGTCGTAC	GCAGTAGGGTACCACACACAGCATG
SEQ ID NO: 3674	**481596**	GTTCGCCGCCATGAACTAAAGCATG	CAAGCGGCGGTACTTGATTTCGTAC
SEQ ID NO: 3675	**482003**	GTCCGACGCACCATTGACGTTTGTA	CAGGCTGCGTGGTAACTGCAAACAT
SEQ ID NO: 3676	**484128**	AGACCGTTCCATCCCAAGCAAGACT	TCTGGCAAGGTAGGGTTCGTTCTGA
SEQ ID NO: 3677	**486429**	ACACCGACCCATCGAGACTAAGAGG	TGTGGCTGGGTAGCTCTGATTCTCC
SEQ ID NO: 3678	**486476**	GCACGCCGCCATCGACAAGAAGAGG	CGTGCGGCGGTAGCTGTTCTTCTCC
SEQ ID NO: 3679	**487291**	CGAGCCGACGCATCAGGAGCATCAT	GCTCGGCTGCGTAGTCCTCGTAGTA
SEQ ID NO: 3680	**487854**	ACAGTCACTCCACACACCATACATA	TGTCAGTGAGGTGTGTGGTATGTAT
SEQ ID NO: 3681	**488428**	TAACTTTGCATGTGTGTGGGTCCCA	ATTGAAACGTACACACACCCAGGGT
SEQ ID NO: 3682	**489627**	TCCGTCCTCCATACACTTCTTTTTG	AGGCAGGAGGTATGTGAAGAAAAAC
SEQ ID NO: 3683	**489915**	CTCAACTCGCATCTCATGGCCTGGT	GAGTTGAGCGTAGAGTACCGGACCA
SEQ ID NO: 3684	**490139**	CCATGAGCATAACGCGGAGCTACCG	GGTACTCGTATTGCGCCTCGATGGC
SEQ ID NO: 3685	**491487**	GGTCCTCGTCCATACAAAGTTTCGG	CCAGGAGCAGGTATGTTTCAAAGCC
SEQ ID NO: 3686	**491535**	AGACATTGAACTTTGCCTCGCAGGA	TCTGTAACTTGAAACGGAGCGTCCT
SEQ ID NO: 3687	**492028**	CGGTGTGTGCATAGTGTGTATACAG	GCCACACACGTATCACACATATGTC
SEQ ID NO: 3688	**492160**	AGTGTGTGCGCATACCTCTGAACTA	TCACACACGCGTATGGAGACTTGAT
SEQ ID NO: 3689	**492634**	CGGCCATCATCAGCACCCACCGGTG	GCCGGTAGTAGTCGTGGGTGGCCAC
SEQ ID NO: 3690	**494062**	GGAGTGTGTATCATTCCGTGTGTGA	CCTCACACATAGTAAGGCACACACT
SEQ ID NO: 3691	**494486**	NA	NA
SEQ ID NO: 3692	**496832**	ATCCGTCCTCATCTCCCTATGGAAA	TAGGCAGGAGTAGAGGGATACCTTT

SEQ ID NO: 3693	**503031**	TGGGTCAACAAGTGTGTGTGAGTAA	ACCCAGTTGTTCACACACACTCATT
SEQ ID NO: 3694	**504161**	CTTAGGACACAAATACAGACGTTGG	GAATCCTGTGTTTATGTCTGCAACC
SEQ ID NO: 3695	**504227**	GTCGCCCACACAACACGTCAAAGGT	CAGCGGGTGTGTTGTGCAGTTTCCA
SEQ ID NO: 3696	**507881**	ACAAAGGACAAGAGGGACGAACCTC	TGTTTCCTGTTCTCCCTGCTTGGAG
SEQ ID NO: 3697	**508064**	TGACTACCGACGACAATCCTCACGC	ACTGATGGCTGCTGTTAGGAGTGCG
SEQ ID NO: 3698	**508165**	TGCTACGCCGACAACCATGCTGTGT	ACGATGCGGCTGTTGGTACGACACA
SEQ ID NO: 3699	**509121**	TATTCGGTCTACAAAGTGGGGTGAG	ATAAGCCAGATGTTTCACCCCACTC
SEQ ID NO: 3700	**509704**	AAGTGCACGACAACCTACGACAGGG	TTCACGTGCTGTTGGATGCTGTCCC
SEQ ID NO: 3701	**516136**	CTGTGTAAGACATGTGTGTCTGTGT	GACACATTCTGTACACACAGACACA
SEQ ID NO: 3702	**518588**	NA	NA
SEQ ID NO: 3703	**518648**	TTTAAACACATAGTAGGAACATGCC	AAATTTGTGTATCATCCTTGTACGG
SEQ ID NO: 3704	**518751**	TACATCACGTACACATACAACACAC	ATGTAGTGCATGTGTATGTTGTGTG
SEQ ID NO: 3705	**518901**	GGCTCCGACGACATAGTCCTGCTGT	CCGAGGCTGCTGTATCAGGACGACA
SEQ ID NO: 3706	**520039**	ACACTCACACACACCCGTACGGACA	TGTGAGTGTGTGTGGGCATGCCTGT
SEQ ID NO: 3707	**521808**	CGAACTCCCAGGTGTGTGTGTTAAC	GCTTGAGGGTCCACACACACAATTG
SEQ ID NO: 3708	**522280**	CCGTCCTCCAGGCTAAGCGTCCACG	GGCAGGAGGTCCGATTCGCAGGTGC
SEQ ID NO: 3709	**522814**	TACCTCGACTCCAGGGGACTGTCGG	ATGGAGCTGAGGTCCCCTGACAGCC
SEQ ID NO: 3710	**523059**	ACCGACACGACCAGGCTTGGAGGTC	TGGCTGTGCTGGTCCGAACCTCCAG
SEQ ID NO: 3711	**523074**	CGTCACACGTCCAGGCTCTACTCCG	GCAGTGTGCAGGTCCGAGATGAGGC
SEQ ID NO: 3712	**523154**	GTCCACGACCCAGGTCCTCAGAGGA	CAGGTGCTGGGTCCAGGAGTCTCCT
SEQ ID NO: 3713	**523496**	TCGCTCGCGCCAGCCCTTGGAGGTG	AGCGAGCGCGGTCGGGAACCTCCAC

SEQ ID NO: 3714	**523786**	AAGGAACCAGCGTGTGTGGAACTGT	TTCCTTGGTCGCACACACCTTGACA
SEQ ID NO: 3715	**524774**	CGGCGCACCAGCACACAGACAGGGA	GCCGCGTGGTCGTGTGTCTGTCCCT
SEQ ID NO: 3716	**524815**	ACCACACTAGCAGGCGTAGGCATAC	TGGTGTGATCGTCCGCATCCGTATG
SEQ ID NO: 3717	**525338**	AATCGCACGCAGGTCAGGGACCGTG	TTAGCGTGCGTCCAGTCCCTGGCAC
SEQ ID NO: 3718	**526251**	GTACCCGCCGCAGGAGAAACCGCTA	CATGGGCGGCGTCCTCTTTGGCGAT
SEQ ID NO: 3719	**527068**	AGACTCCGCCAGATCTCGTTAGATG	TCTGAGGCGGTCTAGAGCAATCTAC
SEQ ID NO: 3720	**527237**	GTGTGTGTGCCAGAAATTTGACTAT	CACACACACGGTCTTTAAACTGATA
SEQ ID NO: 3721	**528041**	TTACCTCTCCAGAGCGACCGGAAGA	AATGGAGAGGTCTCGCTGGCCTTCT
SEQ ID NO: 3722	**528464**	GGACACAGCCAGACACACAGTCGAA	CCTGTGTCGGTCTGTGTGTCAGCTT
SEQ ID NO: 3723	**530393**	CCAGAGGCAGATGGTGGTGAAACTT	GGTCTCCGTCTACCACCACTTTGAA
SEQ ID NO: 3724	**535010**	NA	NA
SEQ ID NO: 3725	**535143**	CTTTTGTCAGGTCGTGCGTGACTTG	GAAAACAGTCCAGCACGCACTGAAC
SEQ ID NO: 3726	**535193**	TAGCGTGTGTGTCAGGGTTCTGCAC	ATCGCACACACAGTCCCAAGACGTG
SEQ ID NO: 3727	**536993**	CTCACGTACACTCAGAGACTCGTTC	GAGTGCATGTGAGTCTCTGAGCAAG
SEQ ID NO: 3728	**537069**	ACACACACGTACTCAGAGTCAGTCA	TGTGTGTGCATGAGTCTCAGTCAGT
SEQ ID NO: 3729	**539326**	TGTACACACACCAGTTCCGAACGTG	ACATGTGTGTGGTCAAGGCTTGCAC
SEQ ID NO: 3730	**540368**	CCGTCCACCAGTCGGTTGTTCGACG	GGCAGGTGGTCAGCCAACAAGCTGC
SEQ ID NO: 3731	**540665**	AAGTGTGTGCAGTGTCTTTCAGGAA	TTCACACACGTCACAGAAAGTCCTT
SEQ ID NO: 3732	**541775**	CCGGGTGCAGTGTCAGTGTGACCAC	GGCCCACGTCACAGTCACACTGGTG
SEQ ID NO: 3733	**546126**	GTAGCAACCACAGGCCGTCCAGATT	CATCGTTGGTGTCCGGCAGGTCTAA
SEQ ID NO: 3734	**546259**	AGCCACGCACAGCTCAAGGAAGAGG	TCGGTGCGTGTCGAGTTCCTTCTCC

SEQ ID NO: 3735	**546820**	ACCACGCACACAGCGCAGGGCGGAG	TGGTGCGTGTGTCGCGTCCCGCCTC
SEQ ID NO: 3736	**546946**	GTCAATCCACAGGTCCCATCCGTAG	CAGTTAGGTGTCCAGGGTAGGCATC
SEQ ID NO: 3737	**547473**	GGTGACCACACAGCATCCCGACTTG	CCACTGGTGTGTCGTAGGGCTGAAC
SEQ ID NO: 3738	**547633**	GGACACTCCACAGCGACACAGTTGG	CCTGTGAGGTGTCGCTGTGTCAACC
SEQ ID NO: 3739	**547723**	AGTCGTCTCGCACAGGCACAACTTC	TCAGCAGAGCGTGTCCGTGTTGAAG
SEQ ID NO: 3740	**549316**	TGCGACCACGACAGGTACCCGACGG	ACGCTGGTGCTGTCCATGGGCTGCC
SEQ ID NO: 3741	**549328**	ACAAACACACAGACCACACATTTAC	TGTTTGTGTGTCTGGTGTGTAAATG
SEQ ID NO: 3742	**550076**	GAACAGGCACAGAGACACACGTCCG	CTTGTCCGTGTCTCTGTGTGCAGGC
SEQ ID NO: 3743	**550410**	ATCGGGAACAGACGTGACCACCTCT	TAGCCCTTGTCTGCACTGGTGGAGA
SEQ ID NO: 3744	**550739**	GGACCTCCACAGACCGCCCATACAT	CCTGGAGGTGTCTGGCGGGTATGTA
SEQ ID NO: 3745	**551683**	AGGTCCGACGACAGAACGCTCAGGT	TCCAGGCTGCTGTCTTGCGAGTCCA
SEQ ID NO: 3746	**552855**	AGAAGGTCTACAGGCACGACACCGA	TCTTCCAGATGTCCGTGCTGTGGCT
SEQ ID NO: 3747	**554859**	ACTACCACCACAGTTGTAGACGAGA	TGATGGTGGTGTCAACATCTGCTCT
SEQ ID NO: 3748	**555171**	CTAGTCGGCGACAGTGTGCGTGTCA	GATCAGCCGCTGTCACACGCACAGT
SEQ ID NO: 3749	**556707**	CGTACACACACGACAGTCTTTCTCT	GCATGTGTGTGCTGTCAGAAAGAGA
SEQ ID NO: 3750	**556900**	TTCTACACACACAGTAGAAACGTAT	AAGATGTGTGTGTCATCTTTGCATA
SEQ ID NO: 3751	**559108**	GTGGTCCAAACGCATTACCCGACTC	CACCAGGTTTGCGTAATGGGCTGAG
SEQ ID NO: 3752	**559932**	ATAAGGAAACCTCGTGGTGAACCCA	TATTCCTTTGGAGCACCACTTGGGT
SEQ ID NO: 3753	**559960**	ATAAGTCCAACCGACCATCAGTGTC	TATTCAGGTTGGCTGGTAGTCACAG
SEQ ID NO: 3754	**560354**	ACTAAACCAACCAACCCTGAATCAG	TGATTTGGTTGGTTGGGACTTAGTC
SEQ ID NO: 3755	**560382**	AGGCGGCAACCCACAGACTCAAGCG	TCCGCCGTTGGGTGTCTGAGTTCGC

SEQ ID NO: 3756	**560557**	GGGCCGAAACCGACACATCGGAGCC	CCCGGCTTTGGCTGTGTAGCCTCGG
SEQ ID NO: 3757	**560624**	GGTTTCCAACCTAACTTCCTGACGT	CCAAAGGTTGGATTGAAGGACTGCA
SEQ ID NO: 3758	**561052**	ATATCGACGCAACCACCGACGGTCT	TATAGCTGCGTTGGTGGCTGCCAGA
SEQ ID NO: 3759	**561131**	GCACACACGTCAACCGCCCGAACAG	CGTGTGTGCAGTTGGCGGGCTTGTC
SEQ ID NO: 3760	**561993**	GATCGGACGACAACCCGACGCAAAG	CTAGCCTGCTGTTGGGCTGCGTTTC
SEQ ID NO: 3761	**564332**	ACCCGCAGAACCTGCCTTAGGTGGA	TGGGCGTCTTGGACGGAATCCACCT
SEQ ID NO: 3762	**567909**	ACCCTAAAACAGACAGTTCGAGTAG	TGGGATTTTGTCTGTCAAGCTCATC
SEQ ID NO: 3763	**570228**	CGGTAACAAACACACGACCACGGTT	GCCATTGTTTGTGTGCTGGTGCCAA
SEQ ID NO: 3764	**571567**	TGCAACGCGAACAACGACTCCATCG	ACGTTGCGCTTGTTGCTGAGGTAGC
SEQ ID NO: 3765	**571777**	TGTTGGGAACATGCGACCGCCGACC	ACAACCCTTGTACGCTGGCGGCTGG
SEQ ID NO: 3766	**572130**	CACCGACACGAACAGGACCTGGTAG	GTGGCTGTGCTTGTCCTGGACCATC
SEQ ID NO: 3767	**572910**	GGACCCACGAACAACTACATTAGAA	CCTGGGTGCTTGTTGATGTAATCTT
SEQ ID NO: 3768	**573396**	GGACGCACCGAACATTTTAGACTAC	CCTGCGTGGCTTGTAAAATCTGATG
SEQ ID NO: 3769	**573795**	TACCGTCCTATAACCCTTTACAAAA	ATGGCAGGATATTGGGAAATGTTTT
SEQ ID NO: 3770	**578602**	CTAAAGAAACTTGTGTTTGTGGCAC	GATTTCTTTGAACACAAACACCGTG
SEQ ID NO: 3771	**578616**	CAAAAAACTTAACAGGTCACGGACA	GTTTTTTGAATTGTCCAGTGCCTGT
SEQ ID NO: 3772	**584574**	GTACGTCCCACGAACTCTCTAAGGG	CATGCAGGGTGCTTGAGAGATTCCC
SEQ ID NO: 3773	**585859**	CGACGAACGACAACTACCGAGGCGC	GCTGCTTGCTGTTGATGGCTCCGCG
SEQ ID NO: 3774	**586188**	AGACACTTGTAACTGCCGCCGACGA	TCTGTGAACATTGACGGCGGCTGCT
SEQ ID NO: 3775	**587987**	GACTATCGCAAACGGCAACCACGGG	CTGATAGCGTTTGCCGTTGGTGCCC
SEQ ID NO: 3776	**590773**	CTCGACTCGACAACGAAACTTTCGG	GAGCTGAGCTGTTGCTTTGAAAGCC

SEQ ID NO: 3777	**592117**	GGGACGAACAACGACTACCGCAGCT	CCCTGCTTGTTGCTGATGGCGTCGA
SEQ ID NO: 3778	**595234**	CCACGTTCTAACGTGGGTGTTGACC	GGTGCAAGATTGCACCCACAACTGG
SEQ ID NO: 3779	**596017**	TGCCGGTCCACCGTGCCCTCGGCGC	ACGGCCAGGTGGCACGGGAGCCGCG
SEQ ID NO: 3780	**596437**	GGTTCCGCCGATCCCGCCGCTTCAG	CCAAGGCGGCTAGGGCGGCGAAGTC
SEQ ID NO: 3781	**596736**	GTATTATAGGAACGTCTACTCTGTG	CATAATATCCTTGCAGATGAGACAC
SEQ ID NO: 3782	**596897**	AGAGGCCACACACCTCCGCTTCAGA	TCTCCGGTGTGTGGAGGCGAAGTCT
SEQ ID NO: 3783	**597435**	TTCTCACTACCACCATCGCATAAAG	AAGAGTGATGGTGGTAGCGTATTTC
SEQ ID NO: 3784	**597446**	TAAAAACCACCACCGCTGTTAGGGT	ATTTTTGGTGGTGGCGACAATCCCA
SEQ ID NO: 3785	**597485**	AGGCACGCCACCACTATCGGGAAGA	TCCGTGCGGTGGTGATAGCCCTTCT
SEQ ID NO: 3786	**597581**	ACAACACCCACCAACAGGGAGCTGT	TGTTGTGGGTGGTTGTCCCTCGACA
SEQ ID NO: 3787	**597629**	GTCCTCACCCACCACCGACCCAGGT	CAGGAGTGGGTGGTGGCTGGGTCCA
SEQ ID NO: 3788	**597910**	AGTCTACCGCCACCCTACCAGAGGT	TCAGATGGCGGTGGGATGGTCTCCA
SEQ ID NO: 3789	**598168**	GGAACACGTCCACCATCAGCCGGAG	CCTTGTGCAGGTGGTAGTCGGCCTC
SEQ ID NO: 3790	**598509**	GACCTCGTCACCACCTTCGGTGGGG	CTGGAGCAGTGGTGGAAGCCACCCC
SEQ ID NO: 3791	**598699**	TATCAACGACCACCATGTAATATCT	ATAGTTGCTGGTGGTACATTATAGA
SEQ ID NO: 3792	**598746**	AGTCGCCGTCCACCTAGACACGCCC	TCAGCGGCAGGTGGATCTGTGCGGG
SEQ ID NO: 3793	**598814**	GAGGACACGGCACCCACCACAGGGG	CTCCTGTGCCGTGGGTGGTGTCCCC
SEQ ID NO: 3794	**598846**	TTTCCGTCGCACCACGGGTTAATTT	AAAGGCAGCGTGGTGCCCAATTAAA
SEQ ID NO: 3795	**598880**	AAGTGTTCCACCACAGCGACTCCGG	TTCACAAGGTGGTGTCGCTGAGGCC
SEQ ID NO: 3796	**598936**	TTGGGTCCACCACTACGCACACGAG	AACCCAGGTGGTGATGCGTGTGCTC
SEQ ID NO: 3797	**598984**	CACGTCCGCCACCTCATGTTGTAGA	GTGCAGGCGGTGGAGTACAACATCT

SEQ ID NO: 3798	**599034**	GTCTCCGTCCCACCTAAGATAGTGG	CAGAGGCAGGGTGGATTCTATCACC
SEQ ID NO: 3799	**599063**	AGAGTCCGTCCACCTGTTAATGTCA	TCTCAGGCAGGTGGACAATTACAGT
SEQ ID NO: 3800	**599494**	ATCAACGACCACCATGTAATATCTT	TAGTTGCTGGTGGTACATTATAGAA
SEQ ID NO: 3801	**599725**	GTCCTAGTCACCACCGGTCCAGTGG	CAGGATCAGTGGTGGCCAGGTCACC
SEQ ID NO: 3802	**599902**	GTGGATGGCACCTACCTACGTACGC	CACCTACCGTGGATGGATGCATGCG
SEQ ID NO: 3803	**599957**	GTATCTCCGCCACCGAAGTAGTTCC	CATAGAGGCGGTGGCTTCATCAAGG
SEQ ID NO: 3804	**600067**	TCCCGTAGCGCACCCACACTCCGAG	AGGGCATCGCGTGGGTGTGAGGCTC
SEQ ID NO: 3805	**600132**	AGTCCGGGCACCTTAACTAGTGGTC	TCAGGCCCGTGGAATTGATCACCAG
SEQ ID NO: 3806	**600168**	ACGACGCTCTGCACCACCACCTGAA	TGCTGCGAGACGTGGTGGTGGACTT
SEQ ID NO: 3807	**600337**	AAGTACTAGCCACCGACGATTCGAG	TTCATGATCGGTGGCTGCTAAGCTC
SEQ ID NO: 3808	**600897**	ACACAACCGCACCTTTAGAAGACTG	TGTGTTGGCGTGGAAATCTTCTGAC
SEQ ID NO: 3809	**600935**	CCACGCCGCACTCAGGGTTAAGTTT	GGTGCGGCGTGAGTCCCAATTCAAA
SEQ ID NO: 3810	**601447**	ACTACCGGACGCACCGAGGACAACA	TGATGGCCTGCGTGGCTCCTGTTGT
SEQ ID NO: 3811	**601787**	GGTCTTCCCACACCGAAACCGTAGT	CCAGAAGGGTGTGGCTTTGGCATCA
SEQ ID NO: 3812	**602104**	AGTCCCGCCACAATAGCGCGTCAAT	TCAGGGCGGTGTTATCGCGCAGTTA
SEQ ID NO: 3813	**602492**	AGCACCACCACAAGACGTCGCGTTA	TCGTGGTGGTGTTCTGCAGCGCAAT
SEQ ID NO: 3814	**602760**	AGGACGCACCACACTCCCAAAGTTG	TCCTGCGTGGTGTGAGGGTTTCAAC
SEQ ID NO: 3815	**603151**	GTAGACACCGTCCACAAATAGGCGG	CATCTGTGGCAGGTGTTTATCCGCC
SEQ ID NO: 3816	**603321**	ACTCCGACGACCACAATAGAAGACC	TGAGGCTGCTGGTGTTATCTTCTGG
SEQ ID NO: 3817	**603413**	GGGCACACGCACACACAGGAACCGG	CCCGTGTGCGTGTGTGTCCTTGGCC
SEQ ID NO: 3818	**603467**	GTCTTCCGCCACAGAGTTTTCCCTA	CAGAAGGCGGTGTCTCAAAAGGGAT

SEQ ID NO: 3819	**603487**	GTACCCGACCCACACTATCAGGATG	CATGGGCTGGGTGTGATAGTCCTAC
SEQ ID NO: 3820	**604786**	TATATATACCCACACGCTCACACAT	ATATATATGGGTGTGCGAGTGTGTA
SEQ ID NO: 3821	**604997**	GTTCACACGCCACACGGGAAACTGG	CAAGTGTGCGGTGTGCCCTTTGACC
SEQ ID NO: 3822	**605001**	TAAGACCGTCCACACAACGTCTTTA	ATTCTGGCAGGTGTGTTGCAGAAAT
SEQ ID NO: 3823	**605012**	GTGTAAGACACCACACACGTCATGT	CACATTCTGTGGTGTGTGCAGTACA
SEQ ID NO: 3824	**605126**	GTAACTGAGACCACACACTTCCGGG	CATTGACTCTGGTGTGTGAAGGCCC
SEQ ID NO: 3825	**605173**	TCCCACCCACACGTTTTACAAGTGG	AGGGTGGGTGTGCAAAATGTTCACC
SEQ ID NO: 3826	**605252**	GAGGATATGCGACCTGCGCCCAGCC	CTCCTATACGCTGGACGCGGGTCGG
SEQ ID NO: 3827	**605306**	GTACGCGTCACACCACACCTGTCCC	CATGCGCAGTGTGGTGTGGACAGGG
SEQ ID NO: 3828	**605634**	ACTACGCAAGCACACTGAGGGTCCA	TGATGCGTTCGTGTGACTCCCAGGT
SEQ ID NO: 3829	**605765**	GTCCCGACCGCACAACTACAGGTGT	CAGGGCTGGCGTGTTGATGTCCACA
SEQ ID NO: 3830	**605769**	CGGACGCACGCACACCACTTGAGGA	GCCTGCGTGCGTGTGGTGAACTCCT
SEQ ID NO: 3831	**605931**	AGTCATGTCGCACACGTACACCTGG	TCAGTACAGCGTGTGCATGTGGACC
SEQ ID NO: 3832	**606472**	GTTTAGCCGCACACGCATGAGACTT	CAAATCGGCGTGTGCGTACTCTGAA
SEQ ID NO: 3833	**606616**	GTGGTTACTACGCACACCTGTCCCG	CACCAATGATGCGTGTGGACAGGGC
SEQ ID NO: 3834	**607152**	GCGCACCGACTCACCACAAATGTAA	CGCGTGGCTGAGTGGTGTTTACATT
SEQ ID NO: 3835	**607489**	GTCACGGAGATCACCAACGACCCTT	CAGTGCCTCTAGTGGTTGCTGGGAA
SEQ ID NO: 3836	**607980**	GTTAAAATCACCTAGTCTACGAGTC	CAATTTTAGTGGATCAGATGCTCAG
SEQ ID NO: 3837	**608297**	CTTAGGAGTCACCACACGACACAAC	GAATCCTCAGTGGTGTGCTGTGTTG
SEQ ID NO: 3838	**608696**	ACTAGAGGGTCACCACACACGCACG	TGATCTCCCAGTGGTGTGTGCGTGC
SEQ ID NO: 3839	**609259**	CAGACACTGTCACCTCTTCTAAGGG	GTCTGTGACAGTGGAGAAGATTCCC

SEQ ID NO: 3840	**610146**	AGCCTCACTCACACACGCGCCGGCG	TCGGAGTGAGTGTGTGCGCGGCCGC
SEQ ID NO: 3841	**610961**	ACACGTGCACACACCCATTTGTAAC	TGTGCACGTGTGTGGGTAAACATTG
SEQ ID NO: 3842	**612354**	ACTCACCACCACTGTAGATCCAGGT	TGAGTGGTGGTGACATCTAGGTCCA
SEQ ID NO: 3843	**614506**	CTACAGAGGCACTCAGACACGGAGG	GATGTCTCCGTGAGTCTGTGCCTCC
SEQ ID NO: 3844	**615033**	ACGTCACACGGCACTCATCCAATGT	TGCAGTGTGCCGTGAGTAGGTTACA
SEQ ID NO: 3845	**615955**	AGTGTGTACGTGCACTTTGAGGTCA	TCACACATGCACGTGAAACTCCAGT
SEQ ID NO: 3846	**616008**	ACACACACACCACTAATCGTACGGA	TGTGTGTGTGGTGATTAGCATGCCT
SEQ ID NO: 3847	**616577**	CAGACGACGTCGCACTCCGGTGTGA	GTCTGCTGCAGCGTGAGGCCACACT
SEQ ID NO: 3848	**618074**	AGAAACATCACTCCGCCGTCCATGG	TCTTTGTAGTGAGGCGGCAGGTACC
SEQ ID NO: 3849	**619661**	GTGGCTGAACACCATCCGCCGCAGG	CACCGACTTGTGGTAGGCGGCGTCC
SEQ ID NO: 3850	**619934**	GGTTTCCGTCACTCCATAAAGGACT	CCAAAGGCAGTGAGGTATTTCCTGA
SEQ ID NO: 3851	**620007**	ACGTTCCGCACACACATGATGATAG	TGCAAGGCGTGTGTGTACTACTATC
SEQ ID NO: 3852	**620020**	TAAAATCACACACACGATGAGTTCG	ATTTTAGTGTGTGTGCTACTCAAGC
SEQ ID NO: 3853	**620411**	GTCGCCCACACACCGCAAAGCCGAG	CAGCGGGTGTGTGGCGTTTCGGCTC
SEQ ID NO: 3854	**620769**	NA	NA
SEQ ID NO: 3855	**620857**	GGACCCGTCACACCACTCCGAGGTA	CCTGGGCAGTGTGGTGAGGCTCCAT
SEQ ID NO: 3856	**620869**	GTAAGTCACCACACCCACCAATCCG	CATTCAGTGGTGTGGGTGGTTAGGC
SEQ ID NO: 3857	**621134**	ACACGTGGACACACCCTAGGAGTCA	TGTGCACCTGTGTGGGATCCTCAGT
SEQ ID NO: 3858	**621199**	ACACGCGGACACACCCACGTGTAAA	TGTGCGCCTGTGTGGGTGCACATTT
SEQ ID NO: 3859	**621200**	ACCCGACACACACCGCGGGAAAGGA	TGGGCTGTGTGTGGCGCCCTTTCCT
SEQ ID NO: 3860	**621547**	CACAGAGACACACCAAAACAGACAC	GTGTCTCTGTGTGGTTTTGTCTGTG

SEQ ID NO: 3861	**621548**	ACACACAGACACACCAAAACAGACA	TGTGTGTCTGTGTGGTTTTGTCTGT
SEQ ID NO: 3862	**621602**	CTCCCACACACACAATCACACTCAC	GAGGGTGTGTGTGTTAGTGTGAGTG
SEQ ID NO: 3863	**622315**	TGCGTCCGCACACCGAGAGCAAGTA	ACGCAGGCGTGTGGCTCTCGTTCAT
SEQ ID NO: 3864	**622329**	GAACCTGAGACACCACACACGAACT	CTTGGACTCTGTGGTGTGTGCTTGA
SEQ ID NO: 3865	**622334**	AGACACTCCACACCGTGCCGCAGAC	TCTGTGAGGTGTGGCACGGCGTCTG
SEQ ID NO: 3866	**622535**	GTCGTCACGGGACACCAACTCGTGT	CAGCAGTGCCCTGTGGTTGAGCACA
SEQ ID NO: 3867	**622706**	AGGAGGGACACACCACGTGCTACCT	TCCTCCCTGTGTGGTGCACGATGGA
SEQ ID NO: 3868	**622779**	GGTGACACCGACACCAAGGTGCCAC	CCACTGTGGCTGTGGTTCCACGGTG
SEQ ID NO: 3869	**622820**	GAGGCCACGACACACGCTTGGTCTC	CTCCGGTGCTGTGTGCGAACCAGAG
SEQ ID NO: 3870	**623133**	GAAGAAGCACACACACAGAACCGGA	CTTCTTCGTGTGTGTGTCTTGGCCT
SEQ ID NO: 3871	**623455**	TTCCGCACACACATGATGATAGTAG	AAGGCGTGTGTGTACTACTATCATC
SEQ ID NO: 3872	**623467**	GTAATCGTAGGACACCGACGCCAGT	CATTAGCATCCTGTGGCTGCGGTCA
SEQ ID NO: 3873	**623490**	AGACGTACGCCGACACCCAGTGTAA	TCTGCATGCGGCTGTGGGTCACATT
SEQ ID NO: 3874	**623744**	ACACACAAACACAGGCACACGTACA	TGTGTGTTTGTGTCCGTGTGCATGT
SEQ ID NO: 3875	**623863**	TGACCAACACACACCGTACCCAGAA	ACTGGTTGTGTGTGGCATGGGTCTT
SEQ ID NO: 3876	**623935**	ACATACTCACACACAGACTTACTCA	TGTATGAGTGTGTGTCTGAATGAGT
SEQ ID NO: 3877	**623961**	TCAGGGCACACACGGGGAATGTCAC	AGTCCCGTGTGTGCCCCTTACAGTG
SEQ ID NO: 3878	**624054**	CACTCACCACACACGGGTACCAGGG	GTGAGTGGTGTGTGCCCATGGTCCC
SEQ ID NO: 3879	**624253**	CCTGTACCACACACCAAGAAAATCG	GGACATGGTGTGTGGTTCTTTTAGC
SEQ ID NO: 3880	**624433**	GTGCGACCGAACACACACCCTATGG	CACGCTGGCTTGTGTGTGGGATACC
SEQ ID NO: 3881	**624563**	GTGCTTACACACACACGGTTCCGGG	CACGAATGTGTGTGTGCCAAGGCCC

SEQ ID NO: 3882	**624724**	ACTACGACTGGACACACCGGATTCC	TGATGCTGACCTGTGTGGCCTAAGG
SEQ ID NO: 3883	**624790**	GGTCACACGCTACACACAGAAGTTT	CCAGTGTGCGATGTGTGTCTTCAAA
SEQ ID NO: 3884	**624841**	GCCCACACTACACAGACCAGTAATG	CGGGTGTGATGTGTCTGGTCATTAC
SEQ ID NO: 3885	**625000**	ACGTACGAACGACACACACACACGA	TGCATGCTTGCTGTGTGTGTGTGCT
SEQ ID NO: 3886	**625054**	TCAAATCACACACACGACGGTCTCG	AGTTTAGTGTGTGTGCTGCCAGAGC
SEQ ID NO: 3887	**625117**	CCTTACACACACACGATATCAAAGT	GGAATGTGTGTGTGCTATAGTTTCA
SEQ ID NO: 3888	**625229**	AAATCACACACACGACGGTCTCGTT	TTTAGTGTGTGTGCTGCCAGAGCAA
SEQ ID NO: 3889	**625382**	CAAATCACACACACGACGGTCTCGT	GTTTAGTGTGTGTGCTGCCAGAGCA
SEQ ID NO: 3890	**625389**	TCACGTTTCACACACGTTATCCTAG	AGTGCAAAGTGTGTGCAATAGGATC
SEQ ID NO: 3891	**625475**	GTAAACACGGACACACCGGGAGTTT	CATTTGTGCCTGTGTGGCCCTCAAA
SEQ ID NO: 3892	**625584**	GCGAACGACACACACACGATCGACA	CGCTTGCTGTGTGTGTGCTAGCTGT
SEQ ID NO: 3893	**625686**	ATAAGACGGACACACCCATCGTCGT	TATTCTGCCTGTGTGGGTAGCAGCA
SEQ ID NO: 3894	**625912**	CACACCTTACACCACACACTCTTAC	GTGTGGAATGTGGTGTGTGAGAATG
SEQ ID NO: 3895	**625950**	CACACACTTACACAGATACTTATAC	GTGTGTGAATGTGTCTATGAATATG
SEQ ID NO: 3896	**626103**	ATACAGGGTACACCAGGTCCGAATC	TATGTCCCATGTGGTCCAGGCTTAG
SEQ ID NO: 3897	**626235**	CTACACGCTGTACACCACGGGGCTG	GATGTGCGACATGTGGTGCCCCGAC
SEQ ID NO: 3898	**626526**	ACACCGCACGTACACAGTCTTGAGG	TGTGGCGTGCATGTGTCAGAACTCC
SEQ ID NO: 3899	**626668**	ACACACGATCGACACACACGTACGA	TGTGTGCTAGCTGTGTGTGCATGCT
SEQ ID NO: 3900	**627520**	GTTTACCACGTACACACGCGCTTGC	CAAATGGTGCATGTGTGCGCGAACG
SEQ ID NO: 3901	**628390**	TCTGCACACACACTCGGTCGGAACG	AGACGTGTGTGTGAGCCAGCCTTGC
SEQ ID NO: 3902	**628780**	CTTTCCACACTTGTGTGTGTCGGTC	GAAAGGTGTGAACACACACAGCCAG

SEQ ID NO: 3903	**628941**	AGTACCACACACACTTTGAGTTTAA	TCATGGTGTGTGTGAAACTCAAATT
SEQ ID NO: 3904	**628947**	CACAATCACACTCACATACACCCTC	GTGTTAGTGTGAGTGTATGTGGGAG
SEQ ID NO: 3905	**629178**	GTTGTGTGTGACACTGAGCCCTGAC	CAACACACACTGTGACTCGGGACTG
SEQ ID NO: 3906	**629323**	GGTGAAGACACACTCTACGGCCCGA	CCACTTCTGTGTGAGATGCCGGGCT
SEQ ID NO: 3907	**629851**	GTGGTGTGTGACACTCTAGGAACTC	CACCACACACTGTGAGATCCTTGAG
SEQ ID NO: 3908	**630213**	ACAGACGTCGGACACTCGTTAGTGG	TGTCTGCAGCCTGTGAGCAATCACC
SEQ ID NO: 3909	**630505**	CGAGTACACACGTACACTTTTGGGT	GCTCATGTGTGCATGTGAAAACCCA
SEQ ID NO: 3910	**630597**	GGATTCCGACACGACAGGTGATACT	CCTAAGGCTGTGCTGTCCACTATGA
SEQ ID NO: 3911	**630634**	GTCCACACTCACACTACAGTAAGAG	CAGGTGTGAGTGTGATGTCATTCTC
SEQ ID NO: 3912	**630635**	GTGCACACTCTACACTCACGGACAC	CACGTGTGAGATGTGAGTGCCTGTG
SEQ ID NO: 3913	**630984**	CGCCGCACCACGACTGGCGGATGGT	GCGGCGTGGTGCTGACCGCCTACCA
SEQ ID NO: 3914	**631372**	ACGAACAGGCACGCAGACAGACGGA	TGCTTGTCCGTGCGTCTGTCTGCCT
SEQ ID NO: 3915	**631731**	AACTCACACGTACACTATACACTTG	TTGAGTGTGCATGTGATATGTGAAC
SEQ ID NO: 3916	**631812**	CAGACACGAGCACGATGATTATTTC	GTCTGTGCTCGTGCTACTAATAAAG
SEQ ID NO: 3917	**631955**	NA	NA
SEQ ID NO: 3918	**632365**	CTGGACACCACGGACACCACCGAGT	GACCTGTGGTGCCTGTGGTGGCTCA
SEQ ID NO: 3919	**632444**	NA	NA
SEQ ID NO: 3920	**632744**	ATCTCGCCCACGACCACGCACGTCG	TAGAGCGGGTGCTGGTGCGTGCAGC
SEQ ID NO: 3921	**633259**	GTAACGACACGCCACGAACTCACGG	CATTGCTGTGCGGTGCTTGAGTGCC
SEQ ID NO: 3922	**633484**	ACTCAACGACCACGAGTGTGGCCAC	TGAGTTGCTGGTGCTCACACCGGTG
SEQ ID NO: 3923	**633594**	NA	NA

SEQ ID NO: 3924	**633734**	AGGGCGACCACGACCTCATGCGTGA	TCCCGCTGGTGCTGGAGTACGCACT
SEQ ID NO: 3925	**633820**	GTGGAGTGGTCACGGTAGACAGTTT	CACCTCACCAGTGCCATCTGTCAAA
SEQ ID NO: 3926	**633861**	GTGCAGGCACACGTACATGACCAGT	CACGTCCGTGTGCATGTACTGGTCA
SEQ ID NO: 3927	**634192**	GTGAGTCCGACGCACGACGTACCTA	CACTCAGGCTGCGTGCTGCATGGAT
SEQ ID NO: 3928	**634546**	GTGCAATCACACGTCCGTACAACGG	CACGTTAGTGTGCAGGCATGTTGCC
SEQ ID NO: 3929	**634623**	GGACACACCCACGTGTAAACACACA	CCTGTGTGGGTGCACATTTGTGTGT
SEQ ID NO: 3930	**635040**	ACGCACTCACGTCACGGAAACGCGA	TGCGTGAGTGCAGTGCCTTTGCGCT
SEQ ID NO: 3931	**635125**	AGAGGTCCTACACGCTCTCGGACGG	TCTCCAGGATGTGCGAGAGCCTGCC
SEQ ID NO: 3932	**635647**	TAAATGCTCACGACACGACCGCCGG	ATTTACGAGTGCTGTGCTGGCGGCC
SEQ ID NO: 3933	**636193**	TACACACGGACACACGCAGGCGCGC	ATGTGTGCCTGTGTGCGTCCGCGCG
SEQ ID NO: 3934	**636475**	GAACACGCACACACGGAAGATCCCG	CTTGTGCGTGTGTGCCTTCTAGGGC
SEQ ID NO: 3935	**636777**	NA	NA
SEQ ID NO: 3936	**636960**	ACGCAGAACACACGACCAAAGGGCA	TGCGTCTTGTGTGCTGGTTTCCCGT
SEQ ID NO: 3937	**637575**	ACGCACGCGCACACGGCAAGAGATC	TGCGTGCGCGTGTGCCGTTCTCTAG
SEQ ID NO: 3938	**637936**	ACACTTCCACACGTCTCATGGTTAT	TGTGAAGGTGTGCAGAGTACCAATA
SEQ ID NO: 3939	**638175**	GTACACACGGACACACGCAGGCGCG	CATGTGTGCCTGTGTGCGTCCGCGC
SEQ ID NO: 3940	**638238**	GCCCGACGCACACGGTCTTCTCGTA	CGGGCTGCGTGTGCCAGAAGAGCAT
SEQ ID NO: 3941	**638444**	CTGAGCCTCACGTAGTCCGACGATG	GACTCGGAGTGCATCAGGCTGCTAC
SEQ ID NO: 3942	**638461**	CTCCTACACACACGTCTTAAGTGAG	GAGGATGTGTGTGCAGAATTCACTC
SEQ ID NO: 3943	**638882**	TACGGACACTTACACGCACACGTAC	ATGCCTGTGAATGTGCGTGTGCATG
SEQ ID NO: 3944	**639122**	AATCACACACACGACGGTCTCGTTC	TTAGTGTGTGTGCTGCCAGAGCAAG

SEQ ID NO: 3945	**639127**	GTACACTCCCACACGTGCGTACATA	CATGTGAGGGTGTGCACGCATGTAT
SEQ ID NO: 3946	**639183**	GTTCGACCACGACACGTCCAAAGGA	CAAGCTGGTGCTGTGCAGGTTTCCT
SEQ ID NO: 3947	**639230**	GTCTCTGTACGCACACGACGGAAAG	CAGAGACATGCGTGTGCTGCCTTTC
SEQ ID NO: 3948	**639349**	ACATTCACTACACGAACACGACGGT	TGTAAGTGATGTGCTTGTGCTGCCA
SEQ ID NO: 3949	**639400**	TTGTGTTGACACGACACCAGGTACG	AACACAACTGTGCTGTGGTCCATGC
SEQ ID NO: 3950	**639460**	AAATCACGTACACGACGACTTTGCT	TTTAGTGCATGTGCTGCTGAAACGA
SEQ ID NO: 3951	**639506**	CCGTCGGAACACGTCACGTCAGAGT	GGCAGCCTTGTGCAGTGCAGTCTCA
SEQ ID NO: 3952	**639782**	GTCTACACCCGACACGAGTAAGAAG	CAGATGTGGGCTGTGCTCATTCTTC
SEQ ID NO: 3953	**640066**	ACACACCCGTACACGGACGAGGGTG	TGTGTGGGCATGTGCCTGCTCCCAC
SEQ ID NO: 3954	**640262**	ACTGATGGGATGCAAGAGGATGTTT	TGACTACCCTACGTTCTCCTACAAA
SEQ ID NO: 3955	**640294**	CGTTAGTCACGACACGTAATTCATA	GCAATCAGTGCTGTGCATTAAGTAT
SEQ ID NO: 3956	**642746**	CGTGTGGTGGAAACGTGACAGACAT	GCACACCACCTTTGCACTGTCTGTA
SEQ ID NO: 3957	**646089**	CGGTGTGTGGAAGAGACCACATGTA	GCCACACACCTTCTCTGGTGTACAT
SEQ ID NO: 3958	**646228**	AGTACGCTTGGAAGATACGTAACAA	TCATGCGAACCTTCTATGCATTGTT
SEQ ID NO: 3959	**650131**	AAAGAACGGAACGACCATTCTAAAG	TTTCTTGCCTTGCTGGTAAGATTTC
SEQ ID NO: 3960	**651580**	ACCCGCAGGAACGACTGGAGCATCT	TGGGCGTCCTTGCTGACCTCGTAGA
SEQ ID NO: 3961	**652704**	CCAGCAGGAACGGAAACGATAGGTG	GGTCGTCCTTGCCTTTGCTATCCAC
SEQ ID NO: 3962	**653559**	ACGTCCGTCCGGAACAGTATAGAGG	TGCAGGCAGGCCTTGTCATATCTCC
SEQ ID NO: 3963	**656230**	NA	NA
SEQ ID NO: 3964	**658108**	CCCGCACTGAAGTGTGTGTCAGCCC	GGGCGTGACTTCACACACAGTCGGG
SEQ ID NO: 3965	**661519**	ACGACTGTGGTGAAAAGAGAGACCG	TGCTGACACCACTTTTCTCTCTGGC

SEQ ID NO: 3966	**661835**	CGGTGTGTGTGAAGTGACGCAAATA	GCCACACACACTTCACTGCGTTTAT
SEQ ID NO: 3967	**661972**	GTACTGTTTGTGAATTGTCTCATCA	CATGACAAACACTTAACAGAGTAGT
SEQ ID NO: 3968	**662026**	ATAGGGGTGAATTGTGTGCGTACTT	TATCCCCACTTAACACACGCATGAA
SEQ ID NO: 3969	**662644**	AGTGTCTGTCGTGAATAATTTAGTC	TCACAGACAGCACTTATTAAATCAG
SEQ ID NO: 3970	**662791**	TCGGTGGTGTGAACCAGTTGATAAA	AGCCACCACACTTGGTCAACTATTT
SEQ ID NO: 3971	**664336**	ACGTGGGTCGGATTTAAGTTTTAGA	TGCACCCAGCCTAAATTCAAAATCT
SEQ ID NO: 3972	**666008**	GTGTTGTGCGGATGTCTTGTCGTTT	CACAACACGCCTACAGAACAGCAAA
SEQ ID NO: 3973	**666576**	GCTACGTTGGGATCGCTAGTCACCC	CGATGCAACCCTAGCGATCAGTGGG
SEQ ID NO: 3974	**668691**	CTCCTACCGGATAGAGTGTGTACTT	GAGGATGGCCTATCTCACACATGAA
SEQ ID NO: 3975	**671921**	CGAGTGTCTTGATGTGTGCGTTCCA	GCTCACAGAACTACACACGCAAGGT
SEQ ID NO: 3976	**672337**	AGTAAGTGTGTGATTAGATGGGTAA	TCATTCACACACTAATCTACCCATT
SEQ ID NO: 3977	**672809**	CGTGGTGGTGATCCTTCTTCCGGTC	GCACCACCACTAGGAAGAAGGCCAG
SEQ ID NO: 3978	**673724**	ACCCGTGTGTGATATGGGGACTACC	TGGGCACACACTATACCCCTGATGG
SEQ ID NO: 3979	**673988**	ATGTGTGTGTGATGTCGTATGTTTT	TACACACACACTACAGCATACAAAA
SEQ ID NO: 3980	**674265**	GCTATTGCGTGATGAAAGTGTGGTC	CGATAACGCACTACTTTCACACCAG
SEQ ID NO: 3981	**674553**	TGACAAAGTGATGAGTCGTACCTTT	ACTGTTTCACTACTCAGCATGGAAA
SEQ ID NO: 3982	**676204**	CTACAGGAAGAAAAGCCGGTCGGTC	GATGTCCTTCTTTTCGGCCAGCCAG
SEQ ID NO: 3983	**682392**	NA	NA
SEQ ID NO: 3984	**685494**	CTGCGGGAGAAGTAGTATCCCCAGT	GACGCCCTCTTCATCATAGGGGTCA
SEQ ID NO: 3985	**687129**	NA	NA
SEQ ID NO: 3986	**689410**	ACACACACACGTAGAATTTTATCCC	TGTGTGTGTGCATCTTAAAATAGGG

SEQ ID NO: 3987	**695496**	NA	NA
SEQ ID NO: 3988	**696025**	GTATATACAGTAGAGATCTTGCTTC	CATATATGTCATCTCTAGAACGAAG
SEQ ID NO: 3989	**698625**	ATTACCCGTAGATGTCGTCCCGACG	TAATGGGCATCTACAGCAGGGCTGC
SEQ ID NO: 3990	**701211**	GTGGTCGTCTCGGAGGCCCTCCACT	CACCAGCAGAGCCTCCGGGAGGTGA
SEQ ID NO: 3991	**701722**	TTCTACGTCGGGAGCCAAAGGTACT	AAGATGCAGCCCTCGGTTTCCATGA
SEQ ID NO: 3992	**701830**	GAGGAGCCGGAGGAATACACACCGT	CTCCTCGGCCTCCTTATGTGTGGCA
SEQ ID NO: 3993	**702235**	ACACAGACACGGAGCTGAAAGACAC	TGTGTCTGTGCCTCGACTTTCTGTG
SEQ ID NO: 3994	**706345**	TGTGTGTACGAGGAGAGTTCTCAGT	ACACACATGCTCCTCTCAAGAGTCA
SEQ ID NO: 3995	**707776**	AGTGTGTGCTGAGGTTGCCCTAACA	TCACACACGACTCCAACGGGATTGT
SEQ ID NO: 3996	**708289**	AGCGGCGTGTGAGGTATCTTGAACT	TCGCCGCACACTCCATAGAACTTGA
SEQ ID NO: 3997	**710054**	CTGTGTGCGTGAGAATACCGGCCAC	GACACACGCACTCTTATGGCCGGTG
SEQ ID NO: 3998	**710741**	TGTACGCCGTTGAGCGTGTGAGTCC	ACATGCGGCAACTCGCACACTCAGG
SEQ ID NO: 3999	**711884**	AAGTTGGTGAGCTGTCGTCTTTCTC	TTCAACCACTCGACAGCAGAAAGAG
SEQ ID NO: 4000	**712194**	CAAGGACTATTCACGCACACCACTA	GTTCCTGATAAGTGCGTGTGGTGAT
SEQ ID NO: 4001	**712825**	CTTGGGGAGTGCGTGAGTCTAAACT	GAACCCCTCACGCACTCAGATTTGA
SEQ ID NO: 4002	**713444**	TCGATGCGTGTGAGTTGATTAGACC	AGCTACGCACACTCAACTAATCTGG
SEQ ID NO: 4003	**714218**	NA	NA
SEQ ID NO: 4004	**714939**	ACCTCGACGGGAGTGTGTTGATCAC	TGGAGCTGCCCTCACACAACTAGTG
SEQ ID NO: 4005	**715150**	CACCGAGTGGAGTGTGTGCGCACAC	GTGGCTCACCTCACACACGCGTGTG
SEQ ID NO: 4006	**715291**	CACACACACGGAGTTCCTGGACCAG	GTGTGTGTGCCTCAAGGACCTGGTC
SEQ ID NO: 4007	**718809**	ACATGAGTGTGAGTCTGACCAACAG	TGTACTCACACTCAGACTGGTTGTC

SEQ ID NO: 4008	**719560**	AGGTGTGGTGAGTATGTCGATCTAT	TCCACACCACTCATACAGCTAGATA
SEQ ID NO: 4009	**719743**	CACCTCGAGTGAGTGTGTCCTATTG	GTGGAGCTCACTCACACAGGATAAC
SEQ ID NO: 4010	**720058**	GGAGGACGAGGACGGGGAGGACGGG	CCTCCTGCTCCTGCCCCTCCTGCCC
SEQ ID NO: 4011	**720646**	CTTAGTAGGTGAGTGTGTCTCCGAC	GAATCATCCACTCACACAGAGGCTG
SEQ ID NO: 4012	**720664**	CCTTTGAGAGGATCACCGGGACTTT	GGAAACTCTCCTAGTGGCCCTGAAA
SEQ ID NO: 4013	**724091**	AGGTCGACGTCCGACGACAACGCGA	TCCAGCTGCAGGCTGCTGTTGCGCT
SEQ ID NO: 4014	**731440**	TGTCGTTACCAGAGTGTGTGCACCC	ACAGCAATGGTCTCACACACGTGGG
SEQ ID NO: 4015	**732258**	TCTGTGTGGAGAGTACTTGTGTAAC	AGACACACCTCTCATGAACACATTG
SEQ ID NO: 4016	**733546**	NA	NA
SEQ ID NO: 4017	**734530**	CGTCACCGCCGAAAGAGAGGAAGAA	GCAGTGGCGGCTTTCTCTCCTTCTT
SEQ ID NO: 4018	**734688**	AGTCCCGACCGAAACTTCCTTAACG	TCAGGGCTGGCTTTGAAGGAATTGC
SEQ ID NO: 4019	**734910**	CTCGGACCCGAAAGAGCTTGTAGTC	GAGCCTGGGCTTTCTCGAACATCAG
SEQ ID NO: 4020	**735466**	AAGAACACCGAAACCGATTTATCTC	TTCTTGTGGCTTTGGCTAAATAGAG
SEQ ID NO: 4021	**735632**	CGCGGAACCGAACGGCCCGGAATGC	GCGCCTTGGCTTGCCGGGCCTTACG
SEQ ID NO: 4022	**735999**	CGACGGCCCGAACGATGACGAAGAC	GCTGCCGGGCTTGCTACTGCTTCTG
SEQ ID NO: 4023	**738121**	GAGCCACACCGAACATATAGTCAAC	CTCGGTGTGGCTTGTATATCAGTTG
SEQ ID NO: 4024	**739112**	CGTCTCGTCATCGAAACTAATGCAT	GCAGAGCAGTAGCTTTGATTACGTA
SEQ ID NO: 4025	**742789**	AGACACGACCCGATCCCGTTAGAGC	TCTGTGCTGGGCTAGGGCAATCTCG
SEQ ID NO: 4026	**743081**	NA	NA
SEQ ID NO: 4027	**743742**	GCAGACGACGCCGATCACTCAAGTT	CGTCTGCTGCGGCTAGTGAGTTCAA
SEQ ID NO: 4028	**744543**	GCACTGCCCGATAAACCGTTTCTGT	CGTGACGGGCTATTTGGCAAAGACA

SEQ ID NO: 4029	**748571**	AACGACCCACGAAGACACTCGAGTC	TTGCTGGGTGCTTCTGTGAGCTCAG
SEQ ID NO: 4030	**749226**	GTCTCCGACCACGAATCGAAGAGTG	CAGAGGCTGGTGCTTAGCTTCTCAC
SEQ ID NO: 4031	**749432**	GTTTCACACACGAATGTCTACAGGG	CAAAGTGTGTGCTTACAGATGTCCC
SEQ ID NO: 4032	**751097**	CAACGACACACGATCGACACACATG	GTTGCTGTGTGCTAGCTGTGTGTAC
SEQ ID NO: 4033	**751338**	GTGCGACCCGACGAACCTTATGTAC	CACGCTGGGCTGCTTGGAATACATG
SEQ ID NO: 4034	**751341**	CGACTTCCGACGAACACCAAGGTGT	GCTGAAGGCTGCTTGTGGTTCCACA
SEQ ID NO: 4035	**751423**	NA	NA
SEQ ID NO: 4036	**752881**	ATCACACACACGATGAGTTCGTTCG	TAGTGTGTGTGCTACTCAAGCAAGC
SEQ ID NO: 4037	**752949**	AGTATTGTTCGAGTGTGTACGCGCA	TCATAACAAGCTCACACATGCGCGT
SEQ ID NO: 4038	**753186**	TCACCGCCGACGATCGAGAGCCTGA	AGTGGCGGCTGCTAGCTCTCGGACT
SEQ ID NO: 4039	**753346**	ACGAACGAACACGATATCGAAACCC	TGCTTGCTTGTGCTATAGCTTTGGG
SEQ ID NO: 4040	**753444**	ACTCTACGACACGACGATGGGAGCC	TGAGATGCTGTGCTGCTACCCTCGG
SEQ ID NO: 4041	**753650**	CCCGTACACACGATAGACCCATGTC	GGGCATGTGTGCTATCTGGGTACAG
SEQ ID NO: 4042	**755122**	ACTCTGTGTCCGAGGGTGTTACCTC	TGAGACACAGGCTCCCACAATGGAG
SEQ ID NO: 4043	**755167**	CCTCGTCGCCGAGATAGGAAACGGG	GGAGCAGCGGCTCTATCCTTTGCCC
SEQ ID NO: 4044	**755169**	GCCCGACCCGAGACGATTAATAGAT	CGGGCTGGGCTCTGCTAATTATCTA
SEQ ID NO: 4045	**756509**	ATGTGGGTCGAGGAGAGTAGCCACC	TACACCCAGCTCCTCTCATCGGTGG
SEQ ID NO: 4046	**757889**	CGACCTCACTCGAGCTGTGATTGGG	GCTGGAGTGAGCTCGACACTAACCC
SEQ ID NO: 4047	**757941**	ACGTCCGCCGCGAGATAGCCCCAGT	TGCAGGCGGCGCTCTATCGGGGTCA
SEQ ID NO: 4048	**758333**	GTCCGACCACTCGAGAATTTCTCTG	CAGGCTGGTGAGCTCTTAAAGAGAC
SEQ ID NO: 4049	**760305**	TTGTCCGCCGAGTCTTCCCAAGCGT	AACAGGCGGCTCAGAAGGGTTCGCA

SEQ ID NO: 4050	**760416**	CAGTGTCCCGAGTGTTCTGTACTTC	GTCACAGGGCTCACAAGACATGAAG
SEQ ID NO: 4051	**760492**	CCCAGGCGAGTGTGTATACGTCTTG	GGGTCCGCTCACACATATGCAGAAC
SEQ ID NO: 4052	**761039**	ATGTTCTGCGAGTTGTCCCTTCCGA	TACAAGACGCTCAACAGGGAAGGCT
SEQ ID NO: 4053	**761083**	CTCCGCCGCGAGTCGCCATGAAGAG	GAGGCGGCGCTCAGCGGTACTTCTC
SEQ ID NO: 4054	**761178**	CTCGCGTCGTGCGAGTGGTGACACA	GAGCGCAGCACGCTCACCACTGTGT
SEQ ID NO: 4055	**762166**	ATAAGGCACGAGTGTGGGCTACATA	TATTCCGTGCTCACACCCGATGTAT
SEQ ID NO: 4056	**763782**	ACTCACACACACGAGACAGATCACA	TGAGTGTGTGTGCTCTGTCTAGTGT
SEQ ID NO: 4057	**764006**	CCACTCCACGAGTCCATGTATGAGG	GGTGAGGTGCTCAGGTACATACTCC
SEQ ID NO: 4058	**764046**	GTACCCGACCACGAGTAGACTCAAG	CATGGGCTGGTGCTCATCTGAGTTC
SEQ ID NO: 4059	**764179**	GGTCACCGACACGAGATCAGTAAGT	CCAGTGGCTGTGCTCTAGTCATTCA
SEQ ID NO: 4060	**764376**	GTACGCCCAGACGAGTGTGTATACG	CATGCGGGTCTGCTCACACATATGC
SEQ ID NO: 4061	**764664**	GTCCTCCTCGACGAGAGCGGCAAGA	CAGGAGGAGCTGCTCTCGCCGTTCT
SEQ ID NO: 4062	**764939**	CCGTTCGTGTACGAGTGTCGTGGAC	GGCAAGCACATGCTCACAGCACCTG
SEQ ID NO: 4063	**765672**	AATGTTGGACCCGTAGTTCTGGAAG	TTACAACCTGGGCATCAAGACCTTC
SEQ ID NO: 4064	**766186**	AACCAGGGACCTCACAGGGCTCGAC	TTGGTCCCTGGAGTGTCCCGAGCTG
SEQ ID NO: 4065	**766480**	GGCCCGGGACCTCCAGATAGACGAC	CCGGGCCCTGGAGGTCTATCTGCTG
SEQ ID NO: 4066	**768177**	CCCAGGGACCGTCAATGGCTCGCGG	GGGTCCCTGGCAGTTACCGAGCGCC
SEQ ID NO: 4067	**768772**	GTGGACACCGGACCACACCCTAGGT	CACCTGTGGCCTGGTGTGGGATCCA
SEQ ID NO: 4068	**768982**	NA	NA
SEQ ID NO: 4069	**769745**	GGTAAGAGACGGACCACGTCGAAAG	CCATTCTCTGCCTGGTGCAGCTTTC
SEQ ID NO: 4070	**771013**	GTATCGGACGGGACACCTTTCGACT	CATAGCCTGCCCTGTGGAAAGCTGA

SEQ ID NO: 4071	**771130**	CGGGCACGGACAGACACACCTTTTT	GCCCGTGCCTGTCTGTGTGGAAAAA
SEQ ID NO: 4072	**771968**	AGTCCGGTGGACACACCCACGTATG	TCAGGCCACCTGTGTGGGTGCATAC
SEQ ID NO: 4073	**772170**	TCTGACACAGGACACACCGGCACGT	AGACTGTGTCCTGTGTGGCCGTGCA
SEQ ID NO: 4074	**772301**	TTCCGACGTAGGACACACGGAGGTC	AAGGCTGCATCCTGTGTGCCTCCAG
SEQ ID NO: 4075	**772687**	GCGCGGACCGGACACACGACTCAAA	CGCGCCTGGCCTGTGTGCTGAGTTT
SEQ ID NO: 4076	**772764**	TGTCAAATGACCAGTCCACCGGGGT	ACAGTTTACTGGTCAGGTGGCCCCA
SEQ ID NO: 4077	**773452**	CATCACCGGACACGGATATCGGAGT	GTAGTGGCCTGTGCCTATAGCCTCA
SEQ ID NO: 4078	**775079**	GTCGCCATCTGACCTGTTTACCGTG	CAGCGGTAGACTGGACAAATGGCAC
SEQ ID NO: 4079	**776720**	GTCCTGGTGTGACACTCCTGGTGGT	CAGGACCACACTGTGAGGACCACCA
SEQ ID NO: 4080	**779655**	GGTCTCCCGGACTAGGGACGTCAAA	CCAGAGGGCCTGATCCCTGCAGTTT
SEQ ID NO: 4081	**780814**	GGAGACCCGGACTCATTTGGTACAC	CCTCTGGGCCTGAGTAAACCATGTG
SEQ ID NO: 4082	**782088**	ACGTCCGACCTGACTTATGAAACGA	TGCAGGCTGGACTGAATACTTTGCT
SEQ ID NO: 4083	**782344**	ATGGTGTGTGACTTTGTATGTTATG	TACCACACACTGAAACATACAATAC
SEQ ID NO: 4084	**783732**	GGAAGACACTGACTTCGTGTGTGTG	CCTTCTGTGACTGAAGCACACACAC
SEQ ID NO: 4085	**783810**	AAAGGTCTGACTCGTACGTGCGTGC	TTTCCAGACTGAGCATGCACGCACG
SEQ ID NO: 4086	**785016**	CGATAAGTTAGACCGGTTTTGCCAC	GCTATTCAATCTGGCCAAAACGGTG
SEQ ID NO: 4087	**785797**	GTGAACGAACAGACCGCACTGCCCA	CACTTGCTTGTCTGGCGTGACGGGT
SEQ ID NO: 4088	**786609**	ATCTACCACAGACCACGTTTCGTTT	TAGATGGTGTCTGGTGCAAAGCAAA
SEQ ID NO: 4089	**787430**	CTTCGGGAGACCTAGACACTTGGGC	GAAGCCCTCTGGATCTGTGAACCCG
SEQ ID NO: 4090	**787651**	ATTCTACCGAGACCGGGACACACCT	TAAGATGGCTCTGGCCCTGTGTGGA
SEQ ID NO: 4091	**789583**	CACACGCACAGACACGCGAGGGCGG	GTGTGCGTGTCTGTGCGCTCCCGCC

SEQ ID NO: 4092	**790863**	TCACACACAGAGACAGTCAGACTAG	AGTGTGTGTCTCTGTCAGTCTGATC
SEQ ID NO: 4093	**790868**	CCGTCACCAGACACGGGCACGGTTA	GGCAGTGGTCTGTGCCCGTGCCAAT
SEQ ID NO: 4094	**791471**	ACGACATACTGAGACACACACACAG	TGCTGTATGACTCTGTGTGTGTGTC
SEQ ID NO: 4095	**791505**	TTAAGATAGAGACACGACACCGACG	AATTCTATCTCTGTGCTGTGGCTGC
SEQ ID NO: 4096	**791726**	GTACGTACCACGGAGACACACACCA	CATGCATGGTGCCTCTGTGTGTGGT
SEQ ID NO: 4097	**791933**	ACTCCACACTAGACAATGACTTCCG	TGAGGTGTGATCTGTTACTGAAGGC
SEQ ID NO: 4098	**793365**	AGAGGCATAGACACACACACTTCGA	TCTCCGTATCTGTGTGTGTGAAGCT
SEQ ID NO: 4099	**796912**	TCCGAGGTCGGACGCCGTCGTGTTA	AGGCTCCAGCCTGCGGCAGCACAAT
SEQ ID NO: 4100	**797056**	ACCAGACACGGACGCGAGTCGCCAC	TGGTCTGTGCCTGCGCTCAGCGGTG
SEQ ID NO: 4101	**797580**	NA	NA
SEQ ID NO: 4102	**797932**	GTCTGTTATGGACGAGGTCCGTACA	CAGACAATACCTGCTCCAGGCATGT
SEQ ID NO: 4103	**798582**	AGGACCAGGACGACCACGTAGAACG	TCCTGGTCCTGCTGGTGCATCTTGC
SEQ ID NO: 4104	**799589**	AAGCTGTGTGACGTGTCGAAGCCCT	TTCGACACACTGCACAGCTTCGGGA
SEQ ID NO: 4105	**800324**	CTGAAGGGACGTTGTTGTCGTTACC	GACTTCCCTGCAACAACAGCAATGG
SEQ ID NO: 4106	**800548**	GAAGCTGTGTGACGTGTCGAAGCCC	CTTCGACACACTGCACAGCTTCGGG
SEQ ID NO: 4107	**800654**	CTTTTTGACGTATGTGTGTATGCAC	GAAAAACTGCATACACACATACGTG
SEQ ID NO: 4108	**803346**	ATCCCAAGACGGTCTTTACAGTTAG	TAGGGTTCTGCCAGAAATGTCAATC
SEQ ID NO: 4109	**803518**	ACACTCGTCCAGACGCACTTGAGGG	TGTGAGCAGGTCTGCGTGAACTCCC
SEQ ID NO: 4110	**805129**	TTATCTTCCGACCACGCGAACCCGG	AATAGAAGGCTGGTGCGCTTGGGCC
SEQ ID NO: 4111	**805560**	CTTTACTGCGACCACGACATGCGGC	GAAATGACGCTGGTGCTGTACGCCG
SEQ ID NO: 4112	**805727**	GGGGACCTCGACACAAATCCAGATT	CCCCTGGAGCTGTGTTTAGGTCTAA

SEQ ID NO: 4113	**805935**	TGTCGAACCACGACCCATGTGGTCC	ACAGCTTGGTGCTGGGTACACCAGG
SEQ ID NO: 4114	**806038**	CTACCACCGCGACCCAAATAGGGGA	GATGGTGGCGCTGGGTTTATCCCCT
SEQ ID NO: 4115	**806273**	CGACTCCTCCGACCGTATAACGTTG	GCTGAGGAGGCTGGCATATTGCAAC
SEQ ID NO: 4116	**806293**	GGTAACCACCGACAAATCCGTCCGT	CCATTGGTGGCTGTTTAGGCAGGCA
SEQ ID NO: 4117	**806328**	TTGTGGCCGACACCGCGACGAAATG	AACACCGGCTGTGGCGCTGCTTTAC
SEQ ID NO: 4118	**806398**	AGACCACGTCCGACCCACTGGAAGG	TCTGGTGCAGGCTGGGTGACCTTCC
SEQ ID NO: 4119	**806454**	AGTTACCACCGACCACTATAACCTA	TCAATGGTGGCTGGTGATATTGGAT
SEQ ID NO: 4120	**806902**	GCCCGTCCCGACATCCGTAGTTAGA	CGGGCAGGGCTGTAGGCATCAATCT
SEQ ID NO: 4121	**807000**	CTTATCCCGACCACGTGTCCAAGGG	GAATAGGGCTGGTGCACAGGTTCCC
SEQ ID NO: 4122	**807048**	AGTCACGCACCGACATGTCTTATCC	TCAGTGCGTGGCTGTACAGAATAGG
SEQ ID NO: 4123	**807073**	GGACGCCACCGACCTCTTTGTAAGA	CCTGCGGTGGCTGGAGAAACATTCT
SEQ ID NO: 4124	**807440**	TTGTCAACCGACAACGACCCACGGG	AACAGTTGGCTGTTGCTGGGTGCCC
SEQ ID NO: 4125	**807650**	ATCCCACCGACCACGAGCATAGATG	TAGGGTGGCTGGTGCTCGTATCTAC
SEQ ID NO: 4126	**807740**	CTGTGTGCCGACAACGAACGACCGA	GACACACGGCTGTTGCTTGCTGGCT
SEQ ID NO: 4127	**807869**	AGGACGACACCGACCTTTAGCTCGA	TCCTGCTGTGGCTGGAAATCGAGCT
SEQ ID NO: 4128	**808147**	GTTGGGTACCGACACACCCGACGTG	CAACCCATGGCTGTGTGGGCTGCAC
SEQ ID NO: 4129	**808367**	GTTTGACTCCGACACCGATTCACGT	CAAACTGAGGCTGTGGCTAAGTGCA
SEQ ID NO: 4130	**808477**	AGAACCACCGACACTTGGAGAGGTA	TCTTGGTGGCTGTGAACCTCTCCAT
SEQ ID NO: 4131	**808719**	GGGTCACCGCGACCGCAAAGCGCGA	CCCAGTGGCGCTGGCGTTTCGCGCT
SEQ ID NO: 4132	**808773**	ACAGCATATCGACACCGCCGAAGGG	TGTCGTATAGCTGTGGCGGCTTCCC
SEQ ID NO: 4133	**809626**	TCTCACGACGCCGACACGGGAGAGG	AGAGTGCTGCGGCTGTGCCCTCTCC

SEQ ID NO: 4134	**810185**	AATTCTAGTCGACCAGTTGTGCCAC	TTAAGATCAGCTGGTCAACACGGTG
SEQ ID NO: 4135	**811020**	CCGCGACGCCGACTTTAAGGGTATC	GGCGCTGCGGCTGAAATTCCCATAG
SEQ ID NO: 4136	**811215**	CGACACACGATCGACACACATGCGA	GCTGTGTGCTAGCTGTGTGTACGCT
SEQ ID NO: 4137	**811262**	CTCGGGCGTCGACAACAGGGCCACA	GAGCCCGCAGCTGTTGTCCCGGTGT
SEQ ID NO: 4138	**812365**	CTGGACACCGACTCACCAAGGGAAA	GACCTGTGGCTGAGTGGTTCCCTTT
SEQ ID NO: 4139	**812399**	ATCCTCCGACGACTAGTCCGACAAG	TAGGAGGCTGCTGATCAGGCTGTTC
SEQ ID NO: 4140	**813147**	GTCACCTATCCGACTGTATAACAAG	CAGTGGATAGGCTGACATATTGTTC
SEQ ID NO: 4141	**813326**	ACATCGTGTGCGACTTGCTACCGGG	TGTAGCACACGCTGAACGATGGCCC
SEQ ID NO: 4142	**813388**	CTGCGTGTGCGACTCTCTCCATCTT	GACGCACACGCTGAGAGAGGTAGAA
SEQ ID NO: 4143	**814253**	GACACCTACCACGACCGTAAATTCT	CTGTGGATGGTGCTGGCATTTAAGA
SEQ ID NO: 4144	**814606**	GGTGGTGGTCGACTACTAAGAGAAG	CCACCACCAGCTGATGATTCTCTTC
SEQ ID NO: 4145	**814697**	GGGACCAACGACCCACGTTTCACGA	CCCTGGTTGCTGGGTGCAAAGTGCT
SEQ ID NO: 4146	**814702**	NA	NA
SEQ ID NO: 4147	**814731**	GTTTCGACCACGACACCAACGTCTT	CAAAGCTGGTGCTGTGGTTGCAGAA
SEQ ID NO: 4148	**815112**	CTCACTCCACGACCCTCTTGGGACG	GAGTGAGGTGCTGGGAGAACCCTGC
SEQ ID NO: 4149	**815478**	CGTGCGTGGCGACGGCAGTATGCGC	GCACGCACCGCTGCCGTCATACGCG
SEQ ID NO: 4150	**815479**	NA	NA
SEQ ID NO: 4151	**815506**	CCCTAGACGACGACCGGAGTACTTG	GGGATCTGCTGCTGGCCTCATGAAC
SEQ ID NO: 4152	**815805**	CGACGTCCCACGACATCAAATTCAG	GCTGCAGGGTGCTGTAGTTTAAGTC
SEQ ID NO: 4153	**815860**	GTAGATGACACCGACGCCACTCTTT	CATCTACTGTGGCTGCGGTGAGAAA
SEQ ID NO: 4154	**816039**	GCTCCGCCACGACGAACCTTATAGT	CGAGGCGGTGCTGCTTGGAATATCA

SEQ ID NO: 4155	**816204**	GGACACACAACGACTTATCCGGAGT	CCTGTGTGTTGCTGAATAGGCCTCA
SEQ ID NO: 4156	**816301**	GTCAACTCCGACGACCCTATCGAGT	CAGTTGAGGCTGCTGGGATAGCTCA
SEQ ID NO: 4157	**816358**	CTACTTTTACGACGGCACGACATTC	GATGAAAATGCTGCCGTGCTGTAAG
SEQ ID NO: 4158	**816374**	CGTGACTCCGACGACAGGTTACGAC	GCACTGAGGCTGCTGTCCAATGCTG
SEQ ID NO: 4159	**816952**	ACACGCCTCCGACGGCCAGCTACGA	TGTGCGGAGGCTGCCGGTCGATGCT
SEQ ID NO: 4160	**817728**	CTACCGCCACGACGGTTTGTAGTAC	GATGGCGGTGCTGCCAAACATCATG
SEQ ID NO: 4161	**817794**	CATACACTCGTACGACACATATGTG	GTATGTGAGCATGCTGTGTATACAC
SEQ ID NO: 4162	**817983**	CCATGGTACGACGTGGGTGTTGAAC	GGTACCATGCTGCACCCACAACTTG
SEQ ID NO: 4163	**818245**	GCGACGTTCCCGACGACGTCCTAGT	CGCTGCAAGGGCTGCTGCAGGATCA
SEQ ID NO: 4164	**818663**	NA	NA
SEQ ID NO: 4165	**818845**	ACTAGCCACCGACGATTCGAGGAAT	TGATCGGTGGCTGCTAAGCTCCTTA
SEQ ID NO: 4166	**818966**	AGGCCTCCGACGACATTAGCGCGTC	TCCGGAGGCTGCTGTAATCGCGCAG
SEQ ID NO: 4167	**819049**	ACGCCAACCGACGAGTCACCTTTAG	TGCGGTTGGCTGCTCAGTGGAAATC
SEQ ID NO: 4168	**819149**	CTCAACAGCGACGACGAGAACGAGG	GAGTTGTCGCTGCTGCTCTTGCTCC
SEQ ID NO: 4169	**819388**	GTCCCGTCACCGACGACGTCCTTGG	CAGGGCAGTGGCTGCTGCAGGAACC
SEQ ID NO: 4170	**819406**	GTACTAGCCACCGACGATTCGAGGA	CATGATCGGTGGCTGCTAAGCTCCT
SEQ ID NO: 4171	**819821**	ATCGAACGCCGACGTAGCTACGTTA	TAGCTTGCGGCTGCATCGATGCAAT
SEQ ID NO: 4172	**820417**	GTTCCAGACCGTTCCATCCCAAGCA	CAAGGTCTGGCAAGGTAGGGTTCGT
SEQ ID NO: 4173	**821481**	NA	NA
SEQ ID NO: 4174	**823031**	GAAAAATTTTTCACGCACACACCGA	CTTTTTAAAAAGTGCGTGTGTGGCT
SEQ ID NO: 4175	**823043**	ATTTGTTTTTGTGTCGGTCTATTAA	TAAACAAAAACACAGCCAGATAATT

SEQ ID NO: 4176	**824049**	ATCCAATTTTTGTGGTTGTGTGTGT	TAGGTTAAAAACACCAACACACACA
SEQ ID NO: 4177	**825883**	GTTTCGGTTTTGGTGGTAATCAGAC	CAAAGCCAAAACCACCATTAGTCTG
SEQ ID NO: 4178	**825910**	TCGGTGTTTTTGTTCCGTGTTCCAC	AGCCACAAAAACAAGGCACAAGGTG
SEQ ID NO: 4179	**827362**	TAAGACAGATTTGGTGTGTTCCCTC	ATTCTGTCTAAACCACACAAGGGAG
SEQ ID NO: 4180	**827625**	GTTCAACATTTGTGGTGGTGTGAGT	CAAGTTGTAAACACCACCACACTCA
SEQ ID NO: 4181	**828058**	ACCAACATTTGTGGTGTGACGTGAA	TGGTTGTAAACACCACACTGCACTT
SEQ ID NO: 4182	**828901**	ATAATCTATTTGTGTGTGGTCGAGG	TATTAGATAAACACACACCAGCTCC
SEQ ID NO: 4183	**830563**	CTTTTCTTTTGTAGTATACCGGCGG	GAAAAGAAAACATCATATGGCCGCC
SEQ ID NO: 4184	**832996**	AGAATAGTCTTTGTGTGAAGTAAGA	TCTTATCAGAAACACACTTCATTCT
SEQ ID NO: 4185	**833865**	GTTTTCTCTTTGTCCGTGGAGAAGT	CAAAAGAGAAACAGGCACCTCTTCA
SEQ ID NO: 4186	**836152**	CCTAGACATTTCTGCGGTGGTGTGA	GGATCTGTAAAGACGCCACCACACT
SEQ ID NO: 4187	**838019**	GTGTGTGCGATTATCGCCGAATTGG	CACACACGCTAATAGCGGCTTAACC
SEQ ID NO: 4188	**839589**	AGAACTATCTTTCATCGGTAAGAGG	TCTTGATAGAAAGTAGCCATTCTCC
SEQ ID NO: 4189	**840070**	TGTGTGTGCTTTCTGTTCACCGTCG	ACACACACGAAAGACAAGTGGCAGC
SEQ ID NO: 4190	**842259**	ACATGAGGTTTTTGTGTGGTCCGAC	TGTACTCCAAAAACACACCAGGCTG
SEQ ID NO: 4191	**843490**	GGTCCCGGTTTGTGTCCTCGGGTTA	CCAGGGCCAAACACAGGAGCCCAAT
SEQ ID NO: 4192	**843508**	ACAATTGTTTGCTGTCGGTGACTCC	TGTTAACAAACGACAGCCACTGAGG
SEQ ID NO: 4193	**843579**	CGTCTCGCTCGTTTGTGAAACCACG	GCAGAGCGAGCAAACACTTTGGTGC
SEQ ID NO: 4194	**844622**	GAATCCGTGTTTGTGGTTTAGTACG	CTTAGGCACAAACACCAAATCATGC
SEQ ID NO: 4195	**844788**	GTGTGGTGTGTTTGTCGTGTGTGGT	CACACCACACAAACAGCACACACCA
SEQ ID NO: 4196	**844796**	AGTAACTACGGTTTGTCGTGGTGGA	TCATTGATGCCAAACAGCACCACCT

SEQ ID NO: 4197	**844847**	TAATCTCAGTTTGTGTGTGCCGGCC	ATTAGAGTCAAACACACACGGCCGG
SEQ ID NO: 4198	**844927**	AAAACGGTTTGTGTTGGAGAGCCTC	TTTTGCCAAACACAACCTCTCGGAG
SEQ ID NO: 4199	**845565**	AATGGAGTTTGACTGTCTTTAGTAC	TTACCTCAAACTGACAGAAATCATG
SEQ ID NO: 4200	**845583**	ACTCAGTAAGTTTGTGGTCCTTCTT	TGAGTCATTCAAACACCAGGAAGAA
SEQ ID NO: 4201	**845782**	CCTATCGCGTTTGTGGTGGCGCCTG	GGATAGCGCAAACACCACCGCGGAC
SEQ ID NO: 4202	**847452**	GTGCGGTGTGTTTCTACAATAAATG	CACGCCACACAAAGATGTTATTTAC
SEQ ID NO: 4203	**847473**	ACAACGTGTGTTTCTGTTAATCACT	TGTTGCACACAAAGACAATTAGTGA
SEQ ID NO: 4204	**847490**	GGTGGTCGGTTTCTCTGATTACGTT	CCACCAGCCAAAGAGACTAATGCAA
SEQ ID NO: 4205	**848480**	CGTCGAGGAGTTTCAGTCTGTGCTT	GCAGCTCCTCAAAGTCAGACACGAA
SEQ ID NO: 4206	**848759**	GCGTGCCGTGTTTCTGCTACCTGTG	CGCACGGCACAAAGACGATGGACAC
SEQ ID NO: 4207	**850211**	GTTTGTGTCGTTTCCTTCAACGTTG	CAAACACAGCAAAGGAAGTTGCAAC
SEQ ID NO: 4208	**851115**	TCTTCATTTTATGTTTGTGTGGGTA	AGAAGTAAAATACAAACACACCCAT
SEQ ID NO: 4209	**851796**	AATGTTTTTATGTGTGGTCGTCGTC	TTACAAAAATACACACCAGCAGCAG
SEQ ID NO: 4210	**852721**	ACAATGTTTTAGTGTGGGTGACTCG	TGTTACAAAATCACACCCACTGAGC
SEQ ID NO: 4211	**853655**	CTATCCGTTTTAGTGTGTGCGTCCC	GATAGGCAAAATCACACACGCAGGG
SEQ ID NO: 4212	**856826**	CTCTTACATTTACGTGTGTGAGTGT	GAGAATGTAAATGCACACACTCACA
SEQ ID NO: 4213	**857747**	AGCAATGTTTACGTGGCTTGTCGAG	TCGTTACAAATGCACCGAACAGCTC
SEQ ID NO: 4214	**858670**	ATCCCGTAATTTCCTGGAGGCGTCT	TAGGGCATTAAAGGACCTCCGCAGA
SEQ ID NO: 4215	**861643**	CAGGTAAATTGGTCGTGTTCTCGGG	GTCCATTTAACCAGCACAAGAGCCC
SEQ ID NO: 4216	**864484**	ACACGTACACACATTTCTACTCTAG	TGTGCATGTGTGTAAAGATGAGATC
SEQ ID NO: 4217	**866224**	AGGAAAATTCTCTGTCGTCCTTTTC	TCCTTTTAAGAGACAGCAGGAAAAG

SEQ ID NO: 4218	**870317**	AATCAAGATTTGTGGTGATGTGAAC	TTAGTTCTAAACACCACTACACTTG
SEQ ID NO: 4219	**870529**	AGTGTGTGTGATTTAACGTAACTCC	TCACACACACTAAATTGCATTGAGG
SEQ ID NO: 4220	**871332**	GTCCGTTGCGATTGTGTCCTACCCT	CAGGCAACGCTAACACAGGATGGGA
SEQ ID NO: 4221	**871752**	GTGAAGCTAGATTGTTGTTGAGATC	CACTTCGATCTAACAACAACTCTAG
SEQ ID NO: 4222	**872012**	ATGTTTGATTCTGTGTTGGTGCGTG	TACAAACTAAGACACAACCACGCAC
SEQ ID NO: 4223	**875743**	AGTCTACCCATTACACGGGTGCACC	TCAGATGGGTAATGTGCCCACGTGG
SEQ ID NO: 4224	**876337**	ATTACGACGACATTAGACAACGAAG	TAATGCTGCTGTAATCTGTTGCTTC
SEQ ID NO: 4225	**876567**	ACGTTGCTTATTCGGTGTGTGTCCC	TGCAACGAATAAGCCACACACAGGG
SEQ ID NO: 4226	**879315**	ATAAATTATTCCGTTGGTGTGTGAA	TATTTAATAAGGCAACCACACACTT
SEQ ID NO: 4227	**880608**	CCCTACGGTATTGACGTTTCAAGAG	GGGATGCCATAACTGCAAAGTTCTC
SEQ ID NO: 4228	**884806**	AAGGTTTTGGGTGTGGTTAAGTCTC	TTCCAAAACCCACACCAATTCAGAG
SEQ ID NO: 4229	**886883**	TACTGTTTTTGGTGTTTATGGAAAC	ATGACAAAAACCACAAATACCTTTG
SEQ ID NO: 4230	**886894**	AAACATTTGGTGGTGGTGTAATCGA	TTTGTAAACCACCACCACATTAGCT
SEQ ID NO: 4231	**888656**	TAGTGCGTGCTTGGTTGTCCGTTCC	ATCACGCACGAACCAACAGGCAAGG
SEQ ID NO: 4232	**889113**	CTCAGCGTCTTGGTCTTCTTCCGGT	GAGTCGCAGAACCAGAAGAAGGCCA
SEQ ID NO: 4233	**889278**	GTAGCCCTTTGCACGCACACACTGT	CATCGGGAAACGTGCGTGTGTGACA
SEQ ID NO: 4234	**889856**	ACGTGTGTGTCTTGGTGTGTTGATT	TGCACACACAGAACCACACAACTAA
SEQ ID NO: 4235	**891697**	GACGGTGGTCGTTGGTTTTTCTTCG	CTGCCACCAGCAACCAAAAAGAAGC
SEQ ID NO: 4236	**892313**	ACTTCTGGTTGGGTAGTTCCTGTGT	TGAAGACCAACCCATCAAGGACACA
SEQ ID NO: 4237	**892591**	CTAACGGCGTTGGTTGTGTATCCCT	GATTGCCGCAACCAACACATAGGGA
SEQ ID NO: 4238	**893051**	CTTACTACTCTTGCGTGTCTGGTCT	GAATGATGAGAACGCACAGACCAGA

SEQ ID NO: 4239	**893513**	CGCTTCGGTTGGTGTGTGAGAACTT	GCGAAGCCAACCACACACTCTTGAA
SEQ ID NO: 4240	**893571**	GTAAGTTGCGTTGGACAGTGTCTCT	CATTCAACGCAACCTGTCACAGAGA
SEQ ID NO: 4241	**893869**	ACGGTGTCTGTTGGTCCCGAAGCAG	TGCCACAGACAACCAGGGCTTCGTC
SEQ ID NO: 4242	**893909**	ACGAGAGTTGTTGGTCGGCGAACTC	TGCTCTCAACAACCAGCCGCTTGAG
SEQ ID NO: 4243	**894647**	AGTTACTAACGTTGGGTGTGGAAGA	TCAATGATTGCAACCCACACCTTCT
SEQ ID NO: 4244	**895897**	CCCTTTTGATCTTTCGGACGACCTG	GGGAAAACTAGAAAGCCTGCTGGAC
SEQ ID NO: 4245	**896962**	NA	NA
SEQ ID NO: 4246	**898180**	AGCGTGCGTTTGACAAAGAACTCAG	TCGCACGCAAACTGTTTCTTGAGTC
SEQ ID NO: 4247	**898742**	AGACCCTTTGACTACGGTGATCGGA	TCTGGGAAACTGATGCCACTAGCCT
SEQ ID NO: 4248	**899962**	CTCTTTTTGACGGTGGTCCCGGTGC	GAGAAAAACTGCCACCAGGGCCACG
SEQ ID NO: 4249	**904118**	GTGTGGTACTTTGTGTGGTCATTCC	CACACCATGAAACACACCAGTAAGG
SEQ ID NO: 4250	**905381**	ATGTCTGTTTGTGGGTCAAACGGAC	TACAGACAAACACCCAGTTTGCCTG
SEQ ID NO: 4251	**905482**	CCCAGTTTGTGCGTGTGAACGAACC	GGGTCAAACACGCACACTTGCTTGG
SEQ ID NO: 4252	**905507**	ATATGTGTTTGTGACGCCCCCTCTT	TATACACAAACACTGCGGGGGAGAA
SEQ ID NO: 4253	**905604**	CAGCCTTTGTGTCGTTGGGTACTCC	GTCGGAAACACAGCAACCCATGAGG
SEQ ID NO: 4254	**905737**	TTTCTGTTTGTGTTGTTCCTCTCCG	AAAGACAAACACAACAAGGAGAGGC
SEQ ID NO: 4255	**906313**	CCTGTGTTTGTGAAGCCTTCCGGCG	GGACACAAACACTTCGGAAGGCCGC
SEQ ID NO: 4256	**906394**	CCGTGGATTGTGGTCGGTTGTTAAA	GGCACCTAACACCAGCCAACAATTT
SEQ ID NO: 4257	**906401**	GTTACGGTCTTTGTGTCCGTTGTGA	CAATGCCAGAAACACAGGCAACACT
SEQ ID NO: 4258	**906629**	AGTCGTCAACTTGTCAATTTAAGTA	TCAGCAGTTGAACAGTTAAATTCAT
SEQ ID NO: 4259	**906791**	AGATATCTCTTGTGGTGTACCTGGT	TCTATAGAGAACACCACATGGACCA

SEQ ID NO: 4260	**906795**	ATACTTGCTTGTTTGTGTGTGCCCA	TATGAACGAACAAACACACACGGGT
SEQ ID NO: 4261	**906800**	CGCGAGTTGTTGTTTAGGGTCAGAT	GCGCTCAACAACAAATCCCAGTCTA
SEQ ID NO: 4262	**906872**	CGTTTACCTTGTGTGGTGCCTCCTC	GCAAATGGAACACACCACGGAGGAG
SEQ ID NO: 4263	**906896**	GTAGTCCACGATTGTGTGTGTGTGT	CATCAGGTGCTAACACACACACACA
SEQ ID NO: 4264	**907104**	TCAAGGTCTTGTTGTGGATATTTCC	AGTTCCAGAACAACACCTATAAAGG
SEQ ID NO: 4265	**907327**	CTATGTGTCTTGTGGTTCTTGTGAT	GATACACAGAACACCAAGAACACTA
SEQ ID NO: 4266	**907434**	CTTTTACGTTGTTGTTCCCAGGTAG	GAAAATGCAACAACAAGGGTCCATC
SEQ ID NO: 4267	**907781**	ATCTCCCTTGTGTGTTACGAGAGAA	TAGAGGGAACACACAATGCTCTCTT
SEQ ID NO: 4268	**907985**	AAGATTCTTGTGTTCGTGTGGCCTC	TTCTAAGAACACAAGCACACCGGAG
SEQ ID NO: 4269	**908076**	CTACTGACGTCTTGTGGTCCTCTAC	GATGACTGCAGAACACCAGGAGATG
SEQ ID NO: 4270	**908255**	AGTGTATACTCTTGTGTGTGTCTGT	TCACATATGAGAACACACACAGACA
SEQ ID NO: 4271	**908311**	CGAATAACTTGTCCGTGTGGGGCAA	GCTTATTGAACAGGCACACCCCGTT
SEQ ID NO: 4272	**908519**	AAGTGGCGTTGTGTCGTCTTCCGTC	TTCACCGCAACACAGCAGAAGGCAG
SEQ ID NO: 4273	**909162**	ATTCGTTCGTTGTGTATTGTTTGGA	TAAGCAAGCAACACATAACAAACCT
SEQ ID NO: 4274	**909165**	AGTCTTGGTTGTTGTGTTTATTTCA	TCAGAACCAACAACACAAATAAAGT
SEQ ID NO: 4275	**909197**	TGGTGTGTTTGTCGTGTGTGGTGTA	ACCACACAAACAGCACACACCACAT
SEQ ID NO: 4276	**909638**	AAACGTCGTGTTGTGGTAACGGGCC	TTTGCAGCACAACACCATTGCCCGG
SEQ ID NO: 4277	**909659**	TGTTGCTGTTGTTGTCCTCGCGAAC	ACAACGACAACAACAGGAGCGCTTG
SEQ ID NO: 4278	**909709**	CTTGGGTTGTGGTATCGTTCTTATC	GAACCCAACACCATAGCAAGAATAG
SEQ ID NO: 4279	**910407**	ATCAGTTCTTGTCTGGTGTGTCCAC	TAGTCAAGAACAGACCACACAGGTG
SEQ ID NO: 4280	**910456**	GTATCACTGGTTGTGTGGCCAAGCT	CATAGTGACCAACACACCGGTTCGA

SEQ ID NO: 4281	**910459**	CCCGACGGTTGTGGTCTTTCGGGTC	GGGCTGCCAACACCAGAAAGCCCAG
SEQ ID NO: 4282	**910528**	ACAAATGTTGTGTGGGTTGTCCTTC	TGTTTACAACACACCCAACAGGAAG
SEQ ID NO: 4283	**910711**	ATCGTTTCGTTGTGGTTGTCGACCG	TAGCAAAGCAACACCAACAGCTGGC
SEQ ID NO: 4284	**910832**	ATCCTGGTTGTGGTTATGGTGGCTC	TAGGACCAACACCAATACCACCGAG
SEQ ID NO: 4285	**911094**	ACTCCGTTGTTGTTGAGTGAGACCC	TGAGGCAACAACAACTCACTCTGGG
SEQ ID NO: 4286	**911352**	ACTGTGGGTTGTCATCGGGACTCGA	TGACACCCAACAGTAGCCCTGAGCT
SEQ ID NO: 4287	**911535**	CGCCGCCGTTGTTCTCGTCTCTTGA	GCGGCGGCAACAAGAGCAGAGAACT
SEQ ID NO: 4288	**912203**	CCATACCGTTGTGTGTGGATACCAG	GGTATGGCAACACACACCTATGGTC
SEQ ID NO: 4289	**917438**	TCCACGCACATGGACTAAGTCAGGC	AGGTGCGTGTACCTGATTCAGTCCG
SEQ ID NO: 4290	**920228**	ATCAACCGATGGTGGTGTATGACGA	TAGTTGGCTACCACCACATACTGCT
SEQ ID NO: 4291	**923631**	GGTGGTGGATGAGTTGTTTATGAAC	CCACCACCTACTCAACAAATACTTG
SEQ ID NO: 4292	**926277**	AGGTTTTATGAAGGAGATCCACCGT	TCCAAAATACTTCCTCTAGGTGGCA
SEQ ID NO: 4293	**926301**	CTTATTTATGGACGCGGAACTCTTG	GAATAAATACCTGCGCCTTGAGAAC
SEQ ID NO: 4294	**928788**	GTGTGGAATGTGTGCTCGCACTTTG	CACACCTTACACACGAGCGTGAAAC
SEQ ID NO: 4295	**928932**	CCTACAAATGTGTGTGATGTCGTAC	GGATGTTTACACACACTACAGCATG
SEQ ID NO: 4296	**929217**	CCGTGTAGAATGTGTACTCCACTTT	GGCACATCTTACACATGAGGTGAAA
SEQ ID NO: 4297	**929642**	ACGAAACAATGTCTGGGTTCGACAG	TGCTTTGTTACAGACCCAAGCTGTC
SEQ ID NO: 4298	**930665**	ATTGTCAATGTGTGTCCTTTCGGTC	TAACAGTTACACACAGGAAAGCCAG
SEQ ID NO: 4299	**930824**	AAAAAATGTCGTCGGTCAACTCCAG	TTTTTTACAGCAGCCAGTTGAGGTC
SEQ ID NO: 4300	**931418**	ACGTATCTGGATGTGTGTATTTGCA	TGCATAGACCTACACACATAAACGT
SEQ ID NO: 4301	**931739**	CACGACCCATGTCGTTGTGTAGTGT	GTGCTGGGTACAGCAACACATCACA

SEQ ID NO: 4302	**931788**	ACACGAAGTACATGTGTGTGCGTAC	TGTGCTTCATGTACACACACGCATG
SEQ ID NO: 4303	**932279**	ACAGATGGATGTGTGTTCGTGTACA	TGTCTACCTACACACAAGCACATGT
SEQ ID NO: 4304	**933278**	ACTCAAAGATGTGTGTGCTCCCGAA	TGAGTTTCTACACACACGAGGGCTT
SEQ ID NO: 4305	**934200**	ATTACTCCGATGTCGTGTGTCGAGC	TAATGAGGCTACAGCACACAGCTCG
SEQ ID NO: 4306	**934202**	ATTAGAGGATGTCGTGTCGTTTATC	TAATCTCCTACAGCACAGCAAATAG
SEQ ID NO: 4307	**935245**	CACCGTGTGTATGTTAATGTCGCTT	GTGGCACACATACAATTACAGCGAA
SEQ ID NO: 4308	**935502**	GGTTTGTATATGTGTGGTCTACGAC	CCAAACATATACACACCAGATGCTG
SEQ ID NO: 4309	**935884**	NA	NA
SEQ ID NO: 4310	**936184**	CGAGACCCTATGTGTGTGCGCGTCG	GCTCTGGGATACACACACGCGCAGC
SEQ ID NO: 4311	**936418**	TAACGACCCTATGTCTGTACTCGGC	ATTGCTGGGATACAGACATGAGCCG
SEQ ID NO: 4312	**936551**	AGTACCCTCTATGTGTGAGTGGAAC	TCATGGGAGATACACACTCACCTTG
SEQ ID NO: 4313	**936602**	TCTGTGTCCGTATGTGTAGATATGT	AGACACAGGCATACACATCTATACA
SEQ ID NO: 4314	**938922**	ATTAGTGTCCTTTGTGTTGAGTATC	TAATCACAGGAAACACAACTCATAG
SEQ ID NO: 4315	**940312**	GATGAGTCGTACCTTTGTTCTACTT	CTACTCAGCATGGAAACAAGATGAA
SEQ ID NO: 4316	**941702**	CAAATCCTTGTGTGTGTCCATCTGT	GTTTAGGAACACACACAGGTAGACA
SEQ ID NO: 4317	**943086**	TCCCGTCCCTTCCTCACTGTGGATG	AGGGCAGGGAAGGAGTGACACCTAC
SEQ ID NO: 4318	**944579**	TTCCCGACCTTCTCGTCCGAAAGAG	AAGGGCTGGAAGAGCAGGCTTTCTC
SEQ ID NO: 4319	**944781**	AGAACTTCACTTCGTGATGTGTGTC	TCTTGAAGTGAAGCACTACACACAG
SEQ ID NO: 4320	**946642**	ACTGGCCCTTCGAGTACGCTGACGA	TGACCGGGAAGCTCATGCGACTGCT
SEQ ID NO: 4321	**946777**	ACCATAAGCTTTGTGTGTCCTCCGG	TGGTATTCGAAACACACAGGAGGCC
SEQ ID NO: 4322	**948531**	CGTGTGCGGCTTGCCCTTCTGCGCG	GCACACGCCGAACGGGAAGACGCGC

SEQ ID NO: 4323	**948612**	GTGTCCCGGCTTGAAGAAGACGCCC	CACAGGGCCGAACTTCTTCTGCGGG
SEQ ID NO: 4324	**950508**	ACATGTACCGCTTCGATCTCTGACA	TGTACATGGCGAAGCTAGAGACTGT
SEQ ID NO: 4325	**950776**	ACCGACCACGCTTACCGGACCGTGT	TGGCTGGTGCGAATGGCCTGGCACA
SEQ ID NO: 4326	**951446**	GACCTCGACCCTTATTCGACGGAGG	CTGGAGCTGGGAATAAGCTGCCTCC
SEQ ID NO: 4327	**952011**	TCTTAAACCTTAGTCGCGTGTGGGG	AGAATTTGGAATCAGCGCACACCCC
SEQ ID NO: 4328	**952360**	CTCGGTTTCTGCTTGCTTCGTTTGT	GAGCCAAAGACGAACGAAGCAAACA
SEQ ID NO: 4329	**955604**	GCGTGCGTGTTCTTGGACCTACCTC	CGCACGCACAAGAACCTGGATGGAG
SEQ ID NO: 4330	**958028**	GCTTTTTCTTCGACCGGGTGGTTAC	CGAAAAAGAAGCTGGCCCACCAATG
SEQ ID NO: 4331	**958055**	CTCTCCGTCTCTTGGATTTTCTCTT	GAGAGGCAGAGAACCTAAAAGAGAA
SEQ ID NO: 4332	**958341**	AACTAGTGTCTCTTGGGTGTCTACA	TTGATCACAGAGAACCCACAGATGT
SEQ ID NO: 4333	**958588**	CTTTTTCTTCGACCGGGTGGTTACT	GAAAAAGAAGCTGGCCCACCAATGA
SEQ ID NO: 4334	**958603**	ACAGGCACTCTTGAGGGGCTACCCA	TGTCCGTGAGAACTCCCCGATGGGT
SEQ ID NO: 4335	**959270**	ACGTCCACACTCTTGAGAAAAGTAG	TGCAGGTGTGAGAACTCTTTTCATC
SEQ ID NO: 4336	**961278**	AGGGACTCTCTTCGCATTCTGTTTG	TCCCTGAGAGAAGCGTAAGACAAAC
SEQ ID NO: 4337	**961497**	CATGAAGTCTTGTGGTTGTAGTCTA	GTACTTCAGAACACCAACATCAGAT
SEQ ID NO: 4338	**961622**	AAGAATAGTCTTTGTGTGAAGTAAG	TTCTTATCAGAAACACACTTCATTC
SEQ ID NO: 4339	**961647**	AAAGGACTCTTCCACCGACGACGGA	TTTCCTGAGAAGGTGGCTGCTGCCT
SEQ ID NO: 4340	**962725**	AGTGTGTCGCGTCTTTGTACAAAAG	TCACACAGCGCAGAAACATGTTTTC
SEQ ID NO: 4341	**962817**	CTCTATGTGTCTTGTGGTTCTTGTG	GAGATACACAGAACACCAAGAACAC
SEQ ID NO: 4342	**962832**	AAAAGTGTCTTTGTTCGTCGGACCA	TTTTCACAGAAACAAGCAGCCTGGT
SEQ ID NO: 4343	**963321**	ACGTCTGGTGTCTTGAGTGGTCTAT	TGCAGACCACAGAACTCACCAGATA

SEQ ID NO: 4344	**964381**	AGACGACCCGTCTTCAGAAAGGCCC	TCTGCTGGGCAGAAGTCTTTCCGGG
SEQ ID NO: 4345	**965850**	AGAACAAGTCTTCGTGTGCGTGTCG	TCTTGTTCAGAAGCACACGCACAGC
SEQ ID NO: 4346	**966284**	AATCCCTCTTAACTACTGAGTCGAG	TTAGGGAGAATTGATGACTCAGCTC
SEQ ID NO: 4347	**969096**	CGTCCACACACTTTCTGCTAGGTTG	GCAGGTGTGTGAAAGACGATCCAAC
SEQ ID NO: 4348	**969268**	GTGTGTGTTAACTTTGTTTTATGTA	CACACACAATTGAAACAAAATACAT
SEQ ID NO: 4349	**969959**	ACGGGGTCACTTGTTGGTGTCTCTC	TGCCCCAGTGAACAACCACAGAGAG
SEQ ID NO: 4350	**970260**	GTGTGTACGTGCACTTTGAGGTCAG	CACACATGCACGTGAAACTCCAGTC
SEQ ID NO: 4351	**970444**	GACAGGCACACTTCCTAACGGTCCT	CTGTCCGTGTGAAGGATTGCCAGGA
SEQ ID NO: 4352	**971935**	AGCAGTCCACTTCGTCACCCTTACC	TCGTCAGGTGAAGCAGTGGGAATGG
SEQ ID NO: 4353	**973326**	CCGTACACACACTTCTAGTAGGGAA	GGCATGTGTGTGAAGATCATCCCTT
SEQ ID NO: 4354	**973408**	TGGTCCCGACTTGCGCCGATCAAGG	ACCAGGGCTGAACGCGGCTAGTTCC
SEQ ID NO: 4355	**974398**	GACCGTCGGTGACTTCCATAGAAGA	CTGGCAGCCACTGAAGGTATCTTCT
SEQ ID NO: 4356	**975629**	AGTTCGACACGACTTCTATTTTGAT	TCAAGCTGTGCTGAAGATAAAACTA
SEQ ID NO: 4357	**976163**	AGGAAAACTTACTCGCATCGTGTAT	TCCTTTTGAATGAGCGTAGCACATA
SEQ ID NO: 4358	**978330**	AGGTCGGTGTACTTTCGGTTCCAGT	TCCAGCCACATGAAAGCCAAGGTCA
SEQ ID NO: 4359	**979066**	GTGGGTTTACTTTCGTATTGTACGT	CACCCAAATGAAAGCATAACATGCA
SEQ ID NO: 4360	**980889**	AAGTCTATCGTACTTTGTGTGTGGA	TTCAGATAGCATGAAACACACACCT
SEQ ID NO: 4361	**980905**	CTAATGCGGTGGTGTGAAGTGGAAA	GATTACGCCACCACACTTCACCTTT
SEQ ID NO: 4362	**980941**	TTCACCGACCTGGGACTTTGGACCA	AAGTGGCTGGACCCTGAAACCTGGT
SEQ ID NO: 4363	**981938**	ACGGCTGTGCTGTGACGGATATAGT	TGCCGACACGACACTGCCTATATCA
SEQ ID NO: 4364	**981952**	GCTCGAGATCCTGGGTGTGTGTCTT	CGAGCTCTAGGACCCACACACAGAA

SEQ ID NO: 4365	**982312**	CTCTGTTACCTGGTGTGGTGTCACC	GAGACAATGGACCACACCACAGTGG
SEQ ID NO: 4366	**982448**	TCGAGGCCCTGGTGAACGGTCCCAC	AGCTCCGGGACCACTTGCCAGGGTG
SEQ ID NO: 4367	**982979**	GGTGGTCGTGCTGCGTTGGTGGGCC	CCACCAGCACGACGCAACCACCCGG
SEQ ID NO: 4368	**983255**	GGTCTAACGGCTGACTTTTATTACC	CCAGATTGCCGACTGAAAATAATGG
SEQ ID NO: 4369	**983598**	ACTCCCTACCTGCTCGTTCACGACC	TGAGGGATGGACGAGCAAGTGCTGG
SEQ ID NO: 4370	**984249**	GCCGCGCGCCTGCAAGCCACTCGTG	CGGCGCGCGGACGTTCGGTGAGCAC
SEQ ID NO: 4371	**985186**	TCTCTCTGTGCTGCCTACGTGCGTG	AGAGAGACACGACGGATGCACGCAC
SEQ ID NO: 4372	**985368**	TTTGTGTCGCTGGTGTCCTTGTACA	AAACACAGCGACCACAGGAACATGT
SEQ ID NO: 4373	**987185**	GCCGCCGCGCTGAGGAAACACTGTC	CGGCGGCGCGACTCCTTTGTGACAG
SEQ ID NO: 4374	**988364**	AGTCACAGCCTGACGACAACAGGTT	TCAGTGTCGGACTGCTGTTGTCCAA
SEQ ID NO: 4375	**988517**	GTCATTCCTCTGGTTGGTGTGGATA	CAGTAAGGAGACCAACCACACCTAT
SEQ ID NO: 4376	**988943**	AGAAACGCGTCTGTGGAATGATTAG	TCTTTGCGCAGACACCTTACTAATC
SEQ ID NO: 4377	**989229**	TCTTTTGTCTGCGTCTGCCAAAAGT	AGAAAACAGACGCAGACGGTTTTCA
SEQ ID NO: 4378	**989473**	AGGAGCCGCTGACCCTTCTTAGCCT	TCCTCGGCGACTGGGAAGAATCGGA
SEQ ID NO: 4379	**990507**	GTATCCTATTCTGGTGTCGTGTCCG	CATAGGATAAGACCACAGCACAGGC
SEQ ID NO: 4380	**990920**	AAACTGAGTCTGGTGGTGTGACAAC	TTTGACTCAGACCACCACACTGTTG
SEQ ID NO: 4381	**990967**	CCCTGTTCTGAAACGGTTAAGTTCG	GGGACAAGACTTTGCCAATTCAAGC
SEQ ID NO: 4382	**991202**	GTACTCTGTTTCTGCGGTTGGTCTA	CATGAGACAAAGACGCCAACCAGAT
SEQ ID NO: 4383	**991578**	GTCTTTGTGTCTGGTACTTCACTTT	CAGAAACACAGACCATGAAGTGAAA
SEQ ID NO: 4384	**991880**	ACTCGTGCTGTCTGCGGTAATATCG	TGAGCACGACAGACGCCATTATAGC
SEQ ID NO: 4385	**992305**	TTCGACGCCGTCTGGGTCGCCCGTG	AAGCTGCGGCAGACCCAGCGGGCAC

SEQ ID NO: 4386	**993678**	TTCCACCGTCTGAGTTTACAGACCG	AAGGTGGCAGACTCAAATGTCTGGC
SEQ ID NO: 4387	**994365**	TGGTGTGGCTGTCGAAAGCCTACGA	ACCACACCGACAGCTTTCGGATGCT
SEQ ID NO: 4388	**995065**	GAGCCGCACGTCTGATTCGCGCGAA	CTCGGCGTGCAGACTAAGCGCGCTT
SEQ ID NO: 4389	**995127**	ATATCAACCTGTGGTGGTGCATGAC	TATAGTTGGACACCACCACGTACTG
SEQ ID NO: 4390	**995282**	AGTATATTCCTGTGACGGTGGTTGT	TCATATAAGGACACTGCCACCAACA
SEQ ID NO: 4391	**995898**	CCCTCGACCTGTCCGTTTAAAACGA	GGGAGCTGGACAGGCAAATTTTGCT
SEQ ID NO: 4392	**996479**	ATTCGGACCTGTGTGGTGTCACTTC	TAAGCCTGGACACACCACAGTGAAG
SEQ ID NO: 4393	**996625**	AGGTAACACCTGTCCCGCAGAATCC	TCCATTGTGGACAGGGCGTCTTAGG
SEQ ID NO: 4394	**997128**	GTCGAGGAGGCTGTCCAGACCTTAG	CAGCTCCTCCGACAGGTCTGGAATC
SEQ ID NO: 4395	**997227**	CCGGTCGTACCTGTGGTCCTGGTCC	GGCCAGCATGGACACCAGGACCAGG
SEQ ID NO: 4396	**997730**	GTCCAAACGCTGTCTGTGTGTACCT	CAGGTTTGCGACAGACACACATGGA
SEQ ID NO: 4397	**998458**	CTCAAATCTGTGTCTGTGCAATCAT	GAGTTTAGACACAGACACGTTAGTA
SEQ ID NO: 4398	**998529**	AGTGGTCTTCTGTTGGTGTCAAACC	TCACCAGAAGACAACCACAGTTTGG
SEQ ID NO: 4399	**998581**	TCAGGCCGTCTGTTTGTGGCGTGAC	AGTCCGGCAGACAAACACCGCACTG
SEQ ID NO: 4400	**998646**	TGACGCGCCGCTGTGTGTCGTCGTT	ACTGCGCGGCGACACACAGCAGCAA
SEQ ID NO: 4401	**998856**	CGACGCTCGTGCTGTGCGCCGGCCC	GCTGCGAGCACGACACGCGGCCGGG
SEQ ID NO: 4402	**999611**	ATTACTGTGTCTGTGGTTACCAACC	TAATGACACAGACACCAATGGTTGG
SEQ ID NO: 4403	**999677**	ATGAGTAACTCTGTGTGCATCTACG	TACTCATTGAGACACACGTAGATGC
SEQ ID NO: 4404	**999720**	GGTCCTTTCTGTGGGCGTGTATCCC	CCAGGAAAGACACCCGCACATAGGG
SEQ ID NO: 4405	**999758**	ACTTCATTCTGTGTGTGTACCCGGG	TGAAGTAAGACACACACATGGGCCC
SEQ ID NO: 4406	**1000338**	ATAATATCTCTGTGTGTGCGGAACT	TATTATAGAGACACACACGCCTTGA

SEQ ID NO: 4407	**1000407**	CGGTAGTCTTCTGTGTGACCTCGCG	GCCATCAGAAGACACACTGGAGCGC
SEQ ID NO: 4408	**1000412**	AGCAGATTCTGTGCTGTGTGACCGA	TCGTCTAAGACACGACACACTGGCT
SEQ ID NO: 4409	**1000540**	ACTGGTTCTCTGTGTCTGTACTCGG	TGACCAAGAGACACAGACATGAGCC
SEQ ID NO: 4410	**1000954**	AGGGGTGTCTGTCTAAACCTTCCTT	TCCCCACAGACAGATTTGGAAGGAA
SEQ ID NO: 4411	**1000965**	CACGGGGTCTGTGTTGGATGTTTAC	GTGCCCCAGACACAACCTACAAATG
SEQ ID NO: 4412	**1001282**	GTGTCCATGTCTGTTCGTCTCGTCT	CACAGGTACAGACAAGCAGAGCAGA
SEQ ID NO: 4413	**1002138**	ATAGTACTGTTCTGTCGGTGTCCTC	TATCATGACAAGACAGCCACAGGAG
SEQ ID NO: 4414	**1002274**	CAGTTACTGTCTGTGGTTCGCCCAG	GTCAATGACAGACACCAAGCGGGTC
SEQ ID NO: 4415	**1002359**	CGGTGTGCGTCTGTCTCCAGTGTCA	GCCACACGCAGACAGAGGTCACAGT
SEQ ID NO: 4416	**1002831**	AGATAGAAGTCTGTCGGTTCCTCCT	TCTATCTTCAGACAGCCAAGGAGGA
SEQ ID NO: 4417	**1002916**	ACCTTGTGTCTGTCGTTCGTGTTAA	TGGAACACAGACAGCAAGCACAATT
SEQ ID NO: 4418	**1003599**	CTTAAAACTGGACGATACAACAATC	GAATTTTGACCTGCTATGTTGTTAG
SEQ ID NO: 4419	**1006663**	CAGCCACACTGACCGGACCGTGTCT	GTCGGTGTGACTGGCCTGGCACAGA
SEQ ID NO: 4420	**1008043**	ATTCAGTATACTGGTGTGTGGGACC	TAAGTCATATGACCACACACCCTGG
SEQ ID NO: 4421	**1009168**	CTCCACCGACTGACGCCTACACGCG	GAGGTGGCTGACTGCGGATGTGCGC
SEQ ID NO: 4422	**1009643**	CAAAGAGACTGTGTGTGTTCTACAT	GTTTCTCTGACACACACAAGATGTA
SEQ ID NO: 4423	**1010474**	ATTCAAACTGTGTGTCTGGAGTCGC	TAAGTTTGACACACAGACCTCAGCG
SEQ ID NO: 4424	**1013844**	AAGTTTTTCCCTACCACGTGCGAGC	TTCAAAAAGGGATGGTGCACGCTCG
SEQ ID NO: 4425	**1014422**	AGCACATTTCCTGTTGTTGTCGTCC	TCGTGTAAAGGACAACAACAGCAGG
SEQ ID NO: 4426	**1015025**	AAATTTTCCTGTGTGTGTACGCGTA	TTTAAAAGGACACACACATGCGCAT
SEQ ID NO: 4427	**1017623**	CGACACGACCTTCCAAGAGGTACCT	GCTGTGCTGGAAGGTTCTCCATGGA

SEQ ID NO: 4428	**1017653**	GTGTGTGTGTTTCCGTCTGTGCAAA	CACACACACAAAGGCAGACACGTTT
SEQ ID NO: 4429	**1018499**	AAAGTGCTTCCGGTTCGATAGTCTC	TTTCACGAAGGCCAAGCTATCAGAG
SEQ ID NO: 4430	**1022942**	GTACGTGTGCGAGTTCCACTTCCAG	CATGCACACGCTCAAGGTGAAGGTC
SEQ ID NO: 4431	**1023969**	CACTACGCTAGTTCCGTGTGTGTCT	GTGATGCGATCAAGGCACACACAGA
SEQ ID NO: 4432	**1024819**	GTAAATTTTCATGCGTGTGCGAATG	CATTTAAAAGTACGCACACGCTTAC
SEQ ID NO: 4433	**1024916**	AGTTTATTTCAACGACGACATCGTT	TCAAATAAAGTTGCTGCTGTAGCAA
SEQ ID NO: 4434	**1025380**	ATCTATGTTTCATGGTGGTGTCTCG	TAGATACAAAGTACCACCACAGAGC
SEQ ID NO: 4435	**1026607**	CTACCCTTCTCATTAGGTGGTGGTG	GATGGGAAGAGTAATCCACCACCAC
SEQ ID NO: 4436	**1029804**	GTTACCTGATTCACCGACCGCAGTA	CAATGGACTAAGTGGCTGGCGTCAT
SEQ ID NO: 4437	**1030374**	GGGTTAGGTTCAGTTTGAAACGTGT	CCCAATCCAAGTCAAACTTTGCACA
SEQ ID NO: 4438	**1031446**	GTATCAACTCTTCACGTAAGGTCTT	CATAGTTGAGAAGTGCATTCCAGAA
SEQ ID NO: 4439	**1034217**	CCAGCTTTCTGTGGTGGTACTGTTA	GGTCGAAAGACACCACCATGACAAT
SEQ ID NO: 4440	**1034850**	CGTGCCGTTTCTCTTTCTCCTTTCA	GCACGGCAAAGAGAAAGAGGAAAGT
SEQ ID NO: 4441	**1035590**	AAAGTTTTCTGTGTGCGTGGTCACC	TTTCAAAAGACACACGCACCAGTGG
SEQ ID NO: 4442	**1037139**	CTCTACGAACTTCTTGAGTTGTTTT	GAGATGCTTGAAGAACTCAACAAAA
SEQ ID NO: 4443	**1037526**	AACTCAGTCTTCTTCGTCGTAACGG	TTGAGTCAGAAGAAGCAGCATTGCC
SEQ ID NO: 4444	**1040552**	GAGTTTCCGTTCTGTGGTTCGTCCT	CTCAAAGGCAAGACACCAAGCAGGA
SEQ ID NO: 4445	**1042137**	AGTTTCCGTTCTGTGGTTCGTCCTT	TCAAAGGCAAGACACCAAGCAGGAA
SEQ ID NO: 4446	**1042684**	ATCCGTTGTTCTCTGTGTGCACCGT	TAGGCAACAAGAGACACACGTGGCA
SEQ ID NO: 4447	**1042844**	TAGGACTGGTTCTCCGTGTGTGTCG	ATCCTGACCAAGAGGCACACACAGC
SEQ ID NO: 4448	**1047235**	AGAGGGCATCCAGGGTACACCACGC	TCTCCCGTAGGTCCCATGTGGTGCG

SEQ ID NO: 4449	**1048202**	CATTTCATCCTCGTCAATTAAGTTC	GTAAAGTAGGAGCAGTTAATTCAAG
SEQ ID NO: 4450	**1048935**	TCGTGTGCGGATCCTTTGCGGTAAG	AGCACACGCCTAGGAAACGCCATTC
SEQ ID NO: 4451	**1049239**	CTAGACAACATCCTCGTCTGACTCA	GATCTGTTGTAGGAGCAGACTGAGT
SEQ ID NO: 4452	**1051690**	CTGCCACGATCCGTCATAAGGGAGT	GACGGTGCTAGGCAGTATTCCCTCA
SEQ ID NO: 4453	**1055267**	ATAACAGCTATCAGAGGTTTTCCAC	TATTGTCGATAGTCTCCAAAAGGTG
SEQ ID NO: 4454	**1056167**	CCCGACACGATCAGAAGAGACATGG	GGGCTGTGCTAGTCTTCTCTGTACC
SEQ ID NO: 4455	**1059686**	AGACTTCGAATCTTCTCCCGGACCG	TCTGAAGCTTAGAAGAGGGCCTGGC
SEQ ID NO: 4456	**1064390**	AGAACGTTCGATCTCCGTGCGTGAC	TCTTGCAAGCTAGAGGCACGCACTG
SEQ ID NO: 4457	**1066481**	AATTTCTTCGTTGGAGTGGTGTGGA	TTAAAGAAGCAACCTCACCACACCT
SEQ ID NO: 4458	**1067236**	GGACGAAGGTTCGTGCGATGTGGGA	CCTGCTTCCAAGCACGCTACACCCT
SEQ ID NO: 4459	**1067450**	TCACATCATTCGGTGTGGGGTGTCT	AGTGTAGTAAGCCACACCCCACAGA
SEQ ID NO: 4460	**1067598**	ACAACCTATTCGGTTCGTGTGTGAA	TGTTGGATAAGCCAAGCACACACTT
SEQ ID NO: 4461	**1068389**	TCCTTGCTTCGGGTGGAGAGCAGAA	AGGAACGAAGCCCACCTCTCGTCTT
SEQ ID NO: 4462	**1073844**	GATGTAGTTATTCGTGTGTGGTCAA	CTACATCAATAAGCACACACCAGTT
SEQ ID NO: 4463	**1074129**	GTAGGTATTCTTCGTGCACACACCA	CATCCATAAGAAGCACGTGTGTGGT
SEQ ID NO: 4464	**1074624**	ACGAACCGAGTTCGTGGTGGTTAGC	TGCTTGGCTCAAGCACCACCAATCG
SEQ ID NO: 4465	**1075730**	TTTTCATTCGTCGTGGTGTGTCACC	AAAAGTAAGCAGCACCACACAGTGG
SEQ ID NO: 4466	**1076081**	TCAACACAGTTCGTGCGTGTACATC	AGTTGTGTCAAGCACGCACATGTAG
SEQ ID NO: 4467	**1076669**	GTCGAGTGTTAGTTCGTGTCGTTTG	CAGCTCACAATCAAGCACAGCAAAC
SEQ ID NO: 4468	**1077133**	ACACACACACATCGGCAGTTAGAGG	TGTGTGTGTGTAGCCGTCAATCTCC
SEQ ID NO: 4469	**1078669**	GTGCCAACATCGACGACACCTGAGC	CACGGTTGTAGCTGCTGTGGACTCG

SEQ ID NO: 4470	**1079797**	ACCGACCACGATCGAGACTTGAGAC	TGGCTGGTGCTAGCTCTGAACTCTG
SEQ ID NO: 4471	**1080427**	CTGTCAGAATCGTGTCTGTGTGCGA	GACAGTCTTAGCACAGACACACGCT
SEQ ID NO: 4472	**1081017**	TTCGAAAATCGTGCGAGTGCATAAT	AAGCTTTTAGCACGCTCACGTATTA
SEQ ID NO: 4473	**1081598**	CTCTGGGTATCGAAGTCTGTTCCGT	GAGACCCATAGCTTCAGACAAGGCA
SEQ ID NO: 4474	**1082797**	GATTCTCCATCGTCGTCGTTGTCGC	CTAAGAGGTAGCAGCAGCAACAGCG
SEQ ID NO: 4475	**1082899**	ACCCTCGCCTCCATGAGCATACGGG	TGGGAGCGGAGGTACTCGTATGCCC
SEQ ID NO: 4476	**1083641**	NA	NA
SEQ ID NO: 4477	**1083867**	CTGTCCGGCTCCTCTTATTTAAGTG	GACAGGCCGAGGAGAATAAATTCAC
SEQ ID NO: 4478	**1083911**	NA	NA
SEQ ID NO: 4479	**1083949**	CTCGTCCTCCTCCATGTACATTATA	GAGCAGGAGGAGGTACATGTAATAT
SEQ ID NO: 4480	**1085462**	TCGTAACGTCGCCTCCTAGAACGTA	AGCATTGCAGCGGAGGATCTTGCAT
SEQ ID NO: 4481	**1085539**	CAGTCGCTCCTCCTCGCTGCCAATG	GTCAGCGAGGAGGAGCGACGGTTAC
SEQ ID NO: 4482	**1085813**	AAACCGACCTCCACGGGACACACGG	TTTGGCTGGAGGTGCCCTGTGTGCC
SEQ ID NO: 4483	**1086244**	TTCCACACCTCCTCGAGAAGGACGT	AAGGTGTGGAGGAGCTCTTCCTGCA
SEQ ID NO: 4484	**1087817**	AACTACTATAGCTCCGTCCTCGTGG	TTGATGATATCGAGGCAGGAGCACC
SEQ ID NO: 4485	**1087894**	GGCCGCCGCTCAGCCAGGCTCCCGG	CCGGCGGCGAGTCGGTCCGAGGGCC
SEQ ID NO: 4486	**1088093**	GAACCGTCTCCTCATTAAGTTAGGG	CTTGGCAGAGGAGTAATTCAATCCC
SEQ ID NO: 4487	**1088269**	ATACCTCGACCTCAGATATTCGGTG	TATGGAGCTGGAGTCTATAAGCCAC
SEQ ID NO: 4488	**1088899**	ACGTGGACTCCTCATCGTCGTGACG	TGCACCTGAGGAGTAGCAGCACTGC
SEQ ID NO: 4489	**1089834**	GGAGCACCCTCACCACAGGCCCGGA	CCTCGTGGGAGTGGTGTCCGGGCCT
SEQ ID NO: 4490	**1090280**	CACCTTCCTCACCTCATAAAGAGGT	GTGGAAGGAGTGGAGTATTTCTCCA

SEQ ID NO: 4491	**1090342**	CTTCCGCCTCACCTCATTGTTGGAG	GAAGGCGGAGTGGAGTAACAACCTC
SEQ ID NO: 4492	**1090733**	CCAAGGCTCACGAGACGCCTGAGGT	GGTTCCGAGTGCTCTGCGGACTCCA
SEQ ID NO: 4493	**1095295**	AGGAACCTCTCAATGTCGTGTGTCA	TCCTTGGAGAGTTACAGCACACAGT
SEQ ID NO: 4494	**1095492**	GGTCCCACGTCTCCTTCTACTGTCG	CCAGGGTGCAGAGGAAGATGACAGC
SEQ ID NO: 4495	**1095769**	GTCCTCTGATCTCATGTCTCTCGTA	CAGGAGACTAGAGTACAGAGAGCAT
SEQ ID NO: 4496	**1096478**	CTTCCTGTCTCATACGACATTGGTG	GAAGGACAGAGTATGCTGTAACCAC
SEQ ID NO: 4497	**1098344**	AGTGCCGCCTCTTTCTCGATCAGTG	TCACGGCGGAGAAAGAGCTAGTCAC
SEQ ID NO: 4498	**1099565**	ATTTTCCTCTGAGGTGTGGTGTCCA	TAAAAGGAGACTCCACACCACAGGT
SEQ ID NO: 4499	**1100002**	CTTGTGCCTCTCTATTTGTGTGCGG	GAACACGGAGAGATAAACACACGCC
SEQ ID NO: 4500	**1101287**	ATCTCACTCCTCTCGGGACAAGTCG	TAGAGTGAGGAGAGCCCTGTTCAGC
SEQ ID NO: 4501	**1102005**	CTTACCTGCTCTGTGGTGGTAGTCA	GAATGGACGAGACACCACCATCAGT
SEQ ID NO: 4502	**1104141**	CATAATATCTCTGTGTGTGCGGAAC	GTATTATAGAGACACACACGCCTTG
SEQ ID NO: 4503	**1105659**	CCACCTCTCTCTATGTGGTGTGACG	GGTGGAGAGAGATACACCACACTGC
SEQ ID NO: 4504	**1108024**	CTAACACCGACTCCGCGGTGCGAAG	GATTGTGGCTGAGGCGCCACGCTTC
SEQ ID NO: 4505	**1108205**	ACTTCGTCACACTCACCTTTTCATT	TGAAGCAGTGTGAGTGGAAAAGTAA
SEQ ID NO: 4506	**1108326**	ACACTCACACACTCATCCTCTCTCC	TGTGAGTGTGTGAGTAGGAGAGAGG
SEQ ID NO: 4507	**1109590**	GTGTGTGTGAACTCAACGGACCCAC	CACACACACTTGAGTTGCCTGGGTG
SEQ ID NO: 4508	**1110302**	ACGTCGTCAACGACTCCGCGGTCGA	TGCAGCAGTTGCTGAGGCGCCAGCT
SEQ ID NO: 4509	**1110520**	TGTGTGTGCGACTCCGAGGACCCTT	ACACACACGCTGAGGCTCCTGGGAA
SEQ ID NO: 4510	**1110803**	CCACCGTCACTCACGAGGACGAGGT	GGTGGCAGTGAGTGCTCCTGCTCCA
SEQ ID NO: 4511	**1111200**	GTCTCCGCCGTACTCATGTCATCGG	CAGAGGCGGCATGAGTACAGTAGCC

SEQ ID NO: 4512	**1113286**	CTGTATCAACTCTTCACGTAAGGTC	GACATAGTTGAGAAGTGCATTCCAG
SEQ ID NO: 4513	**1113483**	GTGTCACTGTCACTCTTTGACGCGA	CACAGTGACAGTGAGAAACTGCGCT
SEQ ID NO: 4514	**1114014**	ACCGTCTCCACTCTCAGGTTGGGTC	TGGCAGAGGTGAGAGTCCAACCCAG
SEQ ID NO: 4515	**1114111**	CTCCGTCCACTCTTAGGGTAGAAGT	GAGGCAGGTGAGAATCCCATCTTCA
SEQ ID NO: 4516	**1114714**	AGTTATGTCTACTCTTGTGTGTGGT	TCAATACAGATGAGAACACACACCA
SEQ ID NO: 4517	**1115781**	GTCCGACACCACTCTAATCCTTTAG	CAGGCTGTGGTGAGATTAGGAAATC
SEQ ID NO: 4518	**1115925**	TCGCCTCTGCTCGTGCGAGTGCGTG	AGCGGAGACGAGCACGCTCACGCAC
SEQ ID NO: 4519	**1116691**	ATTTCACCTCGACCACACTCTTATT	TAAAGTGGAGCTGGTGTGAGAATAA
SEQ ID NO: 4520	**1119528**	CACCCGTCCTCGTATTAAGATACCA	GTGGGCAGGAGCATAATTCTATGGT
SEQ ID NO: 4521	**1120943**	GGTCCCTCACTCGTGCCATGGTTAA	CCAGGGAGTGAGCACGGTACCAATT
SEQ ID NO: 4522	**1121826**	GTCACCTCGCCTCGTTAGTACTGAG	CAGTGGAGCGGAGCAATCATGACTC
SEQ ID NO: 4523	**1121977**	GTCGCCTCTGCTCGTGCGAGTGCGT	CAGCGGAGACGAGCACGCTCACGCA
SEQ ID NO: 4524	**1122008**	GTTCTCAACCTCGTCAATTGTGGTG	CAAGAGTTGGAGCAGTTAACACCAC
SEQ ID NO: 4525	**1122530**	CTCTTTCACTCGCACACGCGACGTC	GAGAAAGTGAGCGTGTGCGCTGCAG
SEQ ID NO: 4526	**1122866**	GTCCGGACACCTCGTCGTGTGTGGT	CAGGCCTGTGGAGCAGCACACACCA
SEQ ID NO: 4527	**1123886**	ATTGAAACTCGTACAATGGGTCGGG	TAACTTTGAGCATGTTACCCAGCCC
SEQ ID NO: 4528	**1124831**	CTGTCTACACACTCGTCTTCAAGAG	GACAGATGTGTGAGCAGAAGTTCTC
SEQ ID NO: 4529	**1125071**	AAAAAACTCGGAAGGTCGCGGTCAA	TTTTTTGAGCCTTCCAGCGCCAGTT
SEQ ID NO: 4530	**1125250**	ACCATCAACTCGTGTGTGTAGTGTT	TGGTAGTTGAGCACACACATCACAA
SEQ ID NO: 4531	**1125507**	GTACGTGTACGCACACTCGCGGCTC	CATGCACATGCGTGTGAGCGCCGAG
SEQ ID NO: 4532	**1126265**	GTACGTGTCCACACTCGTACGTATG	CATGCACAGGTGTGAGCATGCATAC

SEQ ID NO: 4533	**1126716**	GACACACGCACACTCGTTCGGAGCT	CTGTGTGCGTGTGAGCAAGCCTCGA
SEQ ID NO: 4534	**1126947**	NA	NA
SEQ ID NO: 4535	**1127072**	AGACGGTGTGGTTTGTTGCCCTAAC	TCTGCCACACCAAACAACGGGATTG
SEQ ID NO: 4536	**1127237**	TACCGGAGGGTTGTTTTGTGTCTGT	ATGGCCTCCCAACAAAACACAGACA
SEQ ID NO: 4537	**1127274**	CATGATCGGTTTGGTTGGGACGAAT	GTACTAGCCAAACCAACCCTGCTTA
SEQ ID NO: 4538	**1127566**	TAAGAGGTGGTTGGTCGAAATAGAA	ATTCTCCACCAACCAGCTTTATCTT
SEQ ID NO: 4539	**1129021**	CGACTTAGGGTTGTTGTGAAGCGTT	GCTGAATCCCAACAACACTTCGCAA
SEQ ID NO: 4540	**1129284**	ACCAAGAGGTTTATTGTTGACACAC	TGGTTCTCCAAATAACAACTGTGTG
SEQ ID NO: 4541	**1129576**	GCCAAGGGTTGGTCGGATCTACTCT	CGGTTCCCAACCAGCCTAGATGAGA
SEQ ID NO: 4542	**1130271**	TCGTACTCCAGGTTGGAACTTGAGG	AGCATGAGGTCCAACCTTGAACTCC
SEQ ID NO: 4543	**1130402**	GCCCTGGGTTGTGTGATTCCCGTGA	CGGGACCCAACACACTAAGGGCACT
SEQ ID NO: 4544	**1130581**	GACACTTAGGGTTGGTCGTCGCAGT	CTGTGAATCCCAACCAGCAGCGTCA
SEQ ID NO: 4545	**1130724**	CTTATCAGGTTGGTGTGTGTCCACC	GAATAGTCCAACCACACACAGGTGG
SEQ ID NO: 4546	**1130735**	AAGAGGTGGTTGGTCGAAATAGAAC	TTCTCCACCAACCAGCTTTATCTTG
SEQ ID NO: 4547	**1130842**	ATACAACAGGTTGGTGTCTGTCCTG	TATGTTGTCCAACCACAGACAGGAC
SEQ ID NO: 4548	**1130894**	CACTCACCGGTTGGGTGGTCCTTAG	GTGAGTGGCCAACCCACCAGGAATC
SEQ ID NO: 4549	**1131071**	ATTTCTACGGTTGTCTTTCTCTGTG	TAAAGATGCCAACAGAAAGAGACAC
SEQ ID NO: 4550	**1131238**	AGTTAATCGGTTTTTGCTCTGCGGT	TCAATTAGCCAAAAACGAGACGCCA
SEQ ID NO: 4551	**1132093**	AGTCCTTCGGTTGTGTGTGTCGACC	TCAGGAAGCCAACACACACAGCTGG
SEQ ID NO: 4552	**1133227**	GTATTTTGGTTCTGTTCGTTGTCTT	CATAAAACCAAGACAAGCAACAGAA
SEQ ID NO: 4553	**1133719**	ATCTATCGTCGGTTGTTCGAGTCCC	TAGATAGCAGCCAACAAGCTCAGGG

SEQ ID NO: 4554	**1134040**	CTTTGTGGTTCCCAGCGACGTGTAT	GAAACACCAAGGGTCGCTGCACATA
SEQ ID NO: 4555	**1134482**	ACATCGGTGGTTCGGAGAAGGACAC	TGTAGCCACCAAGCCTCTTCCTGTG
SEQ ID NO: 4556	**1135010**	ACGTGGGTCGGTTCACATAATATAA	TGCACCCAGCCAAGTGTATTATATT
SEQ ID NO: 4557	**1136082**	GGACCTAGTGGTTCGGTGTTCAAAC	CCTGGATCACCAAGCCACAAGTTTG
SEQ ID NO: 4558	**1136228**	AGTAAGAATGTTTGGTGTTTTCCTA	TCATTCTTACAAACCACAAAAGGAT
SEQ ID NO: 4559	**1136229**	GTGAATCCGTGTTTGTGGTTTAGTA	CACTTAGGCACAAACACCAAATCAT
SEQ ID NO: 4560	**1136900**	GACGTGGGTCGGTTCACATAATATA	CTGCACCCAGCCAAGTGTATTATAT
SEQ ID NO: 4561	**1137149**	TGGTGGTGGTTACTGCTACGATGTC	ACCACCACCAATGACGATGCTACAG
SEQ ID NO: 4562	**1137319**	CCTATTCGGTTCGTGTGTGAAAAGT	GGATAAGCCAAGCACACACTTTTCA
SEQ ID NO: 4563	**1138388**	CGACGGTGTGTGTTGCAAGGAGACC	GCTGCCACACACAACGTTCCTCTGG
SEQ ID NO: 4564	**1139130**	ACACTGTGTGTGTTGTGGCCTATCG	TGTGACACACACAACACCGGATAGC
SEQ ID NO: 4565	**1139693**	TTAGGCTTGTTGTCGACTTGATCAG	AATCCGAACAACAGCTGAACTAGTC
SEQ ID NO: 4566	**1140100**	ATAATCGTTGTTGTTTTGAGTTCTC	TATTAGCAACAACAAAACTCAAGAG
SEQ ID NO: 4567	**1140152**	TAAAGTGTTGTTTGTCTGGTTTCCC	ATTTCACAACAAACAGACCAAAGGG
SEQ ID NO: 4568	**1140268**	TGACGCGAGTTGTTGTTTAGGGTCA	ACTGCGCTCAACAACAAATCCCAGT
SEQ ID NO: 4569	**1140321**	GTCGTTGTTTGTTTGAGTCCTCCTA	CAGCAACAAACAAACTCAGGAGGAT
SEQ ID NO: 4570	**1140400**	GGAAACGTTGTTGGTTGGATTACAT	CCTTTGCAACAACCAACCTAATGTA
SEQ ID NO: 4571	**1140603**	CACGAGAGTTGTTGGTCGGCGAACT	GTGCTCTCAACAACCAGCCGCTTGA
SEQ ID NO: 4572	**1140616**	ACTCGTGTCGTTGTTTTGTTATCAT	TGAGCACAGCAACAAAACAATAGTA
SEQ ID NO: 4573	**1141515**	NA	NA
SEQ ID NO: 4574	**1142707**	TTGTAGTATTGTTCGAGTGTGTACG	AACATCATAACAAGCTCACACATGC

SEQ ID NO: 4575	**1143226**	TCTGCTATCTGTTCTTGTGTTTACG	AGACGATAGACAAGAACACAAATGC
SEQ ID NO: 4576	**1143598**	AAAATTGTTCCGGTGTGGTGTCCCT	TTTTAACAAGGCCACACCACAGGGA
SEQ ID NO: 4577	**1143635**	GTGTCTTCGGTGTTGGCTTCCGTTC	CACAGAAGCCACAACCGAAGGCAAG
SEQ ID NO: 4578	**1144748**	ATGCGGCGTGTTTTCTGGTAATCCT	TACGCCGCACAAAAGACCATTAGGA
SEQ ID NO: 4579	**1144765**	AATCGTTTGTTCGTGTACAGTGCCC	TTAGCAAACAAGCACATGTCACGGG
SEQ ID NO: 4580	**1144773**	GTCCGTGAGTGTGTTTTCCCGATGT	CAGGCACTCACACAAAAGGGCTACA
SEQ ID NO: 4581	**1145095**	AGGTATGGTGTTTGTAGTCGTGTTC	TCCATACCACAAACATCAGCACAAG
SEQ ID NO: 4582	**1145352**	GTAGTGATGGTGTTTCCCTTCTTCC	CATCACTACCACAAAGGGAAGAAGG
SEQ ID NO: 4583	**1145471**	AGGACCGAGTGTTGTGTGTAACAAA	TCCTGGCTCACAACACACATTGTTT
SEQ ID NO: 4584	**1145659**	GTCACCGCGTGTGTTTAGAAATTCC	CAGTGGCGCACACAAATCTTTAAGG
SEQ ID NO: 4585	**1145787**	CAAAAGTGTTTTGGTGGTGGTAGTA	GTTTTCACAAAACCACCACCATCAT
SEQ ID NO: 4586	**1145979**	GTACCTAGGTGTGTTTCGGTTCCTT	CATGGATCCACACAAAGCCAAGGAA
SEQ ID NO: 4587	**1146015**	GTCCACGTGTGTGTTGGACCGACCC	CAGGTGCACACACAACCTGGCTGGG
SEQ ID NO: 4588	**1146019**	ACACAGACTGTGTTGGGTGAAGAAT	TGTGTCTGACACAACCCACTTCTTA
SEQ ID NO: 4589	**1146086**	ACCCGTGTGTGTTTCGACCGTCCAC	TGGGCACACACAAAGCTGGCAGGTG
SEQ ID NO: 4590	**1146517**	CGCTGGTGTGTTCGTTCGTCCTCCA	GCGACCACACAAGCAAGCAGGAGGT
SEQ ID NO: 4591	**1147593**	ACGGTCGGGTGTTCTCATTATCGGG	TGCCAGCCCACAAGAGTAATAGCCC
SEQ ID NO: 4592	**1147951**	NA	NA
SEQ ID NO: 4593	**1149187**	NA	NA
SEQ ID NO: 4594	**1149817**	CCGACCAAGTTGGTGTCCGGTACCC	GGCTGGTTCAACCACAGGCCATGGG
SEQ ID NO: 4595	**1150502**	GTTTGAAAGTTTCGCTCTCGGGGAA	CAAACTTTCAAAGCGAGAGCCCCTT

SEQ ID NO: 4596	**1153031**	ATAGATCCAGTTCTTTTTGCCCGTC	TATCTAGGTCAAGAAAAACGGGCAG
SEQ ID NO: 4597	**1154465**	GGAAGACTACAGTTCTACACAAGTC	CCTTCTGATGTCAAGATGTGTTCAG
SEQ ID NO: 4598	**1154623**	AACCACGTGAGTTTTTGTGCGTGCC	TTGGTGCACTCAAAAACACGCACGG
SEQ ID NO: 4599	**1155774**	CATTATAGAGTTCGTGTTCGTGTCG	GTAATATCTCAAGCACAAGCACAGC
SEQ ID NO: 4600	**1158639**	GGTGTTGGTGTGGATCCCTACGAAA	CCACAACCACACCTAGGGATGCTTT
SEQ ID NO: 4601	**1158895**	TAAGGTGGTAGTTCACACCGAGAGG	ATTCCACCATCAAGTGTGGCTCTCC
SEQ ID NO: 4602	**1159436**	CGGCGACAGTGTGCGTGTCACCCAG	GCCGCTGTCACACGCACAGTGGGTC
SEQ ID NO: 4603	**1159959**	CCCTGTGGTGGGTTAAGTGCATACC	GGGACACCACCCAATTCACGTATGG
SEQ ID NO: 4604	**1160010**	TGGCCCGGTGGTGTAGTCAGATTAC	ACCGGGCCACCACATCAGTCTAATG
SEQ ID NO: 4605	**1160032**	GTAAGTGTGTAGGTGGGTCCATCCT	CATTCACACATCCACCCAGGTAGGA
SEQ ID NO: 4606	**1160056**	GTGTCGTGTTCGGTGGTGGCTTTCA	CACAGCACAAGCCACCACCGAAAGT
SEQ ID NO: 4607	**1160166**	AACAATGGTGGTGGTCCGGTAGACA	TTGTTACCACCACCAGGCCATCTGT
SEQ ID NO: 4608	**1160189**	CCTCCGACGGTGGTGACGAACCCTA	GGAGGCTGCCACCACTGCTTGGGAT
SEQ ID NO: 4609	**1160191**	CCGTTATGTGTGGTTGGTTACTTTC	GGCAATACACACCAACCAATGAAAG
SEQ ID NO: 4610	**1160193**	ACATGGGGTGGTTTGTCTCTTCGCC	TGTACCCCACCAAACAGAGAAGCGG
SEQ ID NO: 4611	**1160265**	ATTTGTGGTGGCGTAGTGACGTAAC	TAAACACCACCGCATCACTGCATTG
SEQ ID NO: 4612	**1160377**	CCAAGTCGGTGGTGTACATGTGCAT	GGTTCAGCCACCACATGTACACGTA
SEQ ID NO: 4613	**1160448**	NA	NA
SEQ ID NO: 4614	**1160449**	GGTCCTGGGTGGGATACACTATCCT	CCAGGACCCACCCTATGTGATAGGA
SEQ ID NO: 4615	**1160524**	NA	NA
SEQ ID NO: 4616	**1160579**	ACTTGGTGGTGGCTCTCGTTAAACA	TGAACCACCACCGAGAGCAATTTGT

SEQ ID NO: 4617	**1160628**	TTTGCTAGGTGGTGGATCAGGTATA	AAACGATCCACCACCTAGTCCATAT
SEQ ID NO: 4618	**1160849**	ACTGGTTGGTGGGTCGAAACCCTTC	TGACCAACCACCCAGCTTTGGGAAG
SEQ ID NO: 4619	**1160922**	CATTTGGTGGTGGTGTAATCGAATC	GTAAACCACCACCACATTAGCTTAG
SEQ ID NO: 4620	**1160930**	CTGTTCAGGTGCTGGTGAAAAACGC	GACAAGTCCACGACCACTTTTTGCG
SEQ ID NO: 4621	**1160961**	ACACCCTAGGTGGTCGTGGGTTGTC	TGTGGGATCCACCAGCACCCAACAG
SEQ ID NO: 4622	**1161034**	CATGAGGTGTGCGTGCTACGCGCTC	GTACTCCACACGCACGATGCGCGAG
SEQ ID NO: 4623	**1161316**	NA	NA
SEQ ID NO: 4624	**1161617**	TTGTGTCGACGGTGCCGAACGCCCA	AACACAGCTGCCACGGCTTGCGGGT
SEQ ID NO: 4625	**1162541**	TGGCTCCGGTGCTTGTGCTACTTCA	ACCGAGGCCACGAACACGATGAAGT
SEQ ID NO: 4626	**1162574**	ACTAGATGTCGGTGGGTCTATTCTC	TGATCTACAGCCACCCAGATAAGAG
SEQ ID NO: 4627	**1162575**	CGAGTTGCGGTGGTGTTTCTCTGCA	GCTCAACGCCACCACAAAGAGACGT
SEQ ID NO: 4628	**1162647**	AGTGTTCGTGGTGCTACGGAATTTT	TCACAAGCACCACGATGCCTTAAAA
SEQ ID NO: 4629	**1162798**	GAACGTTCGTGGTGCTTGTTCGACT	CTTGCAAGCACCACGAACAAGCTGA
SEQ ID NO: 4630	**1163068**	CCTCGGGGTGCGTGCAGACATTGAA	GGAGCCCCACGCACGTCTGTAACTT
SEQ ID NO: 4631	**1163247**	CCCGTGTGGTGCACGAGTGTCCTGA	GGGCACACCACGTGCTCACAGGACT
SEQ ID NO: 4632	**1163317**	TTATCGTGAGTGTGGATCCAAGGTT	AATAGCACTCACACCTAGGTTCCAA
SEQ ID NO: 4633	**1163387**	TTCCGGTGGTGCAACGATACGGCCT	AAGGCCACCACGTTGCTATGCCGGA
SEQ ID NO: 4634	**1163559**	CCTGGTGGTGCTTGTCGGCACACCC	GGACCACCACGAACAGCCGTGTGGG
SEQ ID NO: 4635	**1163734**	ATTCGGTGGTGCGACTTTCTTCGAG	TAAGCCACCACGCTGAAAGAAGCTC
SEQ ID NO: 4636	**1164453**	GTCGGCGACAGTGTGCGTGTCACCC	CAGCCGCTGTCACACGCACAGTGGG
SEQ ID NO: 4637	**1164832**	CCCTAAGGTGACAGTGTTTTGTATT	GGGATTCCACTGTCACAAAACATAA

SEQ ID NO: 4638	**1165760**	CATACTGAGTGTGCTGTGGTCATCA	GTATGACTCACACGACACCAGTAGT
SEQ ID NO: 4639	**1166104**	TCAAGTAAGGTGACGTGCGTGACTC	AGTTCATTCCACTGCACGCACTGAG
SEQ ID NO: 4640	**1166192**	GCCCGGTTCGTGTGCGGCTTGCCCT	CGGGCCAAGCACACGCCGAACGGGA
SEQ ID NO: 4641	**1166347**	CTTGTCTTGTGGGTGGAATCGAGAA	GAACAGAACACCCACCTTAGCTCTT
SEQ ID NO: 4642	**1166924**	ACTTAGGGTGTGGGTGTCATGATAA	TGAATCCCACACCCACAGTACTATT
SEQ ID NO: 4643	**1166984**	GCATCTGCGTGTGGCCGCAGCCTCG	CGTAGACGCACACCGGCGTCGGAGC
SEQ ID NO: 4644	**1167012**	CGCGTCGGATGTGCGTGGTCAAAGA	GCGCAGCCTACACGCACCAGTTTCT
SEQ ID NO: 4645	**1167206**	GGTGGAGTGTGTGCCTAGTCAACAC	CCACCTCACACACGGATCAGTTGTG
SEQ ID NO: 4646	**1167218**	CCCAGTGTGTGGTTTCACCTCCGAG	GGGTCACACACCAAAGTGGAGGCTC
SEQ ID NO: 4647	**1167233**	CACATTTGTGGTGGCGTGATACTAA	GTGTAAACACCACCGCACTATGATT
SEQ ID NO: 4648	**1167338**	AACATTTGTGGTGGCGTGAGTCTCG	TTGTAAACACCACCGCACTCAGAGC
SEQ ID NO: 4649	**1167339**	AACATTTGTGGGGACGTGAGTCTAG	TTGTAAACACCCCTGCACTCAGATC
SEQ ID NO: 4650	**1167357**	GCGGCGCCGTGTGCGCGTGGATGCA	CGCCGCGGCACACGCGCACCTACGT
SEQ ID NO: 4651	**1167435**	GTCGTGGGTTGTGCGTCATTACTCT	CAGCACCCAACACGCAGTAATGAGA
SEQ ID NO: 4652	**1167485**	CGTACCCGTTGTGGTGTGACGAACA	GCATGGGCAACACCACACTGCTTGT
SEQ ID NO: 4653	**1167528**	GGCGGTGTCTGTGCTCCCTCCAGGA	CCGCCACAGACACGAGGGAGGTCCT
SEQ ID NO: 4654	**1167535**	CTCCCTGTGTGGGTCGAGACATTCC	GAGGGACACACCCAGCTCTGTAAGG
SEQ ID NO: 4655	**1167603**	AGTCTCCGTTGTGGTGCCCGTCCCT	TCAGAGGCAACACCACGGGCAGGGA
SEQ ID NO: 4656	**1167640**	GGTTGTTTGTGGTCCGCTACTCGTC	CCAACAAACACCAGGCGATGAGCAG
SEQ ID NO: 4657	**1167646**	TCGTTTCGTTGTGGTTGTCGACCGA	AGCAAAGCAACACCAACAGCTGGCT
SEQ ID NO: 4658	**1167687**	CTTCTGTTGTGCCTGTTGGAGAGGA	GAAGACAACACGGACAACCTCTCCT

SEQ ID NO: 4659	**1168514**	ACCCTCCGTGTGGAATGTGTGCTCG	TGGGAGGCACACCTTACACACGAGC
SEQ ID NO: 4660	**1168588**	TTCGTAGCGGTGTGGGTGTTACCAA	AAGCATCGCCACACCCACAATGGTT
SEQ ID NO: 4661	**1168792**	NA	NA
SEQ ID NO: 4662	**1168878**	GTTTATACGTGTGTGCCTCCCGCAA	CAAATATGCACACACGGAGGGCGTT
SEQ ID NO: 4663	**1168917**	ACAGTCCGGTGTGAGTCTGGCTAAT	TGTCAGGCCACACTCAGACCGATTA
SEQ ID NO: 4664	**1169091**	CCGTGTAGAGTGTGGATTCGTATTT	GGCACATCTCACACCTAAGCATAAA
SEQ ID NO: 4665	**1169304**	ACAGTGGTGTGTGACATTTTATGGC	TGTCACCACACACTGTAAAATACCG
SEQ ID NO: 4666	**1169377**	TTGGTTTGTGCGTCCAAGTCATCCC	AACCAAACACGCAGGTTCAGTAGGG
SEQ ID NO: 4667	**1169415**	ACATCGTGGTGTGGGTATTATTGGT	TGTAGCACCACACCCATAATAACCA
SEQ ID NO: 4668	**1169502**	CTCCTTGTGTGGTAGTGAGGCTCCA	GAGGAACACACCATCACTCCGAGGT
SEQ ID NO: 4669	**1169641**	CCTTGTGTGTGGTTACTCCTCGGGT	GGAACACACACCAATGAGGAGCCCA
SEQ ID NO: 4670	**1169710**	GTACAACAGTGTGTGGTGTGCCTTC	CATGTTGTCACACACCACACGGAAG
SEQ ID NO: 4671	**1169821**	CCCGTGGTGTGGTGCGAGCGAACCG	GGGCACCACACCACGCTCGCTTGGC
SEQ ID NO: 4672	**1169843**	ATATATGTGTGTGCGGTTAGTTCCC	TATATACACACACGCCAATCAAGGG
SEQ ID NO: 4673	**1169847**	GGGTAAGTGTGTGCTAGAGTGGGTA	CCCATTCACACACGATCTCACCCAT
SEQ ID NO: 4674	**1170082**	CCCGTTGTGTGGTGTCCTATCACCC	GGGCAACACACCACAGGATAGTGGG
SEQ ID NO: 4675	**1170107**	AGAGGAGTGTGTGGTCTGTCGAGTG	TCTCCTCACACACCAGACAGCTCAC
SEQ ID NO: 4676	**1170571**	ACATAGTCGTGTGTGGTTGAAGTCG	TGTATCAGCACACACCAACTTCAGC
SEQ ID NO: 4677	**1170642**	TGGTGTCTTGTGAGTAGGTGGTGTC	ACCACAGAACACTCATCCACCACAG
SEQ ID NO: 4678	**1171016**	AGAATTTCGTGGTGTAGTTGGAATT	TCTTAAAGCACCACATCAACCTTAA
SEQ ID NO: 4679	**1171259**	GCACCTAGGTGTGCGTGTCACCCGA	CGTGGATCCACACGCACAGTGGGCT

SEQ ID NO: 4680	**1171410**	ACGTGTTTCGTGTGACGCATCTAGG	TGCACAAAGCACACTGCGTAGATCC
SEQ ID NO: 4681	**1171412**	ATATTCCTGTGACGGTGGTTGTTTA	TATAAGGACACTGCCACCAACAAAT
SEQ ID NO: 4682	**1171781**	TTTGTGGTGTGACGTGAACTTGGTC	AAACACCACACTGCACTTGAACCAG
SEQ ID NO: 4683	**1171811**	CCCGACCTGTGTGTGTCGAAGGACG	GGGCTGGACACACACAGCTTCCTGC
SEQ ID NO: 4684	**1171851**	CCTCTATGTGTGAGTGGAACTAACC	GGAGATACACACTCACCTTGATTGG
SEQ ID NO: 4685	**1171934**	AAGTGTCGGGTGTTCAGGAAAAACT	TTCACAGCCCACAAGTCCTTTTTGA
SEQ ID NO: 4686	**1172008**	ATGCGGTGGTGTGAAGTGGAAATAG	TACGCCACCACACTTCACCTTTATC
SEQ ID NO: 4687	**1172034**	ATGTGTCCGTGTGAACGTGCTGCTC	TACACAGGCACACTTGCACGACGAG
SEQ ID NO: 4688	**1172091**	ACGGTGTTGGTGTGGATCCCTACGA	TGCCACAACCACACCTAGGGATGCT
SEQ ID NO: 4689	**1172182**	AATACGCTCGGTGTGACGGCCAAAC	TTATGCGAGCCACACTGCCGGTTTG
SEQ ID NO: 4690	**1172216**	ACACATGTGTGTGATGACTCTAGGT	TGTGTACACACACTACTGAGATCCA
SEQ ID NO: 4691	**1172400**	GGTAACGTGTGTGTGTAAAAATATC	CCATTGCACACACACATTTTTATAG
SEQ ID NO: 4692	**1172413**	TCCTTGTTGTGTGAAGTCAACCCGA	AGGAACAACACACTTCAGTTGGGCT
SEQ ID NO: 4693	**1172414**	GTCCTCTGTGTGTGAAAGCCCTCCG	CAGGAGACACACACTTTCGGGAGGC
SEQ ID NO: 4694	**1172630**	AGAAAAGGTGTGTGGTTACTGAAGA	TCTTTTCCACACACCAATGACTTCT
SEQ ID NO: 4695	**1172685**	CCGAGTTGTGTGAGTATCGACAGAA	GGCTCAACACACTCATAGCTGTCTT
SEQ ID NO: 4696	**1172800**	TTTGCGGTGTGATAAGTACCAGACC	AAACGCCACACTATTCATGGTCTGG
SEQ ID NO: 4697	**1172938**	AGTCGGCGTGTGTGACCGAGACACC	TCAGCCGCACACACTGGCTCTGTGG
SEQ ID NO: 4698	**1173167**	ACGTGTAGTCTGTGTGAGTTCCCTC	TGCACATCAGACACACTCAAGGGAG
SEQ ID NO: 4699	**1173176**	ATTGGTGGTGTAGCAGAAAAACGTT	TAACCACCACATCGTCTTTTTGCAA
SEQ ID NO: 4700	**1173193**	CCGTATCGAGTGTGTAATAACGTAA	GGCATAGCTCACACATTATTGCATT

SEQ ID NO: 4701	**1173203**	NA	NA
SEQ ID NO: 4702	**1173220**	NA	NA
SEQ ID NO: 4703	**1173267**	ACCGTCGTGTAGTGTGACGTCTCAT	TGGCAGCACATCACACTGCAGAGTA
SEQ ID NO: 4704	**1173287**	CGCCAGTGGTGTGTGGTCCTTCAGT	GCGGTCACCACACACCAGGAAGTCA
SEQ ID NO: 4705	**1173401**	CTTTGTGGTGTGTCTTGGTTTTGCT	GAAACACCACACAGAACCAAAACGA
SEQ ID NO: 4706	**1173412**	CTACTTGTGGTGTGACTGTTGGACC	GATGAACACCACACTGACAACCTGG
SEQ ID NO: 4707	**1173454**	TACATATGGGTGTGTCTGGTAATAC	ATGTATACCCACACAGACCATTATG
SEQ ID NO: 4708	**1173589**	ATTGTGGGTGTCATGGATAGAAGTA	TAACACCCACAGTACCTATCTTCAT
SEQ ID NO: 4709	**1173602**	CAGGGTGGTGTGCTTTCTCATCGAA	GTCCCACCACACGAAAGAGTAGCTT
SEQ ID NO: 4710	**1173603**	GCATGGTGGTGTGCATTCACTCCCA	CGTACCACCACACGTAAGTGAGGGT
SEQ ID NO: 4711	**1173646**	ATGGTGGGTGTTTTGTATCGTTTGT	TACCACCCACAAAACATAGCAAACA
SEQ ID NO: 4712	**1173817**	ATCTGGGGTGTGTGTAATAGTTCAT	TAGACCCCACACACATTATCAAGTA
SEQ ID NO: 4713	**1173847**	ACTTCTGAGGTGTGGTGAGTATGTC	TGAAGACTCCACACCACTCATACAG
SEQ ID NO: 4714	**1173972**	CTAATTGGTGTTTGTGCTAGTCCAG	GATTAACCACAAACACGATCAGGTC
SEQ ID NO: 4715	**1174437**	AAGTACCCGGTGTGTGAATTCGCAT	TTCATGGGCCACACACTTAAGCGTA
SEQ ID NO: 4716	**1174465**	TGCCTGGGTGTCTGTGCTCGAACAC	ACGGACCCACAGACACGAGCTTGTG
SEQ ID NO: 4717	**1174565**	TACCGTGTAGGGTGTGAACTTACAC	ATGGCACATCCCACACTTGAATGTG
SEQ ID NO: 4718	**1174576**	GGTCCGACCGGTGTCACCAGTCACA	CCAGGCTGGCCACAGTGGTCAGTGT
SEQ ID NO: 4719	**1174737**	ATATGAGGGTGTGCGTTACATACCC	TATACTCCCACACGCAATGTATGGG
SEQ ID NO: 4720	**1174764**	CGTAGGTCGAGGTGTGCTAGTCTCT	GCATCCAGCTCCACACGATCAGAGA
SEQ ID NO: 4721	**1174774**	CTACTTGTGGTGTGTTCTAGACTTC	GATGAACACCACACAAGATCTGAAG

SEQ ID NO: 4722	**1174787**	AGAGCTTGGTGTCCGTGGCACTCAA	TCTCGAACCACAGGCACCGTGAGTT
SEQ ID NO: 4723	**1174817**	AACTTCGGGTGTGTCTCGACCCACT	TTGAAGCCCACACAGAGCTGGGTGA
SEQ ID NO: 4724	**1174819**	TCTATCAGAGGTGTGTTGTGTGACC	AGATAGTCTCCACACAACACACTGG
SEQ ID NO: 4725	**1174853**	ATAACGTGGGTGTAGTAACGGAGTC	TATTGCACCCACATCATTGCCTCAG
SEQ ID NO: 4726	**1174924**	ACCTCTGTCGGTGTGCTTTAGTCCT	TGGAGACAGCCACACGAAATCAGGA
SEQ ID NO: 4727	**1175261**	CGTGTGTCTCGGTGTTGTCCTCAAC	GCACACAGAGCCACAACAGGAGTTG
SEQ ID NO: 4728	**1175448**	GACGATCGGTCGGTGTGTCCTTCGT	CTGCTAGCCAGCCACACAGGAAGCA
SEQ ID NO: 4729	**1175512**	CGGTAAGTTGTGTCCGGTGGGTAAA	GCCATTCAACACAGGCCACCCATTT
SEQ ID NO: 4730	**1175741**	GACCCTTGGTGTCGTTGTTCTGCTA	CTGGGAACCACAGCAACAAGACGAT
SEQ ID NO: 4731	**1175770**	AACCAGCGTGTGTGGAACTGTCGTG	TTGGTCGCACACACCTTGACAGCAC
SEQ ID NO: 4732	**1175844**	CTTATACGGTGTGTGGTCCCTTTCA	GAATATGCCACACACCAGGGAAAGT
SEQ ID NO: 4733	**1176033**	CAATAGCGTGTGTGTAGTCAAGGTC	GTTATCGCACACACATCAGTTCCAG
SEQ ID NO: 4734	**1176076**	GAAGACCTTGTGTGTTGGCGTTCAC	CTTCTGGAACACACAACCGCAAGTG
SEQ ID NO: 4735	**1176145**	ATTACACGGGTGTAGTATAGTATTT	TAATGTGCCCACATCATATCATAAA
SEQ ID NO: 4736	**1176558**	ACTTCTGCTGTGTGCACTGGTTCCC	TGAAGACGACACACGTGACCAAGGG
SEQ ID NO: 4737	**1176836**	AATCCGACGGTGTCGTGTCTCAGGG	TTAGGCTGCCACAGCACAGAGTCCC
SEQ ID NO: 4738	**1176937**	ATTCTTTGTGTGGTTGAGCCTGGTC	TAAGAAACACACCAACTCGGACCAG
SEQ ID NO: 4739	**1176938**	GTTCCGTTATGTGTGGTTGGTTACT	CAAGGCAATACACACCAACCAATGA
SEQ ID NO: 4740	**1177075**	TTAAGACCTGTGTGATGGTGCACCG	AATTCTGGACACACTACCACGTGGC
SEQ ID NO: 4741	**1177154**	ACTTGTTTGTGTGTGTAAATATTGA	TGAACAAACACACACATTTATAACT
SEQ ID NO: 4742	**1177178**	CTCGTGCTTGTGTCAAGAGAGATGG	GAGCACGAACACAGTTCTCTCTACC

SEQ ID NO: 4743	**1177228**	ACGAGCTCCTGTGTGTTATCCGACA	TGCTCGAGGACACACAATAGGCTGT
SEQ ID NO: 4744	**1177239**	ACGTAAAAGTGTGTGGAAAACCCTC	TGCATTTTCACACACCTTTTGGGAG
SEQ ID NO: 4745	**1177338**	CTCTTCTTGTGTAGTGAGGATCCCA	GAGAAGAACACATCACTCCTAGGGT
SEQ ID NO: 4746	**1177367**	CCTTGTCTGTGTTGGGTATGTTGGT	GGAACAGACACAACCCATACAACCA
SEQ ID NO: 4747	**1177443**	GCCCGTGTCGTGTGTTGCTCAGTGA	CGGGCACAGCACACAACGAGTCACT
SEQ ID NO: 4748	**1177547**	TCTTTTGTGTGTCGGAGTGGACATG	AGAAAACACACAGCCTCACCTGTAC
SEQ ID NO: 4749	**1177673**	ACTCATCCGTGTGTGTCGGCAACCC	TGAGTAGGCACACACAGCCGTTGGG
SEQ ID NO: 4750	**1177814**	GTTCGGTTTGTGTTAGAGTCGTCCT	CAAGCCAAACACAATCTCAGCAGGA
SEQ ID NO: 4751	**1177855**	GCATATAGTACTGTGTTTGTGGTCT	CGTATATCATGACACAAACACCAGA
SEQ ID NO: 4752	**1177863**	TTGGGTCGTGTGTAGTGTATGTGTT	AACCCAGCACACATCACATACACAA
SEQ ID NO: 4753	**1177870**	CGGGGATGTGTGTCTCTTCTGCTTA	GCCCCTACACACAGAGAAGACGAAT
SEQ ID NO: 4754	**1177877**	AACTGTAGTGTGTGTTTCCTTACTG	TTGACATCACACACAAAGGAATGAC
SEQ ID NO: 4755	**1177980**	CGACGTATTGTGTGTGATAGGTGCA	GCTGCATAACACACACTATCCACGT
SEQ ID NO: 4756	**1177986**	TCACACCGGTGTGTGGTCTCGGGAA	AGTGTGGCCACACACCAGAGCCCTT
SEQ ID NO: 4757	**1178218**	GTTCAAATGTGTGTCCGTATCGTCG	CAAGTTTACACACAGGCATAGCAGC
SEQ ID NO: 4758	**1178246**	GTATAAGGTATGTGTGTGTAAGGTA	CATATTCCATACACACACATTCCAT
SEQ ID NO: 4759	**1178290**	CTATTTCTGTGTGCCTCGTTTCTTG	GATAAAGACACACGGAGCAAAGAAC
SEQ ID NO: 4760	**1178334**	ACCTCTTGTGTGTGGGGACTGAAAA	TGGAGAACACACACCCCTGACTTTT
SEQ ID NO: 4761	**1178365**	CGTGTCGTATTGTGTGTAGCTCTTT	GCACAGCATAACACACATCGAGAAA
SEQ ID NO: 4762	**1178388**	ATCCTTGTGTGTGTCCATCTGTCCA	TAGGAACACACACAGGTAGACAGGT
SEQ ID NO: 4763	**1178453**	AAGAACACGTGTGTCTGGTAAACGG	TTCTTGTGCACACAGACCATTTGCC

SEQ ID NO: 4764	**1178500**	AGAAGGGTGTGTCGGGATAAAATAC	TCTTCCCACACAGCCCTATTTTATG
SEQ ID NO: 4765	**1178515**	CGTCTATACATGTGTGAGTGTGTAC	GCAGATATGTACACACTCACACATG
SEQ ID NO: 4766	**1178583**	ATTACATGTGTGTGGGTCTTTCTCT	TAATGTACACACACCCAGAAAGAGA
SEQ ID NO: 4767	**1178602**	GGTTCAGTCTGTGTGGTCGTACTTT	CCAAGTCAGACACACCAGCATGAAA
SEQ ID NO: 4768	**1178610**	ACTCGTGGGTGTGTCGATGTCTATA	TGAGCACCCACACAGCTACAGATAT
SEQ ID NO: 4769	**1178616**	ATCAGAGGTGTGTTGTGTGACCTCC	TAGTCTCCACACAACACACTGGAGG
SEQ ID NO: 4770	**1178651**	CTCGTTGGTGTGTATGCGTTTGACT	GAGCAACCACACATACGCAAACTGA
SEQ ID NO: 4771	**1178741**	ACCAGGTCTGTGTGATCGATGTTTA	TGGTCCAGACACACTAGCTACAAAT
SEQ ID NO: 4772	**1178802**	CTGCAGTTGTGTCGTAGTGAACCAC	GACGTCAACACAGCATCACTTGGTG
SEQ ID NO: 4773	**1178843**	CTCGGTGCGTGTGTTACGCGCACGT	GAGCCACGCACACAATGCGCGTGCA
SEQ ID NO: 4774	**1178853**	AATCACTCTGTGTGGTGCTCGTCCG	TTAGTGAGACACACCACGAGCAGGC
SEQ ID NO: 4775	**1178962**	CTATGAAGTGTGTGTACGGAGTCCA	GATACTTCACACACATGCCTCAGGT
SEQ ID NO: 4776	**1179044**	ACTTTCAGTGTGTACGATTGGGCCG	TGAAAGTCACACATGCTAACCCGGC
SEQ ID NO: 4777	**1179052**	AGAACGGCGTGTGTGACAGAAGTCC	TCTTGCCGCACACACTGTCTTCAGG
SEQ ID NO: 4778	**1179139**	GTCGGTGTGGTGTGTCCTCTACCTC	CAGCCACACCACACAGGAGATGGAG
SEQ ID NO: 4779	**1179212**	GTATGTGTGGTGTGTCACGTGTACA	CATACACACCACACAGTGCACATGT
SEQ ID NO: 4780	**1179218**	ATACTCGCTGTGTGTGAACCGTTAC	TATGAGCGACACACACTTGGCAATG
SEQ ID NO: 4781	**1179219**	CGACCCGGTGTGTGAATCATAACAA	GCTGGGCCACACACTTAGTATTGTT
SEQ ID NO: 4782	**1179243**	AAATAGTCGTGTGTGTTTTTTGACA	TTTATCAGCACACACAAAAAACTGT
SEQ ID NO: 4783	**1179312**	CGTTGCGTGTGTGTGTGACCCATCA	GCAACGCACACACACACTGGGTAGT
SEQ ID NO: 4784	**1179387**	ACAAATCCGTGGTGTCGGTAGAAAG	TGTTTAGGCACCACAGCCATCTTTC

SEQ ID NO: 4785	**1179395**	CTAGGCTCAGTGGTGTGGTTTAAAG	GATCCGAGTCACCACACCAAATTTC
SEQ ID NO: 4786	**1179441**	CTGTTTGTGTGTCTTGTCTGTATTG	GACAAACACACAGAACAGACATAAC
SEQ ID NO: 4787	**1179445**	CCGTGTAGAGTGTGTGGACACACTC	GGCACATCTCACACACCTGTGTGAG
SEQ ID NO: 4788	**1179454**	CGTACGGTTTGTGTATAGGTAGACT	GCATGCCAAACACATATCCATCTGA
SEQ ID NO: 4789	**1179456**	ACTCGTGGCTGTGTAGCATCGACCA	TGAGCACCGACACATCGTAGCTGGT
SEQ ID NO: 4790	**1179643**	CCTACAAGTGTGTGTGGTAACACCG	GGATGTTCACACACACCATTGTGGC
SEQ ID NO: 4791	**1179765**	GTGCTTATACGTGTGTCGCTTCCCA	CACGAATATGCACACAGCGAAGGGT
SEQ ID NO: 4792	**1179772**	ATTATGTCGTGTGTTCGGAAGTTCG	TAATACAGCACACAAGCCTTCAAGC
SEQ ID NO: 4793	**1179775**	CCCGTGTAGTGTGTGCACTTAAACT	GGGCACATCACACACGTGAATTTGA
SEQ ID NO: 4794	**1179794**	CTGGATCGTGTGTGTTTGGTTTTGA	GACCTAGCACACACAAACCAAAACT
SEQ ID NO: 4795	**1179795**	AAATTCGTGTGTGTCCTGGTACTAC	TTTAAGCACACACAGGACCATGATG
SEQ ID NO: 4796	**1179798**	GACACCTCGTCGTGTGTGGTCGGTA	CTGTGGAGCAGCACACACCAGCCAT
SEQ ID NO: 4797	**1179828**	ACTGTGTAGAGTGTGTGCGTACGCA	TGACACATCTCACACACGCATGCGT
SEQ ID NO: 4798	**1179831**	CCGTCGTGTAGTGTGTGTATTCGTA	GGCAGCACATCACACACATAAGCAT
SEQ ID NO: 4799	**1179867**	GTCCACACGCGTGTGTGTCAGTAGA	CAGGTGTGCGCACACACAGTCATCT
SEQ ID NO: 4800	**1179890**	ATATTTCGTGTGTTGAGTCTTTGTC	TATAAAGCACACAACTCAGAAACAG
SEQ ID NO: 4801	**1179895**	CTTCTTAAGTGGAAAAAAGAACGAC	GAAGAATTCACCTTTTTTCTTGCTG
SEQ ID NO: 4802	**1179952**	ATCTTACCGTGTGTGTCGTCGAACA	TAGAATGGCACACACAGCAGCTTGT
SEQ ID NO: 4803	**1179961**	AATACTCGTGTGTGTGTCTGCGCAC	TTATGAGCACACACACAGACGCGTG
SEQ ID NO: 4804	**1180032**	CCGTACAGAGTGTGTGTACGCACTT	GGCATGTCTCACACACATGCGTGAA
SEQ ID NO: 4805	**1180148**	ATATGCTACGTGTGTGGACCCATCT	TATACGATGCACACACCTGGGTAGA

SEQ ID NO: 4806	**1180286**	ACCTGCTGTGTGTCTTCTGACGCCC	TGGACGACACACAGAAGACTGCGGG
SEQ ID NO: 4807	**1180493**	AACACGACCAGTGCGTTCGTCCTTT	TTGTGCTGGTCACGCAAGCAGGAAA
SEQ ID NO: 4808	**1180634**	TTTGGGTGTGTAAGTATATATATGT	AAACCCACACATTCATATATATACA
SEQ ID NO: 4809	**1180765**	CGTTCAGGTGTGTAGTAAGGACAGA	GCAAGTCCACACATCATTCCTGTCT
SEQ ID NO: 4810	**1181557**	ACCCGAACAGTGGTAGTGGCACAAC	TGGGCTTGTCACCATCACCGTGTTG
SEQ ID NO: 4811	**1181838**	CTTATCGTCAGTGGTGGTGTTATAC	GAATAGCAGTCACCACCACAATATG
SEQ ID NO: 4812	**1182521**	ATACTCGTTACAGTGGTCGTAGGAC	TATGAGCAATGTCACCAGCATCCTG
SEQ ID NO: 4813	**1182958**	ACTCACGACCAGTGCAGGAGAGACG	TGAGTGCTGGTCACGTCCTCTCTGC
SEQ ID NO: 4814	**1183845**	AGACATGTACGAGTGCTGTGACGTG	TCTGTACATGCTCACGACACTGCAC
SEQ ID NO: 4815	**1183906**	AGTGACAAAGTGATGAGTCGTACCT	TCACTGTTTCACTACTCAGCATGGA
SEQ ID NO: 4816	**1185267**	GTGAGTAGAGAAGTGACGTGCCATA	CACTCATCTCTTCACTGCACGGTAT
SEQ ID NO: 4817	**1185350**	TCATTAAGTAGTGGTGGTGTGAACT	AGTAATTCATCACCACCACACTTGA
SEQ ID NO: 4818	**1186272**	TTTACGGGAGTGTGACAATTTGAAC	AAATGCCCTCACACTGTTAAACTTG
SEQ ID NO: 4819	**1186650**	CTGTGTGAAGTGTGTTAATTGACCT	GACACACTTCACACAATTAACTGGA
SEQ ID NO: 4820	**1186865**	TAACATACTGAGTGTGCTGTGGTCA	ATTGTATGACTCACACGACACCAGT
SEQ ID NO: 4821	**1187462**	CCTCGAGTGAGTGTGTCCTATTGTA	GGAGCTCACTCACACAGGATAACAT
SEQ ID NO: 4822	**1188180**	TCCACCGTGTAGTGTGTGCGAGGAC	AGGTGGCACATCACACACGCTCCTG
SEQ ID NO: 4823	**1188292**	CCCACGAAGTGTGTGTGTCCTACGA	GGGTGCTTCACACACACAGGATGCT
SEQ ID NO: 4824	**1188420**	CATGTTGAGTGTGCACGAGTATTTG	GTACAACTCACACGTGCTCATAAAC
SEQ ID NO: 4825	**1188465**	TCCATATAGAGTGTGTACGTGCACT	AGGTATATCTCACACATGCACGTGA
SEQ ID NO: 4826	**1188717**	TATTGTTCGAGTGTGTACGCGCACT	ATAACAAGCTCACACATGCGCGTGA

SEQ ID NO: 4827	**1189060**	CGTCGGAATAGTGTGAGTGTGTCAA	GCAGCCTTATCACACTCACACAGTT
SEQ ID NO: 4828	**1189579**	CGTTGACGGAGTGTGTTCTCCCTCT	GCAACTGCCTCACACAAGAGGGAGA
SEQ ID NO: 4829	**1189616**	ATCACGGTGAGTGTGAGTACGCCTC	TAGTGCCACTCACACTCATGCGGAG
SEQ ID NO: 4830	**1189736**	GTTCCTCTGTAGTGTGTGCCTACCT	CAAGGAGACATCACACACGGATGGA
SEQ ID NO: 4831	**1189817**	CCCAACGAGTGTGCGTGTACGACTC	GGGTTGCTCACACGCACATGCTGAG
SEQ ID NO: 4832	**1190187**	TTCCGTCGTGTAGTGTGTGTATTCG	AAGGCAGCACATCACACACATAAGC
SEQ ID NO: 4833	**1190880**	CCATGTGCGTTGCAAGTGTGTGTCG	GGTACACGCAACGTTCACACACAGC
SEQ ID NO: 4834	**1191812**	TCCGCGCGGCGTGTGCGAAGGCCAG	AGGCGCGCCGCACACGCTTCCGGTC
SEQ ID NO: 4835	**1192548**	TCGTGTGTCTCCGTTGCCGGCGTAA	AGCACACAGAGGCAACGGCCGCATT
SEQ ID NO: 4836	**1192662**	GTGTGTGTGCCGTTCCAGTTTTTCT	CACACACACGGCAAGGTCAAAAAGA
SEQ ID NO: 4837	**1195159**	AATCTCTTCGTTTGGTGACCCTATA	TTAGAGAAGCAAACCACTGGGATAT
SEQ ID NO: 4838	**1195833**	GGACAGAGTTCGTTGTCGTTGTCTT	CCTGTCTCAAGCAACAGCAACAGAA
SEQ ID NO: 4839	**1196086**	CCCTGGTCGTTGGTTGTCTGACTCC	GGGACCAGCAACCAACAGACTGAGG
SEQ ID NO: 4840	**1196475**	TCAATTGTCGTTGTTTATCGAGAGT	AGTTAACAGCAACAAATAGCTCTCA
SEQ ID NO: 4841	**1196495**	AGACTATATTCGTTGTGTGCTGTAC	TCTGATATAAGCAACACACGACATG
SEQ ID NO: 4842	**1196633**	ATATCGTTTCGTTGTGGTTGTCGAC	TATAGCAAAGCAACACCAACAGCTG
SEQ ID NO: 4843	**1196896**	ATCAAAGTCGTTGCTGTCGTTGTTG	TAGTTTCAGCAACGACAGCAACAAC
SEQ ID NO: 4844	**1196958**	ATCAGGTCGTCGTTTTCTCGGTTAC	TAGTCCAGCAGCAAAAGAGCCAATG
SEQ ID NO: 4845	**1196991**	TGTGTGGTGTCGTTTGTTTTTGTGT	ACACACCACAGCAAACAAAAACACA
SEQ ID NO: 4846	**1199408**	ATTTCTGACGTTGGTCGGAGCCTCA	TAAAGACTGCAACCAGCCTCGGAGT
SEQ ID NO: 4847	**1200265**	CGACGGACCACGTTCTAACGTGGGT	GCTGCCTGGTGCAAGATTGCACCCA

SEQ ID NO: 4848	**1200303**	GTGTTAGTGATACGTTATGTGTGTG	CACAATCACTATGCAATACACACAC
SEQ ID NO: 4849	**1201011**	CTCGACCTCGACGTTGTGTGACAGA	GAGCTGGAGCTGCAACACACTGTCT
SEQ ID NO: 4850	**1201056**	AGTGAGTACTCGTACGTTTGGGTTA	TCACTCATGAGCATGCAAACCCAAT
SEQ ID NO: 4851	**1201148**	TTCACACACACGTTACCTTTTTTAC	AAGTGTGTGTGCAATGGAAAAAATG
SEQ ID NO: 4852	**1201209**	AGAGTTGCCGTGGGTTTAACCGACG	TCTCAACGGCACCCAAATTGGCTGC
SEQ ID NO: 4853	**1201821**	TGTTAGTGATACGTTATGTGTGTGT	ACAATCACTATGCAATACACACACA
SEQ ID NO: 4854	**1201874**	GCTCGACCTCGACGTTAAGTGTTAT	CGAGCTGGAGCTGCAATTCACAATA
SEQ ID NO: 4855	**1201997**	CTCGACTCCGACGTTAATAGACTTC	GAGCTGAGGCTGCAATTATCTGAAG
SEQ ID NO: 4856	**1202077**	CTTCGGCCGTGGGTAACCTGGCCCG	GAAGCCGGCACCCATTGGACCGGGC
SEQ ID NO: 4857	**1202132**	GTGCGCATGCGTGTGAGTAAAAATC	CACGCGTACGCACACTCATTTTTAG
SEQ ID NO: 4858	**1202275**	GGTCGTGGTGCGTGCTACCGACAAA	CCAGCACCACGCACGATGGCTGTTT
SEQ ID NO: 4859	**1202469**	ACCATCGCCGTGCTTCCCTTACGAC	TGGTAGCGGCACGAAGGGAATGCTG
SEQ ID NO: 4860	**1202519**	CCTCGAGGCGTGGTGTAAGGACCTC	GGAGCTCCGCACCACATTCCTGGAG
SEQ ID NO: 4861	**1203085**	GTTACTCCGCCGTGATAGATCGGAC	CAATGAGGCGGCACTATCTAGCCTG
SEQ ID NO: 4862	**1203396**	ATTTGCCGTGGTGGAGTTTTCCGAC	TAAACGGCACCACCTCAAAAGGCTG
SEQ ID NO: 4863	**1203521**	CCTTGTCCGTGGTTTTTGTCCTTCT	GGAACAGGCACCAAAAACAGGAAGA
SEQ ID NO: 4864	**1203590**	TACTGAACGTGCGTGGGCAGAACCC	ATGACTTGCACGCACCCGTCTTGGG
SEQ ID NO: 4865	**1203694**	AAGGAGTGCGTGTCGTTCTGCGTTT	TTCCTCACGCACAGCAAGACGCAAA
SEQ ID NO: 4866	**1203743**	TCTTTGTACCGTGGGTGGTCCTCCT	AGAAACATGGCACCCACCAGGAGGA
SEQ ID NO: 4867	**1204069**	TCGGTCGACCCGTGCGTGTCAGTAC	AGCCAGCTGGGCACGCACAGTCATG
SEQ ID NO: 4868	**1204371**	GTCCCGTCCTCGTGAAAGGTTCTAG	CAGGGCAGGAGCACTTTCCAAGATC

SEQ ID NO: 4869	**1204823**	ACGGTTTATCGTGGGTGTGACTTTA	TGCCAAATAGCACCCACACTGAAAT
SEQ ID NO: 4870	**1204830**	CTACTACGGTGCGTGTTAACCCAAA	GATGATGCCACGCACAATTGGGTTT
SEQ ID NO: 4871	**1205597**	CAAATCTCGTGGTTGGTGAAGTTCT	GTTTAGAGCACCAACCACTTCAAGA
SEQ ID NO: 4872	**1205920**	AGACTTGTGCGTGTATATGAGAACC	TCTGAACACGCACATATACTCTTGG
SEQ ID NO: 4873	**1206734**	GCATCTGACCGTGTGTGTACCCATA	CGTAGACTGGCACACACATGGGTAT
SEQ ID NO: 4874	**1206735**	CAGATTACCGTGTGTGTGCCCTCGA	GTCTAATGGCACACACACGGGAGCT
SEQ ID NO: 4875	**1206960**	CGAGAGTCTGCGTGTCTGTAAAGTC	GCTCTCAGACGCACAGACATTTCAG
SEQ ID NO: 4876	**1206992**	CGCACGAGCCGTGTGTCTGTCTAAA	GCGTGCTCGGCACACAGACAGATTT
SEQ ID NO: 4877	**1207024**	CTTGATGCGTGTGCATCTGTCTGGT	GAACTACGCACACGTAGACAGACCA
SEQ ID NO: 4878	**1207036**	GTCTCATCTGCGTGTGGCTATCTCC	CAGAGTAGACGCACACCGATAGAGG
SEQ ID NO: 4879	**1207141**	AGCCTCGTCCGTGTGAGCGACGGTC	TCGGAGCAGGCACACTCGCTGCCAG
SEQ ID NO: 4880	**1207166**	ACATGACCCGTGTGGGTGTAAAGAG	TGTACTGGGCACACCCACATTTCTC
SEQ ID NO: 4881	**1207294**	AGAACTGTTCGTGTTGTTTGACTAC	TCTTGACAAGCACAACAAACTGATG
SEQ ID NO: 4882	**1207295**	AGACTTTTCGTGTGGGTCGTTCAGG	TCTGAAAAGCACACCCAGCAAGTCC
SEQ ID NO: 4883	**1207316**	AGCCACTGTACGTGTGTGAGCGACA	TCGGTGACATGCACACACTCGCTGT
SEQ ID NO: 4884	**1207358**	TGTCGAAGCGCGTGTGTGTCGTTCC	ACAGCTTCGCGCACACACAGCAAGG
SEQ ID NO: 4885	**1207788**	ACACCGTCCTCGTGTTTTTCAGAGA	TGTGGCAGGAGCACAAAAAGTCTCT
SEQ ID NO: 4886	**1207984**	ATGTGGTGCGTGTACTCTACCTCCG	TACACCACGCACATGAGATGGAGGC
SEQ ID NO: 4887	**1208190**	CTGCTCGCGCGTGTGTCCTTCGGAC	GACGAGCGCGCACACAGGAAGCCTG
SEQ ID NO: 4888	**1208802**	ATCAAAACGTGAGAAAAAACAGGTC	TAGTTTTGCACTCTTTTTTGTCCAG
SEQ ID NO: 4889	**1208971**	AAAGTTTCGTGTGGTTGACGAGACC	TTTCAAAGCACACCAACTGCTCTGG

SEQ ID NO: 4890	**1209012**	GCGTCCTAGGTCGTGTGTGTTCCGC	CGCAGGATCCAGCACACACAAGGCG
SEQ ID NO: 4891	**1209074**	ACTTAGTTACTCGTGTCGGTGGTCC	TGAATCAATGAGCACAGCCACCAGG
SEQ ID NO: 4892	**1209120**	GTACACGTGTGAGCGTGTACGTGTA	CATGTGCACACTCGCACATGCACAT
SEQ ID NO: 4893	**1209357**	CCACACACACGTGGCTTCCAGGTGG	GGTGTGTGTGCACCGAAGGTCCACC
SEQ ID NO: 4894	**1209429**	CATTGCGGTCGGTGCTAAAAAGCAT	GTAACGCCAGCCACGATTTTTCGTA
SEQ ID NO: 4895	**1210332**	GATGTGTGTTCGTGTACACGTGTGT	CTACACACAAGCACATGTGCACACA
SEQ ID NO: 4896	**1212006**	AGGTCGGTCGGTCCGATAAATTCCC	TCCAGCCAGCCAGGCTATTTAAGGG
SEQ ID NO: 4897	**1213019**	CGCCGCCGGTCCTCGCGGGCGCCCG	GCGGCGGCCAGGAGCGCCCGCGGGC
SEQ ID NO: 4898	**1214330**	NA	NA
SEQ ID NO: 4899	**1214608**	NA	NA
SEQ ID NO: 4900	**1216326**	CAACGGCGGTCAAGCTCCACGAGGT	GTTGCCGCCAGTTCGAGGTGCTCCA
SEQ ID NO: 4901	**1216531**	CACTCGAGAGGTCCGGGAACCAAGA	GTGAGCTCTCCAGGCCCTTGGTTCT
SEQ ID NO: 4902	**1218131**	ATGTGGTGGTCAGTAGTAGTAACCA	TACACCACCAGTCATCATCATTGGT
SEQ ID NO: 4903	**1220853**	ATGGGTCTGTCCTCTAAGATGGTGC	TACCCAGACAGGAGATTCTACCACG
SEQ ID NO: 4904	**1222753**	TGTCGGTCGGTGTCCATGACGTTCC	ACAGCCAGCCACAGGTACTGCAAGG
SEQ ID NO: 4905	**1223375**	TCTTCGGTGTGTCCGCTTCGGATCA	AGAAGCCACACAGGCGAAGCCTAGT
SEQ ID NO: 4906	**1223628**	AGTGTGAGTCTGTCCTTTGTGTCTG	TCACACTCAGACAGGAAACACAGAC
SEQ ID NO: 4907	**1223963**	GTCTTCGGTGTGTCCGCTTCGGATC	CAGAAGCCACACAGGCGAAGCCTAG
SEQ ID NO: 4908	**1224822**	GTAACACGGTGTGTCCGTTACTCGT	CATTGTGCCACACAGGCAATGAGCA
SEQ ID NO: 4909	**1225051**	GTCGGTCGGTTGTCATCATCATCTT	CAGCCAGCCAACAGTAGTAGTAGAA
SEQ ID NO: 4910	**1226215**	GCCGTGGTGGTCTTCAGTCCTTTTC	CGGCACCACCAGAAGTCAGGAAAAG

SEQ ID NO: 4911	**1226298**	GCGTCCACCTGTCACGAATGCGATA	CGCAGGTGGACAGTGCTTACGCTAT
SEQ ID NO: 4912	**1226932**	ACCGGTTGGTCTTGGATCTAATAGT	TGGCCAACCAGAACCTAGATTATCA
SEQ ID NO: 4913	**1227035**	TCTCAGGGGTCTTGTGGATGACCAG	AGAGTCCCCAGAACACCTACTGGTC
SEQ ID NO: 4914	**1227173**	TCGCGTACTTGTGTCAGTGGGTGAT	AGCGCATGAACACAGTCACCCACTA
SEQ ID NO: 4915	**1227213**	GTGTCTCTGGGTCTGCATCAAAAGA	CACAGAGACCCAGACGTAGTTTTCT
SEQ ID NO: 4916	**1227785**	GGAGTGGTCGGTCTGGTCAACTTAT	CCTCACCAGCCAGACCAGTTGAATA
SEQ ID NO: 4917	**1229263**	CGTGTAGGTAGGTCTTAACAGTCCC	GCACATCCATCCAGAATTGTCAGGG
SEQ ID NO: 4918	**1229370**	CTTGATAGGTCTGTGTGTTCCAAAA	GAACTATCCAGACACACAAGGTTTT
SEQ ID NO: 4919	**1230462**	GCTAAGGTCGGTCTGTCTACTCGCC	CGATTCCAGCCAGACAGATGAGCGG
SEQ ID NO: 4920	**1230800**	CGGGGTGTGTCTTGAGCATGTCCTT	GCCCCACACAGAACTCGTACAGGAA
SEQ ID NO: 4921	**1232865**	CTTTATCTGTCTTGTGTGTAAGTCC	GAAATAGACAGAACACACATTCAGG
SEQ ID NO: 4922	**1232928**	CCAGTTACTGTCTGTGGTTCGCCCA	GGTCAATGACAGACACCAAGCGGGT
SEQ ID NO: 4923	**1232991**	TACGTTTTCGTGTCTGTGCAGGGAC	ATGCAAAAGCACAGACACGTCCCTG
SEQ ID NO: 4924	**1233353**	TTTTTTGTCTCTGTCGACCCTGTCA	AAAAAACAGAGACAGCTGGGACAGT
SEQ ID NO: 4925	**1233463**	GTATATGCTAGTGTCTGTGTGTGGT	CATATACGATCACAGACACACACCA
SEQ ID NO: 4926	**1233503**	ACATGTCTTGTCTCTGGGTTCTACA	TGTACAGAACAGAGACCCAAGATGT
SEQ ID NO: 4927	**1233510**	ACATTCCTGTCTGTGTGGGTGTCTT	TGTAAGGACAGACACACCCACAGAA
SEQ ID NO: 4928	**1233833**	CTCTTGTGTGTCTGTAGTGTAGAAG	GAGAACACACAGACATCACATCTTC
SEQ ID NO: 4929	**1233856**	GGTCTCTGTCTGTCTGCGTGCGTGT	CCAGAGACAGACAGACGCACGCACA
SEQ ID NO: 4930	**1234389**	CCTCTATGTGTCTGGGTCTCTGTGA	GGAGATACACAGACCCAGAGACACT
SEQ ID NO: 4931	**1234972**	CTACTTTGTGTCTCTGTCGTTCAAG	GATGAAACACAGAGACAGCAAGTTC

SEQ ID NO: 4932	**1237445**	CTAGGGTGAGTCCTTCTTACGTGGT	GATCCCACTCAGGAAGAATGCACCA
SEQ ID NO: 4933	**1241081**	ACGGGTGTGAGTCAAGTGTCCTTCT	TGCCCACACTCAGTTCACAGGAAGA
SEQ ID NO: 4934	**1241829**	CGCCACTCTAGTCCGGGTACCGTAA	GCGGTGAGATCAGGCCCATGGCATT
SEQ ID NO: 4935	**1241960**	CTATACAGGTAGTCCAGGTAGACGA	GATATGTCCATCAGGTCCATCTGCT
SEQ ID NO: 4936	**1242147**	AGGGAGAGAGTCACACACACAGAGA	TCCCTCTCTCAGTGTGTGTGTCTCT
SEQ ID NO: 4937	**1242979**	GTAAAAAAGTCTCGAACAAACGTCC	CATTTTTTCAGAGCTTGTTTGCAGG
SEQ ID NO: 4938	**1244540**	ATCAACATAGTCTTACTCGTAGTCT	TAGTTGTATCAGAATGAGCATCAGA
SEQ ID NO: 4939	**1245753**	TTCCGTGGGTCGAAGTCATAGATCA	AAGGCACCCAGCTTCAGTATCTAGT
SEQ ID NO: 4940	**1246306**	TCACCTCGCCGTCGGTCTATTGAGA	AGTGGAGCGGCAGCCAGATAACTCT
SEQ ID NO: 4941	**1246426**	TGGTGGTGGTCGACTACTAAGAGAA	ACCACCACCAGCTGATGATTCTCTT
SEQ ID NO: 4942	**1246476**	AGACTGAGAGGTCGGTGGTTCTTAT	TCTGACTCTCCAGCCACCAAGAATA
SEQ ID NO: 4943	**1246599**	ACTTGTGGGTCGGACTAAAGTGTCC	TGAACACCCAGCCTGATTTCACAGG
SEQ ID NO: 4944	**1246717**	ACGTTTCTGGTCGTGAGATTTCCGG	TGCAAAGACCAGCACTCTAAAGGCC
SEQ ID NO: 4945	**1247533**	GGGTGTGAGTGTCGCCATCCTCAAA	CCCACACTCACAGCGGTAGGAGTTT
SEQ ID NO: 4946	**1247772**	NA	NA
SEQ ID NO: 4947	**1247987**	CCTGGTGGTCGGATTGGACCGTACT	GGACCACCAGCCTAACCTGGCATGA
SEQ ID NO: 4948	**1248586**	GTAACTTGTTGTCGGTCGTGAATTT	CATTGAACAACAGCCAGCACTTAAA
SEQ ID NO: 4949	**1249160**	NA	NA
SEQ ID NO: 4950	**1249859**	CTTTTTGTCGGTGTTGTCTCTCTTG	GAAAAACAGCCACAACAGAGAGAAC
SEQ ID NO: 4951	**1250064**	NA	NA
SEQ ID NO: 4952	**1250636**	TTCGCGGTCGGTCGTCACTTTCTTT	AAGCGCCAGCCAGCAGTGAAAGAAA

SEQ ID NO: 4953	**1250852**	GACGACTCTGAGTGTCGGGTGTCCC	CTGCTGAGACTCACAGCCCACAGGG
SEQ ID NO: 4954	**1250911**	ACACATCTGTGTCGGTGACTCCCTA	TGTGTAGACACAGCCACTGAGGGAT
SEQ ID NO: 4955	**1250955**	ACTCTGTGTGTGTCGCCGACCCTGG	TGAGACACACACAGCGGCTGGGACC
SEQ ID NO: 4956	**1251001**	AGTCTGTGTGTGTCGATCTCCCGAG	TCAGACACACACAGCTAGAGGGCTC
SEQ ID NO: 4957	**1251244**	AGGTTTCGGTCGTTGTAGCTAGTCG	TCCAAAGCCAGCAACATCGATCAGC
SEQ ID NO: 4958	**1251532**	ACCGTTGGTGTCGTTGTTTCTCCTA	TGGCAACCACAGCAACAAAGAGGAT
SEQ ID NO: 4959	**1251769**	CTGTCGGTGGTCGTTTATGTGTCCA	GACAGCCACCAGCAAATACACAGGT
SEQ ID NO: 4960	**1252066**	ACCTAGTGTGTGTCGTATCATCGCC	TGGATCACACACAGCATAGTAGCGG
SEQ ID NO: 4961	**1252184**	GGTGTGTTTGTCGTGTGTGGTGTAT	CCACACAAACAGCACACACCACATA
SEQ ID NO: 4962	**1252267**	TGAAGCGTGTGTCGTGGTCTCCGAC	ACTTCGCACACAGCACCAGAGGCTG
SEQ ID NO: 4963	**1252476**	ATACATGTGTGTCGTTGTACGTACC	TATGTACACACAGCAACATGCATGG
SEQ ID NO: 4964	**1252549**	ACTAGTGTTGTGTCGTGCAGATTGC	TGATCACAACACAGCACGTCTAACG
SEQ ID NO: 4965	**1253593**	GACTGTCCGAGTGTCGTGTCTCACC	CTGACAGGCTCACAGCACAGAGTGG
SEQ ID NO: 4966	**1256165**	CGTCCCTCACGTCGGTAACCATGTG	GCAGGGAGTGCAGCCATTGGTACAC
SEQ ID NO: 4967	**1257008**	AGACCTGTCCGTCCATTGGTTCAGC	TCTGGACAGGCAGGTAACCAAGTCG
SEQ ID NO: 4968	**1257212**	AGGGCTCCGTCCCTGCATCCAGTGT	TCCCGAGGCAGGGACGTAGGTCACA
SEQ ID NO: 4969	**1257730**	ATCCTCTACCGTCCTTGAGGCAAGG	TAGGAGATGGCAGGAACTCCGTTCC
SEQ ID NO: 4970	**1257768**	CATAGACACCGTCCGCCTCAAGGGA	GTATCTGTGGCAGGCGGAGTTCCCT
SEQ ID NO: 4971	**1258009**	ATCGTTCGTGCGTCCGGAACACCCA	TAGCAAGCACGCAGGCCTTGTGGGT
SEQ ID NO: 4972	**1258631**	AAGGAACCGTCCCTCGTGTCACCGT	TTCCTTGGCAGGGAGCACAGTGGCA
SEQ ID NO: 4973	**1259360**	NA	NA

SEQ ID NO: 4974	**1259897**	CTATCCACCGTCTTAAGGGAACATT	GATAGGTGGCAGAATTCCCTTGTAA
SEQ ID NO: 4975	**1260099**	AATAAGACCGTCAAGTGCGTGTGCC	TTATTCTGGCAGTTCACGCACACGG
SEQ ID NO: 4976	**1260319**	GTGTCTGTTGTCGTCATCTTGAGTA	CACAGACAACAGCAGTAGAACTCAT
SEQ ID NO: 4977	**1260770**	CGGGTGTGTCGTCACGTTCAAGGTA	GCCCACACAGCAGTGCAAGTTCCAT
SEQ ID NO: 4978	**1261005**	CCGTCACTCTCGTCCAGGTAGGTGA	GGCAGTGAGAGCAGGTCCATCCACT
SEQ ID NO: 4979	**1261074**	GTCTTCTCCTCGTCCAACTTCGGTG	CAGAAGAGGAGCAGGTTGAAGCCAC
SEQ ID NO: 4980	**1261788**	GGTGTCGTGTTCGTCATAAACTGTA	CCACAGCACAAGCAGTATTTGACAT
SEQ ID NO: 4981	**1263481**	AGCAGTGTGCGTCTGGTGTCCCACA	TCGTCACACGCAGACCACAGGGTGT
SEQ ID NO: 4982	**1263493**	TCGTGTGGTGTCGTCTCACATTGAT	AGCACACCACAGCAGAGTGTAACTA
SEQ ID NO: 4983	**1263624**	AGTCACTCCCGTCTCCATGTCTTGG	TCAGTGAGGGCAGAGGTACAGAACC
SEQ ID NO: 4984	**1265064**	GGCGACCCACGTCCTCATTCTGCAG	CCGCTGGGTGCAGGAGTAAGACGTC
SEQ ID NO: 4985	**1265490**	TATACACACACACGTCCAGGACCTG	ATATGTGTGTGTGCAGGTCCTGGAC
SEQ ID NO: 4986	**1265810**	CGTAGTTTAACGTCGTTGTGCTCTT	GCATCAAATTGCAGCAACACGAGAA
SEQ ID NO: 4987	**1266004**	AGAACCCGTCGTCGCTACTATTTGA	TCTTGGGCAGCAGCGATGATAAACT
SEQ ID NO: 4988	**1266443**	CACACACACACGTCCATGTATATGT	GTGTGTGTGTGCAGGTACATATACA
SEQ ID NO: 4989	**1267217**	CTCCCGTAACGTCGTTGGTGTGGAC	GAGGGCATTGCAGCAACCACACCTG
SEQ ID NO: 4990	**1267460**	CGACGACCACCGTCGGCACCAGTAC	GCTGCTGGTGGCAGCCGTGGTCATG
SEQ ID NO: 4991	**1267724**	GTGGATTCCGTCGTTCAATGCAGTG	CACCTAAGGCAGCAAGTTACGTCAC
SEQ ID NO: 4992	**1267921**	ATGACTCTACACGTCTCCTGTCTGT	TACTGAGATGTGCAGAGGACAGACA
SEQ ID NO: 4993	**1268367**	GTTATCCGGACGTCTCAGTATCAGT	CAATAGGCCTGCAGAGTCATAGTCA
SEQ ID NO: 4994	**1269281**	CCAGAAACGTCGCACGTGTGTGTCG	GGTCTTTGCAGCGTGCACACACAGC

SEQ ID NO: 4995	**1272531**	AAGTCATCTTAACCCAACGTTAGGT	TTCAGTAGAATTGGGTTGCAATCCA
SEQ ID NO: 4996	**1274324**	NA	NA
SEQ ID NO: 4997	**1275434**	ACGAAGGACTTAACCTAGAGGTTTA	TGCTTCCTGAATTGGATCTCCAAAT
SEQ ID NO: 4998	**1281288**	ACTGTTCCGTTATGTGTGGTTGGTT	TGACAAGGCAATACACACCAACCAA
SEQ ID NO: 4999	**1282666**	TATGTATGGTTATGTGTGGTGATGT	ATACATACCAATACACACCACTACA
SEQ ID NO: 5000	**1283298**	AGAACCGTTTATCCACTCTCTTGAT	TCTTGGCAAATAGGTGAGAGAACTA
SEQ ID NO: 5001	**1284463**	GTTAGTGATACGTTATGTGTGTGTA	CAATCACTATGCAATACACACACAT
SEQ ID NO: 5002	**1284703**	AGAAATCATATTAAAAAACTTGACT	TCTTTAGTATAATTTTTTGAACTGA
SEQ ID NO: 5003	**1284827**	CCGATGTAGTTATTCGTGTGTGGTC	GGCTACATCAATAAGCACACACCAG
SEQ ID NO: 5004	**1292606**	AGGTGTGTGTATAATGAGTATCAAA	TCCACACACATATTACTCATAGTTT
SEQ ID NO: 5005	**1292837**	ACGGTGGTCGATATGTGTGATGGTT	TGCCACCAGCTATACACACTACCAA
SEQ ID NO: 5006	**1294582**	AAAAAATATAACAGAGTCATACTGA	TTTTTTATATTGTCTCAGTATGACT
SEQ ID NO: 5007	**1296087**	ACACGGACACATATACGCTTAGAGT	TGTGCCTGTGTATATGCGAATCTCA
SEQ ID NO: 5008	**1299424**	GTATATGTTTTAGGTGTGTGTACTT	CATATACAAAATCCACACACATGAA
SEQ ID NO: 5009	**1299700**	ACCTAACTTTAGGTCGGTCGGGTCC	TGGATTGAAATCCAGCCAGCCCAGG
SEQ ID NO: 5010	**1301746**	AACGACTGATTAGACTAGAGGCGTC	TTGCTGACTAATCTGATCTCCGCAG
SEQ ID NO: 5011	**1302063**	CTACGAGGTGTTAGACCAGACTCCA	GATGCTCCACAATCTGGTCTGAGGT
SEQ ID NO: 5012	**1302383**	CTGAGTACTACTTAGAAGGCACTAC	GACTCATGATGAATCTTCCGTGATG
SEQ ID NO: 5013	**1304892**	CAGTATCCTGTAGTGGTGGTCATCC	GTCATAGGACATCACCACCAGTAGG
SEQ ID NO: 5014	**1305338**	ATGTGTCACTTAGTGTGTGTCTTTG	TACACAGTGAATCACACACAGAAAC
SEQ ID NO: 5015	**1305673**	CTTTAGCGTTAGTTGTCGTGGTCAT	GAAATCGCAATCAACAGCACCAGTA

SEQ ID NO: 5016	**1307111**	GACTCCGACGTGATAGCGTGCCCAG	CTGAGGCTGCACTATCGCACGGGTC
SEQ ID NO: 5017	**1309732**	TCCTACCGGATAGAGTGTGTACTTA	AGGATGGCCTATCTCACACATGAAT
SEQ ID NO: 5018	**1312000**	AGTTTCCCTAATGCTATGACGCCGT	TCAAAGGGATTACGATACTGCGGCA
SEQ ID NO: 5019	**1313418**	ATTGTTCCTAACTCATCCCGTGTAG	TAACAAGGATTGAGTAGGGCACATC
SEQ ID NO: 5020	**1314493**	GTGTTCGGCTCTAATCTAGTTAGTC	CACAAGCCGAGATTAGATCAATCAG
SEQ ID NO: 5021	**1315077**	GTACTCCCTCTCTAACCTTGTGAGC	CATGAGGGAGAGATTGGAACACTCG
SEQ ID NO: 5022	**1316676**	ACCCGACACCTATCGGAAGGCGCTA	TGGGCTGTGGATAGCCTTCCGCGAT
SEQ ID NO: 5023	**1317016**	GTCACTCCTACCTATTCTACAGAAG	CAGTGAGGATGGATAAGATGTCTTC
SEQ ID NO: 5024	**1317169**	CCTCGCGCGCTATTGCGTGCGTACC	GGAGCGCGCGATAACGCACGCATGG
SEQ ID NO: 5025	**1317704**	ATCGCCGCCTATCCGAGTGTCCGGT	TAGCGGCGGATAGGCTCACAGGCCA
SEQ ID NO: 5026	**1319372**	GTACAGACCGGCTATGACAAAGGCG	CATGTCTGGCCGATACTGTTTCCGC
SEQ ID NO: 5027	**1320425**	GGTCTAGGGCTATACGAAACGTCCG	CCAGATCCCGATATGCTTTGCAGGC
SEQ ID NO: 5028	**1320825**	CTATTCTTCTATGTGTGGGTGTTAC	GATAAGAAGATACACACCCACAATG
SEQ ID NO: 5029	**1321676**	CACACGCACACTAATCCGAAGGGGT	GTGTGCGTGTGATTAGGCTTCCCCA
SEQ ID NO: 5030	**1325249**	AGTTCCCACTATCTACTCCCAGTAG	TCAAGGGTGATAGATGAGGGTCATC
SEQ ID NO: 5031	**1325691**	TTCAACTCTACTATAGTAAATGCCC	AAGTTGAGATGATATCATTTACGGG
SEQ ID NO: 5032	**1327058**	ACTACAAACCTAGGGACTCGTGGGA	TGATGTTTGGATCCCTGAGCACCCT
SEQ ID NO: 5033	**1328027**	CTTGGCCTAGAAGACCAGTAACACC	GAACCGGATCTTCTGGTCATTGTGG
SEQ ID NO: 5034	**1330573**	CCGAGAACCTAGTGTGTGTCTGTTT	GGCTCTTGGATCACACACAGACAAA
SEQ ID NO: 5035	**1331538**	CCCACTACGCTAGTTCCGTGTGTGT	GGGTGATGCGATCAAGGCACACACA
SEQ ID NO: 5036	**1332166**	NA	NA

SEQ ID NO: 5037	**1332666**	CGTTACTCCATACTGGATCTCAATT	GCAATGAGGTATGACCTAGAGTTAA
SEQ ID NO: 5038	**1336925**	TCACACACACGTTACCTTTTTTACA	AGTGTGTGTGCAATGGAAAAAATGT
SEQ ID NO: 5039	**1339074**	GTCTACCCATTACACGACTGCAGTA	CAGATGGGTAATGTGCTGACGTCAT
SEQ ID NO: 5040	**1340147**	TAATATCATTACTGTGTGTCGGTTC	ATTATAGTAATGACACACAGCCAAG
SEQ ID NO: 5041	**1340613**	ACAATGTACTTACTTGGTCTGTTGA	TGTTACATGAATGAACCAGACAACT
SEQ ID NO: 5042	**1340726**	GTGTGTGGTCTTACTAGGTCTCTGG	CACACACCAGAATGATCCAGAGACC
SEQ ID NO: 5043	**1341381**	GTGTGTGCGCATACCTCTGAACTAC	CACACACGCGTATGGAGACTTGATG
SEQ ID NO: 5044	**1342457**	ACACCACACATACATGTACCACGGA	TGTGGTGTGTATGTACATGGTGCCT
SEQ ID NO: 5045	**1342661**	GTTGACCCATACCAAGTCTAGACGT	CAACTGGGTATGGTTCAGATCTGCA
SEQ ID NO: 5046	**1345290**	CCGTATCTTATACCTGTGGTGGAAC	GGCATAGAATATGGACACCACCTTG
SEQ ID NO: 5047	**1349575**	GTGGAACTGCTACAGGCGCCCACCG	CACCTTGACGATGTCCGCGGGTGGC
SEQ ID NO: 5048	**1350036**	CCTGTACGGCTACAAAAGTCTTTGT	GGACATGCCGATGTTTTCAGAAACA
SEQ ID NO: 5049	**1353011**	GACCTCTGTCTCTACACCCGGTAGT	CTGGAGACAGAGATGTGGGCCATCA
SEQ ID NO: 5050	**1353497**	AACACACACCTACTGACGTGTGAGT	TTGTGTGTGGATGACTGCACACTCA
SEQ ID NO: 5051	**1356865**	ATTTAGCACTACGTCATTTCGGATG	TAAATCGTGATGCAGTAAAGCCTAC
SEQ ID NO: 5052	**1358773**	CTGAACGACGACTACACTGCGAACG	GACTTGCTGCTGATGTGACGCTTGC
SEQ ID NO: 5053	**1360716**	AGAACGCCGACTACGACGCCTTGAG	TCTTGCGGCTGATGCTGCGGAACTC
SEQ ID NO: 5054	**1361496**	CGTCACACACGGTAATGAAAATTTA	GCAGTGTGTGCCATTACTTTTAAAT
SEQ ID NO: 5055	**1367391**	GACAGGTGTGGTATTTTTGAGGACC	CTGTCCACACCATAAAAACTCCTGG
SEQ ID NO: 5056	**1367400**	GTCTCGTTGTGTGTAAAGGATCTCC	CAGAGCAACACACATTTCCTAGAGG
SEQ ID NO: 5057	**1367605**	AGTGAGCGTGTGTATGACGGTATAT	TCACTCGCACACATACTGCCATATA

SEQ ID NO: 5058	**1368354**	AGGTCGGTCGTGTAACGTCACAAGT	TCCAGCCAGCACATTGCAGTGTTCA
SEQ ID NO: 5059	**1371474**	GTGTGGTGAAGTAACGAGAACCTTC	CACACCACTTCATTGCTCTTGGAAG
SEQ ID NO: 5060	**1372017**	ATCTCTTTAGTAACGTGCGTGCCTC	TAGAGAAATCATTGCACGCACGGAG
SEQ ID NO: 5061	**1373858**	ACGGACGGTGAGTAAAGTAATCAAA	TGCCTGCCACTCATTTCATTAGTTT
SEQ ID NO: 5062	**1374066**	TTGGGTAGGTAGCTGGGTAACTCTC	AACCCATCCATCGACCCATTGAGAG
SEQ ID NO: 5063	**1374593**	GTTTTCTGAGTATGCGGTGGTCATC	CAAAAGACTCATACGCCACCAGTAG
SEQ ID NO: 5064	**1376928**	AGGATGTCGGTAGGTCGTTTGTAAA	TCCTACAGCCATCCAGCAAACATTT
SEQ ID NO: 5065	**1377405**	TATATAGAGGGTAGGTTCACGATTG	ATATATCTCCCATCCAAGTGCTAAC
SEQ ID NO: 5066	**1377708**	AGTATCGTTACGGTAGGTAGGTCTG	TCATAGCAATGCCATCCATCCAGAC
SEQ ID NO: 5067	**1377730**	AGTCAGTTTGTAGGTGTGTTATGTC	TCAGTCAAACATCCACACAATACAG
SEQ ID NO: 5068	**1378122**	TTCCGGTGTGTAGGTTTTGCTGTTC	AAGGCCACACATCCAAAACGACAAG
SEQ ID NO: 5069	**1379630**	ACAGACCTTGTAGTGGTGGCGTACA	TGTCTGGAACATCACCACCGCATGT
SEQ ID NO: 5070	**1379940**	GAACAAGTGTGTAGGTGAGGAAGTG	CTTGTTCACACATCCACTCCTTCAC
SEQ ID NO: 5071	**1380686**	NA	NA
SEQ ID NO: 5072	**1380687**	TGGGTCGTGTGTAGTGTATGTGTTG	ACCCAGCACACATCACATACACAAC
SEQ ID NO: 5073	**1380707**	AACCTGTGGTAGTCGTGTTTCACTC	TTGGACACCATCAGCACAAAGTGAG
SEQ ID NO: 5074	**1380843**	ATCAGAGTAGGTAGTTCCCGTATCC	TAGTCTCATCCATCAAGGGCATAGG
SEQ ID NO: 5075	**1380862**	ACAGAGTTCTGTAGACTTTGTCCGT	TGTCTCAAGACATCTGAAACAGGCA
SEQ ID NO: 5076	**1380986**	TCCTTATGTGTAGTGGTGGAGGCAC	AGGAATACACATCACCACCTCCGTG
SEQ ID NO: 5077	**1380987**	ACCTTTGTGTAGTGTGTGAGGAGTC	TGGAAACACATCACACACTCCTCAG
SEQ ID NO: 5078	**1381061**	GGTTTTTAGTAGTTCTGTCCGGACC	CCAAAAATCATCAAGACAGGCCTGG

SEQ ID NO: 5079	**1381078**	TTGTTTGTGTAGACGTTGCCCAACT	AACAAACACATCTGCAACGGGTTGA
SEQ ID NO: 5080	**1381941**	CGTCAGTGTGAGTAGAAAGGATTTC	GCAGTCACACTCATCTTTCCTAAAG
SEQ ID NO: 5081	**1382063**	CCGTACGTGGTGTAGTGTGTTCAGC	GGCATGCACCACATCACACAAGTCG
SEQ ID NO: 5082	**1382457**	AGTTCCTCTGTAGTGTGTGCCTACC	TCAAGGAGACATCACACACGGATGG
SEQ ID NO: 5083	**1382911**	CCGTCCTGTGTAGTGGTCCTGACTA	GGCAGGACACATCACCAGGACTGAT
SEQ ID NO: 5084	**1382971**	CGCACAAAGTAGCACCGACGACAGA	GCGTGTTTCATCGTGGCTGCTGTCT
SEQ ID NO: 5085	**1384317**	CTACTCCCAGTAGTGACGCGTTTCG	GATGAGGGTCATCACTGCGCAAAGC
SEQ ID NO: 5086	**1384461**	TGACTAGAGAGAGTAGGTGAGTATC	ACTGATCTCTCTCATCCACTCATAG
SEQ ID NO: 5087	**1385564**	CTTGTGACTCGTATCTGTATCGGAG	GAACACTGAGCATAGACATAGCCTC
SEQ ID NO: 5088	**1387025**	ACACTACCTTCGTATTGGACAGAGT	TGTGATGGAAGCATAACCTGTCTCA
SEQ ID NO: 5089	**1388351**	ACATCACACACGTATCACCACACAC	TGTAGTGTGTGCATAGTGGTGTGTG
SEQ ID NO: 5090	**1388499**	GTTCCCACCGTATAGAGTGTGTGGA	CAAGGGTGGCATATCTCACACACCT
SEQ ID NO: 5091	**1389063**	CGGACACTAGTCGTATACAGGGTAT	GCCTGTGATCAGCATATGTCCCATA
SEQ ID NO: 5092	**1390601**	CAATCGGTCGTAGTGTGTTCCTCTC	GTTAGCCAGCATCACACAAGGAGAG
SEQ ID NO: 5093	**1390707**	GGACCGAGACGACGTAAACCCGGAC	CCTGGCTCTGCTGCATTTGGGCCTG
SEQ ID NO: 5094	**1391169**	AGTGGGTACCGTAGTAGTTACCGTA	TCACCCATGGCATCATCAATGGCAT
SEQ ID NO: 5095	**1392047**	CCGTTGTGTGTACGTCATTCGGAAA	GGCAACACACATGCAGTAAGCCTTT
SEQ ID NO: 5096	**1393523**	GTGTGGAGTGTGTACCCGAACTCGT	CACACCTCACACATGGGCTTGAGCA
SEQ ID NO: 5097	**1395573**	GTGTAGAATGTGTACTCCACTTTGG	CACATCTTACACATGAGGTGAAACC
SEQ ID NO: 5098	**1398639**	TTTGGTACAGTACACTTTCGTGACC	AAACCATGTCATGTGAAAGCACTGG
SEQ ID NO: 5099	**1401207**	ATGTGTCGGGTACGTTACTCGTGTA	TACACAGCCCATGCAATGAGCACAT

SEQ ID NO: 5100	**1401888**	ACGGGCGAGACGTACCGACGACACG	TGCCCGCTCTGCATGGCTGCTGTGC
SEQ ID NO: 5101	**1401916**	CGACCACCGACGTACTTTAGGAATT	GCTGGTGGCTGCATGAAATCCTTAA
SEQ ID NO: 5102	**1402919**	ATTGGACACGTACGAGTGTGTCGGC	TAACCTGTGCATGCTCACACAGCCG
SEQ ID NO: 5103	**1402934**	TGAAGTGTGTGTACGGAGTCCACCC	ACTTCACACACATGCCTCAGGTGGG

Table 5 – Exon regions of a set of genes in female subjects

Att I	Gene Number	Chromosome location	strand	strand start	strand stop	Assigned gene info
	1553	chr1	+	990376.00	990400.00	NM_198576 // AGRN
	1554	chr1	+	1363700.00	1364109.00	---
	1555	chr1	+	1982386.00	1982410.00	---
	1556	chr1	+	2428985.00	2429009.00	NM_014638 // PLCH2
	1557	chr1	+	2734081.00	2734302.00	---
	1558	chr1	+	3397184.00	3397501.00	ENST00000378378 // ARHGEF16
	1559	chr1	+	3801675.00	3801848.00	NM_004402 // DFFB
	1560	chr1	+	6640079.00	6640106.00	NM_005341 // ZBTB48
	1561	chr1	+	11159874.00	11159960.00	---
	1562	chr1	+	11893647.00	11893671.00	NM_001286 // CLCN6
	1563	chr1	+	11893952.00	11893976.00	NM_001286 // CLCN6
	1564	chr1	+	12079417.00	12079496.00	NM_021933 // MIIP
	1565	chr1	+	13910596.00	13910623.00	OTTHUMT00000367736 // PDPN
	1566	chr1	+	14095565.00	14095589.00	ENST00000407521 // PRDM2
	1567	chr1	+	16063134.00	16063296.00	NM_207348 // SLC25A34
	1568	chr1	+	16101387.00	16101411.00	NM_001024215 // FBLIM1
	1569	chr1	+	16483467.00	16483818.00	---
	1570	chr1	+	16510039.00	16510140.00	---
	1571	chr1	+	17952477.00	17952501.00	NM_018125 // ARHGEF10L
	1572	chr1	+	18023346.00	18023370.00	NM_018125 // ARHGEF10L
	1573	chr1	+	23697718.00	23697938.00	NR_033690 // C1orf213
	1574	chr1	+	25916660.00	25916831.00	OTTHUMT00000012834 // OTTHUMG00000004419
	1575	chr1	+	26110238.00	26110262.00	NM_020379 // MAN1C1
	1576	chr1	+	26361797.00	26361821.00	NM_004455 // EXTL1
	1577	chr1	+	28562744.00	28562770.00	NM_016311 // ATPIF1
	1578	chr1	+	29185544.00	29185798.00	NM_000911 // OPRD1
	1579	chr1	+	32050556.00	32050580.00	NM_022164 // TINAGL1
	1580	chr1	+	35250766.00	35250799.00	NM_024009 // GJB3
	1581	chr1	+	35251314.00	35251529.00	NM_024009 // GJB3
	1582	chr1	+	36396857.00	36396881.00	NM_024852 // AGO3
	1583	chr1	+	39720096.00	39720120.00	ENST00000467673 // MACF1
	1584	chr1	+	43108171.00	43108195.00	NM_001080850 // CCDC30
	1585	chr1	+	43317693.00	43317944.00	NM_001242739 // ZNF691

1586	chr1	+	44132084.00	44132108.00	---
1587	chr1	+	44458252.00	44458278.00	NM_152499 // CCDC24
1588	chr1	+	45223239.00	45223263.00	NM_006845 // KIF2C
1589	chr1	+	46669106.00	46669275.00	NM_001013615 // LURAP1
1590	chr1	+	47881758.00	47881944.00	NM_012186 // FOXE3
1591	chr1	+	52518107.00	52518332.00	---
1592	chr1	+	53271171.00	53271195.00	DQ646393 // ZYG11B
1593	chr1	+	55186843.00	55186867.00	NR_037639 // HEATR8-TTC4
1594	chr1	+	57333292.00	57333370.00	NM_000562 // C8A
1595	chr1	+	61892160.00	61892208.00	NM_001134673 // NFIA
1596	chr1	+	63269408.00	63269432.00	NM_032852 // ATG4C
1597	chr1	+	63286814.00	63286875.00	NM_032852 // ATG4C
1598	chr1	+	63902513.00	63902570.00	NM_013339 // ALG6
1599	chr1	+	64515367.00	64515562.00	NM_005012 // ROR1
1600	chr1	+	67390619.00	67390653.00	NM_020948 // MIER1
1601	chr1	+	73776612.00	73776672.00	---
1602	chr1	+	74715179.00	74715203.00	NM_015978 // TNNI3K
1603	chr1	+	75229587.00	75229721.00	NM_138467 // TYW3
1604	chr1	+	76205700.00	76205724.00	NM_000016 // ACADM
1605	chr1	+	83911741.00	83912335.00	---
1606	chr1	+	84791390.00	84791414.00	NM_001010971 // SAMD13
1607	chr1	+	86889875.00	86889926.00	NM_006536 // CLCA2
1608	chr1	+	86919134.00	86919261.00	NM_006536 // CLCA2
1609	chr1	+	86951209.00	86951233.00	NM_001285 // CLCA1
1610	chr1	+	87574072.00	87574396.00	NM_012262 // HS2ST1
1611	chr1	+	87796951.00	87796990.00	ENST00000495705 // LMO4
1612	chr1	+	93712406.00	93712430.00	NM_206886 // CCDC18
1613	chr1	+	94800272.00	94800340.00	OTTHUMT00000029385 // OTTHUMG00000010650
1614	chr1	+	97215091.00	97215167.00	AK299897 // PTBP2
1615	chr1	+	101547656.00	101548525.00	ENST00000451213 // LOC100506051
1616	chr1	+	101616117.00	101616433.00	---
1617	chr1	+	110471967.00	110472290.00	NM_000757 // CSF1
1618	chr1	+	113002550.00	113003739.00	NM_018704 // CTTNBP2NL
1619	chr1	+	113057685.00	113057709.00	NM_004185 // WNT2B
1620	chr1	+	118008956.00	118009010.00	NM_006699 // MAN1A2
1621	chr1	+	118039515.00	118039539.00	NM_006699 // MAN1A2
1622	chr1	+	118496695.00	118496719.00	NM_006784 // WDR3
1623	chr1	+	118738878.00	118738916.00	---

1624	chr1	+	145440540.00	145440596.00	ENST00000488537 // LOC101060503
1625	chr1	+	147380366.00	147381375.00	NM_005267 // GJA8
1626	chr1	+	150049779.00	150049803.00	NM_007259 // VPS45
1627	chr1	+	150933479.00	150933503.00	NM_001145415 // SETDB1
1628	chr1	+	152681632.00	152681656.00	NM_178356 // LCE4A
1629	chr1	+	152733913.00	152734520.00	NM_001025231 // KPRP
1630	chr1	+	152758693.00	152758770.00	ENST00000368771 // LCE1E
1631	chr1	+	153603021.00	153603134.00	NM_006271 // S100A1
1632	chr1	+	154549686.00	154550505.00	NM_000748 // CHRNB2
1633	chr1	+	155006836.00	155006895.00	AK301902 // DCST1
1634	chr1	+	156830623.00	156830647.00	ENST00000368196 // NTRK1
1635	chr1	+	158259602.00	158259737.00	NM_001765 // CD1C
1636	chr1	+	161130244.00	161130268.00	NM_001014443 // USP21
1637	chr1	+	161677023.00	161677051.00	NM_001184866 // FCRLA
1638	chr1	+	161680673.00	161680697.00	NM_001184866 // FCRLA
1639	chr1	+	162740364.00	162740388.00	ENST00000458105 // DDR2
1640	chr1	+	170633546.00	170633580.00	NM_006902 // PRRX1
1641	chr1	+	170967770.00	170967794.00	NM_025063 // MROH9
1642	chr1	+	178516255.00	178516279.00	NR_033186 // C1orf220
1643	chr1	+	180913538.00	180913611.00	NM_020950 // KIAA1614
1644	chr1	+	181759587.00	181759611.00	NM_001205293 // CACNA1E
1645	chr1	+	183515342.00	183515366.00	NM_173156 // SMG7
1646	chr1	+	186007067.00	186007091.00	NM_031935 // HMCN1
1647	chr1	+	186280181.00	186280231.00	NM_005807 // PRG4
1648	chr1	+	200811130.00	200811197.00	NM_203459 // CAMSAP2
1649	chr1	+	203472697.00	203472746.00	NM_014359 // OPTC
1650	chr1	+	203738776.00	203738809.00	ENST00000367215 // LAX1
1651	chr1	+	204942452.00	204942476.00	NM_001005388 // NFASC
1652	chr1	+	206231171.00	206231603.00	ENST00000367126 // AVPR1B
1653	chr1	+	206680879.00	206680906.00	NM_182663 // RASSF5
1654	chr1	+	206903411.00	206903435.00	NM_004759 // MAPKAPK2
1655	chr1	+	209905804.00	209905893.00	NM_005525 // HSD11B1
1656	chr1	+	211563916.00	211564000.00	ENST00000448567 // LINC00467
1657	chr1	+	211859067.00	211859134.00	AK026812 // LOC91548
1658	chr1	+	215752419.00	215752443.00	NM_016121 // KCTD3

1659	chr1	+	225512008.00	225512032.00	NM_001373 // DNAH14
1660	chr1	+	225548402.00	225548426.00	NM_001373 // DNAH14
1661	chr1	+	227834308.00	227834332.00	NM_178549 // ZNF678
1662	chr1	+	228353724.00	228353850.00	NM_001010867 // IBA57
1663	chr1	+	231410847.00	231410871.00	ENST00000469332 // GNPAT
1664	chr1	+	233482275.00	233482299.00	NM_032435 // KIAA1804
1665	chr1	+	237951350.00	237951374.00	NM_001035 // RYR2
1666	chr1	+	242024776.00	242024800.00	NM_006027 // EXO1
1667	chr1	+	245133305.00	245133329.00	NR_026586 // EFCAB2
1668	chr1	+	248285538.00	248286058.00	NR_002141 // OR2M1P
1669	chr1	+	248550928.00	248551830.00	NM_001005471 // OR2T6
1670	chr1	+	248636953.00	248637456.00	---
1671	chr1	-	1228980.00	1229004.00	NM_030649 // ACAP3
1672	chr1	-	1274673.00	1274700.00	ENST00000378888 // DVL1
1673	chr1	-	2139073.00	2139097.00	NM_001146310 // C1orf86
1674	chr1	-	2342083.00	2342164.00	ENST00000502666 // PEX10
1675	chr1	-	6228266.00	6228290.00	NM_015557 // CHD5
1676	chr1	-	6311400.00	6311551.00	NM_207370 // GPR153
1677	chr1	-	7913437.00	7913550.00	NM_021995 // UTS2
1678	chr1	-	9809839.00	9809920.00	NM_001009566 // CLSTN1
1679	chr1	-	10003439.00	10003463.00	ENST00000377213 // LZIC
1680	chr1	-	11026426.00	11026478.00	ENST00000377004 // C1orf127
1681	chr1	-	11169350.00	11169374.00	NM_004958 // MTOR
1682	chr1	-	12998241.00	12998266.00	---
1683	chr1	-	17326600.00	17326624.00	NM_022089 // ATP13A2
1684	chr1	-	18335988.00	18336081.00	---
1685	chr1	-	19812020.00	19812044.00	NM_004930 // CAPZB
1686	chr1	-	20732089.00	20732162.00	NR_033887 // LOC339505
1687	chr1	-	22163343.00	22163367.00	NM_005529 // HSPG2
1688	chr1	-	23645050.00	23645174.00	NM_001102398 // HNRNPR
1689	chr1	-	23765666.00	23765690.00	NM_017707 // ASAP3
1690	chr1	-	24130336.00	24130360.00	AK309129 // HMGCL
1691	chr1	-	24727812.00	24727836.00	NM_001199013 // STPG1
1692	chr1	-	26648668.00	26648692.00	NM_001039775 // AIM1L
1693	chr1	-	26663713.00	26663737.00	ENST00000522923 // AIM1L
1694	chr1	-	26968803.00	26968863.00	---
1695	chr1	-	27687838.00	27687862.00	NM_004672 // MAP3K6

1696	chr1	-	28536488.00	28536563.00	NM_014280 // DNAJC8
1697	chr1	-	29485938.00	29485962.00	NM_005626 // SRSF4
1698	chr1	-	30509644.00	30509828.00	---
1699	chr1	-	32151317.00	32151341.00	NM_001856 // COL16A1
1700	chr1	-	32158076.00	32158100.00	NM_001856 // COL16A1
1701	chr1	-	32207756.00	32207780.00	NM_001703 // BAI2
1702	chr1	-	34498211.00	34498235.00	NM_052896 // CSMD2
1703	chr1	-	36915893.00	36915956.00	NM_145047 // OSCP1
1704	chr1	-	36937322.00	36937346.00	AB209656 // CSF3R
1705	chr1	-	38218569.00	38218593.00	NM_001099439 // EPHA10
1706	chr1	-	40150196.00	40150231.00	NM_016257 // HPCAL4
1707	chr1	-	40367291.00	40367346.00	NM_001033081 // MYCL1
1708	chr1	-	42628577.00	42628639.00	NM_033553 // GUCA2A
1709	chr1	-	42800808.00	42800832.00	NM_014947 // FOXJ3
1710	chr1	-	43222072.00	43222096.00	AF097431 // LEPRE1
1711	chr1	-	43396008.00	43396032.00	ENST00000372500 // SLC2A1
1712	chr1	-	44804843.00	44804952.00	NM_024066 // ERI3
1713	chr1	-	45297914.00	45297938.00	NM_003738 // PTCH2
1714	chr1	-	46088268.00	46088292.00	NM_001114938 // CCDC17
1715	chr1	-	47110853.00	47110877.00	NM_022745 // ATPAF1
1716	chr1	-	51888924.00	51888948.00	ENST00000396122 // EPS15
1717	chr1	-	53685975.00	53686009.00	BC010908 // C1orf123
1718	chr1	-	54635399.00	54636749.00	---
1719	chr1	-	55551776.00	55551800.00	ENST00000472566 // USP24
1720	chr1	-	59354851.00	59354880.00	OTTHUMT00000023040 // OTTHUMG00000008375
1721	chr1	-	61005949.00	61006101.00	---
1722	chr1	-	63005292.00	63005316.00	NM_001271999 // DOCK7
1723	chr1	-	63091037.00	63091061.00	NM_001271999 // DOCK7
1724	chr1	-	68955142.00	68955166.00	NM_001114120 // DEPDC1
1725	chr1	-	70644621.00	70644645.00	NM_017768 // LRRC40
1726	chr1	-	74948969.00	74949020.00	ENST00000294635 // LRRC53
1727	chr1	-	85422142.00	85422262.00	NM_153259 // MCOLN2
1728	chr1	-	86196343.00	86196367.00	NM_152890 // COL24A1
1729	chr1	-	89520996.00	89521020.00	AB208912 // GBP1
1730	chr1	-	91779573.00	91779597.00	NM_001017975 // HFM1
1731	chr1	-	93804256.00	93804280.00	NR_034089 // LOC100131564

1732	chr1	-	93811434.00	93811458.00	ENST00000451302 // LOC100131564
1733	chr1	-	94146841.00	94146865.00	NM_001261409 // BCAR3
1734	chr1	-	95538320.00	95538419.00	NM_144988 // ALG14
1735	chr1	-	106145058.00	106145671.00	---
1736	chr1	-	108247248.00	108247272.00	NM_006113 // VAV3
1737	chr1	-	108313305.00	108313329.00	NM_006113 // VAV3
1738	chr1	-	108328198.00	108328222.00	ENST00000343258 // VAV3
1739	chr1	-	109377118.00	109377142.00	NM_152763 // AKNAD1
1740	chr1	-	110051550.00	110051599.00	NM_020703 // AMIGO1
1741	chr1	-	110924349.00	110924413.00	NM_004696 // SLC16A4
1742	chr1	-	110944154.00	110944199.00	NM_006402 // LAMTOR5
1743	chr1	-	110950212.00	110950420.00	NM_006402 // LAMTOR5
1744	chr1	-	111032760.00	111032861.00	BC042100 // LOC440602
1745	chr1	-	111969059.00	111969112.00	NM_002557 // OVGP1
1746	chr1	-	111983768.00	111983822.00	NM_024102 // WDR77
1747	chr1	-	118456066.00	118456106.00	ENST00000494224 // GDAP2
1748	chr1	-	118530538.00	118530562.00	ENST00000483383 // SPAG17
1749	chr1	-	142951490.00	142951532.00	---
1750	chr1	-	146033632.00	146033656.00	NM_001037501 // NBPF8
1751	chr1	-	146647448.00	146647472.00	ENST00000527849 // LOC101060372
1752	chr1	-	150768881.00	150769243.00	NM_000396 // CTSK
1753	chr1	-	151314589.00	151314613.00	NM_000449 // RFX5
1754	chr1	-	152284586.00	152285327.00	NM_002016 // FLG
1755	chr1	-	153321005.00	153321205.00	BC142636 // PGLYRP4
1756	chr1	-	153517374.00	153517398.00	ENST00000481009 // S100A4
1757	chr1	-	153603488.00	153603541.00	NM_001024210 // S100A13
1758	chr1	-	155213894.00	155213918.00	ENST00000493842 // GBA
1759	chr1	-	156499958.00	156499982.00	NM_178229 // IQGAP3
1760	chr1	-	157805692.00	157805774.00	NM_005894 // CD5L
1761	chr1	-	161161876.00	161161970.00	NM_005099 // ADAMTS4
1762	chr1	-	161953411.00	161953435.00	NM_015441 // OLFML2B
1763	chr1	-	175365833.00	175365857.00	NM_003285 // TNR
1764	chr1	-	177927296.00	177927320.00	NM_033127 // SEC16B
1765	chr1	-	180283827.00	180283853.00	NM_032360 // ACBD6
1766	chr1	-	182635139.00	182635163.00	NM_033345 // RGS8
1767	chr1	-	183933105.00	183933129.00	NM_015101 // COLGALT2
1768	chr1	-	184792832.00	184792858.00	NM_052966 // FAM129A

1769	chr1	-	193654711.00	193654873.00	OTTHUMT00000086757 // OTTHUMG00000035685
1770	chr1	-	195727752.00	195728362.00	---
1771	chr1	-	197564384.00	197564408.00	NM_144977 // DENND1B
1772	chr1	-	201013525.00	201013549.00	NM_000069 // CACNA1S
1773	chr1	-	201334767.00	201334791.00	NM_000364 // TNNT2
1774	chr1	-	201351885.00	201351933.00	ENST00000475136 // LAD1
1775	chr1	-	201390827.00	201390851.00	NM_003281 // TNNI1
1776	chr1	-	201970140.00	201970323.00	---
1777	chr1	-	202913322.00	202913641.00	AK124455 // ADIPOR1
1778	chr1	-	203270218.00	203270406.00	NR_034151 // LOC730227
1779	chr1	-	204009336.00	204009376.00	---
1780	chr1	-	204100312.00	204100336.00	NM_018208 // ETNK2
1781	chr1	-	204218365.00	204218389.00	NM_014935 // PLEKHA6
1782	chr1	-	205569009.00	205569033.00	BC040145 // ELK4
1783	chr1	-	205882948.00	205882972.00	NM_052934 // SLC26A9
1784	chr1	-	208201404.00	208201428.00	NM_025179 // PLXNA2
1785	chr1	-	216896744.00	216896768.00	NM_001438 // ESRRG
1786	chr1	-	220156143.00	220156167.00	NM_004446 // EPRS
1787	chr1	-	220198442.00	220198466.00	---
1788	chr1	-	220160865.00	220160943.00	---
1789	chr1	-	220291195.00	220291287.00	NR_029628 // MIR215
1790	chr1	-	222700336.00	222700389.00	NM_024746 // HHIPL2
1791	chr1	-	222737408.00	222737464.00	NM_005681 // TAF1A
1792	chr1	-	228604260.00	228604398.00	NM_016102 // TRIM17
1793	chr1	-	232538179.00	232538203.00	NM_020808 // SIPA1L2
1794	chr1	-	242612710.00	242612763.00	NM_001195811 // PLD5
1795	chr10	+	736193.00	736263.00	---
1796	chr10	+	2123017.00	2123270.00	---
1797	chr10	+	3802596.00	3802682.00	---
1798	chr10	+	4005215.00	4005287.00	---
1799	chr10	+	5012093.00	5012117.00	ENST00000380859 // AKR1C1
1800	chr10	+	11894086.00	11894193.00	NM_153256 // PROSER2
1801	chr10	+	13639469.00	13639498.00	NM_003675 // PRPF18
1802	chr10	+	25510022.00	25510074.00	NM_020752 // GPR158
1803	chr10	+	29032587.00	29032670.00	---
1804	chr10	+	32636334.00	32636403.00	---
1805	chr10	+	38660023.00	38660056.00	NR_003086 // HSD17B7P2
1806	chr10	+	44467615.00	44467646.00	---
1807	chr10	+	45643031.00	45643115.00	ENST00000427229 // ANKRD30BP3
1808	chr10	+	49893550.00	49893574.00	NM_020945 // WDFY4

1809	chr10	+	50535004.00	50535051.00	NM_001135196 // C10orf71
1810	chr10	+	50902126.00	50902506.00	AK091773 // C10orf53
1811	chr10	+	51562443.00	51562497.00	NM_138634 // MSMB
1812	chr10	+	53822317.00	53822341.00	NM_001098512 // PRKG1
1813	chr10	+	60156831.00	60158251.00	NM_003201 // TFAM
1814	chr10	+	69933981.00	69934194.00	NR_045662 // MYPN
1815	chr10	+	69935081.00	69935216.00	NR_045662 // MYPN
1816	chr10	+	70764806.00	70764830.00	NM_015634 // KIAA1279
1817	chr10	+	71255086.00	71255110.00	ENST00000459981 // TSPAN15
1818	chr10	+	73472383.00	73472407.00	NM_001164375 // C10orf105
1819	chr10	+	73768486.00	73772109.00	NM_004273 // CHST3
1820	chr10	+	75671651.00	75671681.00	NM_001145031 // PLAU
1821	chr10	+	80010772.00	80011621.00	NR_038985 // LINC00856
1822	chr10	+	85902423.00	85902496.00	NM_014394 // GHITM
1823	chr10	+	86332178.00	86332515.00	---
1824	chr10	+	88603177.00	88603262.00	ENST00000480152 // BMPR1A
1825	chr10	+	89311867.00	89311925.00	NM_004897 // MINPP1
1826	chr10	+	91613580.00	91613731.00	---
1827	chr10	+	93542614.00	93542872.00	ENST00000432938 // TNKS2-AS1
1828	chr10	+	95537347.00	95537373.00	NM_005097 // LGI1
1829	chr10	+	96018822.00	96018846.00	NM_016341 // PLCE1
1830	chr10	+	96316955.00	96316979.00	AB102716 // HELLS
1831	chr10	+	96356835.00	96356859.00	NM_018063 // HELLS
1832	chr10	+	97792910.00	97793020.00	---
1833	chr10	+	99350381.00	99350677.00	NM_001009997 // C10orf62
1834	chr10	+	101193319.00	101193603.00	OTTHUMT00000049797 // OTTHUMG00000018883
1835	chr10	+	101993710.00	101993749.00	---
1836	chr10	+	102709839.00	102709863.00	NM_018121 // FAM178A
1837	chr10	+	103295201.00	103295225.00	NM_033637 // BTRC
1838	chr10	+	112653906.00	112653930.00	NM_014456 // PDCD4
1839	chr10	+	114575996.00	114576690.00	NM_145206 // VTI1A
1840	chr10	+	115485222.00	115485271.00	NM_001227 // CASP7
1841	chr10	+	121214487.00	121214511.00	NM_005308 // GRK5
1842	chr10	+	121586720.00	121587147.00	NM_014937 // INPP5F
1843	chr10	+	122357742.00	122357775.00	BC108662 // C10orf85
1844	chr10	+	124058528.00	124058552.00	NM_144587 // BTBD16
1845	chr10	+	124739563.00	124739722.00	NM_153336 // PSTK
1846	chr10	+	125319415.00	125319603.00	---

1847	chr10	+	134901514.00	134901567.00	NM_001083909 // GPR123
1848	chr10	+	134912223.00	134912248.00	NM_001083909 // GPR123
1849	chr10	-	532405.00	532429.00	NM_014974 // DIP2C
1850	chr10	-	3347029.00	3347643.00	---
1851	chr10	-	5437339.00	5437429.00	NM_024803 // TUBAL3
1852	chr10	-	5566998.00	5567389.00	---
1853	chr10	-	13264135.00	13264168.00	NM_145314 // UCMA
1854	chr10	-	13363975.00	13364011.00	GU954549 // SEPHS1
1855	chr10	-	17659110.00	17659228.00	NM_014241 // PTPLA
1856	chr10	-	18940456.00	18940480.00	NM_182543 // NSUN6
1857	chr10	-	21658906.00	21659036.00	OTTHUMT00000047127 // OTTHUMG00000017792
1858	chr10	-	29163327.00	29163431.00	---
1859	chr10	-	29785338.00	29785362.00	AK302077 // SVIL
1860	chr10	-	32310166.00	32310190.00	NM_004521 // KIF5B
1861	chr10	-	33623466.00	33623490.00	NM_003873 // NRP1
1862	chr10	-	43132295.00	43132347.00	ENST00000486614 // ZNF33B
1863	chr10	-	45803192.00	45803247.00	NM_001004297 // OR13A1
1864	chr10	-	49813007.00	49813031.00	NM_001256024 // ARHGAP22
1865	chr10	-	50574294.00	50574368.00	NM_001276451 // DRGX
1866	chr10	-	50964726.00	50964750.00	ENST00000471460 // OGDHL
1867	chr10	-	54785168.00	54785192.00	---
1868	chr10	-	55581917.00	55581941.00	NM_001142763 // PCDH15
1869	chr10	-	61811254.00	61811278.00	ENST00000480699 // ANK3
1870	chr10	-	63212673.00	63212832.00	NM_178505 // TMEM26
1871	chr10	-	64953265.00	64953289.00	ENST00000490669 // JMJD1C
1872	chr10	-	69995098.00	69995129.00	OTTHUMT00000048311 // OTTHUMG00000018345
1873	chr10	-	75158119.00	75158143.00	NM_001156 // ANXA7
1874	chr10	-	75255737.00	75255766.00	NM_001142353 // PPP3CB
1875	chr10	-	75294502.00	75294526.00	NM_152586 // USP54
1876	chr10	-	79595516.00	79595540.00	NM_004747 // DLG5
1877	chr10	-	79785413.00	79785437.00	NM_007055 // POLR3A
1878	chr10	-	80456489.00	80456779.00	---
1879	chr10	-	82295381.00	82295636.00	---
1880	chr10	-	87489319.00	87489352.00	NM_017551 // GRID1
1881	chr10	-	88820021.00	88820045.00	AB209406 // GLUD1
1882	chr10	-	95458072.00	95458096.00	NM_145246 // FRA10AC1

1883	chr10	-	96112096.00	96112120.00	NM_022451 // NOC3L
1884	chr10	-	98311030.00	98311126.00	NM_020123 // TM9SF3
1885	chr10	-	98762074.00	98762098.00	NM_003061 // SLIT1
1886	chr10	-	98790525.00	98790549.00	NM_003061 // SLIT1
1887	chr10	-	99221601.00	99221625.00	NM_022362 // MMS19
1888	chr10	-	99529438.00	99529502.00	NM_003015 // SFRP5
1889	chr10	-	101667753.00	101667802.00	NM_015221 // DNMBP
1890	chr10	-	102266115.00	102266139.00	NM_015490 // SEC31B
1891	chr10	-	105218586.00	105218641.00	NM_001001412 // CALHM1
1892	chr10	-	111644000.00	111644024.00	AK295756 // XPNPEP1
1893	chr10	-	115895654.00	115895702.00	NM_018017 // C10orf118
1894	chr10	-	119875166.00	119875353.00	---
1895	chr10	-	120085667.00	120085755.00	NM_022063 // FAM204A
1896	chr10	-	131170642.00	131171328.00	---
1897	chr10	-	134692958.00	134692982.00	NM_001200049 // TTC40
1898	chr10	-	135380572.00	135380942.00	NR_033789 // SPRNP1
1899	chr11	+	213547.00	213571.00	ENST00000530149 // RIC8A
1900	chr11	+	291978.00	292002.00	NM_025092 // ATHL1
1901	chr11	+	926059.00	926083.00	NM_001242837 // AP2A2
1902	chr11	+	1010564.00	1010588.00	NM_001242837 // AP2A2
1903	chr11	+	1051684.00	1051743.00	---
1904	chr11	+	1158042.00	1158066.00	AJ298317 // MUC5AC
1905	chr11	+	1249909.00	1249933.00	NM_002458 // MUC5B
1906	chr11	+	2393917.00	2393973.00	---
1907	chr11	+	3239728.00	3239768.00	NR_027138 // MRGPRG-AS1
1908	chr11	+	4141089.00	4141113.00	NM_001033 // RRM1
1909	chr11	+	6384029.00	6384307.00	---
1910	chr11	+	9431578.00	9431602.00	NM_006391 // IPO7
1911	chr11	+	9746206.00	9746230.00	NM_015055 // SWAP70
1912	chr11	+	10482797.00	10482821.00	NM_001172430 // AMPD3
1913	chr11	+	18467768.00	18467792.00	NM_002301 // LDHC
1914	chr11	+	20388746.00	20388800.00	NM_001098520 // HTATIP2
1915	chr11	+	22382504.00	22382528.00	NM_020346 // SLC17A6
1916	chr11	+	23818265.00	23818485.00	OTTHUMT00000387785 // OTTHUMG00000166086
1917	chr11	+	29066226.00	29066397.00	---
1918	chr11	+	29288171.00	29288254.00	OTTHUMT00000387986 // OTTHUMG00000166127
1919	chr11	+	43662438.00	43662462.00	---
1920	chr11	+	47236689.00	47236743.00	NM_000107 // DDB2
1921	chr11	+	57243699.00	57244231.00	NM_178570 // RTN4RL2

1922	chr11	+	57364870.00	57364990.00	ENST00000405496 // SERPING1
1923	chr11	+	60470504.00	60470633.00	AK308413 // MS4A8
1924	chr11	+	61532544.00	61532568.00	AK130906 // LOC100129473
1925	chr11	+	62149315.00	62149953.00	---
1926	chr11	+	63803540.00	63803608.00	OTTHUMT00000396285 // OTTHUMG00000167787
1927	chr11	+	63953156.00	63953180.00	BC039299 // STIP1
1928	chr11	+	64127065.00	64127089.00	ENST00000530383 // RPS6KA4
1929	chr11	+	65043437.00	65043461.00	NM_002689 // POLA2
1930	chr11	+	65055098.00	65055122.00	ENST00000533192 // POLA2
1931	chr11	+	65072942.00	65072966.00	---
1932	chr11	+	65359513.00	65359537.00	NM_001099409 // EHBP1L1
1933	chr11	+	66177685.00	66177789.00	ENST00000533759 // LOC100505504
1934	chr11	+	66178346.00	66178444.00	ENST00000533759 // LOC100505504
1935	chr11	+	66252655.00	66252679.00	NM_005700 // DPP3
1936	chr11	+	66252680.00	66252704.00	NM_005700 // DPP3
1937	chr11	+	68370916.00	68370940.00	NM_001164162 // PPP6R3
1938	chr11	+	69300813.00	69300909.00	---
1939	chr11	+	69680151.00	69680450.00	---
1940	chr11	+	70035595.00	70035619.00	NM_018043 // ANO1
1941	chr11	+	70188131.00	70188155.00	---
1942	chr11	+	71806539.00	71806563.00	NM_145309 // LRTOMT
1943	chr11	+	71817051.00	71817075.00	NM_001145308 // LRTOMT
1944	chr11	+	71831926.00	71832196.00	---
1945	chr11	+	71934794.00	71934818.00	---
1946	chr11	+	72354352.00	72354480.00	---
1947	chr11	+	73670718.00	73670769.00	AK128589 // DNAJB13
1948	chr11	+	76750823.00	76750847.00	NM_138706 // B3GNT6
1949	chr11	+	78467290.00	78467525.00	---
1950	chr11	+	82878723.00	82878747.00	AK302606 // PCF11
1951	chr11	+	85989369.00	85989393.00	NM_152991 // EED
1952	chr11	+	92573878.00	92573902.00	NM_001008781 // FAT3
1953	chr11	+	95217154.00	95217333.00	OTTHUMT00000395967 // OTTHUMG00000167737
1954	chr11	+	100845249.00	100845273.00	NM_152432 // ARHGAP42
1955	chr11	+	110306629.00	110306653.00	NM_004109 // FDX1

1956	chr11	+	111430998.00	111431022.00	NM_001258390 // LAYN
1957	chr11	+	111899274.00	111899350.00	NM_001931 // DLAT
1958	chr11	+	112100845.00	112100894.00	ENST00000531175 // PTS
1959	chr11	+	113265679.00	113265801.00	NM_178510 // ANKK1
1960	chr11	+	113933990.00	113934017.00	NM_006006 // ZBTB16
1961	chr11	+	114578248.00	114578274.00	AK057953 // NXPE2
1962	chr11	+	119817139.00	119817230.00	---
1963	chr11	+	123484277.00	123484301.00	NM_020716 // GRAMD1B
1964	chr11	+	123810250.00	123810323.00	ENST00000307033 // OR4D5
1965	chr11	+	124504041.00	124504065.00	NM_032811 // TBRG1
1966	chr11	+	126277210.00	126277234.00	NM_006278 // ST3GAL4
1967	chr11	+	130272389.00	130273062.00	AK091840 // FLJ34521
1968	chr11	+	130597136.00	130597192.00	---
1969	chr11	+	134132691.00	134132715.00	AK299492 // ACAD8
1970	chr11	+	134308421.00	134308445.00	---
1971	chr11	-	790093.00	790122.00	NM_016564 // CEND1
1972	chr11	-	904874.00	904898.00	ENST00000454838 // CHID1
1973	chr11	-	1784878.00	1784968.00	OTTHUMT00000105340 // OTTHUMG00000045359
1974	chr11	-	3111897.00	3111921.00	NM_020896 // OSBPL5
1975	chr11	-	3253409.00	3253615.00	NM_001039165 // MRGPRE
1976	chr11	-	4944762.00	4945528.00	NM_001005237 // OR51G1
1977	chr11	-	6340994.00	6341217.00	ENST00000532354 // PRKCDBP
1978	chr11	-	6462242.00	6462266.00	ENST00000265983 // HPX
1979	chr11	-	9454853.00	9454965.00	---
1980	chr11	-	12986705.00	12986733.00	---
1981	chr11	-	14512184.00	14512208.00	NM_016451 // COPB1
1982	chr11	-	17452256.00	17452280.00	AK297560 // ABCC8
1983	chr11	-	17565864.00	17565888.00	NM_005709 // USH1C
1984	chr11	-	19223508.00	19223580.00	NM_003476 // CSRP3
1985	chr11	-	20142142.00	20142169.00	ENST00000526642 // NAV2-AS1
1986	chr11	-	33127573.00	33127597.00	NM_001326 // CSTF3
1987	chr11	-	33719981.00	33720055.00	ENST00000379011 // C11orf91
1988	chr11	-	33792378.00	33793163.00	AB209039 // FBXO3
1989	chr11	-	34912053.00	34912077.00	NM_015957 // APIP
1990	chr11	-	43456682.00	43456933.00	---
1991	chr11	-	45234554.00	45236209.00	---
1992	chr11	-	46921867.00	46921891.00	NM_002334 // LRP4

1993	chr11	-	47357520.00	47357544.00	NM_000256 // MYBPC3
1994	chr11	-	47371634.00	47371658.00	NM_000256 // MYBPC3
1995	chr11	-	57157379.00	57157404.00	NM_002728 // PRG2
1996	chr11	-	57885980.00	57886712.00	NM_001005211 // OR9I1
1997	chr11	-	58601958.00	58602208.00	NM_145016 // GLYATL2
1998	chr11	-	61124231.00	61124255.00	NM_001161452 // CYB561A3
1999	chr11	-	62392827.00	62392851.00	NM_198334 // GANAB
2000	chr11	-	62592758.00	62592806.00	NM_003164 // STX5
2001	chr11	-	62752247.00	62752460.00	NM_004790 // SLC22A6
2002	chr11	-	63230429.00	63230668.00	NM_054108 // HRASLS5
2003	chr11	-	64084390.00	64084439.00	NM_016404 // TRMT112
2004	chr11	-	64084531.00	64084567.00	NM_016404 // TRMT112
2005	chr11	-	64415691.00	64415715.00	NM_015080 // NRXN2
2006	chr11	-	65307253.00	65307277.00	NM_001130144 // LTBP3
2007	chr11	-	65321174.00	65321198.00	NM_001130144 // LTBP3
2008	chr11	-	65652571.00	65652597.00	NM_198897 // FIBP
2009	chr11	-	66134991.00	66135015.00	NM_001532 // SLC29A2
2010	chr11	-	66203534.00	66203571.00	NM_016050 // MRPL11
2011	chr11	-	67207961.00	67207990.00	OTTHUMT00000396223 // CORO1B
2012	chr11	-	68512488.00	68512512.00	NM_004923 // MTL5
2013	chr11	-	68668025.00	68668049.00	NM_181515 // MRPL21
2014	chr11	-	72065406.00	72065430.00	---
2015	chr11	-	72369062.00	72369086.00	AK095024 // PDE2A
2016	chr11	-	74983836.00	74983860.00	---
2017	chr11	-	76072119.00	76072263.00	ENST00000525277 // PRKRIR
2018	chr11	-	76998214.00	76998238.00	ENST00000527489 // GDPD4
2019	chr11	-	90602307.00	90602342.00	---
2020	chr11	-	92136388.00	92136484.00	---
2021	chr11	-	94163103.00	94163127.00	NM_005591 // MRE11A
2022	chr11	-	94695893.00	94696004.00	NM_016403 // CWC15
2023	chr11	-	94704176.00	94704200.00	NM_016403 // CWC15
2024	chr11	-	94704544.00	94704632.00	NM_016403 // CWC15
2025	chr11	-	104915926.00	104916005.00	ENST00000528513 // CARD16
2026	chr11	-	111709018.00	111709042.00	NM_024740 // ALG9
2027	chr11	-	113704149.00	113704173.00	NM_020886 // USP28
2028	chr11	-	116649715.00	116649739.00	NM_003904 // ZNF259
2029	chr11	-	116756855.00	116757682.00	AK058022 // SIK3-IT1
2030	chr11	-	117096667.00	117096691.00	NM_004716 // PCSK7
2031	chr11	-	118938209.00	118938385.00	---

2032	chr11	-	119060444.00	119060552.00	ENST00000503566 // CCDC153
2033	chr11	-	119294130.00	119294411.00	ENST00000284240 // THY1
2034	chr11	-	123676090.00	123676115.00	ENST00000309154 // OR6M1
2035	chr11	-	124543620.00	124543702.00	NM_170601 // SIAE
2036	chr11	-	124972076.00	124972106.00	NM_001258243 // TMEM218
2037	chr11	-	125874139.00	125874163.00	AB209396 // CDON
2038	chr11	-	130298287.00	130298880.00	ENST00000257359 // ADAMTS8
2039	chr11	-	133668322.00	133669871.00	---
2040	chr11	-	134026881.00	134026905.00	---
2041	chr11	-	134818678.00	134818706.00	---
2042	chr12	+	527717.00	527777.00	NM_032358 // CCDC77
2043	chr12	+	1399118.00	1399142.00	NR_027946 // ERC1
2044	chr12	+	3600631.00	3600745.00	NM_019854 // PRMT8
2045	chr12	+	4853775.00	4853838.00	NM_017417 // GALNT8
2046	chr12	+	6425054.00	6425080.00	NM_018173 // PLEKHG6
2047	chr12	+	6653903.00	6654077.00	---
2048	chr12	+	6878262.00	6878293.00	BC007616 // PTMS
2049	chr12	+	7050630.00	7050654.00	NM_001007026 // ATN1
2050	chr12	+	7262681.00	7262730.00	AL833364 // C1RL-AS1
2051	chr12	+	7342537.00	7342561.00	NM_001131025 // PEX5
2052	chr12	+	12224402.00	12224428.00	NM_138722 // BCL2L14
2053	chr12	+	12379632.00	12379666.00	---
2054	chr12	+	15704550.00	15704574.00	NM_030667 // PTPRO
2055	chr12	+	15710396.00	15710420.00	NM_030667 // PTPRO
2056	chr12	+	15734706.00	15734730.00	NM_030667 // PTPRO
2057	chr12	+	19592869.00	19592893.00	NM_153207 // AEBP2
2058	chr12	+	20885858.00	20885882.00	NM_001145946 // SLCO1C1
2059	chr12	+	21590925.00	21591017.00	AK125461 // PYROXD1
2060	chr12	+	27944688.00	27944795.00	NM_020782 // KLHL42
2061	chr12	+	31477261.00	31477680.00	NR_026806 // FLJ13224
2062	chr12	+	41302249.00	41302273.00	NM_001843 // CNTN1
2063	chr12	+	42748987.00	42749011.00	NM_016488 // PPHLN1
2064	chr12	+	43064214.00	43064238.00	OTTHUMT00000403636 // OTTHUMG00000169347
2065	chr12	+	49919818.00	49919842.00	NM_023071 // SPATS2
2066	chr12	+	50471784.00	50471845.00	NM_020039 // ASIC1
2067	chr12	+	50482390.00	50482414.00	NM_003076 // SMARCD1
2068	chr12	+	50482540.00	50482564.00	AK293932 // SMARCD1
2069	chr12	+	50499671.00	50499695.00	AK295911 // GPD1

2070	chr12	+	51027086.00	51027159.00	---
2071	chr12	+	51236708.00	51236738.00	NM_182559 // TMPRSS12
2072	chr12	+	52700956.00	52701164.00	XR_111293 // LOC100509764
2073	chr12	+	53345480.00	53345504.00	ENST00000546656 // KRT18
2074	chr12	+	54379296.00	54379362.00	NM_017409 // HOXC10
2075	chr12	+	56547326.00	56547428.00	ENST00000551834 // MYL6B
2076	chr12	+	58148883.00	58148945.00	NM_138396 // MARCH9
2077	chr12	+	59206242.00	59206399.00	ENST00000552519 // LOC100506869
2078	chr12	+	64833062.00	64833086.00	NM_007235 // XPOT
2079	chr12	+	72668320.00	72668344.00	ENST00000552503 // TRHDE
2080	chr12	+	79679592.00	79679645.00	NM_005639 // SYT1
2081	chr12	+	80817522.00	80817546.00	ENST00000547376 // PTPRQ
2082	chr12	+	81015866.00	81015890.00	NM_001145026 // PTPRQ
2083	chr12	+	82767848.00	82767872.00	---
2084	chr12	+	89987095.00	89987720.00	OTTHUMT00000406651 // OTTHUMG00000169945
2085	chr12	+	90341942.00	90342024.00	OTTHUMT00000406667 // OTTHUMG00000169952
2086	chr12	+	93896266.00	93896353.00	NM_014050 // MRPL42
2087	chr12	+	95878623.00	95878649.00	---
2088	chr12	+	96606524.00	96606602.00	ENST00000547860 // ELK3
2089	chr12	+	101477561.00	101477585.00	NM_178826 // ANO4
2090	chr12	+	102120508.00	102120586.00	AK226127 // CHPT1
2091	chr12	+	102569409.00	102569433.00	NM_017915 // PARPBP
2092	chr12	+	104049051.00	104049075.00	NM_017564 // STAB2
2093	chr12	+	104379448.00	104379506.00	NM_003211 // TDG
2094	chr12	+	104380756.00	104380800.00	NM_003211 // TDG
2095	chr12	+	108600144.00	108600176.00	NM_014653 // WSCD2
2096	chr12	+	111057686.00	111057710.00	NM_001082538 // TCTN1
2097	chr12	+	119624621.00	119624819.00	OTTHUMT00000401649 // HSPB8
2098	chr12	+	120990321.00	120990345.00	NM_014868 // RNF10
2099	chr12	+	121098060.00	121098130.00	NM_031205 // CABP1
2100	chr12	+	121099952.00	121100133.00	ENST00000498082 // CABP1
2101	chr12	+	122684785.00	122684809.00	NM_001098519 // LRRC43
2102	chr12	+	123030723.00	123030747.00	NM_014708 // KNTC1

2103	chr12	+	123333053.00	123333077.00	ENST00000253083 // HIP1R
2104	chr12	+	123465467.00	123465495.00	ENST00000536502 // ARL6IP4
2105	chr12	+	124284771.00	124284795.00	NM_207437 // DNAH10
2106	chr12	+	124332614.00	124332638.00	NM_207437 // DNAH10
2107	chr12	+	124356022.00	124356046.00	NM_207437 // DNAH10
2108	chr12	+	124362406.00	124362430.00	NM_207437 // DNAH10
2109	chr12	+	124575151.00	124575378.00	---
2110	chr12	+	125562816.00	125562840.00	ENST00000418937 // AACS
2111	chr12	+	125636139.00	125636363.00	---
2112	chr12	+	133657382.00	133657406.00	NM_003440 // ZNF140
2113	chr12	-	1963135.00	1963159.00	NM_172364 // CACNA2D4
2114	chr12	-	3782671.00	3782695.00	NM_001144958 // EFCAB4B
2115	chr12	-	6686980.00	6687004.00	NM_001273 // CHD4
2116	chr12	-	6788000.00	6788024.00	ENST00000537248 // ZNF384
2117	chr12	-	7276727.00	7276770.00	NM_031491 // RBP5
2118	chr12	-	9384207.00	9384292.00	NR_040112 // A2MP1
2119	chr12	-	10826643.00	10826825.00	NM_018423 // STYK1
2120	chr12	-	13095195.00	13095241.00	NM_018654 // GPRC5D
2121	chr12	-	15037155.00	15037179.00	NM_001190839 // MGP
2122	chr12	-	15807283.00	15807307.00	ENST00000541465 // EPS8
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2124	chr12	-	15837143.00	15837167.00	ENST00000536793 // EPS8
2125	chr12	-	22408231.00	22408255.00	NM_003034 // ST8SIA1
2126	chr12	-	30833468.00	30833492.00	NM_006390 // IPO8
2127	chr12	-	30841478.00	30841502.00	OTTHUMT00000402702 // IPO8
2128	chr12	-	30847919.00	30847943.00	OTTHUMT00000402704 // IPO8
2129	chr12	-	30975644.00	30975668.00	---
2130	chr12	-	31542322.00	31542346.00	NM_144973 // DENND5B
2131	chr12	-	34371750.00	34371775.00	OTTHUMT00000403317 // OTTHUMG00000169290
2132	chr12	-	42706871.00	42706938.00	NM_033114 // ZCRB1
2133	chr12	-	48382221.00	48382245.00	AL834148 // COL2A1
2134	chr12	-	48677960.00	48677989.00	---
2135	chr12	-	48961775.00	48961799.00	NM_002289 // LALBA
2136	chr12	-	49491053.00	49491077.00	NM_018113 // LMBR1L

2137	chr12	-	50044970.00	50044994.00	NM_175736 // FMNL3
2138	chr12	-	51386076.00	51386100.00	NM_001174125 // SLC11A2
2139	chr12	-	51592415.00	51592439.00	NR_026893 // POU6F1
2140	chr12	-	53071275.00	53071300.00	ENST00000548765 // KRT1
2141	chr12	-	53532336.00	53532372.00	---
2142	chr12	-	54069996.00	54070021.00	NM_001002031 // ATP5G2
2143	chr12	-	54390461.00	54390565.00	ENST00000513533 // HOXC-AS2
2144	chr12	-	54793653.00	54793677.00	NM_002205 // ITGA5
2145	chr12	-	54797858.00	54797882.00	ENST00000550141 // ITGA5
2146	chr12	-	54936898.00	54937275.00	---
2147	chr12	-	54976540.00	54976573.00	NM_006741 // PPP1R1A
2148	chr12	-	55026053.00	55026155.00	NM_033277 // LACRT
2149	chr12	-	56078936.00	56078960.00	NM_001144996 // ITGA7
2150	chr12	-	56233363.00	56233440.00	NM_002429 // MMP19
2151	chr12	-	56236626.00	56236661.00	NM_002429 // MMP19
2152	chr12	-	56236717.00	56236742.00	NM_002429 // MMP19
2153	chr12	-	56349119.00	56349143.00	NM_001200054 // PMEL
2154	chr12	-	56498410.00	56498566.00	---
2155	chr12	-	56705270.00	56705294.00	ENST00000546937 // CNPY2
2156	chr12	-	56814781.00	56814805.00	NM_003920 // TIMELESS
2157	chr12	-	56826857.00	56826881.00	NM_003920 // TIMELESS
2158	chr12	-	57398702.00	57398743.00	NM_014830 // ZBTB39
2159	chr12	-	58204849.00	58204873.00	NM_006576 // AVIL
2160	chr12	-	58217401.00	58217475.00	NM_005730 // CTDSP2
2161	chr12	-	58239254.00	58239317.00	AK310873 // CTDSP2
2162	chr12	-	62104155.00	62104179.00	NM_178539 // FAM19A2
2163	chr12	-	62529689.00	62529713.00	OTTHUMT00000408102 // FAM19A2
2164	chr12	-	64586453.00	64587574.00	ENST00000398055 // C12orf66
2165	chr12	-	65950660.00	65950759.00	OTTHUMT00000401442 // OTTHUMG00000168872
2166	chr12	-	66786510.00	66786534.00	NM_021150 // GRIP1
2167	chr12	-	66909470.00	66909494.00	NM_021150 // GRIP1
2168	chr12	-	71425760.00	71425828.00	---
2169	chr12	-	72008993.00	72009017.00	NM_144982 // ZFC3H1
2170	chr12	-	75437541.00	75437588.00	NM_001260497 // KCNC2
2171	chr12	-	77259978.00	77260002.00	NM_001321 // CSRP2

2172	chr12	-	80199549.00	80199573.00	ENST00000550007 // PPP1R12A
2173	chr12	-	90018009.00	90018033.00	NM_001001323 // ATP2B1
2174	chr12	-	90049637.00	90049661.00	NM_001001323 // ATP2B1
2175	chr12	-	102590923.00	102590947.00	NM_002674 // PMCH
2176	chr12	-	105837641.00	105837827.00	---
2177	chr12	-	109527434.00	109527811.00	ENST00000543444 // ALKBH2
2178	chr12	-	109724524.00	109724548.00	NM_213596 // FOXN4
2179	chr12	-	109797139.00	109797322.00	OTTHUMT00000403091 // OTTHUMG00000169251
2180	chr12	-	110172072.00	110172386.00	NR_026661 // FAM222A-AS1
2181	chr12	-	110236524.00	110236585.00	NM_021625 // TRPV4
2182	chr12	-	110488818.00	110488842.00	---
2183	chr12	-	110937027.00	110937249.00	ENST00000550267 // VPS29
2184	chr12	-	112037084.00	112037108.00	NM_002973 // ATXN2
2185	chr12	-	112696374.00	112696398.00	NM_001109662 // HECTD4
2186	chr12	-	120565717.00	120565741.00	NM_006836 // GCN1L1
2187	chr12	-	120783976.00	120784028.00	NM_002442 // MSI1
2188	chr12	-	122287640.00	122287694.00	NM_002150 // HPD
2189	chr12	-	123424586.00	123424610.00	BC017348 // ABCB9
2190	chr12	-	131293187.00	131293217.00	NM_001980 // STX2
2191	chr12	-	133351669.00	133351693.00	ENST00000541013 // GOLGA3
2192	chr13	+	19479620.00	19479695.00	BC035261 // LOC100652856
2193	chr13	+	21215507.00	21215531.00	NM_175605 // IFT88
2194	chr13	+	21245142.00	21245166.00	NM_175605 // IFT88
2195	chr13	+	23483028.00	23483059.00	AK130366 // LINC00621
2196	chr13	+	24234548.00	24234572.00	NM_018647 // TNFRSF19
2197	chr13	+	25894707.00	25894731.00	NM_014089 // NUPL1
2198	chr13	+	29242615.00	29242707.00	NM_015932 // POMP
2199	chr13	+	30070488.00	30070535.00	ENST00000400542 // MTUS2
2200	chr13	+	33233368.00	33233392.00	NM_015032 // PDS5B
2201	chr13	+	33590263.00	33590341.00	ENST00000426690 // KL
2202	chr13	+	38122233.00	38122373.00	NR_040244 // LINC00547
2203	chr13	+	38928392.00	38928417.00	NM_016617 // UFM1
2204	chr13	+	39625053.00	39625142.00	---
2205	chr13	+	46287336.00	46288170.00	NM_152719 // SPERT

2206	chr13	+	48653948.00	48654096.00	NR_046511 // MED4-AS1
2207	chr13	+	51503643.00	51503667.00	NM_024570 // RNASEH2B
2208	chr13	+	53261983.00	53262225.00	NM_006704 // SUGT1
2209	chr13	+	90883473.00	90883515.00	NR_030754 // MIR622
2210	chr13	+	100171816.00	100171875.00	ENST00000463709 // TM9SF2
2211	chr13	+	100232424.00	100232622.00	---
2212	chr13	+	102105205.00	102105271.00	NM_004791 // ITGBL1
2213	chr13	+	112968357.00	112973927.00	---
2214	chr13	+	113688207.00	113688231.00	---
2215	chr13	+	113731380.00	113731404.00	NM_001112732 // MCF2L
2216	chr13	+	113738916.00	113738940.00	---
2217	chr13	+	114286123.00	114286147.00	ENST00000465174 // TFDP1
2218	chr13	-	25027760.00	25027784.00	NM_006437 // PARP4
2219	chr13	-	31035734.00	31035758.00	AB208998 // HMGB1
2220	chr13	-	31946948.00	31947372.00	---
2221	chr13	-	41837413.00	41837437.00	AK294343 // MTRF1
2222	chr13	-	44360972.00	44360996.00	NM_017993 // ENOX1
2223	chr13	-	48654039.00	48654063.00	NM_014166 // MED4
2224	chr13	-	48655793.00	48655843.00	NM_014166 // MED4
2225	chr13	-	49000747.00	49000882.00	BC039373 // LPAR6
2226	chr13	-	52707278.00	52707325.00	NM_002498 // NEK3
2227	chr13	-	61987482.00	61987852.00	NM_022843 // PCDH20
2228	chr13	-	76104347.00	76104385.00	NM_203497 // COMMD6
2229	chr13	-	79997910.00	79997940.00	---
2230	chr13	-	80647525.00	80647656.00	---
2231	chr13	-	96508886.00	96508910.00	BC125234 // UGGT2
2232	chr13	-	97644723.00	97644761.00	AK313684 // OXGR1
2233	chr13	-	99538818.00	99538842.00	NM_015296 // DOCK9
2234	chr13	-	111357938.00	111357962.00	ENST00000540785 // CARS2
2235	chr13	-	111552979.00	111553004.00	BC039715 // ANKRD10
2236	chr13	-	111547428.00	111547654.00	OTTHUMT00000106495 // ANKRD10-IT1
2237	chr13	-	112916498.00	112916572.00	---
2238	chr13	-	112926566.00	112926628.00	---
2239	chr13	-	113173298.00	113173322.00	NM_006322 // TUBGCP3
2240	chr13	-	114309133.00	114309199.00	NM_000705 // ATP4B
2241	chr14	+	20942691.00	20942725.00	NM_000270 // PNP
2242	chr14	+	21462715.00	21462739.00	NM_001029991 // METTL17
2243	chr14	+	23299270.00	23299297.00	NM_178336 // MRPL52
2244	chr14	+	24544431.00	24544455.00	NM_006032 // CPNE6

2245	chr14	+	24545526.00	24545550.00	AL137688 // CPNE6
2246	chr14	+	29859552.00	29859680.00	OTTHUMT00000408750 // OTTHUMG00000170374
2247	chr14	+	35523885.00	35523909.00	---
2248	chr14	+	35579908.00	35579932.00	ENST00000553901 // FAM177A1
2249	chr14	+	59866811.00	59866845.00	---
2250	chr14	+	60483414.00	60483438.00	NR_075071 // LRRC9
2251	chr14	+	62278702.00	62278889.00	OTTHUMT00000411881 // OTTHUMG00000171138
2252	chr14	+	64682022.00	64682046.00	NM_182913 // SYNE2
2253	chr14	+	64908841.00	64908865.00	NM_005956 // MTHFD1
2254	chr14	+	64937011.00	64940392.00	NM_004857 // AKAP5
2255	chr14	+	65556666.00	65556727.00	NR_045122 // LOC100506321
2256	chr14	+	68024047.00	68024071.00	NM_020715 // PLEKHH1
2257	chr14	+	69820778.00	69820802.00	NM_001168368 // GALNT16
2258	chr14	+	70918880.00	70918967.00	NM_003813 // ADAM21
2259	chr14	+	74358812.00	74358836.00	NM_001242924 // ZNF410
2260	chr14	+	76044983.00	76045007.00	NM_017791 // FLVCR2
2261	chr14	+	76230960.00	76230984.00	NM_015072 // TTLL5
2262	chr14	+	86029261.00	86029361.00	OTTHUMT00000413195 // FLRT2
2263	chr14	+	86087548.00	86087572.00	NM_013231 // FLRT2
2264	chr14	+	86802758.00	86802819.00	OTTHUMT00000413104 // OTTHUMG00000171356
2265	chr14	+	90729668.00	90729692.00	NM_002802 // PSMC1
2266	chr14	+	94696957.00	94696981.00	NM_058237 // PPP4R4
2267	chr14	+	95797634.00	95797834.00	---
2268	chr14	+	96671129.00	96671287.00	NM_000623 // BDKRB2
2269	chr14	+	100141709.00	100141917.00	NM_001127258 // HHIPL1
2270	chr14	+	100742206.00	100742304.00	ENST00000555735 // YY1
2271	chr14	+	102027925.00	102028710.00	NM_001362 // DIO3
2272	chr14	+	103021054.00	103021952.00	OTTHUMT00000415849 // OTTHUMG00000171913
2273	chr14	+	103571183.00	103571291.00	AK000671 // EXOC3L4
2274	chr14	+	104195161.00	104195228.00	ENST00000556795 // ZFYVE21
2275	chr14	+	104672613.00	104672871.00	---
2276	chr14	+	104689767.00	104690141.00	OTTHUMT00000410577 // OTTHUMG00000170825
2277	chr14	+	104754188.00	104754387.00	OTTHUMT00000410577 // OTTHUMG00000170825

2278	chr14	+	105360551.00	105360575.00	ENST00000251181 // CEP170B
2279	chr14	+	105944996.00	105945020.00	BC034386 // CRIP2
2280	chr14	-	20002225.00	20002277.00	NR_027480 // POTEG
2281	chr14	-	21860027.00	21860051.00	NM_001170629 // CHD8
2282	chr14	-	21876876.00	21876900.00	NM_001170629 // CHD8
2283	chr14	-	23374560.00	23374584.00	NM_001077351 // RBM23
2284	chr14	-	23374608.00	23374632.00	NM_001077351 // RBM23
2285	chr14	-	23394103.00	23394127.00	NM_006109 // PRMT5
2286	chr14	-	23417303.00	23417327.00	ENST00000556421 // MIR4707
2287	chr14	-	23424331.00	23424360.00	NM_001166269 // HAUS4
2288	chr14	-	24032501.00	24032525.00	AK096034 // AP1G2
2289	chr14	-	24657569.00	24657593.00	NR_051979 // IPO4
2290	chr14	-	24787802.00	24787826.00	AF086230 // ADCY4
2291	chr14	-	25103146.00	25103218.00	ENST00000530830 // GZMB
2292	chr14	-	35008767.00	35008834.00	NM_018453 // EAPP
2293	chr14	-	36982328.00	36982357.00	NM_001101341 // SFTA3
2294	chr14	-	39533872.00	39533896.00	OTTHUMT00000409966 // SEC23A
2295	chr14	-	50113343.00	50113367.00	---
2296	chr14	-	50301099.00	50301123.00	NM_004713 // NEMF
2297	chr14	-	50793247.00	50793488.00	OTTHUMT00000410877 // OTTHUMG00000170886
2298	chr14	-	52535891.00	52535915.00	NM_007361 // NID2
2299	chr14	-	55848714.00	55848789.00	NM_014924 // ATG14
2300	chr14	-	58030957.00	58031052.00	NM_001206920 // SLC35F4
2301	chr14	-	60074272.00	60074296.00	ENST00000474911 // RTN1
2302	chr14	-	62583868.00	62583892.00	OTTHUMT00000411702 // OTTHUMG00000171107
2303	chr14	-	65271710.00	65271734.00	NM_001024858 // SPTB
2304	chr14	-	67826502.00	67826526.00	NM_015994 // ATP6V1D
2305	chr14	-	67826841.00	67826865.00	ENST00000216442 // ATP6V1D
2306	chr14	-	70036782.00	70037743.00	AF284217 // CCDC177
2307	chr14	-	71064444.00	71064468.00	NM_005466 // MED6
2308	chr14	-	71275623.00	71275879.00	NM_033141 // MAP3K9
2309	chr14	-	75421910.00	75421945.00	NM_002632 // PGF
2310	chr14	-	75580956.00	75580980.00	NM_033116 // NEK9
2311	chr14	-	76118141.00	76118197.00	ENST00000256319 // C14orf1
2312	chr14	-	89153615.00	89153639.00	NM_183387 // EML5

2313	chr14	-	91007769.00	91007793.00	NM_001010854 // TTC7B
2314	chr14	-	95677056.00	95677080.00	NM_024734 // CLMN
2315	chr14	-	96784128.00	96784152.00	NM_018036 // ATG2B
2316	chr14	-	101543944.00	101543985.00	OTTHUMT00000414541 // OTTHUMG00000045024
2317	chr14	-	105477059.00	105477083.00	NM_017955 // CDCA4
2318	chr14	-	105477802.00	105478189.00	NM_017955 // CDCA4
2319	chr14	-	105533801.00	105533988.00	---
2320	chr14	-	106067241.00	106067520.00	AK130825 // IGH
2321	chr15	+	20767695.00	20767837.00	NR_033351 // GOLGA8F
2322	chr15	+	22997826.00	22997850.00	NM_014608 // CYFIP1
2323	chr15	+	25436864.00	25436888.00	AF400495 // SNRPN
2324	chr15	+	28623805.00	28623947.00	NR_033351 // GOLGA8F
2325	chr15	+	34520808.00	34520855.00	ENST00000557879 // EMC4
2326	chr15	+	38354406.00	38354430.00	OTTHUMT00000418180 // OTTHUMG00000172364
2327	chr15	+	40698391.00	40698415.00	OTTHUMT00000418753 // IVD
2328	chr15	+	40933197.00	40933221.00	NM_170589 // CASC5
2329	chr15	+	40951554.00	40951578.00	NM_170589 // CASC5
2330	chr15	+	41021726.00	41021803.00	NM_002875 // RAD51
2331	chr15	+	41106279.00	41106330.00	AB209224 // ZFYVE19
2332	chr15	+	42110406.00	42110430.00	NM_014994 // MAPKBP1
2333	chr15	+	43622945.00	43622969.00	NM_001159280 // ADAL
2334	chr15	+	43624099.00	43624135.00	NM_001159280 // ADAL
2335	chr15	+	44091847.00	44091871.00	AF370428 // SERF2-C15ORF63
2336	chr15	+	44705543.00	44705567.00	NM_138423 // CASC4
2337	chr15	+	49610359.00	49610383.00	ENST00000561014 // GALK2
2338	chr15	+	49913206.00	49913247.00	ENST00000403028 // DTWD1
2339	chr15	+	57364851.00	57364875.00	ENST00000452095 // TCF12
2340	chr15	+	57999239.00	57999263.00	NR_027390 // POLR2M
2341	chr15	+	61890761.00	61890787.00	---
2342	chr15	+	67709303.00	67709327.00	NM_001031715 // IQCH
2343	chr15	+	69683534.00	69683873.00	OTTHUMT00000416785 // OTTHUMG00000172086
2344	chr15	+	72337542.00	72337612.00	---
2345	chr15	+	74623345.00	74623369.00	NM_025055 // CCDC33
2346	chr15	+	74653910.00	74653942.00	NR_045207 // LOC729739
2347	chr15	+	75042747.00	75042847.00	NM_000761 // CYP1A2
2348	chr15	+	80489600.00	80490205.00	---

2349	chr15	+	82970587.00	82970613.00	NR_033579 // CSPG4P8
2350	chr15	+	83423400.00	83423506.00	ENST00000544685 // LOC100505616
2351	chr15	+	83499445.00	83499784.00	NM_001080435 // WHAMM
2352	chr15	+	85043648.00	85043857.00	NR_038274 // LINC00933
2353	chr15	+	85166117.00	85166310.00	NM_181877 // ZSCAN2
2354	chr15	+	91292890.00	91292914.00	NM_000057 // BLM
2355	chr15	+	91496236.00	91496260.00	NM_018671 // UNC45A
2356	chr15	+	92987879.00	92988097.00	NM_006011 // ST8SIA2
2357	chr15	+	94775191.00	94775215.00	BC041387 // MCTP2
2358	chr15	+	95976344.00	95976404.00	NR_027132 // LINC00924
2359	chr15	+	96992803.00	96992950.00	---
2360	chr15	+	99434840.00	99434864.00	NM_000875 // IGF1R
2361	chr15	+	100332542.00	100332582.00	OTTHUMT00000416903 // OTTHUMG00000172117
2362	chr15	+	101551005.00	101551029.00	NM_024652 // LRRK1
2363	chr15	-	28196997.00	28197021.00	NM_000275 // OCA2
2364	chr15	-	28777980.00	28778122.00	NR_033351 // GOLGA8F
2365	chr15	-	31323241.00	31323265.00	NM_001252020 // TRPM1
2366	chr15	-	31818571.00	31818595.00	NM_130901 // OTUD7A
2367	chr15	-	31862361.00	31862396.00	NM_130901 // OTUD7A
2368	chr15	-	33091119.00	33091143.00	NM_001277313 // FMN1
2369	chr15	-	33486839.00	33486863.00	NM_001277313 // FMN1
2370	chr15	-	38433203.00	38433227.00	---
2371	chr15	-	40331187.00	40331250.00	OTTHUMT00000418264 // SRP14
2372	chr15	-	41388526.00	41388550.00	NM_017553 // INO80
2373	chr15	-	41601569.00	41601935.00	NM_007280 // OIP5
2374	chr15	-	42118615.00	42118720.00	---
2375	chr15	-	42146359.00	42146383.00	NM_016642 // SPTBN5
2376	chr15	-	42245982.00	42246079.00	NM_139265 // EHD4
2377	chr15	-	42378426.00	42378510.00	NM_178034 // PLA2G4D
2378	chr15	-	43023458.00	43023482.00	NM_138477 // CDAN1
2379	chr15	-	48829925.00	48829949.00	NM_000138 // FBN1
2380	chr15	-	49059632.00	49059656.00	NM_001194998 // CEP152
2381	chr15	-	49301472.00	49301496.00	NM_001193489 // SECISBP2L
2382	chr15	-	50875314.00	50875338.00	NM_017672 // TRPM7
2383	chr15	-	55967802.00	55967826.00	NM_173814 // PRTG
2384	chr15	-	56393613.00	56393749.00	NM_022841 // RFX7
2385	chr15	-	59497625.00	59497649.00	NM_004998 // MYO1E
2386	chr15	-	59500925.00	59500949.00	NM_004998 // MYO1E
2387	chr15	-	60695025.00	60695049.00	---
2388	chr15	-	60747555.00	60747579.00	NM_024611 // NARG2

2389	chr15	-	61521419.00	61521443.00	NM_134261 // RORA
2390	chr15	-	64041885.00	64041909.00	NM_003922 // HERC1
2391	chr15	-	64366562.00	64367493.00	ENST00000557835 // FAM96A
2392	chr15	-	64674721.00	64674745.00	OTTHUMT00000418702 // KIAA0101
2393	chr15	-	65257682.00	65257754.00	NM_016630 // SPG21
2394	chr15	-	65678958.00	65678982.00	NM_020962 // IGDCC4
2395	chr15	-	65688312.00	65688336.00	NM_020962 // IGDCC4
2396	chr15	-	66263412.00	66263436.00	---
2397	chr15	-	73635845.00	73635869.00	NM_005477 // HCN4
2398	chr15	-	77344781.00	77344807.00	NM_005724 // TSPAN3
2399	chr15	-	77404479.00	77406397.00	NM_024776 // PEAK1
2400	chr15	-	78403507.00	78403531.00	NM_006383 // CIB2
2401	chr15	-	79054858.00	79054882.00	NM_014272 // ADAMTS7
2402	chr15	-	79224307.00	79224331.00	AK309491 // CTSH
2403	chr15	-	80695847.00	80695895.00	OTTHUMT00000417161 // OTTHUMG00000172167
2404	chr15	-	82769265.00	82769291.00	ENST00000561015 // LOC642423
2405	chr15	-	83145849.00	83145875.00	ENST00000561015 // LOC642423
2406	chr15	-	84841698.00	84841907.00	OTTHUMT00000418799 // OTTHUMG00000172495
2407	chr15	-	84873269.00	84873295.00	ENST00000561015 // LOC642423
2408	chr15	-	85752347.00	85752373.00	ENST00000561015 // LOC642423
2409	chr15	-	90195989.00	90196100.00	NM_198525 // KIF7
2410	chr15	-	90437271.00	90437295.00	NM_005829 // AP3S2
2411	chr15	-	90777146.00	90777173.00	NM_001277764 // CIB1
2412	chr15	-	91525212.00	91525236.00	---
2413	chr15	-	93616229.00	93616253.00	NM_001166283 // RGMA
2414	chr15	-	99190219.00	99190397.00	---
2415	chr15	-	99640978.00	99641053.00	---
2416	chr15	-	101825061.00	101825113.00	OTTHUMT00000416771 // SNRPA1
2417	chr15	-	101826566.00	101826845.00	BC067846 // SNRPA1
2418	chr15	-	102264400.00	102264424.00	NM_152334 // TARSL2
2419	chr16	+	330569.00	330602.00	AB593111 // ARHGDIG
2420	chr16	+	702432.00	702456.00	---
2421	chr16	+	779192.00	779217.00	BC033796 // HAGHL
2422	chr16	+	1819996.00	1820020.00	NM_015133 // MAPK8IP3
2423	chr16	+	2203320.00	2203384.00	NM_014353 // RAB26
2424	chr16	+	3583106.00	3583145.00	AK294318 // CLUAP1

2425	chr16	+	5053429.00	5053513.00	NM_014692 // SEC14L5
2426	chr16	+	8898635.00	8898674.00	NM_000303 // PMM2
2427	chr16	+	9608557.00	9608619.00	OTTHUMT00000435115 // OTTHUMG00000177058
2428	chr16	+	10837686.00	10837711.00	ENST00000574334 // NUBP1
2429	chr16	+	14416122.00	14416349.00	---
2430	chr16	+	19539255.00	19539322.00	NM_001199022 // CCP110
2431	chr16	+	22447235.00	22447273.00	---
2432	chr16	+	27874572.00	27874632.00	---
2433	chr16	+	29811234.00	29811258.00	NM_007317 // KIF22
2434	chr16	+	29845090.00	29845114.00	NM_017458 // MVP
2435	chr16	+	29997089.00	29997143.00	NM_016151 // TAOK2
2436	chr16	+	30015002.00	30015028.00	AY189289 // INO80E
2437	chr16	+	30675813.00	30675837.00	NM_001105079 // FBRS
2438	chr16	+	30997941.00	30997994.00	NM_025193 // HSD3B7
2439	chr16	+	31131516.00	31131573.00	NM_032188 // KAT8
2440	chr16	+	33784691.00	33784715.00	OTTHUMT00000431831 // OTTHUMG00000176371
2441	chr16	+	46943693.00	46943830.00	NM_133443 // GPT2
2442	chr16	+	47699863.00	47699887.00	NM_001031835 // PHKB
2443	chr16	+	49407752.00	49407823.00	ENST00000299191 // C16orf78
2444	chr16	+	50730254.00	50730278.00	---
2445	chr16	+	52132289.00	52132932.00	OTTHUMT00000422566 // OTTHUMG00000173236
2446	chr16	+	53468399.00	53468423.00	NM_005611 // RBL2
2447	chr16	+	55618386.00	55619704.00	NM_017839 // LPCAT2
2448	chr16	+	55794550.00	55794574.00	NR_003276 // CES1P1
2449	chr16	+	56226190.00	56226255.00	NM_020988 // GNAO1
2450	chr16	+	56388925.00	56388949.00	NM_020988 // GNAO1
2451	chr16	+	57673424.00	57673448.00	NM_001145774 // GPR56
2452	chr16	+	68100226.00	68100276.00	NM_017803 // DUS2L
2453	chr16	+	68867225.00	68867249.00	NM_004360 // CDH1
2454	chr16	+	68868617.00	68868852.00	NM_004360 // CDH1
2455	chr16	+	69354048.00	69354179.00	NM_013245 // VPS4A
2456	chr16	+	77896653.00	77896773.00	NM_020927 // VAT1L
2457	chr16	+	78056442.00	78056479.00	ENST00000299642 // CLEC3A
2458	chr16	+	78143680.00	78143726.00	NM_016373 // WWOX
2459	chr16	+	81062200.00	81062224.00	NM_001100624 // CENPN
2460	chr16	+	84012081.00	84012141.00	NM_019065 // NECAB2
2461	chr16	+	86602502.00	86602539.00	NM_005251 // FOXC2
2462	chr16	+	87997045.00	87997069.00	---
2463	chr16	+	89203095.00	89203119.00	NR_045667 // ACSF3

2464	chr16	+	89661888.00	89661912.00	NM_153636 // CPNE7
2465	chr16	+	89927128.00	89927152.00	NM_032451 // SPIRE2
2466	chr16	+	90000849.00	90000873.00	AK127418 // TUBB3
2467	chr16	+	90050943.00	90050989.00	NR_003226 // AFG3L1P
2468	chr16	+	90109616.00	90109672.00	NM_001481 // GAS8
2469	chr16	-	108431.00	108455.00	NM_022450 // RHBDF1
2470	chr16	-	114941.00	114965.00	NM_022450 // RHBDF1
2471	chr16	-	318404.00	318428.00	NM_183337 // RGS11
2472	chr16	-	744276.00	744323.00	NM_153350 // FBXL16
2473	chr16	-	1041895.00	1042560.00	---
2474	chr16	-	1274604.00	1274628.00	NM_012467 // TPSG1
2475	chr16	-	1401854.00	1401879.00	ENST00000007390 // TSR3
2476	chr16	-	1497499.00	1497523.00	NM_001287 // CLCN7
2477	chr16	-	1574558.00	1574582.00	NM_014714 // IFT140
2478	chr16	-	1842439.00	1842515.00	NM_001146006 // IGFALS
2479	chr16	-	2233647.00	2233703.00	NM_020764 // CASKIN1
2480	chr16	-	2834647.00	2834792.00	NM_152891 // PRSS33
2481	chr16	-	2903915.00	2903996.00	NM_022119 // PRSS22
2482	chr16	-	3068164.00	3068441.00	NM_021195 // CLDN6
2483	chr16	-	3543499.00	3543836.00	ENST00000437192 // C16orf90
2484	chr16	-	5083373.00	5083721.00	NM_016256 // NAGPA
2485	chr16	-	8988688.00	8988712.00	NM_003470 // USP7
2486	chr16	-	9050204.00	9050228.00	AK302481 // USP7
2487	chr16	-	11563395.00	11563502.00	AK126539 // LOC400499
2488	chr16	-	11815157.00	11815185.00	---
2489	chr16	-	14096251.00	14096497.00	---
2490	chr16	-	14704526.00	14704550.00	NM_002582 // PARN
2491	chr16	-	15844047.00	15844071.00	NM_002474 // MYH11
2492	chr16	-	16419558.00	16419755.00	AK295599 // LOC100288162
2493	chr16	-	18845692.00	18845716.00	NM_015092 // SMG1
2494	chr16	-	20362035.00	20362059.00	NM_003361 // UMOD
2495	chr16	-	23721511.00	23721535.00	NM_033266 // ERN2
2496	chr16	-	30017568.00	30017617.00	NM_003586 // DOC2A
2497	chr16	-	30686669.00	30686713.00	---
2498	chr16	-	30771105.00	30771129.00	AL122109 // C16orf93
2499	chr16	-	30886603.00	30886634.00	NR_039744 // MIR4519
2500	chr16	-	31102455.00	31102555.00	NM_024006 // VKORC1
2501	chr16	-	48175185.00	48175209.00	NM_033226 // ABCC12
2502	chr16	-	48269047.00	48269071.00	---
2503	chr16	-	52108829.00	52108897.00	OTTHUMT00000422561 // C16orf97
2504	chr16	-	52289367.00	52289394.00	---

2505	chr16	-	52472803.00	52473019.00	NM_001080430 // TOX3
2506	chr16	-	56436940.00	56437005.00	NM_001144 // AMFR
2507	chr16	-	57467988.00	57468104.00	NM_020313 // CIAPIN1
2508	chr16	-	57507335.00	57507381.00	NM_018110 // DOK4
2509	chr16	-	57509041.00	57509122.00	NM_018110 // DOK4
2510	chr16	-	57551982.00	57552125.00	NM_033212 // CCDC102A
2511	chr16	-	58554914.00	58554938.00	NM_016284 // CNOT1
2512	chr16	-	66934093.00	66934359.00	---
2513	chr16	-	66955624.00	66955778.00	NM_001128850 // RRAD
2514	chr16	-	67427284.00	67427428.00	ENST00000393957 // TPPP3
2515	chr16	-	67973915.00	67974308.00	NM_000229 // LCAT
2516	chr16	-	69418501.00	69418608.00	NM_005652 // TERF2
2517	chr16	-	75499537.00	75499749.00	---
2518	chr16	-	81175036.00	81175060.00	NM_052892 // PKD1L2
2519	chr16	-	84228060.00	84228318.00	DQ323994 // LOC654780
2520	chr16	-	87452464.00	87452504.00	NM_015144 // ZCCHC14
2521	chr16	-	88620230.00	88620448.00	AK127438 // LINC00859
2522	chr16	-	88931271.00	88931345.00	NM_001080487 // PABPN1L
2523	chr16	-	90110018.00	90110043.00	NR_027336 // LOC100130015
2524	chr17	+	2929656.00	2929680.00	NM_015085 // RAP1GAP2
2525	chr17	+	2937219.00	2937243.00	NM_015085 // RAP1GAP2
2526	chr17	+	4487835.00	4487861.00	NM_001114974 // SMTNL2
2527	chr17	+	4994843.00	4996108.00	NM_153018 // ZFP3
2528	chr17	+	5286427.00	5286483.00	NM_004703 // RABEP1
2529	chr17	+	5991313.00	5991409.00	NM_015253 // WSCD1
2530	chr17	+	6554997.00	6555160.00	ENST00000391428 // C17orf100
2531	chr17	+	6756949.00	6756973.00	NR_002710 // ALOX12P2
2532	chr17	+	7589938.00	7589962.00	ENST00000316024 // WRAP53
2533	chr17	+	7663231.00	7663255.00	NM_020877 // DNAH2
2534	chr17	+	7734764.00	7734788.00	NM_020877 // DNAH2
2535	chr17	+	7755529.00	7755582.00	NM_001080424 // KDM6B
2536	chr17	+	17997196.00	17997220.00	NM_001388 // DRG2
2537	chr17	+	18397827.00	18397881.00	NM_001040078 // LGALS9C
2538	chr17	+	19215380.00	19215424.00	NM_148921 // EPN2
2539	chr17	+	19314959.00	19314983.00	NM_007148 // RNF112
2540	chr17	+	20347183.00	20347213.00	ENST00000458685 // NOS2P3
2541	chr17	+	27061174.00	27061198.00	NM_178170 // NEK8

2542	chr17	+	28849398.00	28852963.00	NM_004871 // GOSR1
2543	chr17	+	29335266.00	29335687.00	---
2544	chr17	+	31276843.00	31277162.00	---
2545	chr17	+	32583279.00	32583330.00	NM_002982 // CCL2
2546	chr17	+	32961937.00	32962064.00	NM_207313 // TMEM132E
2547	chr17	+	37821614.00	37821719.00	NM_003673 // TCAP
2548	chr17	+	37894598.00	37894622.00	NM_001030002 // GRB7
2549	chr17	+	38501494.00	38501518.00	OTTHUMT00000257140 // RARA
2550	chr17	+	39394323.00	39394562.00	NM_031963 // KRTAP9-8
2551	chr17	+	39976093.00	39976117.00	AK092042 // FKBP10
2552	chr17	+	40120091.00	40120117.00	NM_033133 // CNP
2553	chr17	+	40717786.00	40717810.00	NM_025233 // COASY
2554	chr17	+	41934474.00	41934521.00	NM_145273 // CD300LG
2555	chr17	+	42083403.00	42083588.00	NM_153006 // NAGS
2556	chr17	+	42225254.00	42225461.00	ENST00000319977 // C17orf53
2557	chr17	+	43138737.00	43138800.00	NM_021079 // NMT1
2558	chr17	+	46189977.00	46190003.00	NM_152244 // SNX11
2559	chr17	+	47218619.00	47218668.00	NM_153446 // B4GALNT2
2560	chr17	+	48154008.00	48154032.00	NM_002204 // ITGA3
2561	chr17	+	48252635.00	48252659.00	NM_000023 // SGCA
2562	chr17	+	49365915.00	49365939.00	OTTHUMT00000368673 // UTP18
2563	chr17	+	53398470.00	53402058.00	NM_002126 // HLF
2564	chr17	+	54403587.00	54403708.00	NM_153228 // ANKFN1
2565	chr17	+	55197862.00	55197886.00	NM_003488 // AKAP1
2566	chr17	+	59480467.00	59480491.00	NM_005994 // TBX2
2567	chr17	+	60759613.00	60759637.00	NM_006039 // MRC2
2568	chr17	+	61560504.00	61560528.00	NM_000789 // ACE
2569	chr17	+	61684655.00	61684793.00	NM_016360 // TACO1
2570	chr17	+	72200554.00	72201694.00	ENST00000530646 // RPL38
2571	chr17	+	72436660.00	72436684.00	NM_022036 // GPRC5C
2572	chr17	+	73512890.00	73512915.00	NM_207346 // TSEN54
2573	chr17	+	76230676.00	76230800.00	NM_001204210 // TMEM235
2574	chr17	+	76235881.00	76235933.00	NM_001204210 // TMEM235
2575	chr17	+	76302034.00	76302231.00	---
2576	chr17	+	79495504.00	79495528.00	NM_012418 // FSCN2
2577	chr17	+	79503911.00	79503995.00	NM_012418 // FSCN2
2578	chr17	+	79612060.00	79612478.00	NM_031945 // TSPAN10

2579	chr17	+	79654040.00	79654094.00	NM_004712 // HGS
2580	chr17	+	79857120.00	79857408.00	NM_001002244 // ANAPC11
2581	chr17	-	1399118.00	1399162.00	NM_016532 // INPP5K
2582	chr17	-	1419290.00	1419400.00	NM_130766 // INPP5K
2583	chr17	-	1546737.00	1546880.00	NM_003693 // SCARF1
2584	chr17	-	1578554.00	1578578.00	NM_006445 // PRPF8
2585	chr17	-	4575988.00	4576012.00	NR_046388 // PELP1
2586	chr17	-	7142653.00	7142707.00	NM_024297 // PHF23
2587	chr17	-	7307404.00	7307428.00	NM_152766 // TMEM256
2588	chr17	-	8221419.00	8221778.00	---
2589	chr17	-	16439403.00	16439439.00	---
2590	chr17	-	16470844.00	16470868.00	NM_020653 // ZNF287
2591	chr17	-	16734535.00	16734570.00	NR_029392 // KRT16P2
2592	chr17	-	17716004.00	17716028.00	NM_001005291 // SREBF1
2593	chr17	-	18266805.00	18266829.00	NM_004169 // SHMT1
2594	chr17	-	19250596.00	19250627.00	NM_001243473 // B9D1
2595	chr17	-	19646721.00	19646745.00	NM_001135168 // ALDH3A1
2596	chr17	-	27044257.00	27044281.00	NM_031934 // RAB34
2597	chr17	-	27438498.00	27438522.00	NM_078471 // MYO18A
2598	chr17	-	27943818.00	27943842.00	NM_032854 // CORO6
2599	chr17	-	30205309.00	30205333.00	NM_018428 // UTP6
2600	chr17	-	31340983.00	31341058.00	NM_001094 // ASIC2
2601	chr17	-	31439008.00	31439032.00	NM_001094 // ASIC2
2602	chr17	-	36933993.00	36934052.00	NM_003559 // PIP4K2B
2603	chr17	-	37295917.00	37295941.00	NM_020405 // PLXDC1
2604	chr17	-	37322065.00	37322094.00	NM_001143968 // ARL5C
2605	chr17	-	37588222.00	37588265.00	NM_004774 // MED1
2606	chr17	-	38792225.00	38792315.00	NM_003079 // SMARCE1
2607	chr17	-	40336275.00	40336539.00	NM_001524 // HCRT
2608	chr17	-	41905125.00	41905149.00	NM_001932 // MPP3
2609	chr17	-	41909021.00	41909045.00	NM_001932 // MPP3
2610	chr17	-	42194965.00	42194989.00	NM_005474 // HDAC5
2611	chr17	-	43012694.00	43012718.00	NM_001265577 // KIF18B
2612	chr17	-	44910574.00	44910608.00	---
2613	chr17	-	45206717.00	45206741.00	---
2614	chr17	-	46622497.00	46623395.00	ENST00000330070 // HOXB2
2615	chr17	-	46685314.00	46685343.00	NM_004502 // HOXB7
2616	chr17	-	46799801.00	46799877.00	NM_032391 // PRAC
2617	chr17	-	47307844.00	47307881.00	NM_001143804 // PHOSPHO1

2618	chr17	-	47307997.00	47308049.00	NM_001143804 // PHOSPHO1
2619	chr17	-	47706823.00	47706847.00	AK316366 // SPOP
2620	chr17	-	48193195.00	48193261.00	NM_174920 // SAMD14
2621	chr17	-	48206887.00	48206947.00	NM_174920 // SAMD14
2622	chr17	-	48265751.00	48265775.00	AK297731 // COL1A1
2623	chr17	-	49057172.00	49057196.00	NM_001130528 // SPAG9
2624	chr17	-	54587815.00	54587918.00	---
2625	chr17	-	60002359.00	60002383.00	NM_020748 // INTS2
2626	chr17	-	61915987.00	61916011.00	AK303951 // SMARCD2
2627	chr17	-	67040667.00	67040691.00	NM_080283 // ABCA9
2628	chr17	-	73897796.00	73897828.00	NM_032478 // MRPL38
2629	chr17	-	74043999.00	74044023.00	NM_014230 // SRP68
2630	chr17	-	76454658.00	76454682.00	NM_173628 // DNAH17
2631	chr17	-	77100157.00	77100202.00	NM_001082575 // RBFOX3
2632	chr17	-	79348701.00	79348725.00	---
2633	chr17	-	79792384.00	79792500.00	NM_001007533 // PPP1R27
2634	chr17	-	79804439.00	79804463.00	NM_000918 // P4HB
2635	chr17	-	79866770.00	79866816.00	NM_001184917 // PCYT2
2636	chr17	-	80059559.00	80059583.00	NM_198082 // CCDC57
2637	chr18	+	2590019.00	2590043.00	NM_006101 // NDC80
2638	chr18	+	8798221.00	8798245.00	NM_015210 // SOGA2
2639	chr18	+	9136836.00	9136860.00	NM_015208 // ANKRD12
2640	chr18	+	12311007.00	12311031.00	NM_032525 // TUBB6
2641	chr18	+	19395625.00	19395705.00	NM_020774 // MIB1
2642	chr18	+	21470008.00	21470032.00	NM_198129 // LAMA3
2643	chr18	+	21478959.00	21478983.00	NM_198129 // LAMA3
2644	chr18	+	21532988.00	21533012.00	NM_198129 // LAMA3
2645	chr18	+	21739948.00	21740003.00	NM_012189 // CABYR
2646	chr18	+	32820998.00	32821063.00	NM_001135178 // ZNF397
2647	chr18	+	33234528.00	33234552.00	ENST00000269195 // GALNT1
2648	chr18	+	33836955.00	33837010.00	NM_017947 // MOCOS
2649	chr18	+	34803697.00	34804721.00	NM_020776 // KIAA1328
2650	chr18	+	50918215.00	50918239.00	NM_005215 // DCC
2651	chr18	+	56807116.00	56807140.00	ENST00000587834 // SEC11C
2652	chr18	+	61603193.00	61603262.00	ENST00000238508 // SERPINB10
2653	chr18	+	62083194.00	62083323.00	NR_033881 // LOC284294
2654	chr18	+	77477568.00	77477655.00	NM_004715 // CTDP1
2655	chr18	-	3582173.00	3582197.00	NM_004746 // DLGAP1
2656	chr18	-	6955424.00	6955448.00	NM_005559 // LAMA1

2657	chr18	-	9291038.00	9291150.00	---
2658	chr18	-	10406684.00	10406766.00	---
2659	chr18	-	12351141.00	12351178.00	NM_006796 // AFG3L2
2660	chr18	-	12351307.00	12351381.00	NM_006796 // AFG3L2
2661	chr18	-	19993882.00	19994516.00	NM_172241 // CTAGE1
2662	chr18	-	29429670.00	29429694.00	NM_014939 // TRAPPC8
2663	chr18	-	43460133.00	43460157.00	NM_020964 // EPG5
2664	chr18	-	48351690.00	48351724.00	NM_001127174 // MRO
2665	chr18	-	53789565.00	53789666.00	NR_040025 // LOC100505474
2666	chr18	-	56165283.00	56165328.00	NM_052947 // ALPK2
2667	chr18	-	57053856.00	57053981.00	---
2668	chr18	-	62607350.00	62607407.00	---
2669	chr18	-	64176379.00	64176403.00	NR_073130 // CDH19
2670	chr18	-	66377285.00	66377309.00	NM_019022 // TMX3
2671	chr18	-	67871418.00	67871442.00	NM_173630 // RTTN
2672	chr18	-	67872507.00	67872531.00	NM_173630 // RTTN
2673	chr18	-	70416266.00	70416318.00	NM_138966 // NETO1
2674	chr18	-	72879461.00	72879600.00	---
2675	chr18	-	77344173.00	77344352.00	---
2676	chr19	+	991246.00	991351.00	NM_024100 // WDR18
2677	chr19	+	2425077.00	2425127.00	NM_182973 // TMPRSS9
2678	chr19	+	2841465.00	2841564.00	NM_152791 // ZNF555
2679	chr19	+	2987384.00	2987408.00	AK308771 // TLE6
2680	chr19	+	3543242.00	3543466.00	ENST00000329493 // C19orf71
2681	chr19	+	3933460.00	3933585.00	NM_170678 // NMRK2
2682	chr19	+	4585433.00	4585569.00	---
2683	chr19	+	4910712.00	4910836.00	NM_013282 // UHRF1
2684	chr19	+	6151724.00	6151768.00	NM_030924 // ACSBG2
2685	chr19	+	6165905.00	6165929.00	NM_030924 // ACSBG2
2686	chr19	+	7533864.00	7533919.00	NM_015318 // ARHGEF18
2687	chr19	+	8020663.00	8020772.00	---
2688	chr19	+	9903578.00	9903748.00	---
2689	chr19	+	10406078.00	10406171.00	NM_003259 // ICAM5
2690	chr19	+	12858212.00	12858395.00	NM_004317 // ASNA1
2691	chr19	+	12924343.00	12924449.00	NM_006397 // RNASEH2A
2692	chr19	+	13004385.00	13004409.00	NM_000159 // GCDH
2693	chr19	+	15789262.00	15789286.00	---
2694	chr19	+	17531643.00	17531667.00	ENST00000528997 // MVB12A
2695	chr19	+	18001739.00	18001799.00	NM_000453 // SLC5A5
2696	chr19	+	19037142.00	19037177.00	NR_033677 // DDX49
2697	chr19	+	19212629.00	19212666.00	NM_178526 // SLC25A42

2698	chr19	+	19550937.00	19551033.00	---
2699	chr19	+	33183019.00	33183504.00	NM_001105570 // NUDT19
2700	chr19	+	33281926.00	33281950.00	BC049000 // TDRD12
2701	chr19	+	36036118.00	36036208.00	NM_014364 // GAPDHS
2702	chr19	+	36604385.00	36604466.00	NM_001270948 // OVOL3
2703	chr19	+	36612868.00	36613067.00	ENST00000468156 // TBCB
2704	chr19	+	37025763.00	37025863.00	OTTHUMT00000109556 // OTTHUMG00000048149
2705	chr19	+	38011101.00	38011209.00	NM_001013659 // ZNF793
2706	chr19	+	38795082.00	38795106.00	ENST00000301246 // C19orf33
2707	chr19	+	39006802.00	39006826.00	NM_000540 // RYR1
2708	chr19	+	39658886.00	39658910.00	NM_005884 // PAK4
2709	chr19	+	39976852.00	39976923.00	NM_001001563 // TIMM50
2710	chr19	+	40174816.00	40175291.00	ENST00000412609 // LGALS17A
2711	chr19	+	41620354.00	41620378.00	NM_000774 // CYP2F1
2712	chr19	+	42660143.00	42661632.00	ENST00000559786 // LOC100505639
2713	chr19	+	42872693.00	42872717.00	NM_001271938 // MEGF8
2714	chr19	+	45303854.00	45303887.00	NM_012116 // CBLC
2715	chr19	+	46184996.00	46185069.00	NM_000164 // GIPR
2716	chr19	+	46248504.00	46248528.00	NR_038267 // LOC388553
2717	chr19	+	47761816.00	47761885.00	NM_015603 // CCDC9
2718	chr19	+	47878780.00	47878804.00	NM_014681 // DHX34
2719	chr19	+	48528222.00	48528394.00	NM_022142 // ELSPBP1
2720	chr19	+	49436952.00	49436977.00	NM_014475 // DHDH
2721	chr19	+	49458862.00	49458903.00	ENST00000513545 // BAX
2722	chr19	+	49622855.00	49622879.00	NM_003660 // PPFIA3
2723	chr19	+	49868766.00	49868887.00	NM_014419 // DKKL1
2724	chr19	+	50204609.00	50204633.00	NM_001136052 // CPT1C
2725	chr19	+	50339011.00	50339035.00	NM_030973 // MED25
2726	chr19	+	50796911.00	50796935.00	NM_001077186 // MYH14
2727	chr19	+	51321954.00	51322086.00	NR_038359 // MGC45922
2728	chr19	+	51986565.00	51986594.00	NM_001080405 // CEACAM18
2729	chr19	+	53928352.00	53928381.00	AK295840 // ZNF765
2730	chr19	+	54622083.00	54622110.00	ENST00000467851 // PRPF31
2731	chr19	+	55325158.00	55325194.00	NM_002255 // KIR2DL4
2732	chr19	+	55501034.00	55501058.00	ENST00000381637 // NLRP2

2733	chr19	+	58102100.00	58102125.00	NM_001010879 // ZIK1
2734	chr19	+	58571379.00	58571403.00	NM_003436 // ZNF135
2735	chr19	+	58790524.00	58790647.00	---
2736	chr19	-	1108882.00	1108906.00	NM_014963 // SBNO2
2737	chr19	-	1398971.00	1399021.00	NM_000156 // GAMT
2738	chr19	-	4548275.00	4548415.00	NM_032108 // SEMA6B
2739	chr19	-	6737283.00	6737307.00	OTTHUMT00000407514 // GPR108
2740	chr19	-	7766950.00	7767000.00	NM_002002 // FCER2
2741	chr19	-	8387592.00	8387703.00	NM_198471 // KANK3
2742	chr19	-	11333713.00	11333737.00	NM_020812 // DOCK6
2743	chr19	-	11348138.00	11348162.00	NM_020812 // DOCK6
2744	chr19	-	12474455.00	12474482.00	NM_030824 // ZNF442
2745	chr19	-	12833331.00	12833355.00	NM_001136196 // TNPO2
2746	chr19	-	14198719.00	14199113.00	ENST00000533683 // SAMD1
2747	chr19	-	14909989.00	14910898.00	NM_198944 // OR7C1
2748	chr19	-	14951775.00	14952482.00	NM_001005190 // OR7A10
2749	chr19	-	15233576.00	15233600.00	NM_006844 // ILVBL
2750	chr19	-	15281201.00	15281225.00	NM_000435 // NOTCH3
2751	chr19	-	15343126.00	15343231.00	NM_024794 // EPHX3
2752	chr19	-	16023215.00	16023289.00	NM_021187 // CYP4F11
2753	chr19	-	17186290.00	17186327.00	NM_033417 // HAUS8
2754	chr19	-	17556008.00	17556092.00	NM_001190844 // TMEM221
2755	chr19	-	17571357.00	17571650.00	NM_138454 // NXNL1
2756	chr19	-	18376006.00	18376030.00	NM_001145304 // KIAA1683
2757	chr19	-	18900767.00	18900792.00	NM_000095 // COMP
2758	chr19	-	19752822.00	19752846.00	NM_016573 // GMIP
2759	chr19	-	19764166.00	19764190.00	AK125861 // ATP13A1
2760	chr19	-	33099284.00	33099320.00	---
2761	chr19	-	36234978.00	36235015.00	NM_001040425 // U2AF1L4
2762	chr19	-	36235298.00	36235322.00	NM_001040425 // U2AF1L4
2763	chr19	-	37672876.00	37674273.00	NM_152279 // ZNF585B
2764	chr19	-	37996874.00	37996940.00	---
2765	chr19	-	43687472.00	43687496.00	ENST00000401992 // PSG5
2766	chr19	-	43708916.00	43708966.00	OTTHUMT00000323076 // PSG4
2767	chr19	-	44271775.00	44271799.00	NM_002250 // KCNN4
2768	chr19	-	46299333.00	46299357.00	NM_030785 // RSPH6A

2769	chr19	-	46347321.00	46347345.00	NM_004819 // SYMPK
2770	chr19	-	47226097.00	47226121.00	NM_013403 // STRN4
2771	chr19	-	47941116.00	47941227.00	NM_015063 // SLC8A2
2772	chr19	-	48035502.00	48035526.00	NM_001277075 // ZNF541
2773	chr19	-	48366907.00	48367259.00	OTTHUMT00000409817 // OTTHUMG00000170611
2774	chr19	-	48368566.00	48368598.00	OTTHUMT00000409816 // OTTHUMG00000170611
2775	chr19	-	49939835.00	49939859.00	NM_020309 // SLC17A7
2776	chr19	-	51499273.00	51499314.00	NM_007196 // KLK8
2777	chr19	-	52004623.00	52004789.00	NM_053003 // SIGLEC12
2778	chr19	-	52005006.00	52005032.00	NM_053003 // SIGLEC12
2779	chr19	-	52490028.00	52490079.00	NM_021632 // ZNF350
2780	chr19	-	54671912.00	54671936.00	NM_001145303 // TMC4
2781	chr19	-	55445894.00	55445918.00	NM_139176 // NLRP7
2782	chr19	-	55543918.00	55544212.00	OTTHUMT00000357010 // GP6
2783	chr19	-	55677759.00	55677784.00	NM_001256714 // DNAAF3
2784	chr19	-	55740075.00	55740099.00	NM_173804 // TMEM86B
2785	chr19	-	56089789.00	56090603.00	NM_152600 // ZNF579
2786	chr19	-	58198564.00	58199279.00	AK126625 // ZNF551
2787	chr19	-	58443798.00	58443851.00	AK293723 // ZNF418
2788	chr2	+	10223935.00	10224071.00	OTTHUMT00000323551 // OTTHUMG00000151705
2789	chr2	+	10225291.00	10225326.00	OTTHUMT00000323551 // OTTHUMG00000151705
2790	chr2	+	10917781.00	10917805.00	NM_001039362 // ATP6V1C2
2791	chr2	+	12717200.00	12717224.00	---
2792	chr2	+	15743368.00	15743392.00	NM_004939 // DDX1
2793	chr2	+	25194320.00	25194344.00	ENST00000451291 // DNAJC27-AS1
2794	chr2	+	25224359.00	25224383.00	NR_034113 // DNAJC27-AS1
2795	chr2	+	26410263.00	26410477.00	NM_001168241 // GAREML
2796	chr2	+	26468073.00	26468097.00	ENST00000412805 // HADHB
2797	chr2	+	26785496.00	26785534.00	ENST00000329615 // C2orf70
2798	chr2	+	27015008.00	27015108.00	NM_001809 // CENPA
2799	chr2	+	32422841.00	32422870.00	NM_001193513 // SLC30A6
2800	chr2	+	32502971.00	32503121.00	NM_032312 // YIPF4

2801	chr2	+	35041549.00	35041944.00	---
2802	chr2	+	36606309.00	36606333.00	ENST00000473403 // CRIM1
2803	chr2	+	37429085.00	37429171.00	NR_037879 // LOC100505876
2804	chr2	+	38155976.00	38156000.00	NM_001170792 // RMDN2
2805	chr2	+	39107810.00	39107836.00	NM_001145450 // MORN2
2806	chr2	+	44589054.00	44589078.00	NM_024766 // CAMKMT
2807	chr2	+	46605045.00	46605069.00	NM_001430 // EPAS1
2808	chr2	+	46657318.00	46657342.00	ENST00000432241 // TMEM247
2809	chr2	+	48667811.00	48667835.00	ENST00000431614 // PPP1R21
2810	chr2	+	54937412.00	54937749.00	---
2811	chr2	+	55461622.00	55461694.00	BC042362 // RPS27A
2812	chr2	+	63816292.00	63816438.00	NM_001199111 // MDH1
2813	chr2	+	68882018.00	68882664.00	NM_138964 // PROKR1
2814	chr2	+	71607386.00	71607410.00	NM_014497 // ZNF638
2815	chr2	+	74042533.00	74042640.00	ENST00000409561 // C2orf78
2816	chr2	+	74184257.00	74184351.00	NM_080916 // DGUOK
2817	chr2	+	74650061.00	74650085.00	ENST00000469932 // WDR54
2818	chr2	+	84846923.00	84846947.00	NM_001370 // DNAH6
2819	chr2	+	85046492.00	85046516.00	NM_001370 // DNAH6
2820	chr2	+	85360670.00	85360706.00	NM_031283 // TCF7L1
2821	chr2	+	98264460.00	98264501.00	NM_001862 // COX5B
2822	chr2	+	98887204.00	98887228.00	NM_144992 // VWA3B
2823	chr2	+	99232692.00	99232788.00	NM_014044 // UNC50
2824	chr2	+	99758755.00	99758852.00	BC021264 // C2orf15
2825	chr2	+	100824895.00	100825280.00	AK056640 // LOC150577
2826	chr2	+	102103253.00	102103283.00	OTTHUMT00000339799 // OTTHUMG00000155390
2827	chr2	+	102490199.00	102490223.00	NM_004834 // MAP4K4
2828	chr2	+	102501703.00	102501727.00	NM_004834 // MAP4K4
2829	chr2	+	103013877.00	103014734.00	NM_003855 // IL18R1
2830	chr2	+	103040405.00	103040467.00	NM_003853 // IL18RAP
2831	chr2	+	103040751.00	103040856.00	NM_003853 // IL18RAP
2832	chr2	+	103236509.00	103236533.00	NM_003048 // SLC9A2
2833	chr2	+	108370660.00	108370722.00	OTTHUMT00000330678 // OTTHUMG00000153313
2834	chr2	+	108496525.00	108496549.00	NM_182588 // RGPD4
2835	chr2	+	108881283.00	108881434.00	NM_001008743 // SULT1C3

2836	chr2	+	109492797.00	109492947.00	ENST00000295124 // CCDC138
2837	chr2	+	110725660.00	110725684.00	NR_027145 // LIMS3-LOC440895
2838	chr2	+	111907531.00	111907599.00	AF455755 // BCL2L11
2839	chr2	+	113487208.00	113487232.00	AK092780 // NT5DC4
2840	chr2	+	114334979.00	114335280.00	NR_026818 // FAM138A
2841	chr2	+	120362320.00	120362344.00	NM_001271049 // PCDP1
2842	chr2	+	120387457.00	120387481.00	NM_001271049 // PCDP1
2843	chr2	+	121743973.00	121743997.00	NM_005270 // GLI2
2844	chr2	+	128177406.00	128177430.00	AK298280 // PROC
2845	chr2	+	128177527.00	128177578.00	NM_000312 // PROC
2846	chr2	+	128384734.00	128384758.00	---
2847	chr2	+	130895292.00	130895354.00	NR_033903 // CCDC74B-AS1
2848	chr2	+	132259017.00	132259041.00	NR_026922 // LOC150776
2849	chr2	+	148081555.00	148081629.00	---
2850	chr2	+	159718926.00	159718952.00	HQ179936 // DAPL1
2851	chr2	+	162280055.00	162280094.00	NM_006593 // TBR1
2852	chr2	+	168725600.00	168726465.00	NM_020981 // B3GALT1
2853	chr2	+	169571596.00	169571620.00	NM_001256126 // CERS6
2854	chr2	+	173901495.00	173901519.00	---
2855	chr2	+	173913129.00	173913153.00	ENST00000484645 // RAPGEF4
2856	chr2	+	176995249.00	176995502.00	NM_019558 // HOXD8
2857	chr2	+	183595799.00	183595823.00	NR_073365 // DNAJC10
2858	chr2	+	183597244.00	183597268.00	NR_073365 // DNAJC10
2859	chr2	+	183600997.00	183601021.00	NR_073365 // DNAJC10
2860	chr2	+	189870961.00	189870985.00	NM_000090 // COL3A1
2861	chr2	+	191045226.00	191045666.00	ENST00000340623 // C2orf88
2862	chr2	+	191307393.00	191307531.00	OTTHUMT00000334931 // MFSD6
2863	chr2	+	200332875.00	200332975.00	NR_026830 // SATB2-AS1
2864	chr2	+	201170987.00	201171011.00	NM_001100422 // SPATS2L
2865	chr2	+	201334592.00	201334616.00	---
2866	chr2	+	201467017.00	201467041.00	NM_001159 // AOX1
2867	chr2	+	203175145.00	203176218.00	---
2868	chr2	+	204053269.00	204053293.00	NM_001114132 // NBEAL1
2869	chr2	+	206546738.00	206546762.00	BC009222 // NRP2
2870	chr2	+	206656959.00	206656983.00	NM_201266 // NRP2
2871	chr2	+	206865029.00	206865523.00	---
2872	chr2	+	209203238.00	209203262.00	NM_015040 // PIKFYVE

2873	chr2	+	209214774.00	209214798.00	NM_015040 // PIKFYVE
2874	chr2	+	214182377.00	214182556.00	NM_001025436 // SPAG16
2875	chr2	+	214972929.00	214972953.00	NM_024532 // SPAG16
2876	chr2	+	216182922.00	216182946.00	NM_004044 // ATIC
2877	chr2	+	219496955.00	219496979.00	NM_032726 // PLCD4
2878	chr2	+	219559290.00	219559314.00	NM_015690 // STK36
2879	chr2	+	220341679.00	220341703.00	NM_005876 // SPEG
2880	chr2	+	220350170.00	220350194.00	NM_005876 // SPEG
2881	chr2	+	222688066.00	222688232.00	---
2882	chr2	+	227860174.00	227860230.00	NM_032276 // RHBDD1
2883	chr2	+	228758531.00	228758555.00	NM_178821 // DAW1
2884	chr2	+	232079946.00	232079970.00	ENST00000482392 // ARMC9
2885	chr2	+	233243405.00	233243476.00	NM_001632 // ALPP
2886	chr2	+	234296807.00	234296831.00	NM_003648 // DGKD
2887	chr2	+	238783291.00	238783337.00	OTTHUMT00000328696 // RAMP1
2888	chr2	+	241871867.00	241871891.00	ENST00000430980 // LOC728763
2889	chr2	+	242151522.00	242151546.00	NM_001001891 // ANO7
2890	chr2	+	242283265.00	242283289.00	NM_001008491 // SEPT2
2891	chr2	+	242786547.00	242786571.00	---
2892	chr2	-	3581378.00	3581429.00	---
2893	chr2	-	7005196.00	7005731.00	NM_207315 // CMPK2
2894	chr2	-	8715500.00	8715610.00	OTTHUMT00000323303 // OTTHUMG00000151623
2895	chr2	-	10729810.00	10729834.00	NR_048552 // NOL10
2896	chr2	-	10784474.00	10784498.00	NR_048552 // NOL10
2897	chr2	-	16847301.00	16847325.00	ENST00000445605 // FAM49A
2898	chr2	-	17846202.00	17846226.00	NM_001142286 // SMC6
2899	chr2	-	17889942.00	17889966.00	NM_001142286 // SMC6
2900	chr2	-	18765193.00	18765217.00	AK097848 // NT5C1B
2901	chr2	-	24270237.00	24270281.00	NM_025203 // C2orf44
2902	chr2	-	24300536.00	24300560.00	NM_004881 // TP53I3
2903	chr2	-	24426976.00	24427000.00	AK091859 // ITSN2
2904	chr2	-	26846374.00	26846447.00	ENST00000405346 // CIB4
2905	chr2	-	27361845.00	27361890.00	ENST00000335524 // C2orf53
2906	chr2	-	27434636.00	27434660.00	ENST00000401463 // SLC5A6
2907	chr2	-	31571795.00	31571819.00	NM_000379 // XDH
2908	chr2	-	37121048.00	37121155.00	NM_003162 // STRN

2909	chr2	-	37291897.00	37291921.00	NM_019024 // HEATR5B
2910	chr2	-	39996859.00	39996883.00	NR_028102 // THUMPD2
2911	chr2	-	43793564.00	43793588.00	BX641038 // THADA
2912	chr2	-	44161993.00	44162017.00	NM_133259 // LRPPRC
2913	chr2	-	44548515.00	44548539.00	NM_006036 // PREPL
2914	chr2	-	54128584.00	54128608.00	NM_014614 // PSME4
2915	chr2	-	55470664.00	55470688.00	NM_001005369 // MTIF2
2916	chr2	-	55489469.00	55489493.00	NM_001005369 // MTIF2
2917	chr2	-	55496133.00	55496157.00	NM_001005369 // MTIF2
2918	chr2	-	55920993.00	55921017.00	NM_033109 // PNPT1
2919	chr2	-	56149642.00	56149704.00	ENST00000452337 // EFEMP1
2920	chr2	-	61573414.00	61573438.00	ENST00000460004 // USP34
2921	chr2	-	70188878.00	70190330.00	NM_152792 // ASPRV1
2922	chr2	-	70191531.00	70191555.00	NR_033872 // PCBP1-AS1
2923	chr2	-	74375025.00	74375057.00	ENST00000327428 // BOLA3
2924	chr2	-	74618891.00	74618915.00	ENST00000437375 // DCTN1
2925	chr2	-	74724644.00	74724693.00	NM_001009812 // LBX2
2926	chr2	-	74734706.00	74734730.00	NM_032673 // PCGF1
2927	chr2	-	74747046.00	74747105.00	NM_133637 // DQX1
2928	chr2	-	86071649.00	86071673.00	NM_003896 // ST3GAL5
2929	chr2	-	86073585.00	86073675.00	NM_003896 // ST3GAL5
2930	chr2	-	86075012.00	86075036.00	NM_003896 // ST3GAL5
2931	chr2	-	86406569.00	86406593.00	NM_006839 // IMMT
2932	chr2	-	88888385.00	88888409.00	NM_004836 // EIF2AK3
2933	chr2	-	89130773.00	89130911.00	---
2934	chr2	-	89247314.00	89247338.00	ENST00000496168 // IGKV1-5
2935	chr2	-	96970570.00	96970594.00	NM_014014 // SNRNP200
2936	chr2	-	97520092.00	97520177.00	NM_016466 // ANKRD39
2937	chr2	-	98453565.00	98453589.00	NM_015348 // TMEM131
2938	chr2	-	99346686.00	99346710.00	ENST00000495056 // MGAT4A
2939	chr2	-	99388466.00	99388645.00	OTTHUMT00000329948 // OTTHUMG00000153173
2940	chr2	-	101656696.00	101656720.00	NM_001102426 // TBC1D8
2941	chr2	-	102051434.00	102051478.00	ENST00000492238 // RFX8
2942	chr2	-	105370801.00	105370865.00	NR_038231 // LOC284998
2943	chr2	-	107073482.00	107073506.00	NM_001144013 // RGPD3
2944	chr2	-	111230174.00	111230199.00	NM_033514 // LIMS3

2945	chr2	-	111398615.00	111398639.00	NM_004336 // BUB1
2946	chr2	-	111419094.00	111419118.00	AK023540 // BUB1
2947	chr2	-	113994196.00	113994220.00	NM_003466 // PAX8
2948	chr2	-	122485879.00	122485911.00	NM_032390 // MKI67IP
2949	chr2	-	128015273.00	128015297.00	NM_000122 // ERCC3
2950	chr2	-	136072945.00	136072969.00	NM_032143 // ZRANB3
2951	chr2	-	141598489.00	141598513.00	NM_018557 // LRP1B
2952	chr2	-	144728250.00	144728274.00	NM_001006636 // GTDC1
2953	chr2	-	149018149.00	149018230.00	---
2954	chr2	-	152387519.00	152387543.00	NM_001164507 // NEB
2955	chr2	-	152409955.00	152409979.00	NM_001164507 // NEB
2956	chr2	-	155302335.00	155302382.00	NM_001256368 // LOC100144595
2957	chr2	-	160755303.00	160755327.00	NM_001198759 // LY75-CD302
2958	chr2	-	160759273.00	160759297.00	---
2959	chr2	-	163101403.00	163101427.00	---
2960	chr2	-	163393478.00	163393502.00	NM_033272 // KCNH7
2961	chr2	-	164459895.00	164463823.00	ENST00000333129 // FIGN
2962	chr2	-	169874637.00	169874661.00	NM_003742 // ABCB11
2963	chr2	-	171200137.00	171200161.00	---
2964	chr2	-	171948164.00	171948188.00	ENST00000486857 // TLK1
2965	chr2	-	175112691.00	175112852.00	OTTHUMT00000333877 // OLA1
2966	chr2	-	175445878.00	175445902.00	ENST00000480400 // WIPF1
2967	chr2	-	179404854.00	179404878.00	NM_001267550 // TTN
2968	chr2	-	181962256.00	181962313.00	OTTHUMT00000334382 // OTTHUMG00000154203
2969	chr2	-	187694511.00	187694583.00	NM_182521 // ZSWIM2
2970	chr2	-	188216663.00	188216687.00	NM_005795 // CALCRL
2971	chr2	-	196682502.00	196682526.00	NM_018897 // DNAH7
2972	chr2	-	202614461.00	202614485.00	NM_020919 // ALS2
2973	chr2	-	207602632.00	207602656.00	NM_001039845 // MDH1B
2974	chr2	-	208994519.00	208994551.00	NM_020989 // CRYGC
2975	chr2	-	210908347.00	210908371.00	BC070141 // KANSL1L
2976	chr2	-	212288897.00	212288921.00	NM_005235 // ERBB4
2977	chr2	-	216692082.00	216692136.00	ENST00000413563 // LINC00607
2978	chr2	-	217261654.00	217261683.00	---
2979	chr2	-	219524181.00	219524334.00	NR_073599 // ZNF142
2980	chr2	-	219530703.00	219530727.00	NM_022453 // RNF25
2981	chr2	-	219692011.00	219692061.00	NM_017431 // PRKAG3

2982	chr2	-	219846862.00	219846942.00	NM_017521 // FEV
2983	chr2	-	220246182.00	220246206.00	---
2984	chr2	-	220252044.00	220252068.00	OTTHUMT00000130217 // DNPEP
2985	chr2	-	223086052.00	223086106.00	NM_181457 // PAX3
2986	chr2	-	224463685.00	224463970.00	NM_003469 // SCG2
2987	chr2	-	224642449.00	224642572.00	NM_001039569 // AP1S3
2988	chr2	-	225652088.00	225652112.00	NM_014689 // DOCK10
2989	chr2	-	232347431.00	232347455.00	AK128584 // NCL
2990	chr2	-	238090679.00	238090781.00	---
2991	chr2	-	238259791.00	238259815.00	NM_004369 // COL6A3
2992	chr2	-	241520920.00	241521053.00	---
2993	chr20	+	1277812.00	1277896.00	NM_014723 // SNPH
2994	chr20	+	2674369.00	2674393.00	NM_001110514 // EBF4
2995	chr20	+	2796995.00	2797061.00	NM_001167670 // TMEM239
2996	chr20	+	3732554.00	3732745.00	NM_052970 // HSPA12B
2997	chr20	+	5952654.00	5952679.00	NM_032485 // MCM8
2998	chr20	+	10199490.00	10199552.00	NM_003081 // SNAP25
2999	chr20	+	30347867.00	30347975.00	NM_012112 // TPX2
3000	chr20	+	30408171.00	30408323.00	NM_033118 // MYLK2
3001	chr20	+	30421522.00	30421559.00	NM_033118 // MYLK2
3002	chr20	+	30919034.00	30919063.00	NM_004798 // KIF3B
3003	chr20	+	31039398.00	31039500.00	---
3004	chr20	+	31829867.00	31829925.00	NM_016583 // BPIFA1
3005	chr20	+	32438792.00	32438839.00	NM_176812 // CHMP4B
3006	chr20	+	33567855.00	33567879.00	---
3007	chr20	+	34599063.00	34599161.00	NM_080834 // CNBD2
3008	chr20	+	37209911.00	37210011.00	NM_001018082 // ADIG
3009	chr20	+	42200737.00	42200761.00	NM_170693 // SGK2
3010	chr20	+	42852406.00	42852495.00	---
3011	chr20	+	45702839.00	45702971.00	NM_005244 // EYA2
3012	chr20	+	48599528.00	48599565.00	NM_005985 // SNAI1
3013	chr20	+	55242516.00	55242549.00	---
3014	chr20	+	57009662.00	57009748.00	NM_004738 // VAPB
3015	chr20	+	57430657.00	57430681.00	AJ224867 // GNAS
3016	chr20	+	58513048.00	58513136.00	NM_001190826 // FAM217B
3017	chr20	+	58563962.00	58563986.00	NM_177980 // CDH26
3018	chr20	+	58569459.00	58569483.00	NM_177980 // CDH26
3019	chr20	+	58581787.00	58581811.00	NM_177980 // CDH26
3020	chr20	+	61299685.00	61299709.00	AF104334 // SLCO4A1
3021	chr20	+	61388015.00	61388051.00	ENST00000482259 // NTSR1
3022	chr20	+	61463060.00	61463084.00	AK075240 // COL9A3

3023	chr20	-	633916.00	633941.00	NM_080725 // SRXN1
3024	chr20	-	982738.00	982770.00	NM_001029871 // RSPO4
3025	chr20	-	3235866.00	3235890.00	NM_001009984 // C20orf194
3026	chr20	-	3312961.00	3312985.00	NM_001009984 // C20orf194
3027	chr20	-	4721036.00	4721169.00	NR_024267 // PRNT
3028	chr20	-	4913262.00	4913286.00	NM_005116 // SLC23A2
3029	chr20	-	4951441.00	4951546.00	NM_005116 // SLC23A2
3030	chr20	-	5297141.00	5297360.00	AK289995 // PROKR2
3031	chr20	-	10004993.00	10006154.00	NR_040710 // SNAP25-AS1
3032	chr20	-	10858984.00	10859012.00	---
3033	chr20	-	11851293.00	11851352.00	OTTHUMT00000416683 // LINC00687
3034	chr20	-	18037301.00	18037353.00	NM_021220 // OVOL2
3035	chr20	-	18413885.00	18413909.00	BC036231 // DZANK1
3036	chr20	-	20028412.00	20028481.00	NM_016652 // CRNKL1
3037	chr20	-	24913117.00	24913599.00	---
3038	chr20	-	25123637.00	25123852.00	AK309387 // LOC284798
3039	chr20	-	25275621.00	25275645.00	NM_015600 // ABHD12
3040	chr20	-	25731276.00	25732271.00	---
3041	chr20	-	32266129.00	32266153.00	NM_005225 // E2F1
3042	chr20	-	34215299.00	34215323.00	NR_037188 // CPNE1
3043	chr20	-	35882658.00	35882732.00	NM_021081 // GHRH
3044	chr20	-	37844218.00	37844296.00	NR_027124 // LOC339568
3045	chr20	-	44519631.00	44519860.00	NR_074073 // NEURL2
3046	chr20	-	44540804.00	44540972.00	NM_006227 // PLTP
3047	chr20	-	44590451.00	44590475.00	AK027358 // ZNF335
3048	chr20	-	44845589.00	44845613.00	NM_021248 // CDH22
3049	chr20	-	46987487.00	46987763.00	---
3050	chr20	-	50713927.00	50713951.00	NM_199427 // ZFP64
3051	chr20	-	50781272.00	50781296.00	NM_018197 // ZFP64
3052	chr20	-	56073623.00	56073647.00	NM_001269040 // CTCFL
3053	chr20	-	60790046.00	60790251.00	NM_007232 // HRH3
3054	chr20	-	60971580.00	60971648.00	NM_031215 // CABLES2
3055	chr20	-	61492889.00	61492922.00	NM_006602 // TCFL5
3056	chr20	-	61525806.00	61525888.00	NM_080797 // DIDO1
3057	chr20	-	61880429.00	61880583.00	ENST00000461738 // NKAIN4
3058	chr20	-	62595180.00	62595204.00	NM_020713 // ZNF512B
3059	chr21	+	15673396.00	15673420.00	NR_003087 // ABCC13
3060	chr21	+	30494482.00	30494506.00	EF219158 // MAP3K7CL
3061	chr21	+	30502916.00	30502940.00	BC008567 // MAP3K7CL

3062	chr21	+	31768667.00	31768923.00	NM_181599 // KRTAP13-1
3063	chr21	+	33362448.00	33362487.00	NM_014586 // HUNK
3064	chr21	+	34968079.00	34968124.00	ENST00000480893 // CRYZL1
3065	chr21	+	37443566.00	37443820.00	AK308691 // CBR1
3066	chr21	+	37652596.00	37652620.00	NM_005128 // DOPEY2
3067	chr21	+	37852658.00	37853343.00	---
3068	chr21	+	43474174.00	43474396.00	---
3069	chr21	+	45168915.00	45168939.00	NM_003681 // PDXK
3070	chr21	+	45937677.00	45937713.00	NR_026547 // C21orf90
3071	chr21	+	47537328.00	47537352.00	NM_001849 // COL6A2
3072	chr21	+	47865215.00	47865239.00	NM_006031 // PCNT
3073	chr21	-	15481339.00	15481394.00	NM_198996 // LIPI
3074	chr21	-	26961147.00	26961194.00	NM_017446 // MRPL39
3075	chr21	-	28731445.00	28733357.00	---
3076	chr21	-	33694806.00	33694830.00	NM_014825 // URB1
3077	chr21	-	34901161.00	34901185.00	NM_000819 // GART
3078	chr21	-	34903025.00	34903049.00	OTTHUMT00000140689 // GART
3079	chr21	-	40032476.00	40032500.00	NM_001243428 // ERG
3080	chr21	-	40549446.00	40549470.00	NR_049728 // PSMG1
3081	chr21	-	42517112.00	42517258.00	ENST00000446910 // LINC00323
3082	chr21	-	43236083.00	43236107.00	NM_022115 // PRDM15
3083	chr21	-	44476952.00	44476976.00	NM_000071 // CBS
3084	chr21	-	44484042.00	44484066.00	NM_000071 // CBS
3085	chr22	+	20129020.00	20129044.00	NM_001185024 // ZDHHC8
3086	chr22	+	20194263.00	20194615.00	NR_026919 // LINC00896
3087	chr22	+	21322117.00	21322141.00	NM_144704 // AIFM3
3088	chr22	+	22037474.00	22037498.00	NM_014337 // PPIL2
3089	chr22	+	22661559.00	22661583.00	NR_027293 // LOC96610
3090	chr22	+	23670617.00	23670641.00	OTTHUMT00000320286 // OTTHUMG00000150838
3091	chr22	+	24106466.00	24106581.00	ENST00000402217 // C22orf15
3092	chr22	+	24121613.00	24121639.00	AK125911 // MMP11
3093	chr22	+	24158960.00	24159027.00	NM_003073 // SMARCB1
3094	chr22	+	24808472.00	24808496.00	ENST00000472799 // SPECC1L
3095	chr22	+	25251692.00	25251716.00	---
3096	chr22	+	27061467.00	27061491.00	NR_003491 // MIAT
3097	chr22	+	29169730.00	29169754.00	NM_173510 // CCDC117
3098	chr22	+	30824523.00	30824600.00	NM_016498 // MTFP1

3099	chr22	+	31022480.00	31022504.00	NM_000355 // TCN2
3100	chr22	+	32297743.00	32297767.00	NM_014662 // DEPDC5
3101	chr22	+	32772651.00	32772677.00	NR_038918 // LOC339666
3102	chr22	+	38084319.00	38084343.00	NM_024313 // NOL12
3103	chr22	+	39464766.00	39465940.00	---
3104	chr22	+	42166915.00	42166939.00	NM_152513 // MEI1
3105	chr22	+	44391284.00	44391308.00	ENST00000493621 // SAMM50
3106	chr22	+	45098134.00	45098158.00	NM_181333 // PRR5
3107	chr22	+	45921486.00	45921510.00	NM_006487 // FBLN1
3108	chr22	+	46486936.00	46486996.00	NR_037413 // MIR3619
3109	chr22	+	47071381.00	47071445.00	NM_015124 // GRAMD4
3110	chr22	+	50317628.00	50317779.00	AL713788 // CRELD2
3111	chr22	+	50617516.00	50617552.00	NR_027691 // PANX2
3112	chr22	-	18083563.00	18083845.00	ENST00000484653 // ATP6V1E1
3113	chr22	-	18762630.00	18762729.00	NR_003267 // GGT3P
3114	chr22	-	18924037.00	18924061.00	NM_016335 // PRODH
3115	chr22	-	20367602.00	20367763.00	NM_199127 // GGTLC2
3116	chr22	-	21097178.00	21097202.00	ENST00000494113 // PI4KA
3117	chr22	-	21632794.00	21632834.00	XM_001715205 // LOC100132705
3118	chr22	-	22863470.00	22863494.00	NM_080764 // ZNF280B
3119	chr22	-	24640773.00	24640797.00	NM_001099781 // GGT5
3120	chr22	-	30886186.00	30886210.00	NM_174977 // SEC14L4
3121	chr22	-	32330126.00	32330343.00	AK294232 // C22orf24
3122	chr22	-	32804748.00	32804772.00	ENST00000216038 // RTCB
3123	chr22	-	34680603.00	34680802.00	---
3124	chr22	-	36545262.00	36545293.00	NR_027833 // APOL3
3125	chr22	-	36587392.00	36587525.00	NM_030643 // APOL4
3126	chr22	-	37398170.00	37398206.00	NM_001163857 // TEX33
3127	chr22	-	37891552.00	37891576.00	NM_014550 // CARD10
3128	chr22	-	38485128.00	38485153.00	NM_025045 // BAIAP2L2
3129	chr22	-	38522477.00	38522501.00	ENST00000491986 // PLA2G6
3130	chr22	-	38823111.00	38824056.00	NM_152868 // KCNJ4
3131	chr22	-	39162240.00	39162309.00	ENST00000406622 // SUN2
3132	chr22	-	39265785.00	39266841.00	ENST00000469420 // CBX6
3133	chr22	-	42071066.00	42071186.00	NM_005008 // NHP2L1
3134	chr22	-	42230447.00	42230641.00	---
3135	chr22	-	44161242.00	44161266.00	NM_022785 // EFCAB6

3136	chr22	-	46436980.00	46437055.00	AL137569 // LINC00899
3137	chr22	-	46465608.00	46465751.00	AK123383 // LOC642648
3138	chr22	-	50699284.00	50699341.00	ENST00000497036 // MAPK12
3139	chr22	-	51009616.00	51009640.00	NM_004377 // CPT1B
3140	chr3	+	3845813.00	3845876.00	ENST00000472075 // LRRN1
3141	chr3	+	5244666.00	5244690.00	NM_014674 // EDEM1
3142	chr3	+	10329632.00	10329752.00	NR_004431 // GHRLOS
3143	chr3	+	18805249.00	18805278.00	---
3144	chr3	+	30566241.00	30566298.00	---
3145	chr3	+	31674640.00	31674670.00	ENST00000463044 // STT3B
3146	chr3	+	33863480.00	33863504.00	NM_013374 // PDCD6IP
3147	chr3	+	38040874.00	38040898.00	NM_015873 // VILL
3148	chr3	+	38519949.00	38519973.00	NM_001106 // ACVR2B
3149	chr3	+	39449329.00	39449564.00	ENST00000487876 // SNORA6
3150	chr3	+	42166932.00	42166956.00	NM_001042646 // TRAK1
3151	chr3	+	44773015.00	44773052.00	NM_145044 // ZNF501
3152	chr3	+	44844413.00	44844437.00	NM_020242 // KIF15
3153	chr3	+	44935091.00	44935138.00	NM_003241 // TGM4
3154	chr3	+	46638077.00	46638126.00	ENST00000505797 // TDGF1
3155	chr3	+	47447849.00	47447873.00	NM_015466 // PTPN23
3156	chr3	+	47452177.00	47452201.00	NM_015466 // PTPN23
3157	chr3	+	51197986.00	51198010.00	NM_004947 // DOCK3
3158	chr3	+	51399293.00	51399317.00	NM_004947 // DOCK3
3159	chr3	+	51897025.00	51897357.00	NM_203424 // IQCF2
3160	chr3	+	52012997.00	52013021.00	AK308592 // ABHD14A
3161	chr3	+	52246465.00	52246517.00	OTTHUMT00000350212 // ALAS1
3162	chr3	+	52366221.00	52366245.00	NM_015512 // DNAH1
3163	chr3	+	52378545.00	52378569.00	NM_015512 // DNAH1
3164	chr3	+	58140609.00	58140633.00	NM_001164317 // FLNB
3165	chr3	+	97194251.00	97194275.00	NM_001080448 // EPHA6
3166	chr3	+	101221063.00	101221099.00	---
3167	chr3	+	109056691.00	109056823.00	---
3168	chr3	+	110791320.00	110791344.00	NM_001243288 // PVRL3
3169	chr3	+	111632225.00	111632249.00	NM_001134438 // PHLDB2
3170	chr3	+	112709779.00	112709803.00	ENST00000383678 // GTPBP8
3171	chr3	+	113784250.00	113784274.00	NM_024638 // QTRTD1
3172	chr3	+	121100240.00	121100264.00	NM_014980 // STXBP5L

3173	chr3	+	127258355.00	127258531.00	---
3174	chr3	+	129247696.00	129247903.00	NM_000539 // RHO
3175	chr3	+	129931712.00	129931736.00	NR_027898 // COL6A4P2
3176	chr3	+	130574792.00	130574816.00	OTTHUMT00000356962 // OTTHUMG00000159704
3177	chr3	+	140397167.00	140397359.00	NM_152616 // TRIM42
3178	chr3	+	141298280.00	141298304.00	OTTHUMT00000359716 // RASA2
3179	chr3	+	141462354.00	141462380.00	NR_037702 // RNF7
3180	chr3	+	141499219.00	141499555.00	NM_139209 // GRK7
3181	chr3	+	142735114.00	142735138.00	NM_001080415 // U2SURP
3182	chr3	+	142746040.00	142746064.00	NM_001080415 // U2SURP
3183	chr3	+	147131294.00	147131325.00	NM_003412 // ZIC1
3184	chr3	+	150174872.00	150174897.00	NM_014779 // TSC22D2
3185	chr3	+	153905550.00	153905608.00	NM_001251962 // ARHGEF26
3186	chr3	+	156178139.00	156178163.00	---
3187	chr3	+	174177332.00	174177356.00	OTTHUMT00000347320 // NAALADL2
3188	chr3	+	176415350.00	176415534.00	---
3189	chr3	+	183855837.00	183855861.00	NM_003907 // EIF2B5
3190	chr3	+	184063252.00	184063404.00	NM_144635 // FAM131A
3191	chr3	+	190595730.00	190595780.00	NR_024343 // SNAR-I
3192	chr3	+	191112359.00	191113661.00	NM_174908 // CCDC50
3193	chr3	+	197476436.00	197476501.00	NM_001011537 // FYTTD1
3194	chr3	-	3118247.00	3118298.00	NM_000564 // IL5RA
3195	chr3	-	8669418.00	8669442.00	NR_046358 // SSUH2
3196	chr3	-	9592332.00	9592732.00	ENST00000495730 // LHFPL4
3197	chr3	-	10373961.00	10373985.00	---
3198	chr3	-	10491199.00	10491223.00	NM_001001331 // ATP2B2
3199	chr3	-	15457007.00	15457075.00	AK057791 // METTL6
3200	chr3	-	16580888.00	16581067.00	---
3201	chr3	-	27439204.00	27439228.00	NM_003615 // SLC4A7
3202	chr3	-	33558482.00	33558506.00	NM_015097 // CLASP2
3203	chr3	-	39144335.00	39144359.00	NM_031899 // GORASP1
3204	chr3	-	40440965.00	40441056.00	NR_040100 // ENTPD3-AS1
3205	chr3	-	42304915.00	42305004.00	NM_000729 // CCK
3206	chr3	-	42605387.00	42605411.00	ENST00000493107 // SEC22C

3207	chr3	-	47719714.00	47719738.00	NM_003074 // SMARCC1
3208	chr3	-	47721957.00	47721981.00	NM_003074 // SMARCC1
3209	chr3	-	47960269.00	47960293.00	NM_002375 // MAP4
3210	chr3	-	47973304.00	47973338.00	---
3211	chr3	-	48338219.00	48338252.00	NM_005793 // NME6
3212	chr3	-	48341958.00	48342016.00	ENST00000452211 // NME6
3213	chr3	-	48342146.00	48342192.00	OTTHUMT00000346120 // NME6
3214	chr3	-	48557187.00	48557211.00	NM_004567 // PFKFB4
3215	chr3	-	48619915.00	48619939.00	NM_000094 // COL7A1
3216	chr3	-	48680798.00	48680822.00	ENST00000498057 // CELSR3
3217	chr3	-	49866699.00	49866813.00	ENST00000491060 // TRAIP
3218	chr3	-	50358479.00	50358728.00	AK127945 // HYAL2
3219	chr3	-	50379291.00	50379315.00	NM_015896 // ZMYND10
3220	chr3	-	50403148.00	50403172.00	ENST00000483620 // CACNA2D2
3221	chr3	-	50418179.00	50418203.00	NM_001005505 // CACNA2D2
3222	chr3	-	52786040.00	52786310.00	NM_003157 // NEK4
3223	chr3	-	52794811.00	52794835.00	NM_003157 // NEK4
3224	chr3	-	54952535.00	54952812.00	NM_020678 // LRTM1
3225	chr3	-	57113267.00	57113291.00	NM_001128615 // ARHGEF3
3226	chr3	-	58190507.00	58190531.00	NM_004944 // DNASE1L3
3227	chr3	-	58200719.00	58200777.00	AK131323 // DNASE1L3
3228	chr3	-	58417461.00	58417519.00	NM_000925 // PDHB
3229	chr3	-	64673633.00	64673657.00	ENST00000498707 // ADAMTS9
3230	chr3	-	66465405.00	66465429.00	NM_015541 // LRIG1
3231	chr3	-	67570908.00	67571015.00	NM_001177599 // SUCLG2
3232	chr3	-	67705013.00	67705037.00	NM_001177599 // SUCLG2
3233	chr3	-	97680467.00	97680507.00	NM_001042533 // MINA
3234	chr3	-	98526978.00	98527002.00	NM_080927 // DCBLD2
3235	chr3	-	98600564.00	98600588.00	NM_080927 // DCBLD2
3236	chr3	-	100582680.00	100582704.00	ENST00000475896 // ABI3BP
3237	chr3	-	101405431.00	101405502.00	ENST00000464595 // RPL24
3238	chr3	-	109055219.00	109055270.00	OTTHUMT00000353901 // DPPA4

3239	chr3	-	111996542.00	111996566.00	NM_183061 // SLC9C1
3240	chr3	-	113063457.00	113063481.00	NM_001164496 // WDR52
3241	chr3	-	121437266.00	121437290.00	NM_001256486 // GOLGB1
3242	chr3	-	122178649.00	122178827.00	AK128280 // KPNA1
3243	chr3	-	123247234.00	123247278.00	NM_198402 // PTPLB
3244	chr3	-	123680333.00	123680357.00	ENST00000433542 // CCDC14
3245	chr3	-	124842387.00	124842411.00	---
3246	chr3	-	125626909.00	125626942.00	---
3247	chr3	-	126214905.00	126214951.00	NM_144639 // UROC1
3248	chr3	-	128211891.00	128211978.00	NM_032638 // GATA2
3249	chr3	-	132409436.00	132409460.00	NM_153240 // NPHP3
3250	chr3	-	132411500.00	132411524.00	NM_153240 // NPHP3
3251	chr3	-	134329165.00	134329214.00	NM_178554 // KY
3252	chr3	-	138313083.00	138313107.00	NM_024491 // CEP70
3253	chr3	-	141714045.00	141714069.00	ENST00000492919 // TFDP2
3254	chr3	-	142272084.00	142272108.00	NM_001184 // ATR
3255	chr3	-	145938626.00	145938650.00	NM_001128304 // PLSCR4
3256	chr3	-	150284829.00	150284853.00	ENST00000490945 // SERP1
3257	chr3	-	151017892.00	151017966.00	NM_023915 // GPR87
3258	chr3	-	156261975.00	156261999.00	ENST00000467733 // SSR3
3259	chr3	-	162993072.00	162993096.00	---
3260	chr3	-	164710116.00	164710140.00	NM_001041 // SI
3261	chr3	-	164714368.00	164714392.00	NM_001041 // SI
3262	chr3	-	164776993.00	164777017.00	NM_001041 // SI
3263	chr3	-	180331609.00	180331633.00	OTTHUMT00000349892 // CCDC39
3264	chr3	-	180397497.00	180397521.00	AL122120 // CCDC39
3265	chr3	-	182224878.00	182224908.00	---
3266	chr3	-	183966911.00	183966983.00	OTTHUMT00000346035 // ALG3
3267	chr3	-	189700904.00	189700928.00	NM_018192 // LEPREL1
3268	chr3	-	190578538.00	190578638.00	NM_001146686 // GMNC
3269	chr3	-	195382478.00	195383351.00	---
3270	chr3	-	195622925.00	195622949.00	OTTHUMT00000341500 // TNK2
3271	chr3	-	195801234.00	195801258.00	---
3272	chr3	-	196242150.00	196242237.00	ENST00000397537 // C3orf43
3273	chr4	+	949706.00	949730.00	AK309132 // TMEM175

3274	chr4	+	1976380.00	1976483.00	NR_003004 // SCARNA22
3275	chr4	+	2470958.00	2470982.00	NM_002938 // RNF4
3276	chr4	+	2798225.00	2798249.00	ENST00000510193 // SH3BP2
3277	chr4	+	4861642.00	4862025.00	NM_002448 // MSX1
3278	chr4	+	6303665.00	6304001.00	NM_006005 // WFS1
3279	chr4	+	7743630.00	7743654.00	NM_020777 // SORCS2
3280	chr4	+	15437455.00	15437553.00	NM_001135170 // C1QTNF7
3281	chr4	+	19457061.00	19457266.00	---
3282	chr4	+	26741538.00	26741562.00	NM_018317 // TBC1D19
3283	chr4	+	27010085.00	27010109.00	NM_001169118 // STIM2
3284	chr4	+	34668197.00	34668224.00	OTTHUMT00000360733 // OTTHUMG00000160471
3285	chr4	+	38879711.00	38879735.00	NM_138389 // FAM114A1
3286	chr4	+	39216256.00	39216280.00	NM_025132 // WDR19
3287	chr4	+	39481966.00	39483481.00	NR_026854 // LOC401127
3288	chr4	+	39640790.00	39640913.00	---
3289	chr4	+	42080260.00	42080284.00	NM_006345 // SLC30A9
3290	chr4	+	44700912.00	44701586.00	NM_021927 // GUF1
3291	chr4	+	47527633.00	47527657.00	NM_020453 // ATP10D
3292	chr4	+	48387356.00	48387409.00	AK025264 // SLAIN2
3293	chr4	+	48422466.00	48422490.00	OTTHUMT00000367239 // SLAIN2
3294	chr4	+	52917589.00	52917756.00	ENST00000295213 // SPATA18
3295	chr4	+	53728675.00	53728714.00	NM_023940 // RASL11B
3296	chr4	+	57861524.00	57861548.00	NM_000938 // POLR2B
3297	chr4	+	58020773.00	58020889.00	OTTHUMT00000367708 // OTTHUMG00000162167
3298	chr4	+	68567098.00	68567164.00	NR_015439 // LOC550112
3299	chr4	+	68946262.00	68946586.00	ENST00000500538 // LOC550112
3300	chr4	+	70811964.00	70812259.00	NM_001890 // CSN1S1
3301	chr4	+	74321078.00	74321261.00	ENST00000514279 // AFP
3302	chr4	+	77610718.00	77610742.00	AK027744 // SHROOM3
3303	chr4	+	77631129.00	77631153.00	ENST00000473602 // LOC100996628
3304	chr4	+	79472786.00	79472981.00	NM_005139 // ANXA3
3305	chr4	+	85538721.00	85538747.00	NM_001263 // CDS1
3306	chr4	+	86896763.00	86896880.00	ENST00000502537 // ARHGAP24
3307	chr4	+	87679434.00	87679458.00	NM_080683 // PTPN13
3308	chr4	+	89237934.00	89237959.00	---
3309	chr4	+	90472519.00	90472543.00	---

3310	chr4	+	93225651.00	93225675.00	NM_001510 // GRID2
3311	chr4	+	95129334.00	95129358.00	NR_045644 // SMARCAD1
3312	chr4	+	103516074.00	103516098.00	NM_003998 // NFKB1
3313	chr4	+	119606690.00	119606744.00	NM_020961 // METTL14
3314	chr4	+	141178536.00	141178560.00	NM_032547 // SCOC
3315	chr4	+	141463748.00	141463779.00	NM_153702 // ELMOD2
3316	chr4	+	146434407.00	146434522.00	ENST00000507367 // SMAD1
3317	chr4	+	148993196.00	148993220.00	NM_024605 // ARHGAP10
3318	chr4	+	148703760.00	148703809.00	NR_039962 // MIR4799
3319	chr4	+	151161575.00	151161628.00	NM_001040260 // DCLK2
3320	chr4	+	152200950.00	152201110.00	NM_183375 // PRSS48
3321	chr4	+	152577384.00	152577484.00	NM_001109977 // FAM160A1
3322	chr4	+	154256136.00	154256160.00	NM_015271 // TRIM2
3323	chr4	+	158041722.00	158041810.00	NM_000824 // GLRB
3324	chr4	+	159538283.00	159538307.00	NM_021634 // RXFP1
3325	chr4	+	159547973.00	159547997.00	NM_021634 // RXFP1
3326	chr4	+	162943910.00	162944053.00	---
3327	chr4	+	172737477.00	172737501.00	ENST00000513061 // GALNTL6
3328	chr4	+	174216919.00	174216971.00	NM_017423 // GALNT7
3329	chr4	+	174452893.00	174452917.00	ENST00000504429 // NBLA00301
3330	chr4	+	175219128.00	175219152.00	NM_001040157 // CEP44
3331	chr4	+	175237753.00	175237836.00	ENST00000508483 // CEP44
3332	chr4	+	184250451.00	184250515.00	---
3333	chr4	+	186347459.00	186347533.00	ENST00000501066 // C4orf47
3334	chr4	+	186392814.00	186392864.00	OTTHUMT00000360655 // OTTHUMG00000160454
3335	chr4	+	187658723.00	187658853.00	---
3336	chr4	+	188534535.00	188535020.00	OTTHUMT00000360142 // OTTHUMG00000160300
3337	chr4	-	2945875.00	2945899.00	NM_003703 // NOP14
3338	chr4	-	8073539.00	8073563.00	AK094798 // ABLIM2
3339	chr4	-	10515137.00	10515169.00	NM_052964 // CLNK
3340	chr4	-	15992880.00	15992904.00	NM_006017 // PROM1
3341	chr4	-	16085204.00	16085228.00	ENST00000502501 // PROM1
3342	chr4	-	21764617.00	21764646.00	NM_147182 // KCNIP4

3343	chr4	-	23797514.00	23797538.00	NM_013261 // PPARGC1A
3344	chr4	-	24854812.00	24854875.00	ENST00000512432 // CCDC149
3345	chr4	-	25032422.00	25032487.00	ENST00000382114 // LGI2
3346	chr4	-	25127329.00	25127353.00	NM_016955 // SEPSECS
3347	chr4	-	36617117.00	36617141.00	---
3348	chr4	-	46736875.00	46736963.00	ENST00000355591 // COX7B2
3349	chr4	-	47853890.00	47853914.00	NM_152995 // NFXL1
3350	chr4	-	52883317.00	52883563.00	NM_001024611 // LRRC66
3351	chr4	-	56300843.00	56300867.00	NM_001267843 // CLOCK
3352	chr4	-	56461453.00	56461502.00	NM_006681 // NMU
3353	chr4	-	58524912.00	58524950.00	OTTHUMT00000365846 // OTTHUMG00000161707
3354	chr4	-	68500149.00	68500173.00	NM_018227 // UBA6
3355	chr4	-	69816891.00	69817025.00	NM_024743 // UGT2A3
3356	chr4	-	73434443.00	73434467.00	NM_014243 // ADAMTS3
3357	chr4	-	82353484.00	82353508.00	NM_152545 // RASGEF1B
3358	chr4	-	82355024.00	82355048.00	NM_152545 // RASGEF1B
3359	chr4	-	82368673.00	82368697.00	NM_152545 // RASGEF1B
3360	chr4	-	82377879.00	82377903.00	NM_152545 // RASGEF1B
3361	chr4	-	82378710.00	82378734.00	NM_152545 // RASGEF1B
3362	chr4	-	83276985.00	83277189.00	ENST00000514325 // HNRNPD
3363	chr4	-	83277854.00	83277940.00	ENST00000514325 // HNRNPD
3364	chr4	-	83349471.00	83349542.00	NM_031372 // HNRNPDL
3365	chr4	-	88416208.00	88416261.00	NM_001128310 // SPARCL1
3366	chr4	-	89028346.00	89028404.00	NM_004827 // ABCG2
3367	chr4	-	95219912.00	95220255.00	NM_014485 // HPGDS
3368	chr4	-	100350694.00	100350718.00	NM_001166504 // ADH7
3369	chr4	-	104640915.00	104640962.00	NM_001059 // TACR3
3370	chr4	-	106061683.00	106061773.00	OTTHUMT00000363314 // OTTHUMG00000160994
3371	chr4	-	108038489.00	108038557.00	---
3372	chr4	-	115769419.00	115769443.00	NM_022569 // NDST4
3373	chr4	-	117435602.00	117435688.00	---
3374	chr4	-	122301531.00	122301741.00	NM_198179 // QRFPR
3375	chr4	-	147179863.00	147179887.00	NM_001029998 // SLC10A7
3376	chr4	-	155412547.00	155412910.00	NM_001142553 // DCHS2

3377	chr4	-	156875024.00	156875049.00	ENST00000433477 // CTSO
3378	chr4	-	157051103.00	157051158.00	---
3379	chr4	-	182080234.00	182080301.00	NR_033918 // LINC00290
3380	chr4	-	186436138.00	186437748.00	BX647263 // PDLIM3
3381	chr4	-	186732190.00	186732214.00	NM_001145671 // SORBS2
3382	chr5	+	29165059.00	29165084.00	---
3383	chr5	+	33455692.00	33455716.00	NM_152295 // TARS
3384	chr5	+	33457366.00	33457390.00	NM_152295 // TARS
3385	chr5	+	38427147.00	38427171.00	NM_152403 // EGFLAM
3386	chr5	+	53815410.00	53815554.00	NM_052870 // SNX18
3387	chr5	+	54327250.00	54327459.00	NM_002104 // GZMK
3388	chr5	+	54350780.00	54350944.00	OTTHUMT00000367873 // OTTHUMG00000162201
3389	chr5	+	61602881.00	61602905.00	ENST00000512541 // KIF2A
3390	chr5	+	64925306.00	64925407.00	NR_003545 // TRAPPC13
3391	chr5	+	64942884.00	64942908.00	NM_001093755 // TRAPPC13
3392	chr5	+	72251924.00	72251948.00	NM_138782 // FCHO2
3393	chr5	+	74065078.00	74065102.00	NM_014886 // NSA2
3394	chr5	+	76357532.00	76357561.00	NM_018046 // AGGF1
3395	chr5	+	78407652.00	78407698.00	NM_001713 // BHMT
3396	chr5	+	79086793.00	79086817.00	NM_153610 // CMYA5
3397	chr5	+	79354079.00	79354103.00	NM_003248 // THBS4
3398	chr5	+	81591317.00	81591341.00	ENST00000380167 // FLJ41309
3399	chr5	+	86685185.00	86685209.00	CR749722 // RASA1
3400	chr5	+	87987634.00	87987997.00	XR_112751 // LOC100505949
3401	chr5	+	89930968.00	89930992.00	NM_032119 // GPR98
3402	chr5	+	99489388.00	99489438.00	---
3403	chr5	+	113589212.00	113589448.00	---
3404	chr5	+	115628231.00	115628257.00	NM_016144 // COMMD10
3405	chr5	+	118469053.00	118469077.00	NM_005509 // DMXL1
3406	chr5	+	122909149.00	122909173.00	NM_004384 // CSNK1G3
3407	chr5	+	134228317.00	134228793.00	AK092425 // TXNDC15
3408	chr5	+	135489386.00	135489754.00	NM_005903 // SMAD5
3409	chr5	+	138223351.00	138223375.00	ENST00000517534 // CTNNA1
3410	chr5	+	140572128.00	140574463.00	NM_018930 // PCDHB10
3411	chr5	+	141319314.00	141320657.00	NM_014773 // KIAA0141
3412	chr5	+	143207911.00	143208158.00	---
3413	chr5	+	147582482.00	147582573.00	NM_205841 // SPINK6

3414	chr5	+	148683858.00	148683882.00	ENST00000522492 // AFAP1L1
3415	chr5	+	149359976.00	149361103.00	NM_000112 // SLC26A2
3416	chr5	+	149760075.00	149760099.00	BX537490 // TCOF1
3417	chr5	+	150632802.00	150632832.00	NM_000405 // GM2A
3418	chr5	+	154499020.00	154499150.00	---
3419	chr5	+	156894393.00	156894725.00	AK308830 // NIPAL4
3420	chr5	+	162180836.00	162180913.00	---
3421	chr5	+	167837046.00	167837070.00	---
3422	chr5	+	170215595.00	170215619.00	NM_014211 // GABRP
3423	chr5	+	173531251.00	173531275.00	NM_015980 // HMP19
3424	chr5	+	174253131.00	174253324.00	OTTHUMT00000371789 // OTTHUMG00000163136
3425	chr5	+	174413347.00	174413407.00	OTTHUMT00000371785 // OTTHUMG00000163132
3426	chr5	+	175305743.00	175305767.00	NM_006650 // CPLX2
3427	chr5	+	175581183.00	175581447.00	OTTHUMT00000371913 // OTTHUMG00000163178
3428	chr5	+	176013794.00	176013818.00	NM_001171976 // CDHR2
3429	chr5	+	176522391.00	176522415.00	NM_002011 // FGFR4
3430	chr5	+	176693697.00	176693721.00	OTTHUMT00000372615 // NSD1
3431	chr5	+	176797554.00	176797581.00	ENST00000502731 // RGS14
3432	chr5	+	176825686.00	176825710.00	NM_003052 // SLC34A1
3433	chr5	+	176873825.00	176873852.00	NM_030567 // PRR7
3434	chr5	-	1432582.00	1432631.00	NM_001044 // SLC6A3
3435	chr5	-	1929055.00	1929978.00	---
3436	chr5	-	5047471.00	5047533.00	OTTHUMT00000365650 // OTTHUMG00000161659
3437	chr5	-	10761323.00	10761349.00	NM_004394 // DAP
3438	chr5	-	13891174.00	13891198.00	NM_001369 // DNAH5
3439	chr5	-	16373705.00	16373797.00	---
3440	chr5	-	21842401.00	21842425.00	NM_004061 // CDH12
3441	chr5	-	27423656.00	27423680.00	---
3442	chr5	-	35065699.00	35065723.00	NM_000949 // PRLR
3443	chr5	-	37358225.00	37358249.00	NM_153485 // NUP155
3444	chr5	-	40831426.00	40831496.00	ENST00000274242 // RPL37
3445	chr5	-	43503770.00	43503816.00	ENST00000306862 // C5orf34
3446	chr5	-	54439385.00	54439469.00	NM_152623 // CDC20B
3447	chr5	-	56155536.00	56155698.00	---
3448	chr5	-	56234720.00	56234815.00	NM_152622 // MIER3
3449	chr5	-	60224700.00	60224724.00	NM_000082 // ERCC8

3450	chr5	-	64964069.00	64964093.00	NM_019072 // SGTB
3451	chr5	-	66478949.00	66480305.00	NM_005582 // CD180
3452	chr5	-	66930186.00	66930210.00	---
3453	chr5	-	71374068.00	71374125.00	---
3454	chr5	-	73602967.00	73602994.00	OTTHUMT00000368996 // OTTHUMG00000162459
3455	chr5	-	87974177.00	87974237.00	NR_024383 // LINC00461
3456	chr5	-	88119890.00	88119914.00	---
3457	chr5	-	94863815.00	94863839.00	NM_014639 // TTC37
3458	chr5	-	96502570.00	96502594.00	NM_001159749 // RIOK2
3459	chr5	-	101627108.00	101627132.00	NM_180991 // SLCO4C1
3460	chr5	-	114539735.00	114541654.00	---
3461	chr5	-	114572122.00	114572186.00	NM_005023 // PGGT1B
3462	chr5	-	115146868.00	115146997.00	NM_001801 // CDO1
3463	chr5	-	115815938.00	115815962.00	NM_020796 // SEMA6A
3464	chr5	-	131329842.00	131329866.00	NM_015256 // ACSL6
3465	chr5	-	132113423.00	132113447.00	NM_001098813 // SEPT8
3466	chr5	-	133944712.00	133944736.00	ENST00000503318 // SAR1B
3467	chr5	-	136953348.00	136953372.00	NM_017415 // KLHL3
3468	chr5	-	137474443.00	137474468.00	NM_003551 // NME5
3469	chr5	-	138837349.00	138837390.00	ENST00000515823 // ECSCR
3470	chr5	-	140961908.00	140961932.00	NM_005219 // DIAPH1
3471	chr5	-	141052459.00	141052483.00	NM_022481 // ARAP3
3472	chr5	-	141053181.00	141053205.00	NM_022481 // ARAP3
3473	chr5	-	142782819.00	142782843.00	NM_001204258 // NR3C1
3474	chr5	-	145523025.00	145523049.00	NM_020117 // LARS
3475	chr5	-	145756286.00	145756525.00	---
3476	chr5	-	146991898.00	146991922.00	NM_001270941 // JAKMIP2
3477	chr5	-	151271928.00	151271952.00	NM_001146040 // GLRA1
3478	chr5	-	153857656.00	153857823.00	NM_004821 // HAND1
3479	chr5	-	154300961.00	154300985.00	NM_015465 // GEMIN5
3480	chr5	-	156589850.00	156590617.00	NM_130899 // FAM71B
3481	chr5	-	159738866.00	159738891.00	NM_024565 // CCNJL
3482	chr5	-	160143943.00	160143967.00	NM_025153 // ATP10B
3483	chr5	-	169816462.00	169816663.00	NM_004137 // KCNMB1
3484	chr5	-	176936806.00	176936853.00	NM_024872 // DOK3
3485	chr5	-	178049435.00	178049459.00	CR749504 // CLK4
3486	chr5	-	179226142.00	179226166.00	ENST00000520875 // MGAT4B
3487	chr5	-	179274921.00	179274945.00	ENST00000519318 // C5orf45

3488	chr5	-	179275023.00	179275047.00	ENST00000292586 // C5orf45
3489	chr5	-	180038682.00	180038706.00	ENST00000502603 // FLT4
3490	chr6	+	3118697.00	3118788.00	BC037778 // BPHL
3491	chr6	+	10628047.00	10629534.00	NM_145649 // GCNT2
3492	chr6	+	10703638.00	10703676.00	NM_017906 // PAK1IP1
3493	chr6	+	11487533.00	11487563.00	---
3494	chr6	+	13618374.00	13618441.00	ENST00000420088 // NOL7
3495	chr6	+	22569808.00	22570398.00	NM_138574 // HDGFL1
3496	chr6	+	25279615.00	25279639.00	---
3497	chr6	+	25727140.00	25727454.00	NM_170610 // HIST1H2BA
3498	chr6	+	27342538.00	27342781.00	ENST00000477999 // ZNF391
3499	chr6	+	28198134.00	28198158.00	NM_001199479 // ZSCAN9
3500	chr6	+	28864890.00	28865082.00	ENST00000413667 // HCG14
3501	chr6	+	30564910.00	30564934.00	AB209564 // ABCF1
3502	chr6	+	30888477.00	30888501.00	NM_020442 // VARS2
3503	chr6	+	31902309.00	31902333.00	BC029781 // C2
3504	chr6	+	32007491.00	32007525.00	ENST00000462278 // CYP21A2
3505	chr6	+	33051691.00	33051770.00	ENST00000474044 // HLA-DPB1
3506	chr6	+	33406232.00	33406256.00	NM_006772 // SYNGAP1
3507	chr6	+	35761324.00	35761447.00	OTTHUMT00000040318 // CLPSL1
3508	chr6	+	36907873.00	36908138.00	---
3509	chr6	+	40346499.00	40346597.00	DQ168992 // TDRG1
3510	chr6	+	41470183.00	41470314.00	---
3511	chr6	+	42603256.00	42603280.00	NM_015255 // UBR2
3512	chr6	+	53761299.00	53761351.00	NM_018214 // LRRC1
3513	chr6	+	53762114.00	53762155.00	NM_018214 // LRRC1
3514	chr6	+	55214911.00	55214941.00	NM_207410 // GFRAL
3515	chr6	+	57372292.00	57372316.00	NM_000947 // PRIM2
3516	chr6	+	71276649.00	71276676.00	ENST00000370474 // C6orf57
3517	chr6	+	83905462.00	83905750.00	NM_033411 // RWDD2A
3518	chr6	+	88187096.00	88187120.00	NM_006416 // SLC35A1
3519	chr6	+	88187127.00	88187151.00	NM_006416 // SLC35A1
3520	chr6	+	88773824.00	88773870.00	NM_030960 // SPACA1
3521	chr6	+	109081517.00	109081603.00	NR_033376 // LINC00222

3522	chr6	+	110533355.00	110533438.00	NM_015891 // CDC40
3523	chr6	+	110547375.00	110547399.00	NM_015891 // CDC40
3524	chr6	+	112853419.00	112853452.00	---
3525	chr6	+	126319376.00	126319402.00	NM_001031712 // TRMT11
3526	chr6	+	126667351.00	126667390.00	NM_001012507 // CENPW
3527	chr6	+	132211626.00	132211650.00	NM_006208 // ENPP1
3528	chr6	+	138008254.00	138008358.00	---
3529	chr6	+	138611008.00	138611032.00	NM_020340 // KIAA1244
3530	chr6	+	139355502.00	139355640.00	ENST00000461027 // ABRACL
3531	chr6	+	140407831.00	140407887.00	BC038188 // LOC100507477
3532	chr6	+	147829900.00	147830029.00	NM_001030060 // SAMD5
3533	chr6	+	151334919.00	151334943.00	NM_001242767 // MTHFD1L
3534	chr6	+	155337428.00	155337452.00	ENST00000535231 // LOC100505519
3535	chr6	+	156203100.00	156203523.00	---
3536	chr6	+	163418496.00	163418533.00	ENST00000541974 // PACRG
3537	chr6	+	169072886.00	169072910.00	---
3538	chr6	-	2124939.00	2124965.00	NM_001500 // GMDS
3539	chr6	-	2622926.00	2623533.00	ENST00000296847 // C6orf195
3540	chr6	-	2749440.00	2749498.00	NM_001012418 // MYLK4
3541	chr6	-	11044508.00	11044533.00	NM_017770 // ELOVL2
3542	chr6	-	15248104.00	15248329.00	BC033996 // JARID2-AS1
3543	chr6	-	26250390.00	26250422.00	NM_021018 // HIST1H3F
3544	chr6	-	27782092.00	27782131.00	NM_021066 // HIST1H2AJ
3545	chr6	-	28300130.00	28300169.00	NM_001243242 // ZSCAN31
3546	chr6	-	29576486.00	29576510.00	NM_001470 // GABBR1
3547	chr6	-	29589888.00	29589912.00	NM_001470 // GABBR1
3548	chr6	-	30568372.00	30568396.00	NM_002714 // PPP1R10
3549	chr6	-	30573654.00	30573678.00	ENST00000469365 // PPP1R10
3550	chr6	-	31749540.00	31749564.00	ENST00000491745 // VARS
3551	chr6	-	31832595.00	31832619.00	NM_025257 // SLC44A4
3552	chr6	-	31839129.00	31839153.00	NM_025257 // SLC44A4
3553	chr6	-	32164117.00	32164141.00	NM_004557 // NOTCH4
3554	chr6	-	33864433.00	33864513.00	OTTHUMT00000389707 // OTTHUMG00000166297

3555	chr6	-	40998130.00	40998215.00	NM_173561 // UNC5CL
3556	chr6	-	41349162.00	41349601.00	OTTHUMT00000106561 // OTTHUMG00000046223
3557	chr6	-	41516140.00	41516327.00	ENST00000454812 // LOC101060264
3558	chr6	-	41740584.00	41740658.00	NM_006653 // FRS3
3559	chr6	-	41908939.00	41909099.00	AK055519 // CCND3
3560	chr6	-	44224507.00	44224548.00	NM_178148 // SLC35B2
3561	chr6	-	45530221.00	45530403.00	---
3562	chr6	-	45544075.00	45544252.00	---
3563	chr6	-	46293133.00	46293197.00	NM_005822 // RCAN2
3564	chr6	-	49604530.00	49604567.00	NM_000324 // RHAG
3565	chr6	-	56716640.00	56716664.00	NM_001144770 // DST
3566	chr6	-	56818583.00	56818607.00	NM_001144769 // DST
3567	chr6	-	62526861.00	62526885.00	AK095983 // KHDRBS2
3568	chr6	-	62757806.00	62757866.00	NM_152688 // KHDRBS2
3569	chr6	-	75827211.00	75827235.00	NM_004370 // COL12A1
3570	chr6	-	75840633.00	75840657.00	NM_004370 // COL12A1
3571	chr6	-	75953560.00	75953587.00	NM_001865 // COX7A2
3572	chr6	-	75968505.00	75968610.00	NM_018247 // TMEM30A
3573	chr6	-	80656903.00	80656972.00	NM_022726 // ELOVL4
3574	chr6	-	85466529.00	85466553.00	NM_001080508 // TBX18
3575	chr6	-	100896384.00	100896497.00	NM_005068 // SIM1
3576	chr6	-	109796615.00	109796677.00	NM_014797 // ZBTB24
3577	chr6	-	109850251.00	109850275.00	NM_001145128 // AK9
3578	chr6	-	111656766.00	111656790.00	NM_002912 // REV3L
3579	chr6	-	127634688.00	127634712.00	---
3580	chr6	-	128312479.00	128312503.00	NM_001135648 // PTPRK
3581	chr6	-	131948487.00	131948511.00	ENST00000489888 // MED23
3582	chr6	-	131948782.00	131948806.00	NM_004830 // MED23
3583	chr6	-	134438693.00	134438807.00	NR_037938 // HMGA1P7
3584	chr6	-	135715850.00	135715874.00	OTTHUMT00000392259 // AHI1
3585	chr6	-	135763723.00	135763747.00	NM_001134831 // AHI1
3586	chr6	-	155764418.00	155764542.00	NM_015718 // NOX3
3587	chr6	-	164085418.00	164085679.00	---
3588	chr6	-	165801860.00	165801884.00	NM_001130690 // PDE10A
3589	chr6	-	169343891.00	169343926.00	---
3590	chr6	-	169829003.00	169829067.00	---
3591	chr6_apd_hap1	+	168291.00	168483.00	ENST00000413667 // HCG14
3592	chr6_apd_hap1	+	1108731.00	1111519.00	---
3593	chr6_apd_hap1	+	4338498.00	4338577.00	---

3594	chr6_apd_hap1	-	880029.00	880053.00	---
3595	chr6_apd_hap1	-	893418.00	893442.00	---
3596	chr6_apd_hap1	-	1939461.00	1939552.00	---
3597	chr6_apd_hap1	-	3064290.00	3064314.00	---
3598	chr6_apd_hap1	-	3147350.00	3147374.00	---
3599	chr6_apd_hap1	-	3153882.00	3153906.00	---
3600	chr6_apd_hap1	-	3478855.00	3478879.00	---
3601	chr6_apd_hap1	-	4093551.00	4093575.00	---
3602	chr6_cox_hap2	+	387916.00	388108.00	ENST00000413667 // HCG14
3603	chr6_cox_hap2	+	1380595.00	1383383.00	---
3604	chr6_cox_hap2	+	2076963.00	2076987.00	---
3605	chr6_cox_hap2	+	2388100.00	2388124.00	ENST00000469489 // VARS2
3606	chr6_cox_hap2	+	2400404.00	2400428.00	ENST00000469489 // VARS2
3607	chr6_cox_hap2	+	2644326.00	2644484.00	ENST00000376257 // TCF19
3608	chr6_cox_hap2	+	3050948.00	3051078.00	ENST00000476761 // LTA
3609	chr6_cox_hap2	+	3412065.00	3412089.00	---
3610	chr6_cox_hap2	-	893067.00	893109.00	---
3611	chr6_cox_hap2	-	1095295.00	1095319.00	---
3612	chr6_cox_hap2	-	1108698.00	1108722.00	---
3613	chr6_cox_hap2	-	2080425.00	2080449.00	---
3614	chr6_cox_hap2	-	2085707.00	2085731.00	---
3615	chr6_cox_hap2	-	2633012.00	2633036.00	---
3616	chr6_cox_hap2	-	3259111.00	3259135.00	---
3617	chr6_cox_hap2	-	3342342.00	3342366.00	---
3618	chr6_cox_hap2	-	3348883.00	3348907.00	---
3619	chr6_cox_hap2	-	3634795.00	3634819.00	---
3620	chr6_dbb_hap3	+	1858548.00	1858572.00	---
3621	chr6_dbb_hap3	+	2182604.00	2182628.00	ENST00000469489 // VARS2
3622	chr6_dbb_hap3	+	2426697.00	2426855.00	ENST00000439112 // TCF19
3623	chr6_dbb_hap3	+	3187896.00	3187920.00	---
3624	chr6_dbb_hap3	+	4333030.00	4333109.00	---
3625	chr6_dbb_hap3	-	879843.00	879867.00	---
3626	chr6_dbb_hap3	-	893246.00	893270.00	---
3627	chr6_dbb_hap3	-	1366835.00	1366899.00	---
3628	chr6_dbb_hap3	-	1862010.00	1862034.00	---
3629	chr6_dbb_hap3	-	1867292.00	1867316.00	---
3630	chr6_dbb_hap3	-	2415382.00	2415406.00	---
3631	chr6_dbb_hap3	-	3035122.00	3035146.00	---
3632	chr6_dbb_hap3	-	3118181.00	3118205.00	---

3633	chr6_dbb_hap3	-	3124711.00	3124735.00	---
3634	chr6_dbb_hap3	-	4087925.00	4087949.00	---
3635	chr6_mann_hap4	+	1912983.00	1913007.00	---
3636	chr6_mann_hap4	+	2236558.00	2236582.00	OTTHUMT00000076565 // VARS2
3637	chr6_mann_hap4	+	2477917.00	2478075.00	ENST00000439112 // TCF19
3638	chr6_mann_hap4	+	4509237.00	4509316.00	---
3639	chr6_mann_hap4	-	677269.00	677311.00	---
3640	chr6_mann_hap4	-	879511.00	879535.00	---
3641	chr6_mann_hap4	-	892875.00	892899.00	---
3642	chr6_mann_hap4	-	1371670.00	1371734.00	---
3643	chr6_mann_hap4	-	1916444.00	1916468.00	---
3644	chr6_mann_hap4	-	1921726.00	1921750.00	---
3645	chr6_mann_hap4	-	2466616.00	2466640.00	---
3646	chr6_mann_hap4	-	3506938.00	3506962.00	---
3647	chr6_mcf_hap5	+	168452.00	168644.00	ENST00000413667 // HCG14
3648	chr6_mcf_hap5	+	1946765.00	1946789.00	---
3649	chr6_mcf_hap5	+	2270436.00	2270460.00	ENST00000464084 // VARS2
3650	chr6_mcf_hap5	+	2290729.00	2290799.00	NM_080870 // DPCR1
3651	chr6_mcf_hap5	+	2511496.00	2511654.00	ENST00000376257 // TCF19
3652	chr6_mcf_hap5	+	3282153.00	3282177.00	---
3653	chr6_mcf_hap5	+	4388552.00	4388631.00	---
3654	chr6_mcf_hap5	-	879689.00	879713.00	---
3655	chr6_mcf_hap5	-	893090.00	893114.00	---
3656	chr6_mcf_hap5	-	1950227.00	1950251.00	---
3657	chr6_mcf_hap5	-	1955509.00	1955533.00	---
3658	chr6_mcf_hap5	-	2500195.00	2500219.00	---
3659	chr6_mcf_hap5	-	2617873.00	2618253.00	---
3660	chr6_mcf_hap5	-	3129237.00	3129261.00	---
3661	chr6_mcf_hap5	-	3212473.00	3212497.00	---
3662	chr6_mcf_hap5	-	3219001.00	3219025.00	---
3663	chr6_mcf_hap5	-	3543941.00	3543965.00	---
3664	chr6_mcf_hap5	-	4143424.00	4143448.00	---
3665	chr6_qbl_hap6	+	168291.00	168483.00	ENST00000413667 // HCG14
3666	chr6_qbl_hap6	+	1205278.00	1205318.00	AK125608 // HLA-A
3667	chr6_qbl_hap6	+	1857817.00	1857841.00	---
3668	chr6_qbl_hap6	+	2169010.00	2169034.00	ENST00000469311 // VARS2
3669	chr6_qbl_hap6	+	2181468.00	2181492.00	ENST00000464084 // VARS2

3670	chr6_qbl_hap6	+	2247506.00	2247665.00	ENST00000376296 // MUC21
3671	chr6_qbl_hap6	+	2425425.00	2425583.00	ENST00000376257 // TCF19
3672	chr6_qbl_hap6	+	3196102.00	3196126.00	---
3673	chr6_qbl_hap6	+	4284148.00	4284227.00	---
3674	chr6_qbl_hap6	-	879817.00	879841.00	---
3675	chr6_qbl_hap6	-	893220.00	893244.00	---
3676	chr6_qbl_hap6	-	1366076.00	1366140.00	---
3677	chr6_qbl_hap6	-	1861280.00	1861304.00	---
3678	chr6_qbl_hap6	-	1866561.00	1866585.00	---
3679	chr6_qbl_hap6	-	2375458.00	2375839.00	---
3680	chr6_qbl_hap6	-	2379967.00	2380004.00	---
3681	chr6_qbl_hap6	-	2414099.00	2414123.00	---
3682	chr6_qbl_hap6	-	3132881.00	3132942.00	---
3683	chr6_qbl_hap6	-	3425135.00	3425159.00	---
3684	chr6_ssto_hap7	+	205812.00	206004.00	ENST00000413667 // HCG14
3685	chr6_ssto_hap7	+	1897189.00	1897213.00	---
3686	chr6_ssto_hap7	+	2464510.00	2464668.00	ENST00000441405 // TCF19
3687	chr6_ssto_hap7	+	3235019.00	3235043.00	OTTHUMT00000077115 // C2
3688	chr6_ssto_hap7	+	4532195.00	4532274.00	---
3689	chr6_ssto_hap7	+	4886478.00	4886502.00	NM_006772 // SYNGAP1
3690	chr6_ssto_hap7	-	714822.00	714864.00	---
3691	chr6_ssto_hap7	-	1403560.00	1403624.00	---
3692	chr6_ssto_hap7	-	1900651.00	1900675.00	---
3693	chr6_ssto_hap7	-	1905933.00	1905957.00	---
3694	chr6_ssto_hap7	-	3080352.00	3080376.00	---
3695	chr6_ssto_hap7	-	3165343.00	3165367.00	---
3696	chr6_ssto_hap7	-	3171871.00	3171895.00	---
3697	chr6_ssto_hap7	-	3511843.00	3511867.00	---
3698	chr6_ssto_hap7	-	4142164.00	4142201.00	---
3699	chr6_ssto_hap7	-	4237320.00	4237344.00	---
3700	chr7	+	150571.00	151648.00	AK024243 // LOC100507642
3701	chr7	+	1132439.00	1132463.00	NM_001505 // GPER
3702	chr7	+	1878450.00	1878475.00	AK095485 // LOC100128374
3703	chr7	+	2289046.00	2289097.00	ENST00000487426 // NUDT1
3704	chr7	+	18536070.00	18536094.00	ENST00000474742 // HDAC9
3705	chr7	+	18557410.00	18557434.00	---

3706	chr7	+	21678576.00	21678600.00	NM_001277115 // DNAH11
3707	chr7	+	23224846.00	23224898.00	NM_007342 // NUPL2
3708	chr7	+	24331346.00	24331429.00	NM_000905 // NPY
3709	chr7	+	26303361.00	26303446.00	---
3710	chr7	+	27163662.00	27163824.00	ENST00000517550 // HOXA-AS2
3711	chr7	+	29923511.00	29923876.00	NM_001080529 // WIPF3
3712	chr7	+	39810606.00	39810632.00	NR_026999 // LINC00265
3713	chr7	+	39820834.00	39820858.00	NR_026999 // LINC00265
3714	chr7	+	39991012.00	39991124.00	NM_003718 // CDK13
3715	chr7	+	44143995.00	44144019.00	NM_001129 // AEBP1
3716	chr7	+	44714781.00	44714805.00	NM_002541 // OGDH
3717	chr7	+	57472754.00	57472786.00	NR_036102 // MIR3147
3718	chr7	+	62810144.00	62810345.00	AK128835 // LOC100287704
3719	chr7	+	62854667.00	62855126.00	BC090890 // LOC340239
3720	chr7	+	64115646.00	64115734.00	---
3721	chr7	+	68505220.00	68505252.00	OTTHUMT00000344771 // OTTHUMG00000156611
3722	chr7	+	74009348.00	74009372.00	NM_016328 // GTF2IRD1
3723	chr7	+	76903888.00	76903912.00	NM_020879 // CCDC146
3724	chr7	+	87811371.00	87811395.00	NM_004194 // ADAM22
3725	chr7	+	89927073.00	89927097.00	ENST00000389297 // C7orf63
3726	chr7	+	90014238.00	90014442.00	NM_001042717 // GTPBP10
3727	chr7	+	90043196.00	90043220.00	NM_001185072 // CLDN12
3728	chr7	+	94881129.00	94881153.00	NM_001166160 // PPP1R9A
3729	chr7	+	95606848.00	95606872.00	NM_004411 // DYNC1I1
3730	chr7	+	98552888.00	98552912.00	NM_001244580 // TRRAP
3731	chr7	+	98554106.00	98554130.00	NM_001244580 // TRRAP
3732	chr7	+	98643390.00	98643414.00	---
3733	chr7	+	98946487.00	98946561.00	NM_006409 // ARPC1A
3734	chr7	+	99045423.00	99045448.00	ENST00000430038 // CPSF4
3735	chr7	+	100027693.00	100027821.00	NM_019606 // MEPCE
3736	chr7	+	100211342.00	100211399.00	ENST00000497456 // MOSPD3
3737	chr7	+	100730121.00	100730274.00	ENST00000467847 // TRIM56
3738	chr7	+	101201298.00	101202276.00	NM_133457 // COL26A1

3739	chr7	+	101952419.00	101952446.00	ENST00000536178 // SH2B2
3740	chr7	+	106523027.00	106523184.00	OTTHUMT00000349296 // PIK3CG
3741	chr7	+	107204659.00	107204689.00	NR_073002 // DUS4L
3742	chr7	+	110568375.00	110568418.00	---
3743	chr7	+	116140139.00	116140201.00	NM_001206748 // CAV2
3744	chr7	+	116771975.00	116771999.00	NM_018412 // ST7
3745	chr7	+	116599531.00	116599797.00	NR_002329 // ST7-OT4
3746	chr7	+	124569941.00	124570010.00	---
3747	chr7	+	127234856.00	127234888.00	ENST00000421705 // FSCN3
3748	chr7	+	127235810.00	127236042.00	NM_020369 // FSCN3
3749	chr7	+	128489572.00	128489596.00	NM_001458 // FLNC
3750	chr7	+	128505687.00	128505805.00	NM_004231 // ATP6V1F
3751	chr7	+	129367136.00	129367194.00	NM_005011 // NRF1
3752	chr7	+	131611019.00	131611126.00	---
3753	chr7	+	135862023.00	135862161.00	OTTHUMT00000340910 // OTTHUMG00000155618
3754	chr7	+	138849930.00	138849978.00	NM_024926 // TTC26
3755	chr7	+	139030468.00	139030492.00	NM_197964 // C7orf55
3756	chr7	+	143893065.00	143893116.00	---
3757	chr7	+	150749677.00	150749701.00	NM_004769 // ASIC3
3758	chr7	+	150757184.00	150757208.00	ENST00000490898 // SLC4A2
3759	chr7	+	151776469.00	151776493.00	BC059377 // GALNT11
3760	chr7	+	156451701.00	156452103.00	BC015416 // RNF32
3761	chr7	-	1881379.00	1881423.00	---
3762	chr7	-	2347407.00	2347500.00	ENST00000419693 // SNX8
3763	chr7	-	3341861.00	3342064.00	---
3764	chr7	-	5779075.00	5779099.00	AY177397 // RNF216
3765	chr7	-	6210231.00	6210268.00	NM_004227 // CYTH3
3766	chr7	-	8263135.00	8263159.00	ENST00000457755 // ICA1
3767	chr7	-	16316226.00	16316250.00	ENST00000479493 // ISPD
3768	chr7	-	17497091.00	17497134.00	---
3769	chr7	-	20824607.00	20824631.00	NM_182700 // SP8
3770	chr7	-	22396642.00	22396666.00	OTTHUMT00000326591 // RAPGEF5
3771	chr7	-	23016984.00	23017008.00	NM_032581 // FAM126A
3772	chr7	-	23017936.00	23018017.00	NM_032581 // FAM126A
3773	chr7	-	25219540.00	25219564.00	ENST00000283905 // C7orf31

3774	chr7	-	25219859.00	25219914.00	ENST00000283905 // C7orf31
3775	chr7	-	37956207.00	37956491.00	NM_003014 // SFRP4
3776	chr7	-	39803201.00	39803239.00	---
3777	chr7	-	39807071.00	39807259.00	---
3778	chr7	-	42959021.00	42959741.00	BX641097 // PSMA2
3779	chr7	-	43687109.00	43687133.00	AK309315 // COA1
3780	chr7	-	44068621.00	44068836.00	NR_024116 // RASA4CP
3781	chr7	-	44571379.00	44571428.00	NM_013389 // NPC1L1
3782	chr7	-	44873299.00	44873894.00	NM_012412 // H2AFV
3783	chr7	-	47333379.00	47333403.00	NM_022748 // TNS3
3784	chr7	-	51085182.00	51085206.00	NM_015198 // COBL
3785	chr7	-	52391505.00	52391561.00	---
3786	chr7	-	72298683.00	72298797.00	NM_001145440 // TYW1B
3787	chr7	-	73030453.00	73030477.00	NM_032951 // MLXIPL
3788	chr7	-	81213657.00	81213749.00	AY927634 // LOC100128317
3789	chr7	-	83023613.00	83023637.00	NM_012431 // SEMA3E
3790	chr7	-	84121925.00	84121949.00	ENST00000424555 // SEMA3A
3791	chr7	-	91501390.00	91501655.00	AL832861 // MTERF
3792	chr7	-	91509489.00	91509796.00	ENST00000481516 // MTERF
3793	chr7	-	92463198.00	92463222.00	NM_001259 // CDK6
3794	chr7	-	98775561.00	98775608.00	NM_001145715 // KPNA7
3795	chr7	-	99675103.00	99675127.00	BX647182 // ZNF3
3796	chr7	-	99769738.00	99769802.00	NM_152742 // GPC2
3797	chr7	-	99774965.00	99774989.00	NM_152742 // GPC2
3798	chr7	-	100253448.00	100253489.00	NM_016188 // ACTL6B
3799	chr7	-	100491815.00	100491839.00	NM_015831 // ACHE
3800	chr7	-	105162546.00	105162606.00	NM_019042 // PUS7
3801	chr7	-	106871099.00	106871123.00	NM_006348 // COG5
3802	chr7	-	108962493.00	108962641.00	OTTHUMT00000338048 // OTTHUMG00000155012
3803	chr7	-	111372283.00	111372307.00	NM_014705 // DOCK4
3804	chr7	-	112406143.00	112406680.00	NM_022484 // TMEM168
3805	chr7	-	120450531.00	120450615.00	NM_012338 // TSPAN12
3806	chr7	-	123517895.00	123517951.00	---
3807	chr7	-	127975735.00	127975759.00	ENST00000488249 // RBM28
3808	chr7	-	129691171.00	129691195.00	NM_016478 // ZC3HC1
3809	chr7	-	132333294.00	132333418.00	NM_181775 // PLXNA4
3810	chr7	-	135386716.00	135386740.00	AB208809 // SLC13A4
3811	chr7	-	138604195.00	138604221.00	ENST00000242365 // KIAA1549

3812	chr7	-	140043819.00	140043843.00	AK126589 // SLC37A3
3813	chr7	-	140069418.00	140069442.00	NM_207113 // SLC37A3
3814	chr7	-	140086647.00	140086686.00	---
3815	chr7	-	141366126.00	141366180.00	NM_001080392 // KIAA1147
3816	chr7	-	150642200.00	150642224.00	NM_000238 // KCNH2
3817	chr7	-	150709523.00	150709547.00	NR_073169 // ATG9B
3818	chr7	-	150774536.00	150774560.00	AK023141 // FASTK
3819	chr7	-	151130607.00	151130638.00	NR_037468 // MIR3907
3820	chr7	-	155593239.00	155593279.00	ENST00000297261 // SHH
3821	chr7	-	155599278.00	155599359.00	ENST00000472308 // SHH
3822	chr7	-	156432922.00	156432946.00	NR_026865 // C7orf13
3823	chr7	-	158459853.00	158459877.00	AK301901 // NCAPG2
3824	chr8	+	7752258.00	7752292.00	NM_004942 // DEFB4A
3825	chr8	+	8957411.00	8957473.00	ENST00000520332 // ERI1
3826	chr8	+	11296061.00	11296085.00	NR_026814 // C8orf12
3827	chr8	+	12245799.00	12245834.00	ENST00000433621 // FAM66A
3828	chr8	+	15601010.00	15601034.00	ENST00000508446 // TUSC3
3829	chr8	+	19002018.00	19002415.00	---
3830	chr8	+	19699422.00	19699446.00	ENST00000521008 // INTS10
3831	chr8	+	19936816.00	19937033.00	---
3832	chr8	+	21857123.00	21857147.00	NM_015024 // XPO7
3833	chr8	+	22969233.00	22969257.00	NM_003841 // TNFRSF10C
3834	chr8	+	23646938.00	23646985.00	---
3835	chr8	+	24350016.00	24350040.00	NM_003817 // ADAM7
3836	chr8	+	25319644.00	25319720.00	NM_152562 // CDCA2
3837	chr8	+	27669655.00	27669707.00	BC034641 // ESCO2
3838	chr8	+	27976490.00	27976514.00	ENST00000520110 // ELP3
3839	chr8	+	31887915.00	31887953.00	---
3840	chr8	+	37594263.00	37594515.00	NM_001003790 // ERLIN2
3841	chr8	+	38684836.00	38684860.00	NM_006283 // TACC1
3842	chr8	+	38871527.00	38871551.00	NM_003816 // ADAM9
3843	chr8	+	41517959.00	41518026.00	NR_030161 // MIR486
3844	chr8	+	42591663.00	42591761.00	NM_000749 // CHRNB3
3845	chr8	+	43049083.00	43049107.00	ENST00000520678 // HGSNAT
3846	chr8	+	43212063.00	43212087.00	NM_001002920 // POTEA
3847	chr8	+	61969760.00	61969784.00	ENST00000522621 // CLVS1

3848	chr8	+	63161464.00	63161488.00	ENST00000523367 // NKAIN3
3849	chr8	+	66504973.00	66505006.00	---
3850	chr8	+	72608177.00	72608220.00	---
3851	chr8	+	74888548.00	74888584.00	NM_017866 // TMEM70
3852	chr8	+	89723827.00	89725154.00	---
3853	chr8	+	99960494.00	99960528.00	AK304654 // OSR2
3854	chr8	+	103817745.00	103817777.00	OTTHUMT00000380078 // OTTHUMG00000164736
3855	chr8	+	104195609.00	104195676.00	OTTHUMT00000380258 // BAALC
3856	chr8	+	105361080.00	105361479.00	NM_030788 // DCSTAMP
3857	chr8	+	107726064.00	107726088.00	NM_018002 // OXR1
3858	chr8	+	109483087.00	109483158.00	ENST00000517784 // EMC2
3859	chr8	+	135854566.00	135854695.00	---
3860	chr8	+	137809522.00	137809587.00	OTTHUMT00000377405 // OTTHUMG00000164139
3861	chr8	+	139085262.00	139085364.00	OTTHUMT00000377598 // OTTHUMG00000164175
3862	chr8	+	142528343.00	142528568.00	---
3863	chr8	+	143997884.00	143997910.00	OTTHUMT00000379658 // GML
3864	chr8	+	145150462.00	145150573.00	AK225796 // CYC1
3865	chr8	+	145696012.00	145696036.00	ENST00000531423 // KIFC2
3866	chr8	+	145734840.00	145735221.00	NM_138431 // MFSD3
3867	chr8	+	145744139.00	145744163.00	NM_001272036 // LRRC14
3868	chr8	-	8608884.00	8609002.00	---
3869	chr8	-	10924361.00	10924595.00	---
3870	chr8	-	17726112.00	17726189.00	NM_004467 // FGL1
3871	chr8	-	22777712.00	22777786.00	NM_144962 // PEBP4
3872	chr8	-	23174370.00	23174394.00	---
3873	chr8	-	25744364.00	25744388.00	NM_022659 // EBF2
3874	chr8	-	29004956.00	29004980.00	NM_015254 // KIF13B
3875	chr8	-	33408866.00	33408906.00	NM_024787 // RNF122
3876	chr8	-	36823980.00	36824719.00	---
3877	chr8	-	36925372.00	36925478.00	OTTHUMT00000376635 // OTTHUMG00000163982
3878	chr8	-	41164482.00	41164506.00	AK127331 // SFRP1
3879	chr8	-	41555268.00	41555292.00	BX647936 // ANK1
3880	chr8	-	42050633.00	42050657.00	NM_000930 // PLAT
3881	chr8	-	48793981.00	48794005.00	NM_006904 // PRKDC

3882	chr8	-	53555401.00	53555425.00	ENST00000522957 // RB1CC1
3883	chr8	-	54708287.00	54708311.00	NM_015941 // ATP6V1H
3884	chr8	-	77527477.00	77527553.00	ENST00000521894 // ZFHX4-AS1
3885	chr8	-	79633585.00	79633609.00	ENST00000523959 // IL7
3886	chr8	-	82755035.00	82755089.00	ENST00000521810 // SNX16
3887	chr8	-	86244600.00	86244624.00	ENST00000518233 // CA1
3888	chr8	-	97243518.00	97243553.00	NR_045639 // UQCRB
3889	chr8	-	99118190.00	99118234.00	NM_005836 // HRSP12
3890	chr8	-	100905932.00	100906069.00	NM_004374 // COX6C
3891	chr8	-	100999822.00	100999846.00	NM_015668 // RGS22
3892	chr8	-	101648183.00	101648207.00	NM_152628 // SNX31
3893	chr8	-	108913323.00	108913347.00	NM_178565 // RSPO2
3894	chr8	-	109928109.00	109928178.00	---
3895	chr8	-	112195869.00	112195944.00	OTTHUMT00000380896 // OTTHUMG00000164912
3896	chr8	-	113529281.00	113529305.00	NM_198123 // CSMD3
3897	chr8	-	119728710.00	119729230.00	---
3898	chr8	-	119942938.00	119942964.00	ENST00000517352 // TNFRSF11B
3899	chr8	-	121408220.00	121408290.00	NM_014078 // MRPL13
3900	chr8	-	121667202.00	121667247.00	ENST00000519298 // SNTB1
3901	chr8	-	124657868.00	124657978.00	ENST00000325995 // KLHL38
3902	chr8	-	125183681.00	125183763.00	---
3903	chr8	-	128200292.00	128200316.00	---
3904	chr8	-	131922049.00	131922105.00	NM_001115 // ADCY8
3905	chr8	-	131904907.00	131905011.00	---
3906	chr8	-	134050656.00	134050680.00	NM_001045556 // SLA
3907	chr8	-	134052552.00	134052576.00	ENST00000517549 // SLA
3908	chr8	-	135490783.00	135490807.00	NM_020863 // ZFAT
3909	chr8	-	141754842.00	141754866.00	NM_153831 // PTK2
3910	chr8	-	144658642.00	144658666.00	NM_145201 // NAPRT1
3911	chr8	-	144795718.00	144796106.00	---
3912	chr8	-	145658980.00	145659004.00	NM_013432 // TONSL
3913	chr8	-	145690291.00	145690409.00	NM_138496 // CYHR1
3914	chr8	-	146017533.00	146017557.00	ENST00000528957 // RPL8
3915	chr9	+	433886.00	433910.00	NM_203447 // DOCK8
3916	chr9	+	4299390.00	4299420.00	---
3917	chr9	+	7105465.00	7105489.00	ENST00000420847 // KDM4C

3918	chr9	+	18905855.00	18905879.00	NM_001040272 // ADAMTSL1
3919	chr9	+	27245520.00	27245650.00	---
3920	chr9	+	34522265.00	34522347.00	---
3921	chr9	+	35605986.00	35606077.00	NM_006285 // TESK1
3922	chr9	+	42297720.00	42297799.00	---
3923	chr9	+	42713953.00	42713977.00	BC043420 // CBWD5
3924	chr9	+	42873841.00	42873882.00	OTTHUMT00000037065 // AQP7P3
3925	chr9	+	70912688.00	70912712.00	NM_018491 // CBWD1
3926	chr9	+	70913920.00	70913944.00	NM_018491 // CBWD1
3927	chr9	+	74860142.00	74860166.00	NM_001242505 // GDA
3928	chr9	+	89875373.00	89875410.00	---
3929	chr9	+	91090017.00	91090041.00	NM_006717 // SPIN1
3930	chr9	+	91954784.00	91954808.00	NM_024077 // SECISBP2
3931	chr9	+	97562551.00	97562575.00	AK296699 // C9orf3
3932	chr9	+	98861385.00	98861677.00	NR_033838 // LOC158435
3933	chr9	+	100615703.00	100616113.00	NM_004473 // FOXE1
3934	chr9	+	106761843.00	106762088.00	---
3935	chr9	+	108152260.00	108157357.00	ENST00000374720 // SLC44A1
3936	chr9	+	108468010.00	108468034.00	NM_018112 // TMEM38B
3937	chr9	+	112890007.00	112890282.00	ENST00000471798 // PALM2-AKAP2
3938	chr9	+	115249357.00	115249396.00	BC143424 // KIAA1958
3939	chr9	+	116303634.00	116303658.00	NM_017790 // RGS3
3940	chr9	+	119094655.00	119094679.00	NM_002581 // PAPPA
3941	chr9	+	123912448.00	123912472.00	NM_007018 // CNTRL
3942	chr9	+	125027945.00	125028005.00	AK316266 // MRRF
3943	chr9	+	125760958.00	125760982.00	NM_012197 // RABGAP1
3944	chr9	+	127089656.00	127089680.00	NM_001145001 // NEK6
3945	chr9	+	128118105.00	128118129.00	NM_015635 // GAPVD1
3946	chr9	+	129677075.00	129677099.00	NM_014636 // RALGPS1
3947	chr9	+	129979921.00	129979945.00	ENST00000373434 // RALGPS1
3948	chr9	+	130479931.00	130479955.00	NM_144965 // TTC16
3949	chr9	+	131112779.00	131112828.00	NM_005094 // SLC27A4
3950	chr9	+	131260752.00	131260776.00	NM_153435 // ODF2
3951	chr9	+	131367403.00	131367427.00	NM_001130438 // SPTAN1
3952	chr9	+	131583051.00	131583112.00	NM_004435 // ENDOG
3953	chr9	+	132173384.00	132173428.00	---
3954	chr9	+	132632280.00	132632304.00	ENST00000491731 // USP20
3955	chr9	+	135962347.00	135962463.00	NR_001275 // CELP

3956	chr9	+	138393981.00	138394084.00	NR_051968 // MRPS2
3957	chr9	+	138557102.00	138557201.00	NM_001001676 // LCN9
3958	chr9	+	138557514.00	138557540.00	ENST00000430290 // LCN9
3959	chr9	+	139847485.00	139847514.00	BC031600 // LCN12
3960	chr9	+	139876883.00	139877905.00	NM_207510 // LCNL1
3961	chr9	-	267981.00	268266.00	---
3962	chr9	-	3277374.00	3277398.00	NM_002919 // RFX3
3963	chr9	-	5392522.00	5392591.00	ENST00000473877 // PLGRKT
3964	chr9	-	7798602.00	7798637.00	ENST00000358227 // C9orf123
3965	chr9	-	8460517.00	8460541.00	NM_002839 // PTPRD
3966	chr9	-	8528442.00	8528466.00	BC028038 // PTPRD
3967	chr9	-	10612475.00	10612499.00	NM_002839 // PTPRD
3968	chr9	-	14677398.00	14677454.00	ENST00000497966 // ZDHHC21
3969	chr9	-	18420100.00	18420901.00	---
3970	chr9	-	22213279.00	22213345.00	OTTHUMT00000051934 // OTTHUMG00000019692
3971	chr9	-	27291024.00	27291051.00	NM_020641 // EQTN
3972	chr9	-	32988081.00	32988105.00	NR_036576 // APTX
3973	chr9	-	33001526.00	33001562.00	NR_036578 // APTX
3974	chr9	-	34689931.00	34689977.00	NM_006274 // CCL19
3975	chr9	-	35060453.00	35060517.00	NM_007126 // VCP
3976	chr9	-	35074931.00	35075021.00	NM_004629 // FANCG
3977	chr9	-	35563794.00	35563823.00	NM_001164310 // FAM166B
3978	chr9	-	36246076.00	36246230.00	NM_001128227 // GNE
3979	chr9	-	45394211.00	45394290.00	---
3980	chr9	-	47304476.00	47304508.00	ENST00000477002 // CNTNAP3
3981	chr9	-	66712636.00	66712734.00	---
3982	chr9	-	69892795.00	69892893.00	---
3983	chr9	-	70432988.00	70433012.00	NM_018491 // CBWD1
3984	chr9	-	72046244.00	72046268.00	NM_001163 // APBA1
3985	chr9	-	77684384.00	77684408.00	AK023413 // NMRK1
3986	chr9	-	85622365.00	85622409.00	NM_152573 // RASEF
3987	chr9	-	86356869.00	86356940.00	NM_025211 // GKAP1
3988	chr9	-	89561812.00	89562086.00	NM_002048 // GAS1
3989	chr9	-	98569309.00	98576109.00	NR_023390 // LINC00476
3990	chr9	-	99329099.00	99329123.00	NM_001077181 // CDC14B
3991	chr9	-	101558451.00	101558547.00	NM_173551 // ANKS6
3992	chr9	-	103064506.00	103064530.00	NM_017746 // TEX10

3993	chr9	-	111945038.00	111945062.00	NM_019114 // EPB41L4B
3994	chr9	-	113636131.00	113637519.00	NM_001401 // LPAR1
3995	chr9	-	114510407.00	114510431.00	ENST00000394779 // C9orf84
3996	chr9	-	116848463.00	116848487.00	ENST00000498016 // KIF12
3997	chr9	-	117240969.00	117241019.00	NM_015404 // DFNB31
3998	chr9	-	123593613.00	123593705.00	NM_005047 // PSMD5
3999	chr9	-	130581790.00	130581814.00	ENST00000486329 // ENG
4000	chr9	-	131020012.00	131020036.00	---
4001	chr9	-	131446645.00	131446682.00	---
4002	chr9	-	131503052.00	131503096.00	NM_006336 // ZER1
4003	chr9	-	131600012.00	131600087.00	NM_004059 // CCBL1
4004	chr9	-	132500661.00	132501842.00	NM_004878 // PTGES
4005	chr9	-	136208467.00	136208524.00	NM_133640 // MED22
4006	chr9	-	136380615.00	136380706.00	NM_001080483 // TMEM8C
4007	chr9	-	139159846.00	139159873.00	---
4008	chr9	-	139256600.00	139256632.00	NM_001080849 // DNLZ
4009	chr9	-	139341784.00	139341808.00	NM_014866 // SEC16A
4010	chr9	-	139912015.00	139912039.00	NM_001606 // ABCA2
4011	chr9	-	140118567.00	140118591.00	AK128153 // LOC100130547
4012	chrUn	-	122781.00	122866.00	---
4013	chrUn	+	163596.00	163625.00	---
4014	chrUn	-	32006.00	32160.00	---
4015	chrX	+	3002295.00	3002391.00	NM_004042 // ARSF
4016	chrX	+	13587728.00	13587866.00	NM_015507 // EGFL6
4017	chrX	+	13626463.00	13626527.00	NM_015507 // EGFL6
4018	chrX	+	13641959.00	13641983.00	NM_015507 // EGFL6
4019	chrX	+	21659671.00	21659695.00	NM_001168648 // CNKSR2
4020	chrX	+	22132639.00	22132663.00	NM_000444 // PHEX
4021	chrX	+	24197636.00	24197766.00	NM_003410 // ZFX
4022	chrX	+	29417319.00	29417343.00	NM_014271 // IL1RAPL1
4023	chrX	+	37431226.00	37431694.00	NM_198511 // LANCL3
4024	chrX	+	37953575.00	37953655.00	NM_138780 // SYTL5
4025	chrX	+	41307150.00	41307176.00	NM_022567 // NYX
4026	chrX	+	48341223.00	48341271.00	ENST00000593449 // FTSJ1
4027	chrX	+	48372637.00	48372661.00	NM_022825 // PORCN
4028	chrX	+	48925748.00	48925772.00	NM_033626 // CCDC120
4029	chrX	+	49021530.00	49021554.00	ENST00000425661 // MAGIX
4030	chrX	+	49594364.00	49594433.00	AK092503 // PAGE4

4031	chrX	+	49767764.00	49767844.00	NR_030241 // MIR532
4032	chrX	+	65414977.00	65415001.00	NM_138737 // HEPH
4033	chrX	+	68836169.00	68836514.00	NM_001399 // EDA
4034	chrX	+	77267228.00	77267252.00	AB208828 // ATP7A
4035	chrX	+	78010858.00	78011210.00	NM_005296 // LPAR4
4036	chrX	+	79278698.00	79278722.00	NM_001109878 // TBX22
4037	chrX	+	86087134.00	86087158.00	NM_053281 // DACH2
4038	chrX	+	92964492.00	92965164.00	NM_001171110 // FAM133A
4039	chrX	+	99919831.00	99919902.00	NM_014467 // SRPX2
4040	chrX	+	101484393.00	101484417.00	AK057385 // NXF2
4041	chrX	+	102883444.00	102883687.00	NM_001006640 // TCEAL1
4042	chrX	+	106109153.00	106109177.00	NM_017752 // TBC1D8B
4043	chrX	+	106112741.00	106112765.00	NM_017752 // TBC1D8B
4044	chrX	+	107377331.00	107377388.00	NM_052936 // ATG4A
4045	chrX	+	119297694.00	119297910.00	NM_032498 // RHOXF2
4046	chrX	+	123137563.00	123137587.00	ENST00000469481 // STAG2
4047	chrX	+	128699792.00	128699816.00	NM_000276 // OCRL
4048	chrX	+	128880687.00	128880711.00	ENST00000371105 // XPNPEP2
4049	chrX	+	133594199.00	133594246.00	NM_000194 // HPRT1
4050	chrX	+	136651002.00	136651026.00	ENST00000478471 // ZIC3
4051	chrX	+	148857856.00	148858403.00	NM_016153 // HSFX1
4052	chrX	+	149657872.00	149657909.00	---
4053	chrX	+	149905176.00	149905200.00	NM_003828 // MTMR1
4054	chrX	+	150157313.00	150158872.00	NM_005342 // HMGB3
4055	chrX	+	151870295.00	151870646.00	ENST00000329342 // MAGEA6
4056	chrX	+	153009309.00	153009658.00	NM_000033 // ABCD1
4057	chrX	+	153993204.00	153993230.00	NM_001363 // DKC1
4058	chrX	-	10184652.00	10184721.00	---
4059	chrX	-	15365518.00	15365542.00	ENST00000488351 // FIGF
4060	chrX	-	15801341.00	15801601.00	---
4061	chrX	-	18660126.00	18660273.00	NM_000330 // RS1
4062	chrX	-	19013100.00	19013124.00	NM_001079858 // GPR64
4063	chrX	-	20222047.00	20222071.00	ENST00000474266 // RPS6KA3
4064	chrX	-	24580436.00	24580460.00	NM_004845 // PCYT1B
4065	chrX	-	44202794.00	44202821.00	NM_025184 // EFHC2
4066	chrX	-	44401196.00	44401288.00	NM_173794 // FUNDC1
4067	chrX	-	47436838.00	47436873.00	NM_006950 // SYN1
4068	chrX	-	48595460.00	48595554.00	---

4069	chrX	-	49053998.00	49054026.00	AK094376 // SYP
4070	chrX	-	55207870.00	55208183.00	NM_001190708 // MTRNR2L10
4071	chrX	-	68381943.00	68382138.00	NM_145119 // PJA1
4072	chrX	-	70331116.00	70331140.00	BC071710 // IL2RG
4073	chrX	-	72001689.00	72001838.00	NR_034116 // LINC00684
4074	chrX	-	72434333.00	72434404.00	NM_021963 // NAP1L2
4075	chrX	-	83400486.00	83400510.00	NM_014496 // RPS6KA6
4076	chrX	-	100077679.00	100077727.00	---
4077	chrX	-	100265571.00	100265637.00	NM_024917 // TRMT2B
4078	chrX	-	101142177.00	101142266.00	NR_046008 // ZMAT1
4079	chrX	-	101712608.00	101712632.00	AK057385 // NXF2
4080	chrX	-	102977154.00	102977219.00	NM_001024452 // GLRA4
4081	chrX	-	106331759.00	106331783.00	NM_018301 // RBM41
4082	chrX	-	106359899.00	106359987.00	NM_018301 // RBM41
4083	chrX	-	106362022.00	106362057.00	NM_018301 // RBM41
4084	chrX	-	112025776.00	112025874.00	NM_001113490 // AMOT
4085	chrX	-	118676607.00	118676631.00	---
4086	chrX	-	119759582.00	119759964.00	NM_152692 // C1GALT1C1
4087	chrX	-	129272578.00	129272647.00	NM_004208 // AIFM1
4088	chrX	-	129370243.00	129370267.00	NM_017666 // ZNF280C
4089	chrX	-	129394398.00	129394423.00	NM_017666 // ZNF280C
4090	chrX	-	129645265.00	129645357.00	---
4091	chrX	-	133678492.00	133678655.00	ENST00000457876 // MIR503HG
4092	chrX	-	134654496.00	134654588.00	ENST00000596340 // DDX26B-AS1
4093	chrX	-	138809487.00	138809511.00	NM_173694 // ATP11C
4094	chrX	-	148593125.00	148593149.00	---
4095	chrX	-	151306986.00	151307021.00	NM_001011543 // MAGEA10
4096	chrX	-	151620165.00	151620257.00	ENST00000370311 // GABRA3
4097	chrX	-	153095001.00	153095039.00	ENST00000597323 // PDZD4
4098	chrX	-	154132309.00	154132333.00	NM_000132 // F8
4099	chrY	+	9236094.00	9236118.00	NM_003308 // TSPY1
4100	chrY	+	19671654.00	19671747.00	ENST00000516203 // RNA5SP521
4101	chrY	+	21754554.00	21754692.00	AL832583 // TXLNG2P
4102	chrY	+	27605444.00	27605513.00	NR_001555 // GOLGA2P2Y
4103	chrY	-	2368447.00	2368525.00	NM_001171135 // ZBED1
4104	chrY	-	9355964.00	9357201.00	---

4105	chrY	-	20508031.00	20508124.00	---
4106	chrY	-	23751866.00	23752013.00	---
4107	chrY	-	24443082.00	24443859.00	NR_001541 // TTTY5
4108	chrY	-	26356923.00	26356992.00	NR_001555 // GOLGA2P2Y
4109	chr1	+	224197038.00	224197157.00	AK290103 // LOC100287934
4110	chr17	-	79348701.00	79348725.00	---
4111	chr22	+	30831716.00	30831997.00	AY358802 // LOC646513
4112	chr4	+	77906546.00	77907520.00	AY358789 // LOC100131826
4113	chr6	+	168195981.00	168198876.00	AK125190 // LOC441179
4114	chr8	+	9638020.00	9638472.00	NM_003747 // TNKS
4115	chrY	+	21754554.00	21754692.00	AL832583 // TXLNG2P
4116	chrU	+	72.00	99.00	---
4117	chrU	+	1.00	34.00	---
4118	chrU	+	1.00	68.00	---
4119	chrU	+	35.00	892.00	---
4120	chrU	+	2139.00	2397.00	---
4121	chrU	+	56.00	403.00	---
4122	chrU	+	7.00	412.00	---
4123	chrU	+	111.00	1096.00	---
4124	chrU	+	312.00	649.00	---
4125	chrU	+	22.00	344.00	---
4126	chrU	+	41.00	208.00	---
4127	chrU	+	14.00	700.00	---
4128	chrU	+	34.00	419.00	---
4129	chrU	+	61.00	833.00	---
4130	chrU	+	10.00	260.00	---
4131	chrU	+	36.00	468.00	---
4132	chrU	+	24.00	329.00	---
4133	chrU	+	55.00	884.00	---
4134	chrU	+	1.00	452.00	---
4135	chrU	+	64.00	2441.00	---
4136	chrU	+	64.00	2441.00	---
4137	chrU	+	86.00	373.00	---
4138	chrU	+	86.00	373.00	---
4139	chrU	+	36.00	739.00	---
4140	chrU	+	36.00	739.00	---

Table 6 – Exon regions of a set of genes in male subjects

Gene Number	Gene location	Strand	strand start	strand stop	Assigned gene info.
4141	chr1	+	31031	31102	ENST00000422679 // MIR1302-11
4142	chr1	+	557158	557195	---
4143	chr1	+	860301	860325	ENST00000420190 // SAMD11
4144	chr1	+	898519	898543	NM_198317 // KLHL17
4145	chr1	+	911095	911203	OTTHUMT00000097942 // PLEKHN1
4146	chr1	+	981194	981218	NM_198576 // AGRN
4147	chr1	+	984716	984740	NM_198576 // AGRN
4148	chr1	+	1262713	1263106	NM_001029885 // GLTPD1
4149	chr1	+	1372726	1372810	NM_022834 // VWA1
4150	chr1	+	1385317	1385388	NM_001039211 // ATAD3C
4151	chr1	+	1543079	1543119	AK094692 // LOC284628
4152	chr1	+	1558999	1559023	NM_080875 // MIB2
4153	chr1	+	1959606	1959727	NM_000815 // GABRD
4154	chr1	+	2426362	2426386	NM_014638 // PLCH2
4155	chr1	+	2564034	2564094	---
4156	chr1	+	3541640	3541665	NM_182752 // TPRG1L
4157	chr1	+	4012359	4014791	NR_040065 // LOC728716
4158	chr1	+	4834591	4834618	NM_018836 // AJAP1
4159	chr1	+	6638993	6639022	NM_138697 // TAS1R1
4160	chr1	+	6880247	6880271	NM_015215 // CAMTA1
4161	chr1	+	7430207	7430283	OTTHUMT00000003610 // CAMTA1-IT1
4162	chr1	+	8396140	8396169	ENST00000481265 // SLC45A1
4163	chr1	+	9415768	9415793	ENST00000377399 // SPSB1
4164	chr1	+	9671844	9671904	NM_001130924 // TMEM201
4165	chr1	+	10683274	10683332	AK310726 // PEX14
4166	chr1	+	12439570	12439594	NM_015378 // VPS13D
4167	chr1	+	13922361	13922421	AK307706 // PDPN
4168	chr1	+	14042048	14042085	NM_012231 // PRDM2
4169	chr1	+	15860772	15860796	NM_015291 // DNAJC16
4170	chr1	+	16348369	16348393	BC053869 // CLCNKA
4171	chr1	+	17575639	17575671	NM_016233 // PADI3
4172	chr1	+	17603085	17603109	NM_016233 // PADI3
4173	chr1	+	20411334	20411363	NM_000929 // PLA2G5
4174	chr1	+	22336288	22336312	NM_005747 // CELA3A
4175	chr1	+	22919823	22919847	NM_020526 // EPHA8
4176	chr1	+	22924244	22924268	NM_020526 // EPHA8
4177	chr1	+	23046020	23046072	NR_039832 // MIR4684
4178	chr1	+	24070572	24070670	ENST00000487554 // TCEB3

4179	chr1	+	24973253	24973277	NM_005839 // SRRM1
4180	chr1	+	25350004	25350066	NR_039623 // MIR4425
4181	chr1	+	25889465	25889547	AK309853 // LDLRAP1
4182	chr1	+	25893389	25893413	NM_015627 // LDLRAP1
4183	chr1	+	26137973	26137997	NM_020451 // SEPN1
4184	chr1	+	26883177	26883201	NM_002953 // RPS6KA1
4185	chr1	+	27101082	27101106	NM_006015 // ARID1A
4186	chr1	+	27189975	27190002	NM_006142 // SFN
4187	chr1	+	27624567	27624591	NM_001276252 // WDTC1
4188	chr1	+	27679800	27679824	NM_001193308 // SYTL1
4189	chr1	+	28607834	28607858	NM_031459 // SESN2
4190	chr1	+	29189391	29189415	NM_000911 // OPRD1
4191	chr1	+	29631288	29631312	NM_133178 // PTPRU
4192	chr1	+	32083444	32083468	NM_001525 // HCRTR1
4193	chr1	+	32508268	32508312	NM_006559 // KHDRBS1
4194	chr1	+	33828673	33828818	---
4195	chr1	+	33955176	33955200	NM_145238 // ZSCAN20
4196	chr1	+	35661576	35661663	---
4197	chr1	+	36040558	36040601	NM_178548 // TFAP2E
4198	chr1	+	36439133	36439157	ENST00000491443 // AGO3
4199	chr1	+	36552557	36552645	NM_014466 // TEKT2
4200	chr1	+	36793381	36793405	AY240960 // LOC100127947
4201	chr1	+	37627174	37627220	NR_036217 // MIR4255
4202	chr1	+	37940151	37940175	NM_025079 // ZC3H12A
4203	chr1	+	40431586	40431686	NM_001136493 // MFSD2A
4204	chr1	+	40667609	40667633	ENST00000487606 // RLF
4205	chr1	+	41468821	41468845	NM_001905 // CTPS1
4206	chr1	+	43770579	43770603	NM_005424 // TIE1
4207	chr1	+	43803572	43803598	NM_005373 // MPL
4208	chr1	+	43896949	43896973	NM_015284 // SZT2
4209	chr1	+	43900088	43900112	NM_015284 // SZT2
4210	chr1	+	43905415	43905439	NM_015284 // SZT2
4211	chr1	+	44044538	44044562	NM_002840 // PTPRF
4212	chr1	+	44366424	44366448	AK301829 // ST3GAL3
4213	chr1	+	44386485	44386509	NM_174963 // ST3GAL3
4214	chr1	+	44443475	44443574	BC053601 // ATP6V0B
4215	chr1	+	44684068	44684092	NM_019100 // DMAP1
4216	chr1	+	44684284	44684308	NM_019100 // DMAP1
4217	chr1	+	44877893	44877917	NM_018150 // RNF220
4218	chr1	+	45242359	45242385	NM_001012 // RPS8
4219	chr1	+	45271627	45271651	NM_004073 // PLK3
4220	chr1	+	45276370	45276394	AB209875 // PLK3

4221	chr1	+	46910932	46911315	NR_045483 // LOC729041
4222	chr1	+	47280864	47280888	NM_001099772 // CYP4B1
4223	chr1	+	47489528	47489552	NM_178033 // CYP4X1
4224	chr1	+	48226301	48226918	---
4225	chr1	+	48701486	48701510	NM_001135181 // SLC5A9
4226	chr1	+	49617083	49617132	---
4227	chr1	+	52729459	52729530	NM_007324 // ZFYVE9
4228	chr1	+	52877116	52877194	---
4229	chr1	+	53927153	53927307	NM_033067 // DMRTB1
4230	chr1	+	54356921	54356945	ENST00000534069 // DIO1
4231	chr1	+	54991059	54991126	---
4232	chr1	+	55136523	55136547	NR_037639 // HEATR8-TTC4
4233	chr1	+	56483432	56483473	---
4234	chr1	+	57174480	57174998	NM_006252 // PRKAA2
4235	chr1	+	65296544	65296618	NM_018211 // RAVER2
4236	chr1	+	65613356	65613383	AK309057 // AK4
4237	chr1	+	65614792	65614823	ENST00000474968 // LOC100507855
4238	chr1	+	66074446	66074470	NM_002303 // LEPR
4239	chr1	+	68297991	68298080	NR_040077 // GNG12-AS1
4240	chr1	+	68565419	68565443	NR_040077 // GNG12-AS1
4241	chr1	+	71413125	71413151	---
4242	chr1	+	71867530	71867556	ENST00000599146 // ZRANB2-AS2
4243	chr1	+	74797134	74797158	NM_015978 // TNNI3K
4244	chr1	+	75204430	75204454	NM_138467 // TYW3
4245	chr1	+	75602880	75602916	NM_001001933 // LHX8
4246	chr1	+	75648795	75648828	---
4247	chr1	+	76531727	76531902	OTTHUMT00000026986 // OTTHUMG00000009791
4248	chr1	+	78024589	78024613	NM_174858 // AK5
4249	chr1	+	78332029	78332056	NM_198549 // FAM73A
4250	chr1	+	84767300	84767412	NM_001134663 // SAMD13
4251	chr1	+	84855567	84855614	OTTHUMT00000027247 // SAMD13
4252	chr1	+	85537642	85537666	NM_145172 // WDR63
4253	chr1	+	92417758	92417782	NM_001726 // BRDT
4254	chr1	+	93298579	93298816	AK095815 // RPL5
4255	chr1	+	94921336	94921360	AK296791 // ABCD3
4256	chr1	+	95149016	95149096	---
4257	chr1	+	95712525	95712665	NR_037643 // RWDD3
4258	chr1	+	95978079	95978160	BC067883 // LOC100996635
4259	chr1	+	100598739	100598763	NM_019083 // TRMT13
4260	chr1	+	101598727	101598867	---

4261	chr1	+	101705548	101705661	NM_001400 // S1PR1
4262	chr1	+	109816012	109816036	AK127086 // CELSR2
4263	chr1	+	110088116	110088560	ENST00000527748 // GPR61
4264	chr1	+	110140124	110140384	---
4265	chr1	+	110166637	110166661	NM_001257361 // AMPD2
4266	chr1	+	110215983	110216007	---
4267	chr1	+	111859735	111859995	AK098814 // CHIA
4268	chr1	+	112738132	112738165	---
4269	chr1	+	114223934	114223958	NM_001142782 // MAGI3
4270	chr1	+	117249090	117249118	ENST00000369482 // C1orf137
4271	chr1	+	117297596	117297629	ENST00000369477 // CD2
4272	chr1	+	119897040	119897085	OTTHUMT00000034530 // OTTHUMG00000012409
4273	chr1	+	120143921	120143952	---
4274	chr1	+	120935645	120935756	---
4275	chr1	+	144339817	144340319	BC150590 // LOC100132999
4276	chr1	+	144520647	144520693	BC150590 // LOC100132999
4277	chr1	+	145415288	145415313	NM_213653 // HFE2
4278	chr1	+	146093278	146093439	BC033999 // LOC100506011
4279	chr1	+	150486061	150486085	NM_004425 // ECM1
4280	chr1	+	150589446	150589775	---
4281	chr1	+	150917749	150917773	NM_001243491 // SETDB1
4282	chr1	+	150938340	150938381	---
4283	chr1	+	151227196	151227220	ENST00000368884 // PSMD4
4284	chr1	+	151512809	151512833	NM_020127 // TUFT1
4285	chr1	+	152635877	152635905	ENST00000368784 // LCE2D
4286	chr1	+	153600591	153600615	ENST00000368698 // S100A1
4287	chr1	+	154230249	154230273	ENST00000489076 // UBAP2L
4288	chr1	+	154235852	154235876	NM_001127320 // UBAP2L
4289	chr1	+	154247524	154247548	AK294298 // HAX1
4290	chr1	+	154950156	154950326	ENST00000471245 // CKS1B
4291	chr1	+	154951596	154951641	NM_001826 // CKS1B
4292	chr1	+	154962105	154962129	NM_025207 // FLAD1
4293	chr1	+	155106000	155106024	NM_004428 // EFNA1
4294	chr1	+	155106077	155106183	ENST00000469878 // EFNA1
4295	chr1	+	155152122	155152220	NR_046327 // TRIM46
4296	chr1	+	155253790	155253814	NM_020897 // HCN3
4297	chr1	+	155583219	155583243	NR_046294 // MSTO1
4298	chr1	+	156119533	156119557	ENST00000414683 // SEMA4A
4299	chr1	+	156556381	156556461	NM_001105669 // TTC24
4300	chr1	+	156616899	156616940	NM_021948 // BCAN
4301	chr1	+	156617368	156617425	NM_021948 // BCAN

4302	chr1	+	156894743	156894771	NM_144702 // LRRC71
4303	chr1	+	159752169	159752315	NM_017823 // DUSP23
4304	chr1	+	160914890	160914985	---
4305	chr1	+	161677091	161677117	NM_001184866 // FCRLA
4306	chr1	+	163041970	163041994	AB209019 // RGS4
4307	chr1	+	165187652	165187732	---
4308	chr1	+	165620268	165620321	NM_004528 // MGST3
4309	chr1	+	165623563	165623587	NM_004528 // MGST3
4310	chr1	+	165859442	165859559	NM_012474 // UCK2
4311	chr1	+	167341177	167341201	NM_002697 // POU2F1
4312	chr1	+	167381510	167381534	NM_002697 // POU2F1
4313	chr1	+	167654715	167654741	NM_052862 // RCSD1
4314	chr1	+	171783658	171783739	---
4315	chr1	+	172629235	172629268	NM_000639 // FASLG
4316	chr1	+	173842705	173842741	NM_032522 // ZBTB37
4317	chr1	+	175049320	175049545	NM_022093 // TNN
4318	chr1	+	176197330	176197360	---
4319	chr1	+	176759079	176759103	NM_020318 // PAPPA2
4320	chr1	+	176814094	176814118	ENST00000367662 // PAPPA2
4321	chr1	+	178063628	178063652	NM_170692 // RASAL2
4322	chr1	+	178490359	178490383	NM_032126 // TEX35
4323	chr1	+	179292573	179292597	NM_003101 // SOAT1
4324	chr1	+	179335564	179335588	NR_073544 // AXDND1
4325	chr1	+	180053281	180053305	NM_014810 // CEP350
4326	chr1	+	180123992	180124021	NM_002826 // QSOX1
4327	chr1	+	181740706	181740780	ENST00000517168 // RNA5SP70
4328	chr1	+	183601738	183602287	---
4329	chr1	+	186052049	186052073	NM_031935 // HMCN1
4330	chr1	+	186420763	186420835	---
4331	chr1	+	190462981	190463193	OTTHUMT00000097707 // OTTHUMG00000040635
4332	chr1	+	197413883	197413907	ENST00000367397 // CRB1
4333	chr1	+	198953846	198954524	OTTHUMT00000087439 // OTTHUMG00000035890
4334	chr1	+	200012943	200013013	NM_205860 // NR5A2
4335	chr1	+	201294137	201294198	NM_001005337 // PKP1
4336	chr1	+	201777767	201777828	NR_031599 // MIR1231
4337	chr1	+	201804083	201804107	ENST00000464348 // IPO9
4338	chr1	+	201858154	201858184	NM_198149 // SHISA4
4339	chr1	+	201932764	201932856	NM_006335 // TIMM17A
4340	chr1	+	202152702	202152730	NR_002930 // PTPRVP
4341	chr1	+	202397797	202397821	ENST00000488330 // PPP1R12B

4342	chr1	+	203045691	203045715	NM_015053 // PPFIA4
4343	chr1	+	203444913	203445044	NM_002725 // PRELP
4344	chr1	+	203738776	203738809	ENST00000367215 // LAX1
4345	chr1	+	204083454	204083553	NM_005686 // SOX13
4346	chr1	+	204086723	204086756	NM_005686 // SOX13
4347	chr1	+	204092279	204092303	NM_005686 // SOX13
4348	chr1	+	204942452	204942476	NM_001005388 // NFASC
4349	chr1	+	205033574	205033598	NM_005076 // CNTN2
4350	chr1	+	205569535	205569588	NM_181644 // MFSD4
4351	chr1	+	206650059	206650083	NM_014002 // IKBKE
4352	chr1	+	207245602	207245626	NM_006212 // PFKFB2
4353	chr1	+	207963601	207963625	NM_002389 // CD46
4354	chr1	+	207968761	207968785	NM_002389 // CD46
4355	chr1	+	209786666	209786690	NM_020439 // CAMK1G
4356	chr1	+	212274092	212274116	NM_016448 // DTL
4357	chr1	+	215368315	215368351	NM_001017424 // KCNK2
4358	chr1	+	219347340	219347535	ENST00000483635 // LYPLAL1
4359	chr1	+	224804902	224804926	NM_152495 // CNIH3
4360	chr1	+	226277937	226277963	---
4361	chr1	+	227171380	227171404	AK126200 // ADCK3
4362	chr1	+	228327712	228327736	ENST00000366730 // GUK1
4363	chr1	+	228336399	228336423	NM_001159390 // GUK1
4364	chr1	+	228462103	228462127	NM_052843 // OBSCN
4365	chr1	+	228479655	228479679	NM_052843 // OBSCN
4366	chr1	+	228544762	228544807	---
4367	chr1	+	230728416	230728565	---
4368	chr1	+	230928199	230928228	NM_006615 // CAPN9
4369	chr1	+	234745175	234745211	---
4370	chr1	+	236987492	236987516	NM_000254 // MTR
4371	chr1	+	237944918	237944942	NM_001035 // RYR2
4372	chr1	+	237951350	237951374	NM_001035 // RYR2
4373	chr1	+	237969500	237969524	NM_001035 // RYR2
4374	chr1	+	238648819	238648873	---
4375	chr1	+	242045243	242045279	NM_006027 // EXO1
4376	chr1	+	244747175	244747199	ENST00000366534 // C1orf101
4377	chr1	+	244773807	244773831	AK027205 // C1orf101
4378	chr1	+	245133305	245133329	NR_026586 // EFCAB2
4379	chr1	+	247607232	247607257	ENST00000532083 // NLRP3
4380	chr1	+	247729233	247729259	NM_145278 // GCSAML
4381	chr1	+	248100578	248100658	NM_175911 // OR2L13
4382	chr1	+	248153597	248153636	NR_002145 // OR2L1P
4383	chr1	+	248636953	248637456	---

4384	chr1	+	248676192	248676317	---
4385	chr1	+	249139789	249139813	NM_024836 // ZNF672
4386	chr1	-	16622	16762	NR_024077 // WASH2P
4387	chr1	-	543335	543420	---
4388	chr1	-	1148373	1148447	NM_003327 // TNFRSF4
4389	chr1	-	1148888	1148983	BC040257 // TNFRSF4
4390	chr1	-	1178463	1178487	NM_001014980 // FAM132A
4391	chr1	-	1234987	1235011	AK093954 // ACAP3
4392	chr1	-	1244934	1244958	AK093954 // ACAP3
4393	chr1	-	1274757	1274787	NM_004421 // DVL1
4394	chr1	-	1685653	1685677	AK095043 // NADK
4395	chr1	-	1849696	1849829	NM_178545 // TMEM52
4396	chr1	-	1858129	1858153	BC114926 // C1orf222
4397	chr1	-	1981429	1981558	---
4398	chr1	-	2143759	2143783	---
4399	chr1	-	2424559	2424691	---
4400	chr1	-	2449630	2449654	NM_018216 // PANK4
4401	chr1	-	2575870	2575894	NM_001242672 // TTC34
4402	chr1	-	2979261	2979594	NR_015440 // FLJ42875
4403	chr1	-	3655373	3655744	NR_033711 // TP73-AS1
4404	chr1	-	3656826	3656850	NR_033711 // TP73-AS1
4405	chr1	-	4008933	4009025	---
4406	chr1	-	6186658	6186682	NM_015557 // CHD5
4407	chr1	-	6203887	6203911	NM_015557 // CHD5
4408	chr1	-	6525225	6525249	NM_148965 // TNFRSF25
4409	chr1	-	6713908	6713932	ENST00000485073 // DNAJC11
4410	chr1	-	8280472	8280575	OTTHUMT00000004931 // OTTHUMG00000001770
4411	chr1	-	8421520	8421544	NM_012102 // RERE
4412	chr1	-	9070202	9070258	NM_207420 // SLC2A7
4413	chr1	-	9165592	9165644	NM_024980 // GPR157
4414	chr1	-	9189011	9189040	NM_024980 // GPR157
4415	chr1	-	9713863	9713992	NR_027045 // C1orf200
4416	chr1	-	11086701	11086938	NM_006610 // MASP2
4417	chr1	-	11175673	11175697	ENST00000455339 // MTOR
4418	chr1	-	12640097	12640542	ENST00000482265 // DHRS3
4419	chr1	-	13388756	13388804	NM_001012276 // PRAMEF8
4420	chr1	-	13448259	13448300	NM_001024661 // PRAMEF13
4421	chr1	-	16268436	16268460	NM_001242884 // ZBTB17
4422	chr1	-	16270345	16270369	NM_001242884 // ZBTB17
4423	chr1	-	17345386	17345444	NM_003000 // SDHB
4424	chr1	-	19472488	19472512	ENST00000465036 // UBR4

4425	chr1	-	20501639	20501665	NM_001105572 // PLA2G2C
4426	chr1	-	21503339	21503363	NM_001198801 // EIF4G3
4427	chr1	-	22160371	22160395	NM_005529 // HSPG2
4428	chr1	-	22165349	22165373	NM_005529 // HSPG2
4429	chr1	-	22216922	22216946	NM_005529 // HSPG2
4430	chr1	-	23337327	23337594	ENST00000440767 // LOC729059
4431	chr1	-	23730181	23730441	ENST00000374601 // TCEA3
4432	chr1	-	24742599	24742623	ENST00000468303 // STPG1
4433	chr1	-	25557773	25558446	ENST00000476231 // SYF2
4434	chr1	-	25737942	25737969	OTTHUMT00000101974 // RHCE
4435	chr1	-	26288513	26288563	NM_000437 // PAFAH2
4436	chr1	-	26365537	26365642	NM_001004434 // SLC30A2
4437	chr1	-	26496855	26497028	---
4438	chr1	-	26673166	26673190	NM_001039775 // AIM1L
4439	chr1	-	26691388	26691697	NM_001114759 // ZNF683
4440	chr1	-	26920431	26920528	---
4441	chr1	-	27430280	27430304	AK124218 // SLC9A1
4442	chr1	-	27691328	27691352	NM_004672 // MAP3K6
4443	chr1	-	28907628	28907677	AF277181 // SNHG12
4444	chr1	-	31934171	31934242	---
4445	chr1	-	32124152	32124176	NM_001856 // COL16A1
4446	chr1	-	32224274	32224319	NR_036216 // MIR4254
4447	chr1	-	32256825	32256849	NM_144569 // SPOCD1
4448	chr1	-	32263946	32263970	ENST00000460061 // SPOCD1
4449	chr1	-	32816213	32816264	OTTHUMT00000020212 // OTTHUMG00000007633
4450	chr1	-	33360964	33361017	NM_033504 // TMEM54
4451	chr1	-	33802196	33802311	---
4452	chr1	-	35900631	35900655	NM_024874 // KIAA0319L
4453	chr1	-	37282834	37282858	NM_000831 // GRIK3
4454	chr1	-	38032556	38032580	NM_013285 // GNL2
4455	chr1	-	39391880	39391931	AK097621 // RHBDL2
4456	chr1	-	40319472	40319608	AK304759 // TRIT1
4457	chr1	-	40783370	40783394	BC065715 // COL9A2
4458	chr1	-	40958957	40959360	---
4459	chr1	-	41107407	41107559	NM_014747 // RIMS3
4460	chr1	-	41154797	41157855	NR_024567 // LOC100130557
4461	chr1	-	42776740	42776764	NM_014947 // FOXJ3
4462	chr1	-	42915653	42915677	NM_032257 // ZMYND12
4463	chr1	-	43222072	43222096	AF097431 // LEPRE1
4464	chr1	-	44457358	44457382	OTTHUMT00000386657 // SLC6A9
4465	chr1	-	45297436	45297460	NM_003738 // PTCH2

4466	chr1	-	45516900	45516924	NM_020883 // ZSWIM5
4467	chr1	-	46152741	46152765	---
4468	chr1	-	46655199	46655223	NM_017739 // POMGNT1
4469	chr1	-	46744150	46744226	NM_006369 // LRRC41
4470	chr1	-	47656459	47656710	ENST00000371885 // PDZK1IP1
4471	chr1	-	47765456	47765480	ENST00000433827 // STIL
4472	chr1	-	48865076	48865132	NM_019073 // SPATA6
4473	chr1	-	50917605	50917629	AK094843 // FAF1
4474	chr1	-	50957396	50957420	NM_007051 // FAF1
4475	chr1	-	51768187	51768211	NM_001144832 // TTC39A
4476	chr1	-	52494258	52494282	NM_015913 // TXNDC12
4477	chr1	-	52823257	52823281	NM_032449 // CC2D1B
4478	chr1	-	52896708	52896732	NM_001009881 // ZCCHC11
4479	chr1	-	53377273	53377297	NM_001198961 // ECHDC2
4480	chr1	-	53708129	53708153	NM_004631 // LRP8
4481	chr1	-	54332452	54332516	NR_036639 // YIPF1
4482	chr1	-	62784854	62784880	NM_181712 // KANK4
4483	chr1	-	63466311	63466465	OTTHUMT00000025348 // OTTHUMG00000009147
4484	chr1	-	63787400	63787750	---
4485	chr1	-	64002387	64002418	---
4486	chr1	-	75102042	75102102	ENST00000326665 // C1orf173
4487	chr1	-	79472382	79472406	NM_022159 // ELTD1
4488	chr1	-	85036268	85036308	NM_004388 // CTBS
4489	chr1	-	85136471	85136495	NM_001166417 // SSX2IP
4490	chr1	-	88939791	88939830	---
4491	chr1	-	89571866	89572735	ENST00000464839 // GBP2
4492	chr1	-	89573768	89573847	NM_004120 // GBP2
4493	chr1	-	94027513	94027537	NM_001261408 // BCAR3
4494	chr1	-	94037342	94037366	NM_001261408 // BCAR3
4495	chr1	-	94522231	94522255	NM_000350 // ABCA4
4496	chr1	-	95367343	95367396	ENST00000461018 // CNN3
4497	chr1	-	95670653	95670683	---
4498	chr1	-	96839638	96839681	---
4499	chr1	-	101491301	101491325	NM_001077394 // DPH5
4500	chr1	-	102194198	102194271	---
4501	chr1	-	102462316	102462371	NM_058170 // OLFM3
4502	chr1	-	103385882	103385906	NM_001854 // COL11A1
4503	chr1	-	109608762	109608836	NM_005645 // TAF13
4504	chr1	-	109935683	109935707	NM_001205228 // SORT1
4505	chr1	-	111217450	111217563	NM_002232 // KCNA3
4506	chr1	-	111660155	111660244	NM_178454 // DRAM2

4507	chr1	-	111668036	111668169	ENST00000490780 // DRAM2
4508	chr1	-	111957393	111957904	NM_002557 // OVGP1
4509	chr1	-	112045864	112045964	NM_020683 // ADORA3
4510	chr1	-	115280156	115280180	NM_001007553 // CSDE1
4511	chr1	-	116311348	116311413	NM_001232 // CASQ2
4512	chr1	-	116935510	116935632	AK309389 // ATP1A1OS
4513	chr1	-	117061762	117061811	NM_001144822 // CD58
4514	chr1	-	119474369	119474452	NM_152380 // TBX15
4515	chr1	-	120295200	120295244	NM_005518 // HMGCS2
4516	chr1	-	120336925	120336998	NM_001159352 // REG4
4517	chr1	-	143186909	143186933	---
4518	chr1	-	144364176	144364226	NM_178230 // PPIAL4A
4519	chr1	-	147752774	147752851	---
4520	chr1	-	147955354	147955395	NM_178230 // PPIAL4A
4521	chr1	-	149146739	149146810	---
4522	chr1	-	149576969	149577088	OTTHUMT00000039131 // OTTHUMG00000013949
4523	chr1	-	149691562	149691603	---
4524	chr1	-	149880746	149880816	NM_014849 // SV2A
4525	chr1	-	149900883	149900907	NM_001145862 // MTMR11
4526	chr1	-	149916407	149916873	NM_020205 // OTUD7B
4527	chr1	-	150599613	150599774	NM_207168 // ENSA
4528	chr1	-	150670711	150670997	NM_032132 // HORMAD1
4529	chr1	-	151108067	151108091	NM_001178061 // SEMA6C
4530	chr1	-	151825919	151826019	NM_182578 // THEM5
4531	chr1	-	152984962	152985076	---
4532	chr1	-	153935504	153935534	BC047288 // SLC39A1
4533	chr1	-	154180958	154180993	ENST00000483282 // C1orf43
4534	chr1	-	154574935	154574959	NM_001111 // ADAR
4535	chr1	-	154924366	154924390	NM_020524 // PBXIP1
4536	chr1	-	155243275	155243306	ENST00000368361 // CLK2
4537	chr1	-	155327465	155327489	NM_018489 // ASH1L
4538	chr1	-	155721794	155721818	NM_001037533 // GON4L
4539	chr1	-	155990077	155990101	ENST00000526212 // SSR2
4540	chr1	-	156390155	156390199	NR_029691 // MIR9-1
4541	chr1	-	156475981	156476014	---
4542	chr1	-	156926223	156926247	NM_014784 // ARHGEF11
4543	chr1	-	157485769	157485793	AL832301 // FCRL5
4544	chr1	-	157544671	157544695	NM_031282 // FCRL4
4545	chr1	-	159504810	159504861	ENST00000334857 // OR10J5
4546	chr1	-	159682792	159683123	NM_000567 // CRP
4547	chr1	-	159828677	159828701	NM_001013661 // VSIG8

4548	chr1	-	160232102	160232186	NR_028103 // DCAF8
4549	chr1	-	160991199	160991257	ENST00000289779 // F11R
4550	chr1	-	161023076	161023133	NM_001025598 // ARHGAP30
4551	chr1	-	161059280	161059354	NM_030916 // PVRL4
4552	chr1	-	161092979	161093005	NM_032998 // DEDD
4553	chr1	-	161205532	161205601	BC030972 // NR1I3
4554	chr1	-	161644444	161644556	---
4555	chr1	-	162345080	162345190	ENST00000367935 // C1orf111
4556	chr1	-	164881558	164881704	---
4557	chr1	-	165543284	165543322	ENST00000438275 // LOC400794
4558	chr1	-	167059483	167059509	NM_005814 // GPA33
4559	chr1	-	167803227	167803251	NM_018417 // ADCY10
4560	chr1	-	169437929	169437987	NM_006996 // SLC19A2
4561	chr1	-	169446664	169446843	NM_006996 // SLC19A2
4562	chr1	-	173019898	173019989	NM_005092 // TNFSF18
4563	chr1	-	173629236	173629336	---
4564	chr1	-	173772247	173772342	NM_001127181 // CENPL
4565	chr1	-	175873937	175874215	OTTHUMT00000084671 // OTTHUMG00000034985
4566	chr1	-	176926897	176926921	NM_004319 // ASTN1
4567	chr1	-	177916972	177916996	NM_033127 // SEC16B
4568	chr1	-	179545058	179545085	NM_014625 // NPHS2
4569	chr1	-	180257455	180257488	NM_032360 // ACBD6
4570	chr1	-	182638785	182638851	NM_001102450 // RGS8
4571	chr1	-	185089939	185089963	ENST00000465827 // TRMT1L
4572	chr1	-	186644609	186644721	ENST00000466691 // PTGS2
4573	chr1	-	186645363	186645560	AY151286 // PTGS2
4574	chr1	-	193654711	193654873	OTTHUMT00000086757 // OTTHUMG00000035685
4575	chr1	-	197036357	197036385	NM_001994 // F13B
4576	chr1	-	197521910	197521934	NM_144977 // DENND1B
4577	chr1	-	198868929	198869328	EF413001 // MIR181A1HG
4578	chr1	-	198906415	198906539	NR_040073 // MIR181A1HG
4579	chr1	-	201122923	201122947	ENST00000414605 // TMEM9
4580	chr1	-	202698185	202698209	NM_006618 // KDM5B
4581	chr1	-	203053783	203053853	NM_002479 // MYOG
4582	chr1	-	203143616	203143640	NM_004997 // MYBPH
4583	chr1	-	204120213	204120404	OTTHUMT00000329575 // ETNK2
4584	chr1	-	204237386	204237410	NM_014935 // PLEKHA6
4585	chr1	-	204590403	204590427	ENST00000367175 // LRRN2
4586	chr1	-	205275379	205275434	ENST00000367157 // NUAK2
4587	chr1	-	207083111	207083139	NM_005449 // FAIM3

4588	chr1	-	207139273	207139297	ENST00000324863 // FCAMR
4589	chr1	-	207212077	207212111	---
4590	chr1	-	208219352	208219376	NM_025179 // PLXNA2
4591	chr1	-	208224684	208224708	NM_025179 // PLXNA2
4592	chr1	-	209804021	209804045	NM_000228 // LAMB3
4593	chr1	-	212118195	212118219	NM_015434 // INTS7
4594	chr1	-	213188528	213188562	AK299208 // ANGEL2
4595	chr1	-	216108042	216108066	NM_206933 // USH2A
4596	chr1	-	216221914	216221938	NM_206933 // USH2A
4597	chr1	-	216978629	216978653	NM_001243514 // ESRRG
4598	chr1	-	219255007	219255185	NR_038845 // LOC643723
4599	chr1	-	220195781	220195805	NM_004446 // EPRS
4600	chr1	-	223971948	223971972	NM_001031685 // TP53BP2
4601	chr1	-	224001915	224001939	ENST00000472180 // TP53BP2
4602	chr1	-	226043591	226043615	NM_014698 // TMEM63A
4603	chr1	-	228109321	228109614	NM_003395 // WNT9A
4604	chr1	-	228582917	228582941	NM_145214 // TRIM11
4605	chr1	-	229667528	229667552	ENST00000486755 // ABCB10
4606	chr1	-	230912629	230912733	---
4607	chr1	-	231124824	231124865	---
4608	chr1	-	235992301	235992325	NR_102436 // LYST
4609	chr1	-	245778076	245778171	---
4610	chr1	-	246093176	246093200	NM_001167740 // SMYD3
4611	chr1	-	247012990	247013014	NM_015446 // AHCTF1
4612	chr1	-	247335242	247335289	NM_003431 // ZNF124
4613	chr1	-	247472103	247472502	AK303258 // ZNF496
4614	chr1	-	247691680	247691724	NR_027309 // GCSAML-AS1
4615	chr1	-	247886731	247886755	ENST00000366485 // OR14A2
4616	chr1	-	247887222	247887283	ENST00000366485 // OR14A2
4617	chr10	+	696302	696359	NR_027152 // PRR26
4618	chr10	+	1058577	1058601	NM_012341 // GTPBP4
4619	chr10	+	1063096	1063120	NM_012341 // GTPBP4
4620	chr10	+	1081387	1081425	NR_027709 // IDI2-AS1
4621	chr10	+	1206493	1206574	NR_015376 // LINC00200
4622	chr10	+	3186096	3186175	NR_038284 // PITRM1-AS1
4623	chr10	+	4951761	4951786	BC040210 // AKR1C1
4624	chr10	+	5006009	5006033	ENST00000380859 // AKR1C1
4625	chr10	+	5804585	5804609	NM_017782 // FAM208B
4626	chr10	+	5950899	5950923	NM_032807 // FBXO18
4627	chr10	+	6373726	6374572	---
4628	chr10	+	7830190	7830214	NM_001001973 // ATP5C1
4629	chr10	+	8116142	8116946	NM_001002295 // GATA3

4630	chr10	+	11372210	11372388	ENST00000379261 // CELF2
4631	chr10	+	12111090	12111114	ENST00000263035 // DHTKD1
4632	chr10	+	12238057	12238081	NM_006023 // CDC123
4633	chr10	+	12272949	12272973	NM_006023 // CDC123
4634	chr10	+	13213058	13213082	NM_182751 // MCM10
4635	chr10	+	13786545	13786669	---
4636	chr10	+	14921854	14921976	OTTHUMT00000046950 // SUV39H2
4637	chr10	+	17726834	17726858	NM_003473 // STAM
4638	chr10	+	23399178	23399237	NM_012228 // MSRB2
4639	chr10	+	23632964	23633012	---
4640	chr10	+	25764466	25764688	ENST00000482641 // GPR158
4641	chr10	+	26855981	26856005	NM_019043 // APBB1IP
4642	chr10	+	28878702	28878726	NR_024557 // WAC
4643	chr10	+	29524099	29524860	---
4644	chr10	+	30722960	30722984	NM_005204 // MAP3K8
4645	chr10	+	30728297	30728321	AB209539 // MAP3K8
4646	chr10	+	30736729	30736818	NM_005204 // MAP3K8
4647	chr10	+	30739229	30739406	NM_005204 // MAP3K8
4648	chr10	+	30725532	30725567	AB209539 // MAP3K8
4649	chr10	+	35441262	35441286	ENST00000496626 // CREM
4650	chr10	+	36731254	36731288	OTTHUMT00000047582 // OTTHUMG00000017963
4651	chr10	+	38755168	38755311	---
4652	chr10	+	42667594	42667624	---
4653	chr10	+	43953546	43953577	---
4654	chr10	+	44101881	44101967	NM_145312 // ZNF485
4655	chr10	+	47762140	47762164	NM_001271702 // ANXA8
4656	chr10	+	50025402	50025426	NM_020945 // WDFY4
4657	chr10	+	50028400	50028424	NM_020945 // WDFY4
4658	chr10	+	50524206	50524271	NM_001135196 // C10orf71
4659	chr10	+	50822463	50822487	NM_020549 // CHAT
4660	chr10	+	50887695	50887720	NM_182554 // C10orf53
4661	chr10	+	62547835	62547859	NM_001786 // CDK1
4662	chr10	+	65225028	65226298	NR_027182 // JMJD1C-AS1
4663	chr10	+	69935081	69935216	NR_045662 // MYPN
4664	chr10	+	69917927	69918165	---
4665	chr10	+	70411630	70411679	NM_030625 // TET1
4666	chr10	+	70507294	70507318	NM_018237 // CCAR1
4667	chr10	+	70661086	70661110	NM_024045 // DDX50
4668	chr10	+	70723101	70723184	NM_004728 // DDX21
4669	chr10	+	71637094	71637118	---

4670	chr10	+	72289764	72289808	NM_014431 // PALD1
4671	chr10	+	72434361	72434692	NM_139155 // ADAMTS14
4672	chr10	+	72975595	72975628	---
4673	chr10	+	73464836	73464860	NM_022124 // CDH23
4674	chr10	+	74033830	74033870	ENST00000473155 // DDIT4
4675	chr10	+	74035468	74035692	NM_019058 // DDIT4
4676	chr10	+	75012974	75013011	---
4677	chr10	+	75521881	75521905	ENST00000411652 // SEC24C
4678	chr10	+	75676348	75676391	NM_002658 // PLAU
4679	chr10	+	75878331	75878355	NM_014000 // VCL
4680	chr10	+	76980742	76980768	ENST00000468285 // VDAC2
4681	chr10	+	77102999	77103092	OTTHUMT00000383920 // ZNF503-AS1
4682	chr10	+	78317052	78317077	NM_032024 // C10orf11
4683	chr10	+	81056484	81056508	ENST00000478357 // ZMIZ1
4684	chr10	+	85901268	85901294	NM_014394 // GHITM
4685	chr10	+	85912723	85912747	NM_014394 // GHITM
4686	chr10	+	88466292	88466316	NM_007078 // LDB3
4687	chr10	+	88635777	88635802	NM_004329 // BMPR1A
4688	chr10	+	88649346	88649490	ENST00000363306 // RNU1-19P
4689	chr10	+	89367742	89367783	---
4690	chr10	+	90435318	90435342	ENST00000496797 // LIPF
4691	chr10	+	90751072	90751096	AK311424 // FAS
4692	chr10	+	91484821	91484845	NM_016195 // KIF20B
4693	chr10	+	91497623	91497647	NM_016195 // KIF20B
4694	chr10	+	92656087	92656146	NM_001104546 // RPP30
4695	chr10	+	93542614	93542872	ENST00000432938 // TNKS2-AS1
4696	chr10	+	96234316	96234410	---
4697	chr10	+	96356835	96356859	NM_018063 // HELLS
4698	chr10	+	97792910	97793020	---
4699	chr10	+	97791722	97791746	NM_001159747 // CC2D2B
4700	chr10	+	99212173	99212216	NM_032327 // ZDHHC16
4701	chr10	+	99337558	99337590	NM_020349 // ANKRD2
4702	chr10	+	99338009	99338091	NM_020349 // ANKRD2
4703	chr10	+	101151276	101151312	NM_020348 // CNNM1
4704	chr10	+	101287752	101288201	---
4705	chr10	+	101591843	101591867	NM_000392 // ABCC2
4706	chr10	+	101611580	101611604	NM_000392 // ABCC2
4707	chr10	+	102140580	102140604	---
4708	chr10	+	103880410	103880730	---
4709	chr10	+	104125274	104125298	NM_004193 // GBF1
4710	chr10	+	104408976	104409010	ENST00000487927 // TRIM8

4711	chr10	+	104417163	104418013	NM_030912 // TRIM8
4712	chr10	+	104495635	104495659	NM_178858 // SFXN2
4713	chr10	+	113236152	113236332	---
4714	chr10	+	114063037	114063069	NM_058222 // TECTB
4715	chr10	+	115342988	115343012	NM_004132 // HABP2
4716	chr10	+	116416275	116416319	---
4717	chr10	+	116698181	116698247	NM_139169 // TRUB1
4718	chr10	+	118389517	118389541	NM_005396 // PNLIPRP2
4719	chr10	+	120004874	120004939	---
4720	chr10	+	124006770	124006794	ENST00000465600 // TACC2
4721	chr10	+	124740074	124740169	NM_153336 // PSTK
4722	chr10	+	134145645	134145669	NM_030626 // LRRC27
4723	chr10	+	135163611	135163635	NM_145202 // PRAP1
4724	chr10	-	1089270	1089332	NM_004508 // IDI1
4725	chr10	-	1090081	1090111	NM_004508 // IDI1
4726	chr10	-	4927192	4927216	NR_026743 // AKR1C6P
4727	chr10	-	13736009	13736033	NM_018027 // FRMD4A
4728	chr10	-	21107715	21107739	BC110452 // NEBL
4729	chr10	-	22193467	22193538	NM_022365 // DNAJC1
4730	chr10	-	23556124	23556155	ENST00000376500 // C10orf67
4731	chr10	-	27546625	27546700	---
4732	chr10	-	28233854	28233878	NM_018076 // ARMC4
4733	chr10	-	29084824	29085040	NR_038374 // LINC00837
4734	chr10	-	30654302	30654463	ENST00000488290 // MTPAP
4735	chr10	-	30656698	30656743	ENST00000488290 // MTPAP
4736	chr10	-	32217685	32217709	NM_018287 // ARHGAP12
4737	chr10	-	34558607	34558631	NM_019619 // PARD3
4738	chr10	-	35409347	35409429	---
4739	chr10	-	44880514	44880539	NM_199168 // CXCL12
4740	chr10	-	45561786	45561970	BC026193 // ZNF22
4741	chr10	-	46956303	46956328	---
4742	chr10	-	49701566	49701590	NM_001256026 // ARHGAP22
4743	chr10	-	50948824	50948848	NM_018245 // OGDHL
4744	chr10	-	51230573	51230710	ENST00000470172 // AGAP8
4745	chr10	-	52003055	52003079	NM_019893 // ASAH2
4746	chr10	-	52603761	52603785	NM_014576 // A1CF
4747	chr10	-	55568390	55568414	ENST00000395438 // PCDH15
4748	chr10	-	61043138	61043162	NM_198215 // FAM13C
4749	chr10	-	61043305	61043329	ENST00000513377 // FAM13C
4750	chr10	-	63170286	63170383	NM_178505 // TMEM26
4751	chr10	-	64575732	64575781	NM_000399 // EGR2
4752	chr10	-	71332189	71332800	NM_020999 // NEUROG3

4753	chr10	-	72083698	72083724	NM_207119 // LRRC20
4754	chr10	-	73533267	73533292	NM_022153 // C10orf54
4755	chr10	-	74098006	74098055	NM_001002762 // DNAJB12
4756	chr10	-	74127220	74127244	NM_006077 // MICU1
4757	chr10	-	79614070	79614094	NM_004747 // DLG5
4758	chr10	-	81390546	81390588	OTTHUMT00000048971 // OTTHUMG00000018570
4759	chr10	-	81928768	81928792	NM_001157 // ANXA11
4760	chr10	-	82098191	82098222	AK125908 // DYDC1
4761	chr10	-	90708645	90708669	NM_001141945 // ACTA2
4762	chr10	-	93666855	93667421	NM_152429 // FGFBP3
4763	chr10	-	95082902	95082926	NM_013451 // MYOF
4764	chr10	-	95083084	95083108	NM_013451 // MYOF
4765	chr10	-	97023639	97023796	NM_020992 // PDLIM1
4766	chr10	-	97031400	97031539	NM_020992 // PDLIM1
4767	chr10	-	97050583	97050613	NM_020992 // PDLIM1
4768	chr10	-	97170449	97170473	NM_006434 // SORBS1
4769	chr10	-	97181728	97181752	NM_006434 // SORBS1
4770	chr10	-	99228788	99228812	NM_022362 // MMS19
4771	chr10	-	99240005	99240029	OTTHUMT00000049711 // MMS19
4772	chr10	-	99625329	99625356	NM_018058 // CRTAC1
4773	chr10	-	100150771	100150795	NM_032709 // PYROXD2
4774	chr10	-	100174910	100174963	NM_032709 // PYROXD2
4775	chr10	-	101668722	101668861	NM_015221 // DNMBP
4776	chr10	-	102048780	102048805	NM_016112 // PKD2L1
4777	chr10	-	103529942	103530046	NM_033165 // FGF8
4778	chr10	-	103867887	103867976	NM_001113407 // LDB1
4779	chr10	-	104474116	104474140	NM_004311 // ARL3
4780	chr10	-	105063672	105063696	NM_001011663 // PCGF6
4781	chr10	-	105420813	105420837	NM_014631 // SH3PXD2A
4782	chr10	-	108380200	108380224	NM_052918 // SORCS1
4783	chr10	-	110209781	110209857	---
4784	chr10	-	111643568	111643592	ENST00000507328 // XPNPEP1
4785	chr10	-	115355387	115355411	NM_006175 // NRAP
4786	chr10	-	115471375	115471587	---
4787	chr10	-	118423280	118423496	BC021737 // C10orf82
4788	chr10	-	118423563	118423630	BC021737 // C10orf82
4789	chr10	-	118765006	118765030	NM_001127211 // KIAA1598
4790	chr10	-	119878360	119878420	---
4791	chr10	-	123681869	123681916	NM_001001976 // ATE1
4792	chr10	-	134325218	134325662	---
4793	chr10	-	134899035	134899137	---

4794	chr10	-	134900016	134900196	---
4795	chr10	-	135082275	135082299	NM_001109 // ADAM8
4796	chr10	-	135083985	135084009	NM_001109 // ADAM8
4797	chr10	-	135139461	135139624	NM_015722 // CALY
4798	chr10	-	135139794	135139818	ENST00000467611 // CALY
4799	chr10	-	135164094	135164185	---
4800	chr11	+	199819	199843	AL133658 // ODF3
4801	chr11	+	314015	314135	NM_003641 // IFITM1
4802	chr11	+	356611	356802	---
4803	chr11	+	369880	369904	NM_178537 // B4GALNT4
4804	chr11	+	404490	404514	OTTHUMT00000383852 // PKP3
4805	chr11	+	451468	451492	ENST00000531520 // PTDSS2
4806	chr11	+	460419	460443	ENST00000525059 // PTDSS2
4807	chr11	+	561834	561891	NM_003475 // RASSF7
4808	chr11	+	811649	811826	ENST00000524867 // SNORA52
4809	chr11	+	1051684	1051743	---
4810	chr11	+	1087902	1087926	NM_002457 // MUC2
4811	chr11	+	1219503	1219527	AJ001402 // MUC5AC
4812	chr11	+	1278782	1278806	NM_002458 // MUC5B
4813	chr11	+	1857460	1857484	NM_138567 // SYT8
4814	chr11	+	1861760	1861873	NM_003282 // TNNI2
4815	chr11	+	1950317	1950341	ENST00000492075 // TNNT3
4816	chr11	+	2425060	2425084	NM_005706 // TSSC4
4817	chr11	+	3845440	3845464	AK308525 // PGAP2
4818	chr11	+	4112848	4112872	NM_003156 // STIM1
4819	chr11	+	4674665	4674709	NM_152430 // OR51E1
4820	chr11	+	5009350	5009414	ENST00000380390 // MMP26
4821	chr11	+	5842534	5842578	ENST00000317037 // OR52N2
4822	chr11	+	7441753	7441777	NM_175733 // SYT9
4823	chr11	+	7598626	7598650	AK097449 // PPFIBP2
4824	chr11	+	8708072	8710039	NM_000990 // RPL27A
4825	chr11	+	10328422	10328576	NM_001124 // ADM
4826	chr11	+	12159945	12159969	NM_014632 // MICAL2
4827	chr11	+	18422414	18422438	NM_005566 // LDHA
4828	chr11	+	18500818	18501022	NM_144972 // LDHAL6A
4829	chr11	+	18762007	18762108	---
4830	chr11	+	22279250	22279274	NM_213599 // ANO5
4831	chr11	+	30252563	30252595	NM_000510 // FSHB
4832	chr11	+	31805338	31805408	ENST00000350638 // ELP4
4833	chr11	+	32126332	32126481	NM_002901 // RCN1
4834	chr11	+	32459210	32459241	ENST00000478367 // WT1-AS
4835	chr11	+	33693772	33694454	NM_012194 // KIAA1549L

4836	chr11	+	36616076	36616128	NR_077243 // C11orf74
4837	chr11	+	41857963	41857987	---
4838	chr11	+	43411308	43411332	NM_018259 // TTC17
4839	chr11	+	45377363	45377418	---
4840	chr11	+	45944660	45944685	NM_152312 // GYLTL1B
4841	chr11	+	46396271	46396295	ENST00000524869 // DGKZ
4842	chr11	+	46397089	46397113	NM_201532 // DGKZ
4843	chr11	+	46398084	46398108	NM_201532 // DGKZ
4844	chr11	+	46868010	46868039	NR_038909 // LRP4-AS1
4845	chr11	+	47436733	47436768	BX647491 // SLC39A13
4846	chr11	+	55653497	55653597	BC005014 // TRIM51
4847	chr11	+	57217656	57217757	ENST00000516261 // RNA5SP341
4848	chr11	+	57236079	57236103	---
4849	chr11	+	57428926	57429175	NM_006831 // CLP1
4850	chr11	+	58707029	58707053	---
4851	chr11	+	59496051	59496132	BX538158 // STX3
4852	chr11	+	60154202	60154245	NM_021201 // MS4A7
4853	chr11	+	60197148	60197241	NM_023945 // MS4A5
4854	chr11	+	60260302	60260391	ENST00000530007 // MS4A12
4855	chr11	+	60610130	60610154	NM_024098 // CCDC86
4856	chr11	+	60617432	60617464	NM_024098 // CCDC86
4857	chr11	+	60640635	60640667	NM_207341 // ZP1
4858	chr11	+	60689527	60689556	NM_024092 // TMEM109
4859	chr11	+	61165202	61165245	ENST00000544795 // TMEM216
4860	chr11	+	61505627	61505675	NM_006133 // DAGLA
4861	chr11	+	61553285	61553309	NM_013279 // MYRF
4862	chr11	+	61583774	61583798	ENST00000257261 // FADS2
4863	chr11	+	61631535	61631559	ENST00000521849 // FADS2
4864	chr11	+	61730879	61730903	NM_001139443 // BEST1
4865	chr11	+	62529208	62529233	ENST00000527435 // POLR2G
4866	chr11	+	62623803	62623827	NM_001012662 // SLC3A2
4867	chr11	+	63065083	63065139	NM_001039752 // SLC22A10
4868	chr11	+	63067034	63067085	NM_001039752 // SLC22A10
4869	chr11	+	63071639	63071663	NM_001039752 // SLC22A10
4870	chr11	+	63671533	63671557	NM_017490 // MARK2
4871	chr11	+	64064374	64064410	NM_033310 // KCNK4
4872	chr11	+	64360251	64360317	NM_144585 // SLC22A12
4873	chr11	+	64808841	64808940	NM_013299 // SAC3D1
4874	chr11	+	64884670	64884705	BC104003 // ZNHIT2
4875	chr11	+	64950281	64950305	NR_040008 // CAPN1
4876	chr11	+	64950627	64950651	NM_001198868 // CAPN1
4877	chr11	+	65293607	65293631	NM_020680 // SCYL1

4878	chr11	+	65340382	65340415	NM_001098785 // FAM89B
4879	chr11	+	65417093	65417117	NM_153253 // SIPA1
4880	chr11	+	65631245	65631269	AK095326 // MUS81
4881	chr11	+	65780336	65780387	NM_001323 // CST6
4882	chr11	+	66049799	66049824	NR_073078 // CNIH2
4883	chr11	+	66130811	66131049	OTTHUMT00000391898 // OTTHUMG00000166921
4884	chr11	+	66366621	66366719	NM_005125 // CCS
4885	chr11	+	66612652	66612707	NM_005133 // RCE1
4886	chr11	+	66627156	66627363	NM_024036 // LRFN4
4887	chr11	+	66982934	66982958	---
4888	chr11	+	67160186	67160210	NM_004584 // RAD9A
4889	chr11	+	67180172	67180438	---
4890	chr11	+	67352550	67352576	BC044846 // GSTP1
4891	chr11	+	67375957	67375981	AK055875 // NDUFV1
4892	chr11	+	68779906	68780008	---
4893	chr11	+	68851445	68851469	NM_139075 // TPCN2
4894	chr11	+	69062917	69062941	NM_138768 // MYEOV
4895	chr11	+	69062989	69063037	AJ223366 // MYEOV
4896	chr11	+	70049582	70049699	NM_003824 // FADD
4897	chr11	+	70176355	70176379	NM_177423 // PPFIA1
4898	chr11	+	70210481	70210505	AK124621 // PPFIA1
4899	chr11	+	71232146	71232170	ENST00000526622 // NADSYN1
4900	chr11	+	71548490	71548558	NM_001002035 // DEFB108B
4901	chr11	+	73610222	73610246	NM_001267803 // PAAF1
4902	chr11	+	75428941	75429001	NM_025098 // MOGAT2
4903	chr11	+	75470573	75470670	---
4904	chr11	+	76727792	76727816	NM_018367 // ACER3
4905	chr11	+	76799063	76799088	AK094150 // CAPN5
4906	chr11	+	76833679	76833745	NM_004055 // CAPN5
4907	chr11	+	76877118	76877142	NM_000260 // MYO7A
4908	chr11	+	76903213	76903237	NM_000260 // MYO7A
4909	chr11	+	82891757	82891781	ENST00000528336 // PCF11
4910	chr11	+	85366670	85366751	NM_032273 // TMEM126A
4911	chr11	+	86662805	86662829	ENST00000532234 // PRSS23
4912	chr11	+	91536458	91536493	OTTHUMT00000447346 // OTTHUMG00000167330
4913	chr11	+	93474763	93474831	ENST00000528288 // C11orf54
4914	chr11	+	93534591	93534615	ENST00000525613 // MED17
4915	chr11	+	93803602	93803707	NM_001098672 // HEPHL1
4916	chr11	+	94231183	94231207	AL833977 // ANKRD49
4917	chr11	+	94823173	94823270	NM_015036 // ENDOD1

4918	chr11	+	103022901	103022925	NM_001377 // DYNC2H1
4919	chr11	+	105481452	105481476	NM_001112812 // GRIA4
4920	chr11	+	105695442	105695496	---
4921	chr11	+	108170313	108170337	ENST00000534625 // ATM
4922	chr11	+	111169978	111170185	ENST00000398035 // C11orf93
4923	chr11	+	111319345	111319369	XR_110541 // LOC644277
4924	chr11	+	111951313	111951719	AK094203 // C11orf57
4925	chr11	+	112046231	112046255	NM_031938 // BCO2
4926	chr11	+	112064529	112064553	AK091783 // BCO2
4927	chr11	+	112094724	112094748	AB096252 // BCO2
4928	chr11	+	112161972	112162041	OTTHUMT00000393663 // OTTHUMG00000167191
4929	chr11	+	112237175	112237227	---
4930	chr11	+	113117007	113117031	ENST00000534516 // NCAM1
4931	chr11	+	113131060	113131084	ENST00000525355 // NCAM1
4932	chr11	+	113650470	113650517	ENST00000453129 // CLDN25
4933	chr11	+	114279054	114280923	NM_016090 // RBM7
4934	chr11	+	117049452	117049476	ENST00000324225 // SIDT2
4935	chr11	+	118220696	118220720	ENST00000533462 // CD3G
4936	chr11	+	119043614	119043644	NM_024618 // NLRX1
4937	chr11	+	119059459	119059553	NR_033122 // PDZD3
4938	chr11	+	120980177	120980201	NM_005422 // TECTA
4939	chr11	+	121502770	121502794	NM_003105 // SORL1
4940	chr11	+	123306142	123306175	OTTHUMT00000387401 // OTTHUMG00000166002
4941	chr11	+	124609840	124609864	NM_006176 // NRGN
4942	chr11	+	124615416	124615505	NM_006176 // NRGN
4943	chr11	+	124735308	124735332	NM_022370 // ROBO3
4944	chr11	+	125280148	125280202	NM_022062 // PKNOX2
4945	chr11	+	125450676	125451054	ENST00000530540 // EI24
4946	chr11	+	125513699	125513723	NM_001114122 // CHEK1
4947	chr11	+	125781299	125781357	NM_013264 // DDX25
4948	chr11	+	126143099	126143123	ENST00000527875 // FOXRED1
4949	chr11	+	126278544	126278568	ENST00000528605 // ST3GAL4
4950	chr11	+	128628165	128628189	NM_002017 // FLI1
4951	chr11	+	128761378	128761456	NM_000890 // KCNJ5
4952	chr11	+	130058031	130058055	NM_021978 // ST14
4953	chr11	+	130272389	130273062	AK091840 // FLJ34521
4954	chr11	+	131781003	131781027	NM_016522 // NTM
4955	chr11	+	132154198	132154237	OTTHUMT00000316006 // NTM-IT3
4956	chr11	+	133897642	133897977	OTTHUMT00000393569 // OTTHUMG00000167171

4957	chr11	+	134014202	134014257	NM_032801 // JAM3
4958	chr11	+	134180629	134180653	BC063875 // GLB1L3
4959	chr11	+	134352589	134352613	NR_033852 // LOC283177
4960	chr11	-	504934	504958	NM_002939 // RNH1
4961	chr11	-	565697	567484	NR_038262 // MIR210HG
4962	chr11	-	568098	568143	NR_029623 // MIR210
4963	chr11	-	614253	614380	NM_001572 // IRF7
4964	chr11	-	621876	621903	NM_021924 // CDHR5
4965	chr11	-	689741	689803	OTTHUMT00000383847 // DEAF1
4966	chr11	-	771400	771426	NM_182612 // PDDC1
4967	chr11	-	801894	801918	ENST00000527357 // PIDD
4968	chr11	-	804260	804284	NM_145886 // PIDD
4969	chr11	-	1028912	1028936	NM_005961 // MUC6
4970	chr11	-	1605825	1605856	NM_001005922 // KRTAP5-1
4971	chr11	-	2189121	2189145	NM_199292 // TH
4972	chr11	-	2442316	2442340	NM_014555 // TRPM5
4973	chr11	-	3033466	3033490	NM_139273 // CARS
4974	chr11	-	3116026	3116050	AK124919 // OSBPL5
4975	chr11	-	3141776	3141800	NM_020896 // OSBPL5
4976	chr11	-	4869431	4869466	ENST00000322101 // OR51S1
4977	chr11	-	4944762	4945528	NM_001005237 // OR51G1
4978	chr11	-	5246713	5246815	NM_000518 // HBB
4979	chr11	-	5246906	5246933	NM_000518 // HBB
4980	chr11	-	6206543	6206568	OTTHUMT00000384691 // OTTHUMG00000165532
4981	chr11	-	6471158	6471182	AK126685 // TRIM3
4982	chr11	-	6501232	6501258	NM_001242854 // ARFIP2
4983	chr11	-	8248490	8248514	NR_073006 // LMO1
4984	chr11	-	8496426	8496450	NM_030906 // STK33
4985	chr11	-	8704161	8704185	---
4986	chr11	-	8737194	8737218	NM_005418 // ST5
4987	chr11	-	8793341	8793365	---
4988	chr11	-	8798076	8798100	OTTHUMT00000386564 // ST5
4989	chr11	-	9979688	9979712	---
4990	chr11	-	10562671	10562742	NM_016422 // RNF141
4991	chr11	-	11398730	11398888	NM_198516 // GALNT18
4992	chr11	-	17522621	17522645	NM_005709 // USH1C
4993	chr11	-	18051072	18051126	NM_004179 // TPH1
4994	chr11	-	18103016	18103040	NM_138421 // SAAL1
4995	chr11	-	18284207	18284235	---
4996	chr11	-	18736094	18736118	NM_173588 // IGSF22
4997	chr11	-	19203646	19204213	NM_003476 // CSRP3

4998	chr11	-	19423419	19423453	---
4999	chr11	-	20181546	20181782	NM_001029865 // DBX1
5000	chr11	-	23826055	23826181	OTTHUMT00000387786 // OTTHUMG00000166087
5001	chr11	-	26708025	26708088	NM_178498 // SLC5A12
5002	chr11	-	26730891	26730915	NM_178498 // SLC5A12
5003	chr11	-	26732874	26732904	NM_178498 // SLC5A12
5004	chr11	-	27393892	27393916	NM_018490 // LGR4
5005	chr11	-	31824809	31824833	AB209177 // PAX6
5006	chr11	-	33025244	33025394	---
5007	chr11	-	33731607	33731631	NM_203330 // CD59
5008	chr11	-	33731719	33731743	NM_203330 // CD59
5009	chr11	-	35282476	35282500	NM_004171 // SLC1A2
5010	chr11	-	35551602	35551626	AK297092 // PAMR1
5011	chr11	-	42210157	42210181	NR_038309 // LOC100507205
5012	chr11	-	44286417	44286729	NM_021926 // ALX4
5013	chr11	-	45674131	45674155	NM_003654 // CHST1
5014	chr11	-	45928696	45928728	ENST00000449465 // C11orf94
5015	chr11	-	46292116	46292154	---
5016	chr11	-	47359271	47359295	NM_000256 // MYBPC3
5017	chr11	-	47862018	47862042	NM_015231 // NUP160
5018	chr11	-	55371850	55371874	NM_001004700 // OR4C11
5019	chr11	-	55734975	55735006	ENST00000312345 // OR10AG1
5020	chr11	-	57166987	57167039	Z26248 // PRG2
5021	chr11	-	58491708	58491732	ENST00000531084 // GLYAT
5022	chr11	-	59051455	59051485	---
5023	chr11	-	59189474	59190342	NM_001001954 // OR5A2
5024	chr11	-	59927265	59927335	---
5025	chr11	-	61058272	61058296	NM_152718 // VWCE
5026	chr11	-	61094996	61095020	AK302924 // DDB1
5027	chr11	-	61557973	61558061	NM_014206 // TMEM258
5028	chr11	-	61583774	61583798	OTTHUMT00000398587 // FADS1
5029	chr11	-	62201040	62201154	NM_024060 // AHNAK
5030	chr11	-	62334447	62334473	NM_001404 // EEF1G
5031	chr11	-	62473399	62473423	ENST00000403550 // BSCL2
5032	chr11	-	62566017	62566041	NM_006362 // NXF1
5033	chr11	-	62678606	62678637	NM_000738 // CHRM1
5034	chr11	-	62763583	62763607	NM_004254 // SLC22A8
5035	chr11	-	62933683	62933707	NM_199352 // SLC22A25
5036	chr11	-	64457878	64457902	NM_015080 // NRXN2
5037	chr11	-	64532809	64532833	NM_004630 // SF1
5038	chr11	-	64578334	64578358	NM_130803 // MEN1

5039	chr11	-	64739381	64739405	AK093130 // C11orf85
5040	chr11	-	64885129	64885170	NM_014205 // ZNHIT2
5041	chr11	-	65256368	65256448	---
5042	chr11	-	65315216	65315240	NM_001130144 // LTBP3
5043	chr11	-	65622331	65622355	NM_005507 // CFL1
5044	chr11	-	65766130	65766156	NM_001242481 // EIF1AD
5045	chr11	-	66035259	66035302	---
5046	chr11	-	66103795	66103820	NM_004292 // RIN1
5047	chr11	-	66103967	66103991	NM_004292 // RIN1
5048	chr11	-	66241630	66241686	---
5049	chr11	-	66639279	66639303	NM_000920 // PC
5050	chr11	-	67612687	67615441	---
5051	chr11	-	67980075	67980099	ENST00000434573 // SUV420H1
5052	chr11	-	69861025	69861272	OTTHUMT00000393502 // OTTHUMG00000167160
5053	chr11	-	72468835	72468859	NM_006645 // STARD10
5054	chr11	-	72549870	72549894	NM_014824 // FCHSD2
5055	chr11	-	73802366	73802390	---
5056	chr11	-	74108858	74108954	ENST00000545890 // PGM2L1
5057	chr11	-	75917375	75917402	NM_004626 // WNT11
5058	chr11	-	76367593	76367723	OTTHUMT00000383014 // OTTHUMG00000165260
5059	chr11	-	84822707	84822731	NM_001142699 // DLG2
5060	chr11	-	85336232	85336256	ENST00000526147 // DLG2
5061	chr11	-	85396131	85397172	NM_152723 // CCDC89
5062	chr11	-	86383206	86383230	NM_001014811 // ME3
5063	chr11	-	89165974	89165998	NM_016931 // NOX4
5064	chr11	-	93271045	93271079	ENST00000527149 // SMCO4
5065	chr11	-	101326217	101326241	ENST00000532184 // TRPC6
5066	chr11	-	101771193	101771254	NM_178127 // ANGPTL5
5067	chr11	-	102401331	102401431	NM_002423 // MMP7
5068	chr11	-	103714470	103714649	---
5069	chr11	-	104869645	104869721	NM_004347 // CASP5
5070	chr11	-	104896953	104896977	NM_001257118 // CASP1
5071	chr11	-	110454324	110454439	NM_020809 // ARHGAP20
5072	chr11	-	112043292	112043323	---
5073	chr11	-	113318299	113318323	ENST00000543292 // DRD2
5074	chr11	-	114392465	114392665	NM_152315 // NXPE1
5075	chr11	-	114453064	114453251	NM_001077639 // NXPE4
5076	chr11	-	117072505	117072606	NR_045215 // LOC100652768
5077	chr11	-	117089833	117089857	NM_004716 // PCSK7
5078	chr11	-	117342670	117342694	NM_020693 // DSCAML1

5079	chr11	-	118773721	118773745	NM_182557 // BCL9L
5080	chr11	-	118774136	118774160	NM_182557 // BCL9L
5081	chr11	-	118781594	118781618	---
5082	chr11	-	118873844	118874122	NR_003040 // RPL23AP64
5083	chr11	-	119063895	119063953	NM_001145018 // CCDC153
5084	chr11	-	119183334	119183358	NM_006500 // MCAM
5085	chr11	-	119229864	119229937	ENST00000525189 // USP2
5086	chr11	-	121986991	121987015	---
5087	chr11	-	122932587	122932611	OTTHUMT00000387538 // HSPA8
5088	chr11	-	124765760	124765784	NM_019055 // ROBO4
5089	chr11	-	125002744	125002786	OTTHUMT00000386862 // OTTHUMG00000165882
5090	chr11	-	125853845	125853869	NM_001243597 // CDON
5091	chr11	-	126135443	126135467	ENST00000531104 // SRPR
5092	chr11	-	129758320	129758344	OTTHUMT00000386071 // NFRKB
5093	chr11	-	129812413	129812437	NM_020228 // PRDM10
5094	chr11	-	133230666	133231827	---
5095	chr11	-	134118218	134118302	NM_014174 // THYN1
5096	chr11	-	134281714	134281749	NM_018644 // B3GAT1
5097	chr12	+	655966	655990	ENST00000535680 // B4GALNT3
5098	chr12	+	812115	812163	---
5099	chr12	+	2743495	2743519	NM_199460 // CACNA1C
5100	chr12	+	2910931	2910955	---
5101	chr12	+	2921819	2921843	NM_018463 // ITFG2
5102	chr12	+	3192918	3193209	ENST00000539631 // TSPAN9
5103	chr12	+	3702911	3703088	NM_019854 // PRMT8
5104	chr12	+	5513352	5513465	OTTHUMT00000400482 // OTTHUMG00000168648
5105	chr12	+	6571433	6571479	NM_018009 // TAPBPL
5106	chr12	+	6637854	6637878	NM_014865 // NCAPD2
5107	chr12	+	6833370	6833394	NM_001164095 // COPS7A
5108	chr12	+	6950582	6950642	AB209283 // GNB3
5109	chr12	+	6982900	6982924	BC011980 // LRRC23
5110	chr12	+	7037523	7037547	NM_001940 // ATN1
5111	chr12	+	7169030	7169054	ENST00000403949 // C1S
5112	chr12	+	7295734	7295758	---
5113	chr12	+	7470687	7470763	NM_001080454 // ACSM4
5114	chr12	+	9452023	9452047	NR_024374 // LOC642846
5115	chr12	+	13215365	13215389	---
5116	chr12	+	13364446	13364470	NM_001423 // EMP1
5117	chr12	+	18491401	18491425	NM_004570 // PIK3C2G
5118	chr12	+	21660091	21660190	ENST00000545113 // GOLT1B

5119	chr12	+	25232660	25232684	NM_006152 // LRMP
5120	chr12	+	26348606	26348639	NM_005086 // SSPN
5121	chr12	+	27175479	27175508	ENST00000282892 // MED21
5122	chr12	+	27908205	27908359	NM_021821 // MRPS35
5123	chr12	+	31107011	31107036	BC084571 // TSPAN11
5124	chr12	+	31242579	31242603	ENST00000543026 // DDX11
5125	chr12	+	32491804	32491884	NM_001714 // BICD1
5126	chr12	+	32655180	32655204	NM_139241 // FGD4
5127	chr12	+	32791613	32791637	NM_139241 // FGD4
5128	chr12	+	34358651	34358689	ENST00000362784 // RNA5SP357
5129	chr12	+	40808882	40808906	HM801842 // MUC19
5130	chr12	+	40834868	40834892	HM801842 // MUC19
5131	chr12	+	42835617	42835641	NM_201515 // PPHLN1
5132	chr12	+	47629244	47629471	NM_138371 // PCED1B
5133	chr12	+	49521668	49521733	NM_006082 // TUBA1B
5134	chr12	+	49717831	49717855	OTTHUMT00000404346 // TROAP
5135	chr12	+	50017742	50017766	NR_052006 // PRPF40B
5136	chr12	+	50135071	50135095	ENST00000548809 // TMBIM6
5137	chr12	+	50135400	50135424	ENST00000548713 // TMBIM6
5138	chr12	+	51086756	51086780	NM_173602 // DIP2B
5139	chr12	+	51441882	51441906	OTTHUMT00000404704 // LETMD1
5140	chr12	+	51844542	51844566	DQ996398 // SLC4A8
5141	chr12	+	52188325	52188349	NM_014191 // SCN8A
5142	chr12	+	52407514	52407563	NM_181711 // GRASP
5143	chr12	+	52501248	52501704	X87825 // OR7E47P
5144	chr12	+	52604735	52604790	NR_027358 // LINC00592
5145	chr12	+	52995284	52995351	ENST00000551089 // LOC100127967
5146	chr12	+	53007177	53007294	ENST00000551089 // LOC100127967
5147	chr12	+	53447763	53447787	NM_015319 // TENC1
5148	chr12	+	53499730	53499754	NM_003578 // SOAT2
5149	chr12	+	53553370	53553424	OTTHUMT00000406889 // OTTHUMG00000170026
5150	chr12	+	53898418	53898442	ENST00000549572 // TARBP2
5151	chr12	+	54537836	54537862	---
5152	chr12	+	54680226	54680250	ENST00000546500 // HNRNPA1
5153	chr12	+	54680446	54680470	ENST00000546500 // HNRNPA1
5154	chr12	+	54930061	54930085	ENST00000548980 // NCKAP1L
5155	chr12	+	56524283	56524307	ENST00000550986 // ESYT1
5156	chr12	+	57623426	57623450	NM_005412 // SHMT2
5157	chr12	+	58008341	58008365	NM_182947 // ARHGEF25

5158	chr12	+	58019044	58019068	NM_133489 // SLC26A10
5159	chr12	+	58166403	58166430	NM_015433 // METTL21B
5160	chr12	+	58176591	58176616	NM_001172696 // TSFM
5161	chr12	+	59832097	59832121	---
5162	chr12	+	62986477	62986501	NM_015026 // MON2
5163	chr12	+	64199018	64199042	NM_014254 // TMEM5
5164	chr12	+	64877887	64877911	ENST00000545025 // TBK1
5165	chr12	+	65953394	65953461	OTTHUMT00000401464 // OTTHUMG00000168876
5166	chr12	+	66057002	66057079	OTTHUMT00000401556 // OTTHUMG00000168900
5167	chr12	+	66346377	66352342	AB209853 // HMGA2
5168	chr12	+	68042540	68042913	NM_003583 // DYRK2
5169	chr12	+	69044374	69044653	OTTHUMT00000257823 // RAP1B
5170	chr12	+	69210693	69210717	NM_002392 // MDM2
5171	chr12	+	69233334	69233358	NM_002392 // MDM2
5172	chr12	+	69233572	69233596	NM_002392 // MDM2
5173	chr12	+	71965140	71965164	ENST00000547310 // LGR5
5174	chr12	+	72058652	72058735	OTTHUMT00000404797 // THAP2
5175	chr12	+	72234884	72234908	ENST00000474468 // TBC1D15
5176	chr12	+	75817051	75817075	NM_152436 // GLIPR1L2
5177	chr12	+	75824637	75824722	NM_001270396 // GLIPR1L2
5178	chr12	+	77239509	77239533	NM_015336 // ZDHHC17
5179	chr12	+	79844372	79844651	NM_005639 // SYT1
5180	chr12	+	80651733	80651757	NM_173591 // OTOGL
5181	chr12	+	81537188	81537212	ENST00000548387 // ACSS3
5182	chr12	+	81545804	81545828	NM_024560 // ACSS3
5183	chr12	+	93881515	93881539	ENST00000548545 // MRPL42
5184	chr12	+	94697621	94697645	NR_037687 // PLXNC1
5185	chr12	+	96259791	96259819	NM_003095 // SNRPF
5186	chr12	+	96915642	96915666	AK056076 // C12orf55
5187	chr12	+	98988174	98988367	BX647062 // SLC25A3
5188	chr12	+	100995496	100995520	NM_174942 // GAS2L3
5189	chr12	+	101433812	101433836	NM_178826 // ANO4
5190	chr12	+	101437352	101437376	NM_178826 // ANO4
5191	chr12	+	101699709	101699733	NM_014503 // UTP20
5192	chr12	+	102090725	102090751	ENST00000550385 // CHPT1
5193	chr12	+	102091517	102091543	NM_020244 // CHPT1
5194	chr12	+	102173673	102173707	ENST00000364298 // RNA5SP368
5195	chr12	+	102517722	102517775	NM_017915 // PARPBP
5196	chr12	+	103972291	103972569	---
5197	chr12	+	104151727	104151751	---

5198	chr12	+	104213388	104213494	---
5199	chr12	+	104378891	104378925	---
5200	chr12	+	104461771	104461812	NM_013320 // HCFC2
5201	chr12	+	104645431	104645455	NM_001093771 // TXNRD1
5202	chr12	+	106838282	106838306	NM_018082 // POLR3B
5203	chr12	+	107090148	107090172	NM_032491 // RFX4
5204	chr12	+	109491816	109491840	---
5205	chr12	+	109637218	109637242	NM_001093 // ACACB
5206	chr12	+	109661678	109661702	NM_001093 // ACACB
5207	chr12	+	109831149	109831173	NM_001101421 // MYO1H
5208	chr12	+	109949058	109949082	NM_130466 // UBE3B
5209	chr12	+	110788494	110788518	NM_001681 // ATP2A2
5210	chr12	+	112187005	112187029	NM_001136538 // ACAD10
5211	chr12	+	112915482	112915506	NM_002834 // PTPN11
5212	chr12	+	113229610	113229634	NM_001143854 // RPH3A
5213	chr12	+	113398997	113399021	NM_006187 // OAS3
5214	chr12	+	113717972	113717996	NM_001143819 // TPCN1
5215	chr12	+	113733788	113733812	NM_001143819 // TPCN1
5216	chr12	+	114845996	114846089	NR_038440 // TBX5-AS1
5217	chr12	+	116400449	116400536	---
5218	chr12	+	119916931	119916993	NM_178499 // CCDC60
5219	chr12	+	120530829	120530853	NM_207311 // CCDC64
5220	chr12	+	120933908	120933963	NM_001037495 // DYNLL1
5221	chr12	+	120935935	120935962	NM_001037494 // DYNLL1
5222	chr12	+	121015041	121015065	NM_014868 // RNF10
5223	chr12	+	121416462	121416486	HM116541 // HNF1A
5224	chr12	+	122064808	122064877	NM_032790 // ORAI1
5225	chr12	+	122437776	122437800	NM_144668 // WDR66
5226	chr12	+	122622974	122622998	NM_014938 // MLXIP
5227	chr12	+	123461743	123462492	AK303095 // OGFOD2
5228	chr12	+	124303766	124303790	NM_207437 // DNAH10
5229	chr12	+	124409713	124409737	NM_207437 // DNAH10
5230	chr12	+	124418001	124418025	NM_207437 // DNAH10
5231	chr12	+	125478453	125478546	NM_080626 // BRI3BP
5232	chr12	+	125638475	125638533	---
5233	chr12	+	129694673	129694805	---
5234	chr12	+	131143314	131143351	OTTHUMT00000458698 // OTTHUMG00000168322
5235	chr12	+	132198925	132198949	AB208921 // SFSWAP
5236	chr12	+	132404054	132404078	NM_003565 // ULK1
5237	chr12	+	132407636	132407660	NM_003565 // ULK1
5238	chr12	+	133033925	133033954	---

5239	chr12	+	133079743	133079767	---
5240	chr12	+	133144080	133144104	NM_001142641 // FBRSL1
5241	chr12	-	1489331	1490329	---
5242	chr12	-	1769131	1769159	---
5243	chr12	-	2799325	2799352	NR_045725 // CACNA1C-AS1
5244	chr12	-	2936392	2936459	NM_031474 // NRIP2
5245	chr12	-	6094774	6094798	NM_000552 // VWF
5246	chr12	-	6677137	6677161	ENST00000538697 // NOP2
5247	chr12	-	6705267	6705291	NM_001273 // CHD4
5248	chr12	-	7527220	7527244	NM_174941 // CD163L1
5249	chr12	-	8024472	8024496	AK126026 // SLC2A14
5250	chr12	-	8391320	8391344	NR_024254 // FAM86FP
5251	chr12	-	9210153	9210215	AK123808 // LINC00612
5252	chr12	-	9216974	9217594	BC028195 // LINC00612
5253	chr12	-	10005927	10005988	NM_005127 // CLEC2B
5254	chr12	-	10089414	10089468	---
5255	chr12	-	10241748	10241772	NM_016511 // CLEC1A
5256	chr12	-	10279249	10279273	NM_197947 // CLEC7A
5257	chr12	-	10279438	10279621	CR749536 // CLEC7A
5258	chr12	-	10282773	10282797	NM_197947 // CLEC7A
5259	chr12	-	12339964	12339988	NM_002336 // LRP6
5260	chr12	-	12640015	12640039	NM_030640 // DUSP16
5261	chr12	-	15822730	15822754	NM_004447 // EPS8
5262	chr12	-	16753430	16753454	AK294651 // LMO3
5263	chr12	-	21654221	21654297	NM_002907 // RECQL
5264	chr12	-	25308285	25308309	NM_018272 // CASC1
5265	chr12	-	25967018	25967105	---
5266	chr12	-	31613269	31613293	NM_144973 // DENND5B
5267	chr12	-	31743675	31743699	NM_144973 // DENND5B
5268	chr12	-	31903128	31904196	---
5269	chr12	-	38668253	38668351	---
5270	chr12	-	42555010	42555034	BX649019 // YAF2
5271	chr12	-	48089850	48090056	ENST00000548296 // RPAP3
5272	chr12	-	48133033	48133057	ENST00000490387 // RAPGEF3
5273	chr12	-	48876868	48876900	---
5274	chr12	-	49166146	49166170	NM_015270 // ADCY6
5275	chr12	-	49463607	49463763	NM_144593 // RHEBL1
5276	chr12	-	49504637	49504661	NM_018113 // LMBR1L
5277	chr12	-	49521668	49521730	NM_006082 // TUBA1B
5278	chr12	-	49578625	49578676	NM_006009 // TUBA1A
5279	chr12	-	49626651	49627915	ENST00000549023 // LOC100293962

5280	chr12	-	49675940	49676761	---
5281	chr12	-	50281170	50281194	NM_012306 // FAIM2
5282	chr12	-	50345302	50345416	---
5283	chr12	-	51590633	51590673	NM_002702 // POU6F1
5284	chr12	-	51751144	51751225	NM_007210 // GALNT6
5285	chr12	-	52579476	52579533	BX537567 // KRT80
5286	chr12	-	52668466	52668855	OTTHUMT00000405179 // OTTHUMG00000169629
5287	chr12	-	53183864	53184120	NM_057088 // KRT3
5288	chr12	-	53203092	53203116	ENST00000549295 // KRT4
5289	chr12	-	53468577	53468701	ENST00000550564 // SPRYD3
5290	chr12	-	53901201	53901229	NM_003717 // NPFF
5291	chr12	-	54107609	54107633	NR_026554 // CALCOCO1
5292	chr12	-	55028597	55028623	NM_033277 // LACRT
5293	chr12	-	56665537	56665561	NM_004077 // CS
5294	chr12	-	56881281	56881305	ENST00000491880 // GLS2
5295	chr12	-	57081837	57082056	NM_006601 // PTGES3
5296	chr12	-	57480361	57480551	---
5297	chr12	-	57866253	57866277	NM_032496 // ARHGAP9
5298	chr12	-	57910428	57910537	NM_001195053 // DDIT3
5299	chr12	-	58021454	58021478	NM_001478 // B4GALNT1
5300	chr12	-	59271226	59271250	NM_001136051 // LRIG3
5301	chr12	-	59307525	59307549	ENST00000548968 // LRIG3
5302	chr12	-	63327704	63327785	ENST00000548414 // PPM1H
5303	chr12	-	65952554	65952578	OTTHUMT00000401446 // OTTHUMG00000168872
5304	chr12	-	66267622	66267920	ENST00000504038 // LOC100129940
5305	chr12	-	68099629	68099776	---
5306	chr12	-	69235131	69235453	AK094838 // MDM2
5307	chr12	-	71054743	71054767	NM_002849 // PTPRR
5308	chr12	-	71078536	71078560	NM_002849 // PTPRR
5309	chr12	-	71551428	71551452	NM_004616 // TSPAN8
5310	chr12	-	72050148	72050172	BC073843 // ZFC3H1
5311	chr12	-	72050445	72050469	BC073843 // ZFC3H1
5312	chr12	-	72054167	72054191	OTTHUMT00000404762 // ZFC3H1
5313	chr12	-	76377602	76377626	---
5314	chr12	-	80980442	80980498	---
5315	chr12	-	88775690	88775715	---
5316	chr12	-	92384084	92384125	NR_046160 // C12orf79
5317	chr12	-	93835707	93835740	NM_003348 // UBE2N
5318	chr12	-	95397490	95397534	ENST00000327772 // NDUFA12

5319	chr12	-	95770994	95771108	---
5320	chr12	-	95774863	95775508	---
5321	chr12	-	101824939	101825020	---
5322	chr12	-	102163884	102163908	NM_024312 // GNPTAB
5323	chr12	-	102869436	102869510	NM_001111283 // IGF1
5324	chr12	-	104277487	104277581	NR_027249 // GNN
5325	chr12	-	104347211	104347235	BC044618 // C12orf73
5326	chr12	-	106676724	106676759	---
5327	chr12	-	108126883	108127415	NM_012406 // PRDM4
5328	chr12	-	108851577	108851635	---
5329	chr12	-	108917760	108917784	OTTHUMT00000404097 // SART3
5330	chr12	-	109124054	109124078	ENST00000546571 // CORO1C
5331	chr12	-	109530840	109531051	ENST00000536358 // ALKBH2
5332	chr12	-	110100697	110100766	---
5333	chr12	-	110171149	110171214	---
5334	chr12	-	110820825	110820849	OTTHUMT00000347079 // ANAPC7
5335	chr12	-	110872900	110872924	NM_005719 // ARPC3
5336	chr12	-	110872967	110872991	NM_005719 // ARPC3
5337	chr12	-	110929640	110929807	NM_016226 // VPS29
5338	chr12	-	110929850	110929895	NM_016226 // VPS29
5339	chr12	-	112037084	112037108	NM_002973 // ATXN2
5340	chr12	-	112037353	112037377	NM_002973 // ATXN2
5341	chr12	-	112546633	112546657	ENST00000261745 // NAA25
5342	chr12	-	112475419	112475493	---
5343	chr12	-	112608957	112608981	NM_001109662 // HECTD4
5344	chr12	-	114676791	114677177	OTTHUMT00000404204 // OTTHUMG00000169468
5345	chr12	-	114679533	114679575	---
5346	chr12	-	115135176	115135218	---
5347	chr12	-	117476760	117476819	NR_031766 // TESC
5348	chr12	-	119212292	119212322	---
5349	chr12	-	120765530	120765556	NM_000928 // PLA2G1B
5350	chr12	-	122287640	122287694	NM_002150 // HPD
5351	chr12	-	122710392	122710416	OTTHUMT00000347104 // DIABLO
5352	chr12	-	122825496	122825520	NM_002956 // CLIP1
5353	chr12	-	123414624	123414648	NM_019625 // ABCB9
5354	chr12	-	123808284	123808308	NM_001167856 // SBNO1
5355	chr12	-	124107274	124107298	NM_001414 // EIF2B1
5356	chr12	-	124456456	124456543	ENST00000539761 // CCDC92
5357	chr12	-	124832862	124832886	ENST00000473999 // NCOR2
5358	chr12	-	124862842	124862866	NM_006312 // NCOR2
5359	chr12	-	124873343	124873367	OTTHUMT00000318177 // NCOR2

5360	chr12	-	125051910	125051934	NM_006312 // NCOR2
5361	chr12	-	125668816	125668846	---
5362	chr12	-	127174884	127175003	---
5363	chr12	-	127758920	127759007	---
5364	chr12	-	128508333	128508362	OTTHUMT00000399705 // OTTHUMG00000168427
5365	chr12	-	131478370	131478415	OTTHUMT00000399377 // OTTHUMG00000168346
5366	chr12	-	132642711	132642742	---
5367	chr12	-	133404462	133404486	---
5368	chr12	-	133411980	133412086	---
5369	chr12	-	133706862	133707017	NM_001277291 // ZNF891
5370	chr13	+	19762893	19762917	---
5371	chr13	+	23507816	23508500	---
5372	chr13	+	23898518	23898608	NM_000231 // SGCG
5373	chr13	+	25877258	25877282	ENST00000481980 // NUPL1
5374	chr13	+	26125517	26125541	NM_016529 // ATP8A2
5375	chr13	+	26127996	26128020	NM_016529 // ATP8A2
5376	chr13	+	27737001	27737060	ENST00000440657 // USP12-AS1
5377	chr13	+	28197467	28197548	NM_015972 // POLR1D
5378	chr13	+	28494180	28494208	NM_000209 // PDX1
5379	chr13	+	29242615	29242707	NM_015932 // POMP
5380	chr13	+	29246476	29246548	NM_015932 // POMP
5381	chr13	+	29252251	29252365	NM_015932 // POMP
5382	chr13	+	32041023	32041073	---
5383	chr13	+	32798388	32798412	NM_023037 // FRY
5384	chr13	+	33334747	33334771	NM_015032 // PDS5B
5385	chr13	+	40637747	40637774	---
5386	chr13	+	44032610	44032650	OTTHUMT00000044716 // ENOX1-AS2
5387	chr13	+	45944512	45944536	ENST00000522859 // TPT1-AS1
5388	chr13	+	46627000	46627050	NR_046226 // CPB2-AS1
5389	chr13	+	49720578	49720602	AK056071 // FNDC3A
5390	chr13	+	49841641	49841773	NM_030911 // CDADC1
5391	chr13	+	50092181	50092268	NM_001040443 // PHF11
5392	chr13	+	50101359	50101458	ENST00000488605 // PHF11
5393	chr13	+	50571631	50571709	NM_213590 // TRIM13
5394	chr13	+	51102371	51102395	AJ412062 // DLEU1
5395	chr13	+	74993322	74993365	NR_047005 // LINC00381
5396	chr13	+	78036681	78036706	---
5397	chr13	+	78293812	78293842	ENST00000377236 // SLAIN1
5398	chr13	+	98606232	98606256	ENST00000482642 // IPO5

5399	chr13	+	103472905	103472929	AF339793 // BIVM
5400	chr13	+	109704740	109704764	NM_001198950 // MYO16
5401	chr13	+	110706374	110706526	OTTHUMT00000045758 // OTTHUMG00000017341
5402	chr13	+	113909314	113909338	NM_001008895 // CUL4A
5403	chr13	+	113977921	113977945	ENST00000332556 // LAMP1
5404	chr13	+	114006012	114006280	ENST00000419199 // GRTP1-AS1
5405	chr13	+	114586721	114586782	OTTHUMT00000045944 // LINC00453
5406	chr13	+	115089278	115089317	NM_032436 // CHAMP1
5407	chr13	-	20735049	20735135	NM_021954 // GJA3
5408	chr13	-	21007942	21007973	NR_039721 // MIR4499
5409	chr13	-	23471484	23472307	NR_033774 // BASP1P1
5410	chr13	-	24465401	24465425	ENST00000382137 // C1QTNF9B
5411	chr13	-	25460472	25460496	NR_047594 // CENPJ
5412	chr13	-	31624068	31624123	---
5413	chr13	-	32981501	32981750	BC068049 // N4BP2L1
5414	chr13	-	33701648	33701672	NM_178006 // STARD13
5415	chr13	-	36871801	36871825	NM_001198910 // CCDC169-SOHLH2
5416	chr13	-	37524108	37524171	NM_013338 // ALG5
5417	chr13	-	39605734	39605758	NM_025138 // PROSER1
5418	chr13	-	40175021	40175345	NM_005780 // LHFP
5419	chr13	-	41344959	41344983	ENST00000435009 // MRPS31
5420	chr13	-	43463349	43463375	NM_001002264 // EPSTI1
5421	chr13	-	45202705	45202791	---
5422	chr13	-	45515383	45515415	NM_012345 // NUFIP1
5423	chr13	-	46785448	46785472	ENST00000398576 // LCP1
5424	chr13	-	47345417	47345504	NM_001984 // ESD
5425	chr13	-	48528309	48528333	NM_003850 // SUCLA2
5426	chr13	-	48562545	48562569	ENST00000470760 // SUCLA2
5427	chr13	-	50235305	50235334	NM_032565 // EBPL
5428	chr13	-	51959359	51959383	OTTHUMT00000045028 // INTS6
5429	chr13	-	52377758	52377782	ENST00000497151 // DHRS12
5430	chr13	-	52686406	52686430	NM_199289 // NEK5
5431	chr13	-	52976678	52976710	NM_018676 // THSD1
5432	chr13	-	53286884	53286967	NM_007015 // LECT1
5433	chr13	-	57711822	57711858	---
5434	chr13	-	73333266	73333290	NM_014953 // DIS3
5435	chr13	-	73348103	73348127	NM_014953 // DIS3
5436	chr13	-	95899299	95899323	NM_005845 // ABCC4
5437	chr13	-	96240141	96240165	ENST00000485031 // DZIP1

5438	chr13	-	97601635	97601713	---
5439	chr13	-	98856127	98856394	---
5440	chr13	-	99356567	99356591	NM_005073 // SLC15A1
5441	chr13	-	99361848	99361872	NM_005073 // SLC15A1
5442	chr13	-	101828701	101828725	NM_052867 // NALCN
5443	chr13	-	111110030	111110065	ENST00000458403 // COL4A2-AS2
5444	chr13	-	111110438	111110511	ENST00000458403 // COL4A2-AS2
5445	chr13	-	111298893	111298917	AK301907 // CARS2
5446	chr13	-	111330331	111330355	ENST00000543487 // CARS2
5447	chr13	-	112985379	112985536	OTTHUMT00000045824 // OTTHUMG00000017366
5448	chr13	-	113805026	113805117	---
5449	chr13	-	113845135	113845159	AK309321 // PCID2
5450	chr13	-	113862854	113862878	NM_001258213 // PCID2
5451	chr13	-	114133230	114133390	---
5452	chr13	-	114535700	114535724	NM_000820 // GAS6
5453	chr14	+	20345393	20345468	ENST00000298642 // OR4K2
5454	chr14	+	20773897	20774191	---
5455	chr14	+	21070862	21070888	AK093210 // LOC254028
5456	chr14	+	21464111	21464135	ENST00000555640 // METTL17
5457	chr14	+	23001452	23001510	---
5458	chr14	+	23842286	23842313	NM_022789 // IL25
5459	chr14	+	23847976	23848000	BC029729 // CMTM5
5460	chr14	+	23945269	23945354	NM_001042635 // NGDN
5461	chr14	+	23946625	23946687	AK124318 // NGDN
5462	chr14	+	24545805	24545829	AL137688 // CPNE6
5463	chr14	+	24563615	24563639	NM_004563 // PCK2
5464	chr14	+	24608044	24608092	NM_006263 // PSME1
5465	chr14	+	24624872	24624896	NM_017999 // RNF31
5466	chr14	+	24677098	24677129	OTTHUMT00000409995 // TSSK4
5467	chr14	+	24775702	24775772	ENST00000267425 // NOP9
5468	chr14	+	24868087	24868268	NM_025081 // NYNRIN
5469	chr14	+	24898501	24898584	ENST00000251343 // KHNYN
5470	chr14	+	24899148	24899183	NM_015299 // KHNYN
5471	chr14	+	27305612	27305660	OTTHUMT00000409034 // OTTHUMG00000170416
5472	chr14	+	28887752	28887784	OTTHUMT00000408803 // OTTHUMG00000170385
5473	chr14	+	29299639	29299704	OTTHUMT00000408705 // OTTHUMG00000170368
5474	chr14	+	35783704	35785665	ENST00000554457 // PSMA6
5475	chr14	+	35786480	35786504	NM_002791 // PSMA6

5476	chr14	+	37125447	37125589	---
5477	chr14	+	38405462	38405486	BC038110 // TTC6
5478	chr14	+	39648245	39648280	ENST00000554902 // PNN
5479	chr14	+	39648610	39648634	NM_002687 // PNN
5480	chr14	+	51054608	51054698	NM_015915 // ATL1
5481	chr14	+	51087367	51087429	NM_015915 // ATL1
5482	chr14	+	52294395	52294419	ENST00000556522 // GNG2
5483	chr14	+	52340674	52340698	BC041446 // GNG2
5484	chr14	+	53684517	53684578	---
5485	chr14	+	55611840	55611973	NR_003225 // LGALS3
5486	chr14	+	55612042	55612105	NR_003225 // LGALS3
5487	chr14	+	58738655	58738694	NR_038123 // PSMA3
5488	chr14	+	58814390	58814414	NM_002892 // ARID4A
5489	chr14	+	58908640	58908674	---
5490	chr14	+	59114265	59114738	NR_046093 // DACT1
5491	chr14	+	60733933	60733991	ENST00000525399 // PPM1A
5492	chr14	+	61448142	61448166	NR_033344 // SLC38A6
5493	chr14	+	62213691	62213715	NM_001530 // HIF1A
5494	chr14	+	62567462	62567785	NM_031914 // SYT16
5495	chr14	+	69446549	69446576	---
5496	chr14	+	71865063	71865124	NR_001276 // SNORD56B
5497	chr14	+	73550232	73550256	NM_021239 // RBM25
5498	chr14	+	73575894	73575918	---
5499	chr14	+	73614315	73614339	ENST00000556066 // PSEN1
5500	chr14	+	73673044	73673068	ENST00000555867 // PSEN1
5501	chr14	+	73718751	73718775	NM_173462 // PAPLN
5502	chr14	+	74086544	74086569	NM_001037162 // ACOT6
5503	chr14	+	74416815	74416839	NM_182480 // COQ6
5504	chr14	+	74707890	74707969	NM_182894 // VSX2
5505	chr14	+	76091002	76091055	NM_017791 // FLVCR2
5506	chr14	+	76070531	76070621	ENST00000364226 // RNA5SP387
5507	chr14	+	76211868	76211892	NM_015072 // TTLL5
5508	chr14	+	76673039	76673206	ENST00000261530 // GPATCH2L
5509	chr14	+	77295447	77295471	AK125722 // C14orf166B
5510	chr14	+	77310774	77310798	ENST00000393774 // C14orf166B
5511	chr14	+	77391094	77391118	---
5512	chr14	+	85995371	85995446	OTTHUMT00000413192 // OTTHUMG00000171371
5513	chr14	+	88936347	88936371	OTTHUMT00000410283 // SPATA7
5514	chr14	+	90485693	90485717	NM_018319 // TDP1
5515	chr14	+	90731457	90731505	NM_002802 // PSMC1
5516	chr14	+	91592787	91592883	NR_003709 // SNORA11B

5517	chr14	+	93305793	93306084	NM_005113 // GOLGA5
5518	chr14	+	93359618	93359819	---
5519	chr14	+	93995636	93995660	NM_020818 // UNC79
5520	chr14	+	94405916	94405944	OTTHUMT00000412854 // OTTHUMG00000171299
5521	chr14	+	95107106	95107166	NR_015340 // SERPINA13P
5522	chr14	+	96709041	96710230	NM_000623 // BDKRB2
5523	chr14	+	96887765	96887840	ENST00000554313 // AK7
5524	chr14	+	96904188	96904243	NM_152327 // AK7
5525	chr14	+	96968717	96968741	NM_032632 // PAPOLA
5526	chr14	+	98047602	98047862	OTTHUMT00000413540 // OTTHUMG00000171465
5527	chr14	+	99961844	99961868	NM_001099402 // CCNK
5528	chr14	+	100599058	100599082	NM_016337 // EVL
5529	chr14	+	101192871	101192912	ENST00000392848 // DLK1
5530	chr14	+	101419707	101419747	NR_003195 // SNORD114-3
5531	chr14	+	101442162	101442223	NR_003211 // SNORD114-18
5532	chr14	+	101454498	101454544	NR_003220 // SNORD114-27
5533	chr14	+	101491356	101491413	NR_029872 // MIR380
5534	chr14	+	101491912	101491968	NR_031713 // MIR1197
5535	chr14	+	101492357	101492432	NR_030406 // MIR758
5536	chr14	+	101495979	101496014	NR_030174 // MIR494
5537	chr14	+	101506419	101506454	NR_030266 // MIR376A2
5538	chr14	+	101513663	101513695	NR_030256 // MIR539
5539	chr14	+	101521599	101521650	NR_030408 // MIR668
5540	chr14	+	101538347	101538665	NR_047664 // MEG9
5541	chr14	+	101742829	101744314	---
5542	chr14	+	102263844	102263868	---
5543	chr14	+	102387532	102387556	---
5544	chr14	+	102515016	102515040	---
5545	chr14	+	102783854	102783878	NM_001267827 // ZNF839
5546	chr14	+	103396955	103396979	NM_030943 // AMN
5547	chr14	+	103573761	103573851	NM_001077594 // EXOC3L4
5548	chr14	+	103801454	103801478	NM_183004 // EIF5
5549	chr14	+	104605549	104605597	NM_015656 // KIF26A
5550	chr14	+	105169696	105169790	NM_022489 // INF2
5551	chr14	+	105225883	105225946	NM_006427 // SIVA1
5552	chr14	+	105371475	105371501	OTTHUMT00000410294 // OTTHUMG00000170764
5553	chr14	+	105956635	105956753	ENST00000443229 // C14orf80
5554	chr14	-	20232073	20232166	---
5555	chr14	-	20614286	20614314	---

5556	chr14	-	21465840	21465969	---
5557	chr14	-	21491070	21491094	ENST00000557167 // NDRG2
5558	chr14	-	21927301	21928160	NM_032846 // RAB2B
5559	chr14	-	23047812	23047867	---
5560	chr14	-	23233420	23233447	---
5561	chr14	-	23424331	23424360	NM_001166269 // HAUS4
5562	chr14	-	23445676	23445700	NM_032876 // AJUBA
5563	chr14	-	23479324	23479362	ENST00000299088 // C14orf93
5564	chr14	-	23572903	23573015	BC153822 // LOC100128908
5565	chr14	-	24029269	24029293	ENST00000554892 // AP1G2
5566	chr14	-	24034219	24034243	AK307696 // AP1G2
5567	chr14	-	24038795	24038824	NM_032452 // JPH4
5568	chr14	-	24583932	24584193	BX161381 // NRL
5569	chr14	-	24610124	24610148	NM_016049 // EMC9
5570	chr14	-	24613427	24613451	NM_002818 // PSME2
5571	chr14	-	24655625	24655649	NR_051979 // IPO4
5572	chr14	-	24708894	24708992	NM_001099274 // TINF2
5573	chr14	-	24765964	24766024	NM_001136050 // DHRS1
5574	chr14	-	25479767	25479831	BC009499 // STXBP6
5575	chr14	-	26949293	26949346	NM_002515 // NOVA1
5576	chr14	-	35253084	35253108	NM_013448 // BAZ1A
5577	chr14	-	36041825	36041849	NM_014990 // RALGAPA1
5578	chr14	-	37198721	37198771	NM_030631 // SLC25A21
5579	chr14	-	37203739	37203766	NM_030631 // SLC25A21
5580	chr14	-	42512819	42513018	---
5581	chr14	-	45237203	45237229	---
5582	chr14	-	47613376	47613400	NM_001113498 // MDGA2
5583	chr14	-	49410653	49410717	---
5584	chr14	-	49544175	49544223	---
5585	chr14	-	50295341	50295365	NM_004713 // NEMF
5586	chr14	-	50296038	50296062	---
5587	chr14	-	51134595	51134619	NM_021818 // SAV1
5588	chr14	-	51428368	51428717	AK127576 // FLJ45671
5589	chr14	-	55448277	55448301	NM_007086 // WDHD1
5590	chr14	-	61447572	61447600	OTTHUMT00000412833 // TRMT5
5591	chr14	-	62570105	62570499	OTTHUMT00000411702 // OTTHUMG00000171107
5592	chr14	-	64009519	64009822	NM_006246 // PPP2R5E
5593	chr14	-	65216064	65216088	NM_001024858 // SPTB
5594	chr14	-	65438761	65438785	NM_198686 // RAB15
5595	chr14	-	65543112	65543136	NR_073137 // MAX
5596	chr14	-	65544721	65544748	NR_073137 // MAX

5597	chr14	-	68117971	68118011	NM_006370 // VTI1B
5598	chr14	-	68236335	68236359	NM_015346 // ZFYVE26
5599	chr14	-	70826250	70826294	NM_016468 // COX16
5600	chr14	-	73376164	73376196	---
5601	chr14	-	74973969	74973993	NM_000428 // LTBP2
5602	chr14	-	75576547	75576571	NM_033116 // NEK9
5603	chr14	-	75593418	75593442	NM_033116 // NEK9
5604	chr14	-	76968504	76968588	---
5605	chr14	-	77279145	77279170	NM_015305 // ANGEL1
5606	chr14	-	77490916	77491650	NM_024496 // IRF2BPL
5607	chr14	-	77808137	77808297	NM_213601 // TMED8
5608	chr14	-	78063599	78063658	NM_004863 // SPTLC2
5609	chr14	-	81972458	81972482	NM_005065 // SEL1L
5610	chr14	-	82282669	82282706	---
5611	chr14	-	88431853	88431877	NM_000153 // GALC
5612	chr14	-	88500936	88501026	OTTHUMT00000410155 // OTTHUMG00000170739
5613	chr14	-	89083140	89083164	NM_183387 // EML5
5614	chr14	-	89750772	89750796	---
5615	chr14	-	90099595	90099788	OTTHUMT00000411021 // OTTHUMG00000170975
5616	chr14	-	91059936	91059960	NM_001010854 // TTC7B
5617	chr14	-	92181330	92181410	---
5618	chr14	-	96790063	96790124	---
5619	chr14	-	100840351	100840375	ENST00000557722 // WARS
5620	chr14	-	101034277	101034308	NM_001159531 // BEGAIN
5621	chr14	-	101822458	101822488	---
5622	chr14	-	102547254	102547754	NM_001017963 // HSP90AA1
5623	chr14	-	102974995	102975050	NM_152326 // ANKRD9
5624	chr14	-	104149285	104150244	---
5625	chr14	-	104178360	104178384	AK124498 // XRCC3
5626	chr14	-	104251158	104251182	NM_015316 // PPP1R13B
5627	chr14	-	104346302	104346415	---
5628	chr14	-	105059675	105059718	ENST00000556573 // TMEM179
5629	chr14	-	105618580	105618604	NM_002226 // JAG2
5630	chr14	-	105678466	105678490	NM_001519 // BRF1
5631	chr14	-	105781718	105781742	NM_001242786 // BRF1
5632	chr14	-	106115128	106115207	OTTHUMT00000380292 // OTTHUMG00000164792
5633	chr14	-	106354409	106354436	ENST00000390572 // IGHD2-21
5634	chr14	-	106363815	106363843	---
5635	chr14	-	106973686	106973733	---

5636	chr15	+	22921594	22921618	AK125936 // CYFIP1
5637	chr15	+	23264919	23264946	---
5638	chr15	+	24646620	24646655	---
5639	chr15	+	25355611	25355635	BX648788 // SNRPN
5640	chr15	+	25338999	25339120	BC080646 // SNRPN
5641	chr15	+	25427176	25427235	AF400492 // SNRPN
5642	chr15	+	25438701	25438768	AF400496 // SNRPN
5643	chr15	+	25448966	25449020	AF400497 // SNRPN
5644	chr15	+	26378855	26378879	---
5645	chr15	+	27113890	27113933	NM_000810 // GABRA5
5646	chr15	+	31110171	31110196	---
5647	chr15	+	31696126	31696156	AK127052 // LOC100499221
5648	chr15	+	33491534	33491568	---
5649	chr15	+	34310527	34310551	BC041805 // CHRM5
5650	chr15	+	36003994	36004035	NR_038251 // DPH6-AS1
5651	chr15	+	36793789	36793898	---
5652	chr15	+	38826390	38826484	---
5653	chr15	+	40322589	40322613	NM_001013703 // EIF2AK4
5654	chr15	+	40532140	40532164	NM_020168 // PAK6
5655	chr15	+	41102220	41102244	AB209224 // ZFYVE19
5656	chr15	+	41247633	41247725	NM_024111 // CHAC1
5657	chr15	+	41861139	41861163	NM_006293 // TYRO3
5658	chr15	+	42111021	42111045	NM_014994 // MAPKBP1
5659	chr15	+	42944736	42944760	NM_020759 // STARD9
5660	chr15	+	43477697	43477763	NM_012142 // CCNDBP1
5661	chr15	+	43888732	43888756	AK296472 // CKMT1B
5662	chr15	+	43891098	43891122	NM_020990 // CKMT1B
5663	chr15	+	43891593	43891617	AK295776 // CKMT1A
5664	chr15	+	43989508	43989543	---
5665	chr15	+	43990912	43990936	NM_001015001 // CKMT1A
5666	chr15	+	45258398	45258424	ENST00000340827 // C15orf43
5667	chr15	+	45557801	45557850	NM_004212 // SLC28A2
5668	chr15	+	45722760	45722835	ENST00000396650 // C15orf48
5669	chr15	+	45981242	45981371	NM_021199 // SQRDL
5670	chr15	+	45983183	45983222	NM_021199 // SQRDL
5671	chr15	+	48059258	48059282	NM_153617 // SEMA6D
5672	chr15	+	48284909	48284967	---
5673	chr15	+	50648131	50648262	NR_024490 // GABPB1-AS1
5674	chr15	+	51692391	51692436	NM_181789 // GLDN
5675	chr15	+	51661268	51661307	OTTHUMT00000418933 // OTTHUMG00000172523
5676	chr15	+	57600118	57600655	---

5677	chr15	+	57668173	57668197	---
5678	chr15	+	57998305	57998329	AY334562 // GCOM1
5679	chr15	+	58813510	58813839	---
5680	chr15	+	59186176	59186261	---
5681	chr15	+	59752184	59752276	NM_152450 // FAM81A
5682	chr15	+	62745840	62745864	OTTHUMT00000416579 // TLN2
5683	chr15	+	62990011	62990035	NM_015059 // TLN2
5684	chr15	+	63076107	63076131	BX648146 // TLN2
5685	chr15	+	63335835	63335859	AK092051 // TPM1
5686	chr15	+	63845705	63845729	ENST00000558925 // USP3
5687	chr15	+	63855141	63855165	NM_006537 // USP3
5688	chr15	+	64736877	64736901	OTTHUMT00000418129 // TRIP4
5689	chr15	+	65209624	65209648	NM_182703 // ANKDD1A
5690	chr15	+	65218303	65218328	NM_182703 // ANKDD1A
5691	chr15	+	65944069	65944093	NM_004727 // SLC24A1
5692	chr15	+	67709303	67709327	NM_001031715 // IQCH
5693	chr15	+	67819352	67819423	ENST00000342683 // C15orf61
5694	chr15	+	69728058	69728082	NM_138555 // KIF23
5695	chr15	+	72039254	72039278	NM_024817 // THSD4
5696	chr15	+	72102896	72102961	NM_016346 // NR2E3
5697	chr15	+	72110110	72110358	NM_014249 // NR2E3
5698	chr15	+	72947038	72947067	NM_001038640 // GOLGA6A
5699	chr15	+	74559020	74559044	NM_025055 // CCDC33
5700	chr15	+	75550899	75550928	NM_001038640 // GOLGA6A
5701	chr15	+	75557670	75557714	NM_001164404 // GOLGA6C
5702	chr15	+	75560644	75560691	NM_001038640 // GOLGA6A
5703	chr15	+	75584920	75584967	NM_001038640 // GOLGA6A
5704	chr15	+	76462157	76462181	ENST00000388942 // C15orf27
5705	chr15	+	78837229	78837282	NM_002789 // PSMA4
5706	chr15	+	81041978	81042005	NM_021214 // ABHD17C
5707	chr15	+	83657870	83657911	NM_031452 // FAM103A1
5708	chr15	+	83659420	83659730	NM_031452 // FAM103A1
5709	chr15	+	85229856	85229918	---
5710	chr15	+	90118724	90118748	ENST00000268138 // TICRR
5711	chr15	+	90144730	90144754	NM_152259 // TICRR
5712	chr15	+	90161394	90161418	NM_152259 // TICRR
5713	chr15	+	90768778	90768802	ENST00000561252 // SEMA4B
5714	chr15	+	90898584	90898608	ENST00000560038 // ZNF774
5715	chr15	+	91030236	91030260	NM_003870 // IQGAP1
5716	chr15	+	91044895	91044919	NM_003870 // IQGAP1
5717	chr15	+	91181720	91181744	NM_022769 // CRTC3
5718	chr15	+	91424533	91424617	NM_002569 // FURIN

5719	chr15	+	91448549	91448573	NM_006122 // MAN2A2
5720	chr15	+	91454620	91454644	NM_006122 // MAN2A2
5721	chr15	+	91809963	91810101	ENST00000553727 // SV2B
5722	chr15	+	92960777	92960914	---
5723	chr15	+	96992803	96992950	---
5724	chr15	+	98827316	98827525	OTTHUMT00000415222 // OTTHUMG00000171823
5725	chr15	+	99872156	99872180	ENST00000558890 // LRRC28
5726	chr15	+	101567507	101567531	NM_024652 // LRRK1
5727	chr15	+	102513425	102513450	NR_003659 // WASH3P
5728	chr15	-	24587900	24587932	---
5729	chr15	-	27403418	27403541	---
5730	chr15	-	28361898	28361922	NM_004667 // HERC2
5731	chr15	-	28419650	28419674	NM_004667 // HERC2
5732	chr15	-	28424297	28424321	NM_004667 // HERC2
5733	chr15	-	29443982	29444006	NM_015307 // FAM189A1
5734	chr15	-	31848950	31849692	AK126002 // OTUD7A
5735	chr15	-	32743141	32743207	NM_001277308 // GOLGA8O
5736	chr15	-	34177826	34177870	ENST00000558136 // AVEN
5737	chr15	-	38856981	38857005	NM_005739 // RASGRP1
5738	chr15	-	40328013	40328482	NM_003134 // SRP14
5739	chr15	-	40584076	40584100	NM_004573 // PLCB2
5740	chr15	-	41518657	41518715	AK302864 // EXD1
5741	chr15	-	41799773	41799815	NM_002344 // LTK
5742	chr15	-	42146359	42146383	NM_016642 // SPTBN5
5743	chr15	-	42362199	42362223	NM_178034 // PLA2G4D
5744	chr15	-	42375421	42375498	NM_178034 // PLA2G4D
5745	chr15	-	42836292	42836322	NM_153260 // LRRC57
5746	chr15	-	43738704	43738728	NM_001141980 // TP53BP1
5747	chr15	-	43903123	43903147	NM_153700 // STRC
5748	chr15	-	43904190	43904214	NM_153700 // STRC
5749	chr15	-	44165896	44165920	NM_032892 // FRMD5
5750	chr15	-	45398807	45398831	NM_014080 // DUOX2
5751	chr15	-	45421228	45421325	NM_144565 // DUOXA1
5752	chr15	-	45421438	45421462	ENST00000559644 // DUOXA1
5753	chr15	-	47426252	47426280	---
5754	chr15	-	48106286	48106373	OTTHUMT00000416879 // OTTHUMG00000172113
5755	chr15	-	48779585	48779609	NM_000138 // FBN1
5756	chr15	-	48797242	48797266	NM_000138 // FBN1
5757	chr15	-	49182980	49183004	NM_203349 // SHC4
5758	chr15	-	49659692	49659716	NM_152647 // FAM227B

5759	chr15	-	51018283	51018310	ENST00000559527 // SPPL2A
5760	chr15	-	51040209	51040233	ENST00000560288 // SPPL2A
5761	chr15	-	53905908	53905932	NR_102334 // WDR72
5762	chr15	-	59190731	59190755	AK131242 // SLTM
5763	chr15	-	59971614	59971688	ENST00000477543 // BNIP2
5764	chr15	-	62936970	62937310	BC014404 // MGC15885
5765	chr15	-	62980030	62980094	---
5766	chr15	-	63445591	63446199	NM_015920 // RPS27L
5767	chr15	-	63619359	63619415	NM_001218 // CA12
5768	chr15	-	63922866	63922890	ENST00000561348 // HERC1
5769	chr15	-	64356612	64356636	ENST00000559306 // DAPK2
5770	chr15	-	64364814	64365113	NM_032231 // FAM96A
5771	chr15	-	64665906	64665943	---
5772	chr15	-	65809589	65809613	OTTHUMT00000418495 // DPP8
5773	chr15	-	65809734	65809758	AK296915 // DPP8
5774	chr15	-	67546936	67546960	NM_024666 // AAGAB
5775	chr15	-	70345290	70345314	AB209672 // TLE3
5776	chr15	-	72490081	72490111	NM_001012642 // GRAMD2
5777	chr15	-	72524036	72524060	BC094767 // PKM
5778	chr15	-	74374862	74374891	NM_001038640 // GOLGA6A
5779	chr15	-	74495421	74495445	NM_001142618 // STRA6
5780	chr15	-	74709683	74709781	NM_003612 // SEMA7A
5781	chr15	-	75893498	75893531	NM_005701 // SNUPN
5782	chr15	-	76352012	76352037	AK311204 // NRG4
5783	chr15	-	77336716	77338334	NM_005724 // TSPAN3
5784	chr15	-	78578683	78578707	ENST00000559940 // WDR61
5785	chr15	-	78913605	78913629	NM_000743 // CHRNA3
5786	chr15	-	78917552	78917576	NM_000750 // CHRNB4
5787	chr15	-	80125868	80125896	OTTHUMT00000416722 // OTTHUMG00000172076
5788	chr15	-	80253415	80253446	NM_004049 // BCL2A1
5789	chr15	-	80736628	80737354	ENST00000548231 // LOC100133746
5790	chr15	-	81195439	81195505	OTTHUMT00000417729 // OTTHUMG00000172298
5791	chr15	-	81631052	81631076	NM_001080532 // TMC3
5792	chr15	-	83438504	83438528	NM_001007122 // FSD2
5793	chr15	-	88472256	88472280	AK309695 // NTRK3
5794	chr15	-	88476306	88476330	NM_001012338 // NTRK3
5795	chr15	-	89006191	89006806	AK074053 // MRPL46
5796	chr15	-	89442279	89442303	NM_005928 // MFGE8
5797	chr15	-	89763003	89763074	NM_000326 // RLBP1

5798	chr15	-	89873452	89873476	NM_002693 // POLG
5799	chr15	-	89876760	89876784	NM_002693 // POLG
5800	chr15	-	89901823	89901879	---
5801	chr15	-	90192466	90192490	NM_198525 // KIF7
5802	chr15	-	90233822	90233863	NM_003847 // PEX11A
5803	chr15	-	90293922	90293951	NM_018670 // MESP1
5804	chr15	-	91298504	91298542	---
5805	chr15	-	91551118	91551142	NM_018668 // VPS33B
5806	chr15	-	95831392	95831421	---
5807	chr15	-	97725803	97725886	---
5808	chr15	-	99190539	99190587	---
5809	chr15	-	100802608	100802632	NM_139057 // ADAMTS17
5810	chr15	-	100614292	100614378	---
5811	chr15	-	101590948	101590984	---
5812	chr15	-	101811350	101811744	NM_203472 // VIMP
5813	chr15	-	102191988	102192023	ENST00000560013 // TM2D3
5814	chr15	-	102192073	102192097	ENST00000560013 // TM2D3
5815	chr15	-	102500059	102500130	ENST00000422679 // MIR1302-11
5816	chr16	+	216722	216765	NM_001003938 // HBM
5817	chr16	+	223600	223690	NM_000517 // HBA2
5818	chr16	+	310676	310700	---
5819	chr16	+	311357	311381	---
5820	chr16	+	603564	603887	NM_005632 // SOLH
5821	chr16	+	646344	646379	ENST00000509637 // RAB40C
5822	chr16	+	708617	708641	NM_145294 // WDR90
5823	chr16	+	772085	772125	NM_023933 // FAM173A
5824	chr16	+	778800	778825	NM_032304 // HAGHL
5825	chr16	+	845287	845311	NM_022092 // CHTF18
5826	chr16	+	1413121	1413196	NM_032520 // GNPTG
5827	chr16	+	1718131	1718155	NM_020825 // CRAMP1L
5828	chr16	+	2025235	2025259	NM_006453 // TBL3
5829	chr16	+	2130248	2130272	NM_000548 // TSC2
5830	chr16	+	2202991	2203018	NM_014353 // RAB26
5831	chr16	+	2225327	2225393	NM_032271 // TRAF7
5832	chr16	+	2282470	2282519	NM_004424 // E4F1
5833	chr16	+	2285268	2285292	NM_004424 // E4F1
5834	chr16	+	2563881	2563988	NM_001694 // ATP6V0C
5835	chr16	+	2579743	2579767	ENST00000302956 // CEMP1
5836	chr16	+	2749826	2749851	NM_018992 // KCTD5
5837	chr16	+	2819666	2819749	AL833672 // SRRM2
5838	chr16	+	2986581	2986698	AK057022 // FLYWCH1
5839	chr16	+	2988338	2988362	NM_032296 // FLYWCH1

5840	chr16	+	3017997	3018021	NM_024507 // KREMEN2
5841	chr16	+	3712781	3712805	AK300914 // DNASE1
5842	chr16	+	10996014	10996038	NM_000246 // CIITA
5843	chr16	+	11387067	11387129	---
5844	chr16	+	14995521	14995902	OTTHUMT00000409539 // MIR3179-1
5845	chr16	+	16418751	16418775	NR_036447 // PKD1P1
5846	chr16	+	16429933	16429957	NR_036447 // PKD1P1
5847	chr16	+	19934892	19935025	---
5848	chr16	+	22189455	22189509	ENST00000330898 // SDR42E2
5849	chr16	+	23223391	23223415	NM_001039 // SCNN1G
5850	chr16	+	24366223	24366288	NM_006539 // CACNG3
5851	chr16	+	24566940	24567012	NM_006910 // RBBP6
5852	chr16	+	24567142	24567195	NM_006910 // RBBP6
5853	chr16	+	24570925	24570949	NM_006910 // RBBP6
5854	chr16	+	24576130	24576154	NM_006910 // RBBP6
5855	chr16	+	24582297	24583448	NM_006910 // RBBP6
5856	chr16	+	28997470	28997495	NM_014387 // LAT
5857	chr16	+	29086165	29086267	NR_003369 // RRN3P2
5858	chr16	+	29465961	29466031	NM_001014999 // SLX1A
5859	chr16	+	29761725	29761769	---
5860	chr16	+	29999361	29999462	NM_016151 // TAOK2
5861	chr16	+	30205303	30205373	NM_001014999 // SLX1A
5862	chr16	+	30521683	30521707	NM_002209 // ITGAL
5863	chr16	+	30677838	30677862	NM_001105079 // FBRS
5864	chr16	+	30722095	30722119	NM_006662 // SRCAP
5865	chr16	+	30732039	30732063	NM_006662 // SRCAP
5866	chr16	+	31484545	31484569	NM_015927 // TGFB1I1
5867	chr16	+	31717316	31717355	ENST00000254109 // CLUHP3
5868	chr16	+	31925827	31926410	NM_003414 // ZNF267
5869	chr16	+	31927743	31927769	NM_003414 // ZNF267
5870	chr16	+	32070641	32070697	OTTHUMT00000432529 // OTTHUMG00000176557
5871	chr16	+	32759385	32759468	AK300387 // LOC100289574
5872	chr16	+	33778692	33778735	OTTHUMT00000431831 // OTTHUMG00000176371
5873	chr16	+	48370317	48370358	ENST00000416006 // LONP2
5874	chr16	+	50104092	50104116	NM_182922 // HEATR3
5875	chr16	+	50112680	50112768	NM_182922 // HEATR3
5876	chr16	+	50778744	50778768	NM_015247 // CYLD
5877	chr16	+	52306829	52306853	AK093211 // LOC283854
5878	chr16	+	53190259	53190283	NM_025134 // CHD9

5879	chr16	+	55358040	55358655	ENST00000290552 // IRX6
5880	chr16	+	55584900	55584992	NM_017839 // LPCAT2
5881	chr16	+	55690575	55690604	NM_001172504 // SLC6A2
5882	chr16	+	55725850	55725964	NM_001172504 // SLC6A2
5883	chr16	+	55735779	55735803	NM_001172504 // SLC6A2
5884	chr16	+	56368692	56368716	NM_020988 // GNAO1
5885	chr16	+	56380439	56380907	NM_138736 // GNAO1
5886	chr16	+	56279456	56279516	NR_037499 // MIR3935
5887	chr16	+	56868304	56868328	NM_014669 // NUP93
5888	chr16	+	56904074	56904098	NM_000339 // SLC12A3
5889	chr16	+	56995943	56995997	NM_000078 // CETP
5890	chr16	+	57085471	57085495	NM_032206 // NLRC5
5891	chr16	+	57103805	57103829	NM_032206 // NLRC5
5892	chr16	+	57406481	57406535	NM_002996 // CX3CL1
5893	chr16	+	57438719	57438746	NM_002987 // CCL17
5894	chr16	+	57576563	57576591	ENST00000349457 // GPR114
5895	chr16	+	57790350	57790374	NM_005886 // KATNB1
5896	chr16	+	58538115	58538139	NR_040072 // NDRG4
5897	chr16	+	59765276	59765307	---
5898	chr16	+	66511479	66511528	NM_001178020 // BEAN1
5899	chr16	+	66887328	66887359	NM_005182 // CA7
5900	chr16	+	67003629	67003662	NM_024922 // CES3
5901	chr16	+	67198215	67198239	---
5902	chr16	+	67679074	67679098	NM_001013838 // RLTPR
5903	chr16	+	67679630	67679654	NM_001013838 // RLTPR
5904	chr16	+	67855054	67855078	NM_018430 // TSNAXIP1
5905	chr16	+	68225722	68225849	EU887610 // NFATC3
5906	chr16	+	72139134	72139158	NM_014003 // DHX38
5907	chr16	+	73126980	73127109	NR_027756 // HCCAT5
5908	chr16	+	77775886	77775910	NM_001105663 // NUDT7
5909	chr16	+	83711991	83712015	NM_001257 // CDH13
5910	chr16	+	83998745	83999057	NM_182981 // OSGIN1
5911	chr16	+	84486931	84486955	NM_014861 // ATP2C2
5912	chr16	+	85111110	85111134	NM_014732 // KIAA0513
5913	chr16	+	85682307	85682331	NM_014615 // GSE1
5914	chr16	+	86052363	86052405	---
5915	chr16	+	86716091	86716330	---
5916	chr16	+	86771482	86774207	---
5917	chr16	+	88218802	88218919	AK123554 // LOC100506735
5918	chr16	+	88219596	88220357	AK123554 // LOC100506735
5919	chr16	+	88580824	88580903	NM_153813 // ZFPM1
5920	chr16	+	88593290	88593321	NM_153813 // ZFPM1

5921	chr16	+	89168761	89168787	OTTHUMT00000395822 // ACSF3
5922	chr16	+	89258711	89258836	NM_004933 // CDH15
5923	chr16	+	89287405	89287511	NM_001201407 // ZNF778
5924	chr16	+	89364559	89364693	---
5925	chr16	+	89627636	89627660	NM_000977 // RPL13
5926	chr16	+	89998308	89998332	AK122757 // TUBB3
5927	chr16	+	89999194	89999218	---
5928	chr16	+	90000948	90000972	AK127418 // TUBB3
5929	chr16	+	90021602	90021639	NM_207514 // DEF8
5930	chr16	-	67906	67930	ENST00000470725 // WASH4P
5931	chr16	-	776173	776197	AK128538 // CCDC78
5932	chr16	-	780453	780477	NM_022493 // NARFL
5933	chr16	-	1272229	1272328	NM_012467 // TPSG1
5934	chr16	-	1470700	1470724	ENST00000442039 // C16orf91
5935	chr16	-	1872313	1872337	NM_005326 // HAGH
5936	chr16	-	2002878	2003015	NM_005061 // RPL3L
5937	chr16	-	2029080	2029104	NM_144603 // NOXO1
5938	chr16	-	2143068	2143092	NM_001009944 // PKD1
5939	chr16	-	2155815	2155839	ENST00000486339 // LOC101060429
5940	chr16	-	2834108	2834478	NM_152891 // PRSS33
5941	chr16	-	3105857	3105946	BC045731 // LOC100507419
5942	chr16	-	3283795	3283819	NM_003454 // ZNF200
5943	chr16	-	3432408	3432591	NM_017810 // ZSCAN32
5944	chr16	-	3447520	3447544	NM_017810 // ZSCAN32
5945	chr16	-	3633142	3633412	NM_032444 // SLX4
5946	chr16	-	4308096	4308190	NM_003223 // TFAP4
5947	chr16	-	4457513	4457537	NM_001201479 // CORO7-PAM16
5948	chr16	-	4812296	4812323	NM_021646 // ZNF500
5949	chr16	-	11824547	11824605	NM_015914 // TXNDC11
5950	chr16	-	11827839	11827926	NM_015914 // TXNDC11
5951	chr16	-	16276687	16276711	NM_001171 // ABCC6
5952	chr16	-	21875338	21875362	---
5953	chr16	-	28009621	28009719	---
5954	chr16	-	30017568	30017617	NM_003586 // DOC2A
5955	chr16	-	30037992	30038160	NM_031478 // FAM57B
5956	chr16	-	30389755	30389812	NM_052838 // SEPT1
5957	chr16	-	30545637	30545669	NM_023931 // ZNF747
5958	chr16	-	30709457	30709719	NM_001256932 // LOC730183
5959	chr16	-	31072488	31073054	NM_001172668 // ZNF668
5960	chr16	-	31097784	31097808	NM_001039503 // PRSS53
5961	chr16	-	31144572	31144624	NM_002773 // PRSS8

5962	chr16	-	31519113	31519138	NM_022744 // C16orf58
5963	chr16	-	33351953	33351987	OTTHUMT00000432132 // OTTHUMG00000176466
5964	chr16	-	46992939	46993012	NM_005880 // DNAJA2
5965	chr16	-	47192819	47192843	NM_030790 // ITFG1
5966	chr16	-	48117952	48117976	NM_033226 // ABCC12
5967	chr16	-	48173144	48173168	NM_033226 // ABCC12
5968	chr16	-	48281438	48281462	ENST00000537808 // ABCC11
5969	chr16	-	50178502	50178539	---
5970	chr16	-	58001032	58001056	NM_001297 // CNGB1
5971	chr16	-	58004977	58005001	NM_001297 // CNGB1
5972	chr16	-	58193526	58194033	ENST00000563307 // CSNK2A2
5973	chr16	-	58752137	58752168	NM_002080 // GOT2
5974	chr16	-	66048122	66048197	---
5975	chr16	-	67218902	67218943	NM_178516 // EXOC3L1
5976	chr16	-	67432476	67432623	NM_013304 // ZDHHC1
5977	chr16	-	67763583	67763689	NM_020850 // RANBP10
5978	chr16	-	67768806	67768835	NM_020850 // RANBP10
5979	chr16	-	68011590	68011614	NM_022357 // DPEP3
5980	chr16	-	68027048	68027072	NM_022355 // DPEP2
5981	chr16	-	68344249	68344392	NM_032178 // SLC7A6OS
5982	chr16	-	68508515	68508565	---
5983	chr16	-	69599738	69599771	NR_031719 // MIR1538
5984	chr16	-	75238114	75238140	NM_001025200 // CTRB2
5985	chr16	-	75282103	75282224	NM_001170719 // BCAR1
5986	chr16	-	75320628	75320663	---
5987	chr16	-	75567035	75567079	NM_024533 // CHST5
5988	chr16	-	75569026	75569055	NM_024533 // CHST5
5989	chr16	-	75661676	75661700	NM_001130089 // KARS
5990	chr16	-	77328934	77328958	NM_199355 // ADAMTS18
5991	chr16	-	81155192	81155216	NM_052892 // PKD1L2
5992	chr16	-	84982632	84982656	---
5993	chr16	-	85433952	85434192	---
5994	chr16	-	85768799	85768823	ENST00000284245 // C16orf74
5995	chr16	-	85833061	85833094	NM_006067 // EMC8
5996	chr16	-	87296234	87296468	---
5997	chr16	-	87350715	87350739	ENST00000253461 // C16orf95
5998	chr16	-	87874658	87874757	NM_003486 // SLC7A5
5999	chr16	-	88218508	88218536	AK123554 // LOC100506735
6000	chr16	-	88752774	88752805	NM_178310 // SNAI3
6001	chr16	-	89350996	89351748	NM_001256182 // ANKRD11
6002	chr16	-	89774863	89774888	NM_004913 // VPS9D1

6003	chr16	-	89775320	89775359	NM_004913 // VPS9D1
6004	chr16	-	89845216	89845240	NM_000135 // FANCA
6005	chr17	+	1646163	1646187	NM_000934 // SERPINF2
6006	chr17	+	2268538	2268562	NM_014853 // SGSM2
6007	chr17	+	5329562	5329618	NM_001160243 // RPAIN
6008	chr17	+	5984001	5984346	NM_015253 // WSCD1
6009	chr17	+	6014107	6014229	NM_015253 // WSCD1
6010	chr17	+	6347774	6347800	NM_019013 // FAM64A
6011	chr17	+	6757625	6757649	NR_002710 // ALOX12P2
6012	chr17	+	6943335	6943438	NM_201566 // SLC16A13
6013	chr17	+	7246711	7246785	NM_014716 // ACAP1
6014	chr17	+	7284373	7284423	NM_001251902 // TNK1
6015	chr17	+	7320346	7320719	NM_020795 // NLGN2
6016	chr17	+	7482120	7482144	NM_001416 // EIF4A1
6017	chr17	+	7811783	7811807	NM_001005273 // CHD3
6018	chr17	+	7812504	7812528	NM_001005273 // CHD3
6019	chr17	+	7836471	7836622	NM_053051 // CNTROB
6020	chr17	+	8414465	8414506	---
6021	chr17	+	9536270	9536294	NM_145054 // WDR16
6022	chr17	+	9541970	9541994	NM_145054 // WDR16
6023	chr17	+	9578259	9578283	NM_153210 // USP43
6024	chr17	+	9739712	9739736	NM_004246 // GLP2R
6025	chr17	+	9793659	9793683	ENST00000262441 // GLP2R
6026	chr17	+	11672460	11672484	NM_001372 // DNAH9
6027	chr17	+	11828496	11828520	ENST00000581682 // DNAH9
6028	chr17	+	15637356	15637381	OTTHUMT00000444649 // TBC1D26
6029	chr17	+	15668924	15668951	NR_033865 // CDRT15P2
6030	chr17	+	16893444	16893485	OTTHUMT00000131475 // OTTHUMG00000059263
6031	chr17	+	16926501	16926546	---
6032	chr17	+	18054727	18054751	NM_016239 // MYO15A
6033	chr17	+	18058481	18058505	NM_016239 // MYO15A
6034	chr17	+	18064140	18064164	BX538062 // MYO15A
6035	chr17	+	18075854	18075878	AK297179 // MYO15A
6036	chr17	+	18326486	18326602	NR_001443 // LOC339240
6037	chr17	+	18333070	18333104	ENST00000326333 // KRT17P2
6038	chr17	+	18394599	18394636	NM_001040078 // LGALS9C
6039	chr17	+	18622274	18622348	---
6040	chr17	+	18769194	18769218	NM_002767 // PRPSAP2
6041	chr17	+	18991029	18991062	---
6042	chr17	+	18996841	18996873	AK026312 // LOC79999
6043	chr17	+	19117196	19117229	---

6044	chr17	+	19283286	19283393	AB209611 // MAPK7
6045	chr17	+	19483547	19483639	---
6046	chr17	+	20859598	20859622	ENST00000437829 // LOC339260
6047	chr17	+	20979761	20979795	---
6048	chr17	+	21191333	21191371	ENST00000529517 // LOC100996792
6049	chr17	+	27900074	27900100	NM_138349 // TP53I13
6050	chr17	+	27934822	27934846	NM_152345 // ANKRD13B
6051	chr17	+	28295816	28295840	NR_026738 // EFCAB5
6052	chr17	+	29070127	29070205	---
6053	chr17	+	30362597	30362621	NM_052888 // LRRC37B
6054	chr17	+	33331004	33331028	AK125853 // LIG3
6055	chr17	+	34409030	34409055	---
6056	chr17	+	34945775	34945824	NM_024835 // GGNBP2
6057	chr17	+	35294877	35294917	NM_005568 // LHX1
6058	chr17	+	35851640	35851732	ENST00000394386 // DUSP14
6059	chr17	+	36286589	36286614	ENST00000539424 // LOC101060506
6060	chr17	+	36613722	36613746	ENST00000443378 // ARHGAP23
6061	chr17	+	37864688	37864712	NM_004448 // ERBB2
6062	chr17	+	37882757	37882804	NR_039881 // MIR4728
6063	chr17	+	38345051	38345075	AK294642 // RAPGEFL1
6064	chr17	+	38418819	38418884	NM_133264 // WIPF2
6065	chr17	+	38420835	38421277	NM_133264 // WIPF2
6066	chr17	+	39969032	39969078	NM_021939 // FKBP10
6067	chr17	+	39993754	39993838	ENST00000448203 // KLHL10
6068	chr17	+	40937439	40937463	NM_032387 // WNK4
6069	chr17	+	40939363	40939387	NM_032387 // WNK4
6070	chr17	+	40949027	40949051	NM_032387 // WNK4
6071	chr17	+	41570161	41570185	NM_004941 // DHX8
6072	chr17	+	43214415	43214476	NM_001135704 // ACBD4
6073	chr17	+	43923255	43924096	NM_175882 // SPPL2C
6074	chr17	+	43924328	43924429	NM_175882 // SPPL2C
6075	chr17	+	46189937	46189964	NM_152244 // SNX11
6076	chr17	+	46781379	46781639	OTTHUMT00000440736 // OTTHUMG00000178141
6077	chr17	+	46810457	46810481	---
6078	chr17	+	47656208	47656595	NM_007225 // NXPH3
6079	chr17	+	47892872	47892896	AK294602 // KAT7
6080	chr17	+	48141488	48141512	NM_002204 // ITGA3
6081	chr17	+	48157645	48157669	NM_002204 // ITGA3
6082	chr17	+	48355930	48355984	NM_153229 // TMEM92

6083	chr17	+	48435681	48435705	NM_022167 // XYLT2
6084	chr17	+	48551577	48551601	NM_025149 // ACSF2
6085	chr17	+	48602413	48602437	OTTHUMT00000347824 // MYCBPAP
6086	chr17	+	48944884	48945293	NR_038458 // TOB1-AS1
6087	chr17	+	48971131	48971217	ENST00000514358 // TOB1-AS1
6088	chr17	+	56164452	56164581	NM_080677 // DYNLL2
6089	chr17	+	57348297	57348321	NM_182569 // GDPD1
6090	chr17	+	57338109	57338187	---
6091	chr17	+	58506772	58506834	ENST00000269127 // C17orf64
6092	chr17	+	60767286	60767310	NM_006039 // MRC2
6093	chr17	+	61906893	61906917	NM_002805 // PSMC5
6094	chr17	+	63097202	63097313	---
6095	chr17	+	71908291	71908369	---
6096	chr17	+	72211819	72211843	AK296511 // TTYH2
6097	chr17	+	72427369	72427851	ENST00000392627 // GPRC5C
6098	chr17	+	72741482	72741534	NM_001006638 // RAB37
6099	chr17	+	72742651	72742675	NM_001006638 // RAB37
6100	chr17	+	73402160	73402224	NR_037449 // MIR3678
6101	chr17	+	73565122	73565146	NM_004524 // LLGL2
6102	chr17	+	73611655	73611679	NR_003587 // MYO15B
6103	chr17	+	74076902	74076964	AK122638 // ZACN
6104	chr17	+	74946042	74946066	NM_144677 // MGAT5B
6105	chr17	+	76083063	76083087	NM_001142640 // TNRC6C
6106	chr17	+	76127417	76127616	NM_152468 // TMC8
6107	chr17	+	76128901	76128942	NM_152468 // TMC8
6108	chr17	+	76134691	76134723	NM_152468 // TMC8
6109	chr17	+	76142496	76142523	ENST00000340363 // C17orf99
6110	chr17	+	78023909	78023985	NM_017950 // CCDC40
6111	chr17	+	78355911	78355935	AK127358 // RNF213
6112	chr17	+	79077710	79077734	NM_017450 // BAIAP2
6113	chr17	+	79425895	79425919	NM_001080519 // BAHCC1
6114	chr17	+	79680477	79680529	ENST00000574129 // SLC25A10
6115	chr17	+	79858054	79858256	NM_001002244 // ANAPC11
6116	chr17	+	79905023	79905445	---
6117	chr17	+	80010070	80010094	NM_212492 // GPS1
6118	chr17	+	80676385	80676432	NR_046408 // FN3KRP
6119	chr17	+	80888474	80888498	NM_005993 // TBCD
6120	chr17	+	80895728	80895752	AJ006417 // TBCD
6121	chr17	-	729250	729275	NM_022463 // NXN
6122	chr17	-	1463050	1463075	AK303986 // PITPNA
6123	chr17	-	1615075	1615689	NR_028502 // MIR22HG

6124	chr17	-	1684708	1684732	NM_052928 // SMYD4
6125	chr17	-	2233570	2233610	NR_003072 // SNORD91A
6126	chr17	-	2304243	2304388	ENST00000174618 // MNT
6127	chr17	-	2318671	2318726	AK093990 // LOC284009
6128	chr17	-	3433355	3433494	NM_001258205 // TRPV3
6129	chr17	-	3489171	3489195	NM_080704 // TRPV1
6130	chr17	-	3665218	3665242	NM_002208 // ITGAE
6131	chr17	-	3716403	3716567	ENST00000389005 // C17orf85
6132	chr17	-	3850889	3850913	NM_005173 // ATP2A3
6133	chr17	-	4455482	4455506	NM_001105538 // MYBBP1A
6134	chr17	-	4637901	4637946	NM_022059 // CXCL16
6135	chr17	-	4804822	4804895	NM_000080 // CHRNE
6136	chr17	-	4862538	4862764	NM_004890 // SPAG7
6137	chr17	-	4936128	4936152	NM_001104577 // SLC52A1
6138	chr17	-	5026343	5026367	NM_014519 // ZNF232
6139	chr17	-	7120706	7120730	NM_001128827 // DLG4
6140	chr17	-	7169385	7169434	---
6141	chr17	-	7192962	7193025	NM_015982 // YBX2
6142	chr17	-	7834329	7834456	NM_021210 // TRAPPC1
6143	chr17	-	8135084	8135108	NM_025099 // CTC1
6144	chr17	-	8138108	8138132	NM_025099 // CTC1
6145	chr17	-	8455436	8455460	NM_001256012 // MYH10
6146	chr17	-	10254091	10254115	AK294316 // MYH13
6147	chr17	-	15212010	15212056	NM_031898 // TEKT3
6148	chr17	-	15492051	15492226	NM_006382 // CDRT1
6149	chr17	-	16012147	16012171	NM_006311 // NCOR1
6150	chr17	-	16734535	16734570	NR_029392 // KRT16P2
6151	chr17	-	17717168	17717236	NR_030361 // MIR33B
6152	chr17	-	17801931	17801984	NM_001033551 // TOM1L2
6153	chr17	-	17875577	17875601	NM_001033551 // TOM1L2
6154	chr17	-	18176351	18176375	OTTHUMT00000132059 // TOP3A
6155	chr17	-	18924022	18925160	NM_006613 // GRAP
6156	chr17	-	18925277	18925394	NM_006613 // GRAP
6157	chr17	-	19067651	19067684	---
6158	chr17	-	19364016	19364047	---
6159	chr17	-	19607454	19607478	NM_152908 // SLC47A2
6160	chr17	-	19642897	19642921	NM_001135168 // ALDH3A1
6161	chr17	-	19648856	19648880	NM_001135167 // ALDH3A1
6162	chr17	-	20747408	20747556	---
6163	chr17	-	20922397	20922448	NM_015276 // USP22
6164	chr17	-	21780958	21781004	---
6165	chr17	-	26874030	26874105	NM_005148 // UNC119

6166	chr17	-	26898310	26898366	AY359112 // PIGS
6167	chr17	-	27093614	27093684	NM_001077498 // FAM222B
6168	chr17	-	27188684	27188728	NR_039885 // MIR4732
6169	chr17	-	27421059	27421083	NM_078471 // MYO18A
6170	chr17	-	27943326	27943352	NM_032854 // CORO6
6171	chr17	-	28001049	28001073	---
6172	chr17	-	29634931	29634970	AK297087 // EVI2B
6173	chr17	-	32509007	32509117	---
6174	chr17	-	34092936	34093506	NM_024302 // MMP28
6175	chr17	-	34199401	34199463	NM_002985 // CCL5
6176	chr17	-	34205545	34205577	NM_002985 // CCL5
6177	chr17	-	35562692	35562716	NM_198834 // ACACA
6178	chr17	-	35981455	35981550	NM_007010 // DDX52
6179	chr17	-	36697705	36699268	AK295027 // SRCIN1
6180	chr17	-	37224167	37224191	NM_020405 // PLXDC1
6181	chr17	-	37557842	37557872	NM_032875 // FBXL20
6182	chr17	-	37764046	37764182	ENST00000302584 // NEUROD2
6183	chr17	-	38179613	38179637	NM_014815 // MED24
6184	chr17	-	39273506	39273952	NM_033059 // KRTAP4-11
6185	chr17	-	39593664	39593777	NM_006771 // KRT38
6186	chr17	-	40021646	40021684	ENST00000319121 // KLHL11
6187	chr17	-	40272767	40272791	NM_021078 // KAT2A
6188	chr17	-	40861923	40861947	NM_001991 // EZH1
6189	chr17	-	40962786	40962906	NM_003766 // BECN1
6190	chr17	-	41132339	41132363	NM_001142653 // PTGES3L
6191	chr17	-	41623050	41623081	AK298872 // ETV4
6192	chr17	-	42288442	42288466	NM_014233 // UBTF
6193	chr17	-	42338977	42339001	NM_000342 // SLC4A1
6194	chr17	-	42433180	42433204	NM_198475 // FAM171A2
6195	chr17	-	43364272	43364342	NM_003954 // MAP3K14
6196	chr17	-	43487629	43487653	AK300880 // ARHGAP27
6197	chr17	-	45400601	45401363	---
6198	chr17	-	45916210	45916309	NM_138355 // SCRN2
6199	chr17	-	46710987	46711113	---
6200	chr17	-	46703115	46703171	NM_024017 // HOXB9
6201	chr17	-	46846465	46846489	NM_001130918 // TTLL6
6202	chr17	-	47394986	47395087	NM_001145365 // ZNF652
6203	chr17	-	47921449	47921475	NM_170685 // TAC4
6204	chr17	-	53046034	53046062	NM_004375 // COX11
6205	chr17	-	54966568	54966746	NM_005082 // TRIM25
6206	chr17	-	55962709	55962733	NR_073495 // CUEDC1
6207	chr17	-	56065523	56065600	NM_007146 // VEZF1

6208	chr17	-	56296831	56296855	NM_001165927 // MKS1
6209	chr17	-	56585523	56585547	NM_004687 // MTMR4
6210	chr17	-	56606549	56606615	NR_037155 // SEPT4
6211	chr17	-	56643158	56643182	NM_198393 // TEX14
6212	chr17	-	56756893	56757050	---
6213	chr17	-	58075565	58075589	NR_002924 // TBC1D3P1-DHX40P1
6214	chr17	-	59876462	59876561	NM_032043 // BRIP1
6215	chr17	-	60023654	60023678	NM_005121 // MED13
6216	chr17	-	62020267	62020291	NM_000334 // SCN4A
6217	chr17	-	62130207	62130231	NM_001433 // ERN1
6218	chr17	-	63553980	63554088	NM_004655 // AXIN2
6219	chr17	-	65713622	65713732	---
6220	chr17	-	66263333	66263766	NM_001174166 // SLC16A6
6221	chr17	-	66938134	66938158	NM_007168 // ABCA8
6222	chr17	-	70022039	70022118	OTTHUMT00000255305 // OTTHUMG00000132237
6223	chr17	-	70588350	70588438	NR_036488 // LINC00673
6224	chr17	-	71390349	71390373	NM_001144952 // SDK2
6225	chr17	-	71394519	71394543	NM_001144952 // SDK2
6226	chr17	-	73149865	73149890	BC039343 // HN1
6227	chr17	-	73772536	73773289	NM_005324 // H3F3B
6228	chr17	-	73826512	73826536	NM_199242 // UNC13D
6229	chr17	-	73888839	73888872	NM_173547 // TRIM65
6230	chr17	-	74023311	74023335	NM_001988 // EVPL
6231	chr17	-	74303554	74303578	NM_032134 // QRICH2
6232	chr17	-	74309934	74309958	NM_002766 // PRPSAP1
6233	chr17	-	74401339	74401386	NM_022066 // UBE2O
6234	chr17	-	74714597	74714797	NM_015167 // JMJD6
6235	chr17	-	76122392	76122416	NM_001127198 // TMC6
6236	chr17	-	76170973	76171015	NM_003258 // TK1
6237	chr17	-	76816066	76816090	NM_025090 // USP36
6238	chr17	-	76899262	76899297	NM_001243541 // LOC100653515
6239	chr17	-	77926501	77926525	NM_019020 // TBC1D16
6240	chr17	-	78187613	78187641	NM_000199 // SGSH
6241	chr17	-	78188431	78188513	NM_000199 // SGSH
6242	chr17	-	79225099	79225123	NM_138570 // SLC38A10
6243	chr17	-	79514795	79515015	AK054713 // C17orf70
6244	chr17	-	79817736	79817760	ENST00000467086 // P4HB
6245	chr17	-	79880481	79880911	NM_002359 // MAFG
6246	chr17	-	79892109	79892165	AK303852 // PYCR1
6247	chr17	-	79892269	79892293	NM_006907 // PYCR1
6248	chr17	-	79900181	79900228	NM_001145113 // MYADML2

6249	chr17	-	80606313	80606341	NM_019613 // WDR45B
6250	chr17	-	80901720	80901849	NM_001009905 // B3GNTL1
6251	chr17_ctg5_hap1	-	1505015	1505050	---
6252	chr18	+	641426	641450	NM_014410 // CLUL1
6253	chr18	+	8296384	8296408	NM_001105244 // PTPRM
6254	chr18	+	8379173	8379197	NM_001105244 // PTPRM
6255	chr18	+	9250153	9250186	---
6256	chr18	+	10020559	10020821	---
6257	chr18	+	13752365	13752389	NM_003799 // RNMT
6258	chr18	+	20735797	20735851	NM_138375 // CABLES1
6259	chr18	+	21594385	21594410	NM_001135993 // TTC39C
6260	chr18	+	23772509	23773242	NM_144662 // PSMA8
6261	chr18	+	24386466	24386684	---
6262	chr18	+	29171904	29171934	NM_000371 // TTR
6263	chr18	+	29671846	29672181	NM_016271 // RNF138
6264	chr18	+	29797774	29797878	NM_005925 // MEP1B
6265	chr18	+	30349780	30349922	OTTHUMT00000336609 // OTTHUMG00000154695
6266	chr18	+	32409010	32409034	NM_001392 // DTNA
6267	chr18	+	32621557	32621607	NM_014268 // MAPRE2
6268	chr18	+	33243640	33243742	NM_020474 // GALNT1
6269	chr18	+	33709863	33709887	NM_001242875 // ELP2
6270	chr18	+	33744729	33744753	ENST00000541294 // ELP2
6271	chr18	+	43204598	43204622	NM_007163 // SLC14A2
6272	chr18	+	43417817	43417841	NM_213602 // SIGLEC15
6273	chr18	+	50831951	50831975	NM_005215 // DCC
6274	chr18	+	52262212	52262304	NM_173629 // DYNAP
6275	chr18	+	55134413	55134444	OTTHUMT00000357265 // ONECUT2
6276	chr18	+	56532571	56532617	NM_018181 // ZNF532
6277	chr18	+	56822927	56822999	NM_033280 // SEC11C
6278	chr18	+	72956535	72956568	ENST00000560661 // TSHZ1
6279	chr18	-	2507853	2507951	---
6280	chr18	-	6239771	6239811	NM_173464 // L3MBTL4
6281	chr18	-	6729759	6729866	---
6282	chr18	-	6963957	6963981	ENST00000490190 // LAMA1
6283	chr18	-	6974949	6974973	NM_005559 // LAMA1
6284	chr18	-	7117671	7117695	NM_005559 // LAMA1
6285	chr18	-	10699010	10699034	NM_022068 // PIEZO2
6286	chr18	-	11471228	11471266	---
6287	chr18	-	11918854	11918900	---
6288	chr18	-	12533453	12533499	---

6289	chr18	-	15315575	15315754	---
6290	chr18	-	19109309	19109550	NM_052911 // ESCO1
6291	chr18	-	19994593	19994801	NM_172241 // CTAGE1
6292	chr18	-	21162043	21162078	---
6293	chr18	-	21752392	21752416	NM_018030 // OSBPL1A
6294	chr18	-	23539022	23539203	---
6295	chr18	-	25562996	25563045	NM_001792 // CDH2
6296	chr18	-	25616435	25616499	AK302831 // CDH2
6297	chr18	-	26665297	26665330	---
6298	chr18	-	28713868	28714021	NM_024421 // DSC1
6299	chr18	-	28719712	28719808	NM_024421 // DSC1
6300	chr18	-	29206297	29206321	NM_004775 // B4GALT6
6301	chr18	-	33696674	33696716	NM_012319 // SLC39A6
6302	chr18	-	34408646	34408702	NM_015476 // TPGS2
6303	chr18	-	36738955	36739034	---
6304	chr18	-	43596021	43596102	ENST00000591729 // PSTPIP2
6305	chr18	-	47310217	47310283	NM_006111 // ACAA2
6306	chr18	-	54278245	54278324	NR_024546 // TXNL1
6307	chr18	-	54293604	54293687	NR_024546 // TXNL1
6308	chr18	-	71740700	71740862	NM_152676 // FBXO15
6309	chr18	-	72114045	72114454	NM_001044369 // FAM69C
6310	chr18	-	76556276	76556392	---
6311	chr19	+	1053505	1053529	NM_019112 // ABCA7
6312	chr19	+	1064930	1064954	NM_019112 // ABCA7
6313	chr19	+	1276014	1276038	ENST00000469144 // C19orf24
6314	chr19	+	1373127	1373157	NM_032853 // MUM1
6315	chr19	+	1383551	1383576	AK289671 // NDUFS7
6316	chr19	+	1495305	1495363	NM_138393 // REEP6
6317	chr19	+	1922884	1922951	ENST00000472442 // SCAMP4
6318	chr19	+	2273163	2273251	NM_004152 // OAZ1
6319	chr19	+	2344394	2344422	NM_152988 // SPPL2B
6320	chr19	+	3278029	3278100	NR_033342 // CELF5
6321	chr19	+	3728447	3728471	NM_001267560 // TJP3
6322	chr19	+	4359944	4359968	NM_032868 // MPND
6323	chr19	+	5144851	5144875	NM_015015 // KDM4B
6324	chr19	+	6372478	6372758	NM_032306 // ALKBH7
6325	chr19	+	6828433	6828457	NM_005428 // VAV1
6326	chr19	+	6887595	6887619	NM_001974 // EMR1
6327	chr19	+	6890492	6890535	NM_001974 // EMR1
6328	chr19	+	7030623	7030654	NM_001164425 // MBD3L3
6329	chr19	+	7532103	7532236	NM_015318 // ARHGEF18
6330	chr19	+	7535056	7535178	NM_015318 // ARHGEF18

6331	chr19	+	7680560	7680584	NM_001080429 // CAMSAP3
6332	chr19	+	7694681	7694718	NR_033242 // PET100
6333	chr19	+	7912639	7912694	NM_001159944 // EVI5L
6334	chr19	+	7982719	7982744	NM_001195259 // TGFBR3L
6335	chr19	+	8315962	8315987	NM_024552 // CERS4
6336	chr19	+	8553581	8553653	NM_005968 // HNRNPM
6337	chr19	+	9475538	9475562	NM_003451 // ZNF177
6338	chr19	+	9903578	9903748	---
6339	chr19	+	9947511	9947548	NR_038422 // PIN1
6340	chr19	+	10222980	10223004	ENST00000471843 // P2RY11
6341	chr19	+	10662836	10662867	NR_031603 // MIR1238
6342	chr19	+	10738596	10738677	NM_020428 // SLC44A2
6343	chr19	+	10747045	10747114	NM_020428 // SLC44A2
6344	chr19	+	10795100	10795124	NM_004516 // ILF3
6345	chr19	+	10812804	10812828	NM_031209 // QTRT1
6346	chr19	+	10923018	10923042	NM_001005360 // DNM2
6347	chr19	+	11348126	11348155	AF271350 // C19orf80
6348	chr19	+	12924144	12924261	NM_006397 // RNASEH2A
6349	chr19	+	12984647	12984671	NM_014975 // MAST1
6350	chr19	+	13080448	13080474	NM_152654 // DAND5
6351	chr19	+	14640394	14640466	NM_138501 // TECR
6352	chr19	+	15945927	15945983	AK024303 // UCA1
6353	chr19	+	16176916	16177075	OTTHUMT00000460155 // OTTHUMG00000182228
6354	chr19	+	16963892	16963916	NM_015260 // SIN3B
6355	chr19	+	17396507	17396567	NM_152363 // ANKLE1
6356	chr19	+	17535741	17535765	NM_138401 // MVB12A
6357	chr19	+	17599657	17599724	NM_198580 // SLC27A1
6358	chr19	+	17892584	17892608	NM_001161357 // FCHO1
6359	chr19	+	18001739	18001799	NM_000453 // SLC5A5
6360	chr19	+	18496969	18496998	NM_004864 // GDF15
6361	chr19	+	18886517	18886604	NM_015321 // CRTC1
6362	chr19	+	19031397	19031455	NM_019070 // DDX49
6363	chr19	+	23102549	23102576	---
6364	chr19	+	32083208	32083239	FJ211597 // THEG5
6365	chr19	+	33298462	33298486	BC049000 // TDRD12
6366	chr19	+	34663555	34663668	NM_001114093 // LSM14A
6367	chr19	+	34984442	34984527	NM_001080436 // WTIP
6368	chr19	+	35556203	35556249	NM_182983 // HPN
6369	chr19	+	35634158	35634220	NM_022006 // FXYD7
6370	chr19	+	35739635	35739761	NM_015925 // LSR
6371	chr19	+	36108190	36108215	NM_015302 // HAUS5

6372	chr19	+	36198889	36199153	---
6373	chr19	+	36223768	36223792	NM_014727 // KMT2B
6374	chr19	+	36260609	36260633	---
6375	chr19	+	36616802	36616836	NM_001281 // TBCB
6376	chr19	+	38969137	38969161	NM_000540 // RYR1
6377	chr19	+	39949842	39949866	NM_003169 // SUPT5H
6378	chr19	+	40149164	40149306	NM_001190441 // LGALS16
6379	chr19	+	40176144	40176168	ENST00000455832 // LGALS17A
6380	chr19	+	41117219	41117243	NM_001042544 // LTBP4
6381	chr19	+	41281292	41281316	NM_006533 // MIA
6382	chr19	+	41312490	41312514	NR_037791 // RAB4B-EGLN2
6383	chr19	+	41313728	41313760	NR_037791 // RAB4B-EGLN2
6384	chr19	+	42221608	42221637	NM_004363 // CEACAM5
6385	chr19	+	42798793	42798817	NM_015125 // CIC
6386	chr19	+	42874893	42874917	NM_001271938 // MEGF8
6387	chr19	+	43905648	43905712	NM_031451 // TEX101
6388	chr19	+	44716703	44716729	NM_182490 // ZNF227
6389	chr19	+	45147433	45147457	NM_006505 // PVR
6390	chr19	+	45162169	45162197	NM_001135770 // PVR
6391	chr19	+	46180241	46180265	NM_000164 // GIPR
6392	chr19	+	46522190	46522276	NR_030412 // MIR769
6393	chr19	+	46891892	46891916	NM_006247 // PPP5C
6394	chr19	+	47880009	47880033	AK123046 // DHX34
6395	chr19	+	48775001	48775065	NM_153608 // ZNF114
6396	chr19	+	48825235	48825419	---
6397	chr19	+	48975701	48975791	AK299590 // CYTH2
6398	chr19	+	49436993	49437018	NM_014475 // DHDH
6399	chr19	+	49652547	49652571	NM_003660 // PPFIA3
6400	chr19	+	49867203	49867239	NM_014419 // DKKL1
6401	chr19	+	50124800	50124824	NM_020719 // PRR12
6402	chr19	+	50128117	50128209	NM_020719 // PRR12
6403	chr19	+	50148643	50148667	NM_021228 // SCAF1
6404	chr19	+	50161541	50161565	NM_021228 // SCAF1
6405	chr19	+	50204609	50204633	NM_001136052 // CPT1C
6406	chr19	+	50208272	50208296	NM_152359 // CPT1C
6407	chr19	+	50213864	50213888	AK299866 // CPT1C
6408	chr19	+	50354173	50354203	AK294366 // PTOV1
6409	chr19	+	50354457	50354484	NM_017432 // PTOV1
6410	chr19	+	50363731	50363755	NM_017432 // PTOV1
6411	chr19	+	50381418	50381442	NM_024682 // TBC1D17
6412	chr19	+	50919678	50919702	NM_001256849 // POLD1
6413	chr19	+	50920303	50920327	NM_001256849 // POLD1

6414	chr19	+	50969485	50969509	NM_004533 // MYBPC2
6415	chr19	+	50985408	50985462	NM_206538 // EMC10
6416	chr19	+	51361729	51361783	NM_001648 // KLK3
6417	chr19	+	52195902	52195934	NR_029843 // MIR99B
6418	chr19	+	53016686	53016710	NM_001099694 // ZNF578
6419	chr19	+	54185432	54185475	NR_030186 // MIR520F
6420	chr19	+	54612514	54612561	ENST00000482960 // NDUFA3
6421	chr19	+	54704768	54704829	ENST00000445961 // RPS9
6422	chr19	+	54927964	54927988	AK293468 // TTYH1
6423	chr19	+	55220726	55220766	NR_003061 // LILRP2
6424	chr19	+	55315346	55315376	NM_002255 // KIR2DL4
6425	chr19	+	55344216	55344253	NM_012314 // KIR2DS4
6426	chr19	+	55898063	55898087	NM_001136136 // RPL28
6427	chr19	+	55898289	55898456	NM_001136136 // RPL28
6428	chr19	+	56170584	56170614	NM_007279 // U2AF2
6429	chr19	+	56171545	56171577	NM_007279 // U2AF2
6430	chr19	+	56171912	56171938	NM_007279 // U2AF2
6431	chr19	+	57746808	57746888	NM_001015878 // AURKC
6432	chr19	+	58003336	58003367	ENST00000523439 // ZNF419
6433	chr19	+	58095518	58095678	ENST00000597850 // ZIK1
6434	chr19	+	58130780	58130809	NM_003435 // ZNF134
6435	chr19	+	58547341	58547367	NM_182572 // ZSCAN1
6436	chr19	+	58740106	58740130	NM_014480 // ZNF544
6437	chr19	+	58926932	58927012	NM_173548 // ZNF584
6438	chr19	+	58927246	58927292	BC017651 // ZNF584
6439	chr19	+	58989043	58989150	NM_017908 // ZNF446
6440	chr19	-	472395	472495	NM_182577 // ODF3L2
6441	chr19	-	622162	622229	NM_005035 // POLRMT
6442	chr19	-	868417	868444	NM_005481 // MED16
6443	chr19	-	871133	871157	NM_005481 // MED16
6444	chr19	-	871625	871649	BC017282 // MED16
6445	chr19	-	889732	889793	NM_005481 // MED16
6446	chr19	-	900074	900125	NM_138774 // R3HDM4
6447	chr19	-	1237844	1237882	ENST00000215376 // C19orf26
6448	chr19	-	1247804	1247854	---
6449	chr19	-	1619380	1619404	NM_003200 // TCF3
6450	chr19	-	1885474	1885502	NM_031213 // ABHD17A
6451	chr19	-	2328566	2328598	NM_016199 // LSM7
6452	chr19	-	2737064	2737247	NM_144564 // SLC39A3
6453	chr19	-	3014569	3014593	NM_003260 // TLE2
6454	chr19	-	3633493	3633517	NM_012398 // PIP5K1C
6455	chr19	-	3648623	3648648	NM_001195733 // PIP5K1C

6456	chr19	-	4102590	4102719	ENST00000601786 // MAP2K2
6457	chr19	-	4332019	4332044	NM_017720 // STAP2
6458	chr19	-	4531689	4531785	NM_001013706 // PLIN5
6459	chr19	-	4556031	4556093	NM_032108 // SEMA6B
6460	chr19	-	5231580	5231604	NM_002850 // PTPRS
6461	chr19	-	6424486	6424513	NM_003685 // KHSRP
6462	chr19	-	6475289	6475358	NM_024898 // DENND1C
6463	chr19	-	6730086	6730110	NM_001080452 // GPR108
6464	chr19	-	7040124	7040155	NM_001164425 // MBD3L3
6465	chr19	-	7058585	7058616	NM_001164425 // MBD3L3
6466	chr19	-	8389852	8389976	NM_198471 // KANK3
6467	chr19	-	9000478	9000502	NM_024690 // MUC16
6468	chr19	-	9005639	9005663	NM_024690 // MUC16
6469	chr19	-	10429844	10429870	NM_133452 // RAVER1
6470	chr19	-	11492623	11492723	NM_000121 // EPOR
6471	chr19	-	11513296	11513320	AK293404 // RGL3
6472	chr19	-	11568951	11569098	NM_001420 // ELAVL3
6473	chr19	-	12132908	12132940	OTTHUMT00000344146 // ZNF433
6474	chr19	-	12476640	12476677	OTTHUMT00000344111 // ZNF442
6475	chr19	-	12799904	12799932	NM_032301 // FBXW9
6476	chr19	-	13211745	13211815	NM_005583 // LYL1
6477	chr19	-	13213382	13213949	NM_005583 // LYL1
6478	chr19	-	14073963	14074000	NM_002918 // RFX1
6479	chr19	-	14094377	14094401	NM_002918 // RFX1
6480	chr19	-	14910951	14911022	ENST00000248073 // OR7C1
6481	chr19	-	16631665	16631704	NM_006387 // CHERP
6482	chr19	-	16633889	16634055	NM_006387 // CHERP
6483	chr19	-	16636284	16636308	NM_006387 // CHERP
6484	chr19	-	16664638	16664708	NM_024881 // SLC35E1
6485	chr19	-	17004059	17004083	NM_015692 // CPAMD8
6486	chr19	-	17025257	17025281	NM_015692 // CPAMD8
6487	chr19	-	17088297	17088321	NM_015692 // CPAMD8
6488	chr19	-	17403546	17403570	NM_024527 // ABHD8
6489	chr19	-	17405129	17405269	NM_024527 // ABHD8
6490	chr19	-	18314713	18314860	NM_002866 // RAB3A
6491	chr19	-	18893737	18893762	NM_000095 // COMP
6492	chr19	-	19006809	19006838	NM_001492 // GDF1
6493	chr19	-	19050717	19050741	NM_001145722 // HOMER3
6494	chr19	-	19115317	19115367	NM_001017392 // SUGP2
6495	chr19	-	19680930	19681018	NM_025245 // PBX4
6496	chr19	-	19729360	19729389	NM_025245 // PBX4
6497	chr19	-	19766427	19766451	NM_020410 // ATP13A1

6498	chr19	-	20844321	20844348	NM_001076675 // ZNF626
6499	chr19	-	28340914	28340975	---
6500	chr19	-	32562606	32562819	---
6501	chr19	-	33360646	33360678	NM_014270 // SLC7A9
6502	chr19	-	35549963	35550058	NR_024562 // HPN-AS1
6503	chr19	-	35914971	35915294	---
6504	chr19	-	35989467	35989491	---
6505	chr19	-	35997030	35997054	NM_001126056 // DMKN
6506	chr19	-	36604687	36604718	NM_006233 // POLR2I
6507	chr19	-	37096078	37096110	NM_001145649 // ZNF529
6508	chr19	-	37178320	37178344	---
6509	chr19	-	38147074	38147161	GU388430 // ZFP30
6510	chr19	-	38345771	38345836	BC042630 // LOC100631378
6511	chr19	-	38713659	38713683	AK094632 // DPF1
6512	chr19	-	39327369	39327393	NM_001533 // HNRNPL
6513	chr19	-	39374368	39374392	NR_034146 // SIRT2
6514	chr19	-	39402467	39402491	ENST00000571838 // LOC643669
6515	chr19	-	39505044	39505082	---
6516	chr19	-	40354033	40354057	NM_003890 // FCGBP
6517	chr19	-	40772008	40772032	ENST00000441941 // AKT2
6518	chr19	-	40829913	40829983	NR_046202 // C19orf47
6519	chr19	-	40886772	40887062	NM_144685 // HIPK4
6520	chr19	-	40899778	40899826	NM_020956 // PRX
6521	chr19	-	40914091	40914132	NM_020956 // PRX
6522	chr19	-	40927669	40928724	ENST00000357949 // SERTAD1
6523	chr19	-	41195946	41196022	AK299484 // NUMBL
6524	chr19	-	41383805	41383830	NM_000764 // CYP2A7
6525	chr19	-	41903090	41903225	NM_020158 // EXOSC5
6526	chr19	-	42492361	42492385	---
6527	chr19	-	42906113	42906137	NM_005357 // LIPE
6528	chr19	-	43708916	43708966	OTTHUMT00000323076 // PSG4
6529	chr19	-	44057600	44057650	NM_006297 // XRCC1
6530	chr19	-	44130077	44130101	NM_145296 // CADM4
6531	chr19	-	45016948	45016978	NM_001102599 // CEACAM20
6532	chr19	-	45667479	45667505	NM_024108 // TRAPPC6A
6533	chr19	-	45911015	45911039	NM_001983 // ERCC1
6534	chr19	-	46299333	46299357	NM_030785 // RSPH6A
6535	chr19	-	46313903	46314025	NM_030785 // RSPH6A
6536	chr19	-	46387598	46388911	NM_015649 // IRF2BP1
6537	chr19	-	46969821	46969985	NM_018215 // PNMAL1
6538	chr19	-	47137997	47138350	---
6539	chr19	-	47960803	47960827	NM_015063 // SLC8A2

6540	chr19	-	48547197	48547265	NM_019855 // CABP5
6541	chr19	-	48640980	48641004	AK303644 // LIG1
6542	chr19	-	48800790	48800814	AK128144 // CCDC114
6543	chr19	-	49016405	49016441	NM_001080434 // LMTK3
6544	chr19	-	49063565	49063611	---
6545	chr19	-	49254148	49254172	NM_000148 // FUT1
6546	chr19	-	49314267	49314320	NM_001190 // BCAT2
6547	chr19	-	49341321	49341369	NM_020904 // PLEKHA4
6548	chr19	-	49551999	49552109	NM_033183 // CGB8
6549	chr19	-	51848437	51848462	NM_001985 // ETFB
6550	chr19	-	52391177	52391207	NM_032679 // ZNF577
6551	chr19	-	53466055	53466090	NM_001031665 // ZNF816
6552	chr19	-	53792885	53792916	NM_033341 // BIRC8
6553	chr19	-	54598493	54598548	NM_206818 // OSCAR
6554	chr19	-	54868282	54868306	AK093559 // LAIR1
6555	chr19	-	55602389	55602442	NM_017607 // PPP1R12C
6556	chr19	-	55741182	55741206	NM_014931 // PPP6R1
6557	chr19	-	55743322	55743346	NM_014931 // PPP6R1
6558	chr19	-	59063273	59063303	NM_014453 // CHMP2A
6559	chr19	-	59063443	59063530	NM_014453 // CHMP2A
6560	chr2	+	1565110	1565599	---
6561	chr2	+	3481817	3481841	ENST00000489032 // TRAPPC12
6562	chr2	+	3749974	3750027	NM_018436 // ALLC
6563	chr2	+	12864792	12864916	OTTHUMT00000323585 // TRIB2
6564	chr2	+	12877510	12877549	NR_036072 // MIR3125
6565	chr2	+	14775876	14778967	NM_145175 // FAM84A
6566	chr2	+	15731789	15731813	NM_004939 // DDX1
6567	chr2	+	16061731	16061762	---
6568	chr2	+	23914627	23914716	NM_052920 // KLHL29
6569	chr2	+	24248302	24248326	BX647146 // MFSD2B
6570	chr2	+	26513177	26513201	NM_000183 // HADHB
6571	chr2	+	27071184	27071212	NM_001253723 // DPYSL5
6572	chr2	+	27320401	27320458	NM_000221 // KHK
6573	chr2	+	27445496	27445520	NM_004341 // CAD
6574	chr2	+	27656574	27656598	NM_013392 // NRBP1
6575	chr2	+	27760308	27760392	OTTHUMT00000324535 // OTTHUMG00000151939
6576	chr2	+	28812373	28812397	NM_153021 // PLB1
6577	chr2	+	30457146	30457255	ENST00000484150 // LBH
6578	chr2	+	32582487	32582511	NM_016252 // BIRC6
6579	chr2	+	32698065	32698089	---
6580	chr2	+	32853138	32853162	NM_017735 // TTC27

6581	chr2	+	33154060	33154162	AK095182 // LINC00486
6582	chr2	+	33413772	33413796	NM_206943 // LTBP1
6583	chr2	+	35041549	35041944	---
6584	chr2	+	37002182	37002207	NM_053276 // VIT
6585	chr2	+	37443278	37443335	---
6586	chr2	+	39156057	39156081	NM_001145451 // ARHGEF33
6587	chr2	+	42098411	42098499	---
6588	chr2	+	42980514	42980538	AK127245 // MTA3
6589	chr2	+	43989470	43989494	NM_172069 // PLEKHH2
6590	chr2	+	44903764	44903788	---
6591	chr2	+	45188239	45188372	---
6592	chr2	+	47454058	47454142	OTTHUMT00000323596 // OTTHUMG00000151712
6593	chr2	+	48032786	48032841	NM_000179 // MSH6
6594	chr2	+	54342804	54342828	NM_138448 // ACYP2
6595	chr2	+	54937412	54937749	---
6596	chr2	+	58748034	58748058	NR_033873 // FLJ30838
6597	chr2	+	58922942	58922966	---
6598	chr2	+	64456363	64456387	ENST00000436950 // LOC100507006
6599	chr2	+	64834109	64834268	BC131701 // LOC339807
6600	chr2	+	65385796	65385994	---
6601	chr2	+	65466989	65467015	NM_001005386 // ACTR2
6602	chr2	+	65473353	65473415	AK301634 // ACTR2
6603	chr2	+	67492276	67492313	---
6604	chr2	+	67440541	67440608	---
6605	chr2	+	69297787	69297811	NM_032208 // ANTXR1
6606	chr2	+	70045793	70045817	NM_001153 // ANXA4
6607	chr2	+	70121126	70121150	NM_006857 // SNRNP27
6608	chr2	+	71190393	71190417	NM_001692 // ATP6V1B1
6609	chr2	+	71661873	71661897	NM_014497 // ZNF638
6610	chr2	+	73151394	73151418	OTTHUMT00000327593 // EMX1
6611	chr2	+	74097300	74097387	ENST00000487811 // STAMBP
6612	chr2	+	74361618	74361782	ENST00000401851 // MGC10955
6613	chr2	+	74648847	74648877	ENST00000461531 // WDR54
6614	chr2	+	74782528	74782552	NM_001381 // DOK1
6615	chr2	+	74782707	74782750	NM_001381 // DOK1
6616	chr2	+	80875448	80875472	NM_004389 // CTNNA2
6617	chr2	+	84881832	84881856	NM_001370 // DNAH6
6618	chr2	+	85460929	85460953	OTTHUMT00000329002 // TCF7L1
6619	chr2	+	85617574	85617598	NM_032213 // ELMOD3
6620	chr2	+	85768292	85768328	ENST00000465151 // MAT2A

6621	chr2	+	85823953	85823978	NM_016494 // RNF181
6622	chr2	+	85925526	85925550	OTTHUMT00000382894 // GNLY
6623	chr2	+	86042253	86042456	NR_038888 // LOC284950
6624	chr2	+	95969092	95969116	---
6625	chr2	+	96687135	96687190	NR_003698 // FAHD2CP
6626	chr2	+	96937167	96939518	NM_004804 // CIAO1
6627	chr2	+	97312141	97312165	NM_001113382 // FER1L5
6628	chr2	+	97364460	97364484	NM_001113382 // FER1L5
6629	chr2	+	97585520	97585624	---
6630	chr2	+	99136440	99136464	NM_004027 // INPP4A
6631	chr2	+	101554270	101554294	NM_002518 // NPAS2
6632	chr2	+	103048759	103048816	NR_039930 // MIR4772
6633	chr2	+	103236509	103236533	NM_003048 // SLC9A2
6634	chr2	+	103603794	103603836	OTTHUMT00000329502 // OTTHUMG00000153094
6635	chr2	+	105941487	105941579	OTTHUMT00000329578 // OTTHUMG00000153107
6636	chr2	+	110674118	110674142	NR_027467 // LIMS3
6637	chr2	+	110693839	110693863	NR_027145 // LIMS3-LOC440895
6638	chr2	+	110695599	110695623	NR_027145 // LIMS3-LOC440895
6639	chr2	+	111490646	111490670	ENST00000448863 // ACOXL
6640	chr2	+	111886210	111886285	---
6641	chr2	+	111903540	111903752	NM_001204113 // BCL2L11
6642	chr2	+	111911390	111911462	NM_207003 // BCL2L11
6643	chr2	+	111963825	111964057	OTTHUMT00000331955 // OTTHUMG00000153644
6644	chr2	+	113033174	113033394	ENST00000409871 // ZC3H6
6645	chr2	+	113321905	113321929	ENST00000484574 // POLR1B
6646	chr2	+	113742640	113742989	NM_019618 // IL36G
6647	chr2	+	113873117	113873216	---
6648	chr2	+	113993387	113993411	---
6649	chr2	+	114335873	114335961	NR_026818 // FAM138A
6650	chr2	+	114336163	114336374	NR_026818 // FAM138A
6651	chr2	+	114394925	114394956	ENST00000465711 // RABL2A
6652	chr2	+	119739057	119739081	NM_006770 // MARCO
6653	chr2	+	119750008	119750033	NM_006770 // MARCO
6654	chr2	+	119751984	119752053	NM_006770 // MARCO
6655	chr2	+	120129897	120130038	NM_020548 // DBI
6656	chr2	+	120362320	120362344	NM_001271049 // PCDP1
6657	chr2	+	120373238	120373262	NM_001271049 // PCDP1
6658	chr2	+	120437129	120437153	NM_001105198 // TMEM177
6659	chr2	+	128459867	128461161	NM_032740 // SFT2D3

6660	chr2	+	132047602	132047628	NR_030728 // LOC440910
6661	chr2	+	132286005	132286029	---
6662	chr2	+	132479982	132480007	ENST00000355171 // C2orf27A
6663	chr2	+	134877560	134877692	OTTHUMT00000332272 // MGAT5
6664	chr2	+	135596260	135596296	NM_138326 // ACMSD
6665	chr2	+	139326941	139328114	NM_001001664 // SPOPL
6666	chr2	+	143799648	143799672	NM_003937 // KYNU
6667	chr2	+	143848962	143848986	OTTHUMT00000332175 // ARHGAP15
6668	chr2	+	149522552	149522576	NM_015630 // EPC2
6669	chr2	+	149528365	149528389	NM_015630 // EPC2
6670	chr2	+	150069604	150069628	NM_177964 // LYPD6B
6671	chr2	+	152226540	152226716	NM_007115 // TNFAIP6
6672	chr2	+	152302993	152303017	NM_018151 // RIF1
6673	chr2	+	153481789	153481813	OTTHUMT00000333588 // FMNL2
6674	chr2	+	159542415	159542511	---
6675	chr2	+	160242878	160242981	---
6676	chr2	+	160619402	160619461	NM_022826 // MARCH7
6677	chr2	+	162224387	162224411	NM_005805 // PSMD14
6678	chr2	+	163625457	163625486	---
6679	chr2	+	166430907	166430931	OTTHUMT00000333608 // CSRNP3
6680	chr2	+	170350276	170350346	NM_152384 // BBS5
6681	chr2	+	170489908	170490030	BC001555 // PPIG
6682	chr2	+	170666715	170666758	ENST00000494051 // SSB
6683	chr2	+	171686017	171686041	NM_013445 // GAD1
6684	chr2	+	171717393	171717417	NM_000817 // GAD1
6685	chr2	+	172848113	172848255	NM_003642 // HAT1
6686	chr2	+	172970661	172970867	---
6687	chr2	+	176972014	176972041	ENST00000249504 // HOXD11
6688	chr2	+	176981352	176981520	ENST00000249501 // HOXD10
6689	chr2	+	176995528	176995626	NM_019558 // HOXD8
6690	chr2	+	179255892	179255916	NM_032523 // OSBPL6
6691	chr2	+	179260360	179260384	NM_032523 // OSBPL6
6692	chr2	+	179326016	179326067	NM_001042702 // DFNB59
6693	chr2	+	182792940	182792964	NM_001130445 // SSFA2
6694	chr2	+	182913552	182913625	ENST00000410486 // RNA5SP113
6695	chr2	+	187373873	187374006	NM_018471 // ZC3H15
6696	chr2	+	187558700	187558785	ENST00000304698 // FAM171B
6697	chr2	+	188418891	188418916	OTTHUMT00000334636 // OTTHUMG00000154263
6698	chr2	+	190531276	190532079	NM_019048 // ASNSD1
6699	chr2	+	190649291	190649315	NM_000534 // PMS1

6700	chr2	+	201390859	201390916	NM_152524 // SGOL2
6701	chr2	+	201616253	201616277	NR_001557 // AOX2P
6702	chr2	+	201843518	201843641	---
6703	chr2	+	202082315	202082339	NM_032977 // CASP10
6704	chr2	+	203000749	203000773	ENST00000409515 // LOC100652824
6705	chr2	+	203051719	203051743	NM_001277372 // LOC100652824
6706	chr2	+	203623962	203624059	NM_173511 // FAM117B
6707	chr2	+	207027098	207027160	ENST00000482103 // SNORA41
6708	chr2	+	207820189	207820272	NM_173077 // CPO
6709	chr2	+	208104925	208105022	OTTHUMT00000337057 // OTTHUMG00000154787
6710	chr2	+	208983868	208983923	NR_038437 // LOC100507443
6711	chr2	+	217311407	217311431	---
6712	chr2	+	219267388	219267444	NR_029500 // MIR26B
6713	chr2	+	219294353	219294377	NM_007127 // VIL1
6714	chr2	+	219524492	219524516	NM_001257344 // BCS1L
6715	chr2	+	219561859	219561883	NM_015690 // STK36
6716	chr2	+	219842269	219842851	NR_024385 // LINC00608
6717	chr2	+	220097500	220097524	ENST00000475202 // ANKZF1
6718	chr2	+	220326074	220326098	AK129604 // SPEG
6719	chr2	+	220356566	220356590	NM_005876 // SPEG
6720	chr2	+	220370561	220370609	AB209592 // GMPPA
6721	chr2	+	220493952	220493976	NM_005070 // SLC4A3
6722	chr2	+	220602203	220602452	OTTHUMT00000131979 // OTTHUMG00000059376
6723	chr2	+	228190290	228190314	ENST00000418961 // MFF
6724	chr2	+	228375547	228375571	ENST00000486932 // AGFG1
6725	chr2	+	228399664	228399719	NM_001135187 // AGFG1
6726	chr2	+	228752355	228752445	---
6727	chr2	+	231265023	231265047	AK023116 // SP140L
6728	chr2	+	232079804	232079828	ENST00000482392 // ARMC9
6729	chr2	+	232135635	232135659	ENST00000481520 // ARMC9
6730	chr2	+	233200943	233200967	NR_046477 // DIS3L2
6731	chr2	+	233632853	233632877	OTTHUMT00000330488 // GIGYF2
6732	chr2	+	234119028	234119052	OTTHUMT00000330175 // ATG16L1
6733	chr2	+	234377133	234377157	NM_003648 // DGKD
6734	chr2	+	238121322	238121553	---
6735	chr2	+	238870424	238870497	---
6736	chr2	+	239070242	239070308	ENST00000486834 // FAM132B
6737	chr2	+	239076154	239076178	BC047423 // FAM132B
6738	chr2	+	239237327	239237351	NM_015650 // TRAF3IP1

6739	chr2	+	241514104	241514128	ENST00000481757 // RNPEPL1
6740	chr2	+	241625636	241625697	---
6741	chr2	+	241626641	241627012	AK096937 // LOC285191
6742	chr2	+	241929120	241929144	OTTHUMT00000324140 // OTTHUMG00000151855
6743	chr2	+	242135285	242135309	NM_001001666 // ANO7
6744	chr2	+	242162792	242162816	ENST00000487192 // ANO7
6745	chr2	+	242164557	242164581	NM_001001891 // ANO7
6746	chr2	+	242285724	242285748	ENST00000481500 // SEPT2
6747	chr2	+	242402907	242402931	---
6748	chr2	+	242660654	242660678	ENST00000482774 // ING5
6749	chr2	+	242681857	242681881	NM_152783 // D2HGDH
6750	chr2	+	242741367	242741444	NM_022134 // GAL3ST2
6751	chr2	+	242814054	242815400	NM_173821 // CXXC11
6752	chr2	-	260400	260424	AK096440 // SH3YL1
6753	chr2	-	287857	287885	NM_001002919 // FAM150B
6754	chr2	-	675637	675661	AK125009 // TMEM18
6755	chr2	-	747956	747986	---
6756	chr2	-	1154009	1154159	---
6757	chr2	-	1748242	1748266	NM_012293 // PXDN
6758	chr2	-	2886702	2886727	---
6759	chr2	-	6778861	6778927	OTTHUMT00000459418 // OTTHUMG00000151631
6760	chr2	-	6989518	6989972	NM_207315 // CMPK2
6761	chr2	-	9048790	9048832	NM_138799 // MBOAT2
6762	chr2	-	9628958	9630163	ENST00000310823 // ADAM17
6763	chr2	-	9683339	9683411	NM_003183 // ADAM17
6764	chr2	-	10220963	10220989	ENST00000477304 // CYS1
6765	chr2	-	11584831	11585218	NM_198256 // E2F6
6766	chr2	-	20733972	20734000	---
6767	chr2	-	23746962	23747184	OTTHUMT00000324302 // OTTHUMG00000151895
6768	chr2	-	23971870	23971894	NM_017552 // ATAD2B
6769	chr2	-	24291227	24291304	NM_016047 // SF3B14
6770	chr2	-	24422773	24422974	---
6771	chr2	-	25042613	25042637	NM_004036 // ADCY3
6772	chr2	-	25551542	25551581	NR_031570 // MIR1301
6773	chr2	-	26537495	26537519	ENST00000459892 // GPR113
6774	chr2	-	27236824	27236920	AK125769 // LOC100129724
6775	chr2	-	27587834	27587858	ENST00000478311 // EIF2B4
6776	chr2	-	27615914	27616141	NR_002201 // FTH1P3
6777	chr2	-	27667332	27667356	NM_015662 // IFT172

6778	chr2	-	27717600	27717626	ENST00000476197 // FNDC4
6779	chr2	-	30959449	30959473	ENST00000450650 // CAPN13
6780	chr2	-	30974038	30974062	NM_144575 // CAPN13
6781	chr2	-	32144947	32144979	---
6782	chr2	-	37334632	37334668	NM_002759 // EIF2AK2
6783	chr2	-	37374016	37374040	NM_002759 // EIF2AK2
6784	chr2	-	37398618	37398696	NM_001032377 // SULT6B1
6785	chr2	-	39046054	39046078	NM_198963 // DHX57
6786	chr2	-	39053068	39053092	NM_198963 // DHX57
6787	chr2	-	39111703	39111806	---
6788	chr2	-	39492391	39492415	NM_003618 // MAP4K3
6789	chr2	-	39993202	39993226	NR_028102 // THUMPD2
6790	chr2	-	48132901	48132925	NM_001190274 // FBXO11
6791	chr2	-	48873673	48873697	ENST00000420913 // LHCGR
6792	chr2	-	52722945	52722973	OTTHUMT00000325653 // OTTHUMG00000152267
6793	chr2	-	54087031	54087055	NM_006794 // GPR75
6794	chr2	-	54117304	54117328	NM_014614 // PSME4
6795	chr2	-	55276289	55276313	NM_207521 // RTN4
6796	chr2	-	55571564	55571588	NM_001135597 // CCDC88A
6797	chr2	-	61729308	61729332	OTTHUMT00000325987 // XPO1
6798	chr2	-	62364693	62364722	---
6799	chr2	-	63711762	63711786	NM_015910 // WDPCP
6800	chr2	-	64859014	64861695	NM_014755 // SERTAD2
6801	chr2	-	70417852	70417879	ENST00000428751 // C2orf42
6802	chr2	-	71357350	71357380	NM_032601 // MCEE
6803	chr2	-	74702552	74702697	ENST00000497232 // CCDC142
6804	chr2	-	74752254	74752278	NM_133637 // DQX1
6805	chr2	-	74754118	74754142	NM_181575 // AUP1
6806	chr2	-	75278463	75278566	NM_001058 // TACR1
6807	chr2	-	85775558	85775582	NM_000821 // GGCX
6808	chr2	-	86385613	86385637	ENST00000474969 // IMMT
6809	chr2	-	88529113	88529181	---
6810	chr2	-	95512287	95512384	---
6811	chr2	-	96850724	96851955	NM_020151 // STARD7
6812	chr2	-	97268523	97268547	NM_001115016 // KANSL3
6813	chr2	-	97613582	97613606	NM_001122646 // FAM178B
6814	chr2	-	97617434	97617458	ENST00000520074 // FAM178B
6815	chr2	-	99725865	99725889	NM_025244 // TSGA10
6816	chr2	-	101024697	101024721	ENST00000487860 // CHST10
6817	chr2	-	101910478	101910520	NM_173647 // RNF149
6818	chr2	-	106055020	106055163	NM_201557 // FHL2

6819	chr2	-	106209827	106210278	NR_038891 // LOC285000
6820	chr2	-	109545739	109545828	NM_022336 // EDAR
6821	chr2	-	110904364	110904388	NM_000272 // NPHP1
6822	chr2	-	110926075	110926099	NM_000272 // NPHP1
6823	chr2	-	114605711	114605781	---
6824	chr2	-	122042661	122042685	NM_014553 // TFCP2L1
6825	chr2	-	124439715	124439791	---
6826	chr2	-	127809912	127809936	NM_139343 // BIN1
6827	chr2	-	130886700	130886783	---
6828	chr2	-	130900264	130900295	AL133619 // CCDC74B
6829	chr2	-	131175587	131175618	NR_046258 // LOC100216479
6830	chr2	-	136110960	136110984	---
6831	chr2	-	146360667	146360701	OTTHUMT00000332189 // OTTHUMG00000153710
6832	chr2	-	151343347	151343371	ENST00000497865 // RND3
6833	chr2	-	152727072	152727096	NM_001005747 // CACNB4
6834	chr2	-	158182207	158182396	NM_020711 // ERMN
6835	chr2	-	158183724	158183784	ENST00000411762 // ERMN
6836	chr2	-	158271495	158271770	NM_004288 // CYTIP
6837	chr2	-	160826685	160826709	NM_007366 // PLA2R1
6838	chr2	-	161141286	161141310	NM_016836 // RBMS1
6839	chr2	-	161349440	161349464	ENST00000477486 // RBMS1
6840	chr2	-	161777345	161777517	---
6841	chr2	-	163393478	163393502	NM_033272 // KCNH7
6842	chr2	-	166870254	166870278	NM_001165963 // SCN1A
6843	chr2	-	169850229	169850253	NM_003742 // ABCB11
6844	chr2	-	170175307	170175331	NM_004525 // LRP2
6845	chr2	-	170505700	170505815	NM_001085447 // CCDC173
6846	chr2	-	170681154	170681257	NM_014168 // METTL5
6847	chr2	-	171538943	171538995	AK127400 // LOC100130256
6848	chr2	-	175213385	175213613	NM_004882 // CIR1
6849	chr2	-	175436469	175436493	NM_003387 // WIPF1
6850	chr2	-	175962208	175962232	NM_001880 // ATF2
6851	chr2	-	176041833	176042035	NM_001689 // ATP5G3
6852	chr2	-	178110676	178111323	---
6853	chr2	-	179655526	179655550	NM_001267550 // TTN
6854	chr2	-	179888008	179888105	---
6855	chr2	-	180345752	180345776	---
6856	chr2	-	180799200	180799244	---
6857	chr2	-	188348727	188348751	ENST00000481389 // TFPI
6858	chr2	-	190445203	190445231	NM_014585 // SLC40A1
6859	chr2	-	191841714	191841738	NM_007315 // STAT1

6860	chr2	-	191844498	191844522	NM_007315 // STAT1
6861	chr2	-	195890995	195891086	OTTHUMT00000334988 // OTTHUMG00000154373
6862	chr2	-	196933125	196933149	OTTHUMT00000335204 // DNAH7
6863	chr2	-	197010664	197010755	NM_004226 // STK17B
6864	chr2	-	197645486	197645510	---
6865	chr2	-	202617940	202617964	NM_020919 // ALS2
6866	chr2	-	202922013	202922170	---
6867	chr2	-	203653563	203653587	NM_138468 // ICA1L
6868	chr2	-	204309407	204309527	AB053311 // RAPH1
6869	chr2	-	207011655	207011722	NM_005006 // NDUFS1
6870	chr2	-	207985608	207985704	OTTHUMT00000336782 // KLF7-IT1
6871	chr2	-	208633997	208634140	NM_003468 // FZD5
6872	chr2	-	208938831	208938880	---
6873	chr2	-	208989017	208989054	NM_006891 // CRYGD
6874	chr2	-	208989260	208989297	NM_006891 // CRYGD
6875	chr2	-	209130730	209130774	ENST00000451391 // IDH1
6876	chr2	-	213768128	213768160	---
6877	chr2	-	216806416	216806442	---
6878	chr2	-	218675006	218675030	NM_022648 // TNS1
6879	chr2	-	218677100	218677124	NM_022648 // TNS1
6880	chr2	-	218749847	218749871	NM_022648 // TNS1
6881	chr2	-	219866369	219866411	NR_029867 // MIR375
6882	chr2	-	220078932	220078956	BC043423 // ABCB6
6883	chr2	-	220154598	220154622	NM_002846 // PTPRN
6884	chr2	-	220251678	220251702	NM_012100 // DNPEP
6885	chr2	-	224878598	224878653	ENST00000432738 // SERPINE2
6886	chr2	-	227968713	227968737	NM_000092 // COL4A4
6887	chr2	-	228551008	228551032	NM_025243 // SLC19A3
6888	chr2	-	229548256	229548379	---
6889	chr2	-	230664048	230664072	NM_004238 // TRIP12
6890	chr2	-	231988504	231988837	NM_000867 // HTR2B
6891	chr2	-	232322995	232323019	NM_005381 // NCL
6892	chr2	-	233347859	233347883	NM_004826 // ECEL1
6893	chr2	-	237246856	237246880	NR_073043 // IQCA1
6894	chr2	-	237253244	237253268	NR_073043 // IQCA1
6895	chr2	-	238037376	238037631	---
6896	chr2	-	238241957	238241981	OTTHUMT00000315795 // COL6A3
6897	chr2	-	238242147	238242171	NM_004369 // COL6A3
6898	chr2	-	239079066	239079090	NM_030768 // ILKAP
6899	chr2	-	239359717	239360324	---
6900	chr2	-	240016709	240016733	NM_006037 // HDAC4

6901	chr2	-	240834688	240834712	OTTHUMT00000326148 // NDUFA10
6902	chr2	-	241663428	241663452	NM_001244008 // KIF1A
6903	chr2	-	242486497	242486541	---
6904	chr2	-	242673838	242673870	---
6905	chr20	+	123270	123317	NM_030931 // DEFB126
6906	chr20	+	389250	389274	NM_006462 // RBCK1
6907	chr20	+	2083414	2083439	NM_080836 // STK35
6908	chr20	+	2193589	2193762	OTTHUMT00000077577 // OTTHUMG00000031689
6909	chr20	+	2384092	2384116	NM_198994 // TGM6
6910	chr20	+	3092304	3092335	NR_038395 // UBOX5-AS1
6911	chr20	+	3546004	3546028	NM_139321 // ATRN
6912	chr20	+	3577041	3577065	NM_139321 // ATRN
6913	chr20	+	3584877	3584901	NM_139321 // ATRN
6914	chr20	+	3843001	3843059	NM_020746 // MAVS
6915	chr20	+	5165514	5165567	NM_003818 // CDS2
6916	chr20	+	17823227	17823301	---
6917	chr20	+	18744114	18744395	NM_080820 // DTD1
6918	chr20	+	20209135	20209159	---
6919	chr20	+	20348936	20350406	NM_002196 // INSM1
6920	chr20	+	22671106	22671131	---
6921	chr20	+	23335121	23335364	NM_013248 // NXT1
6922	chr20	+	23342819	23342848	AK293942 // GZF1
6923	chr20	+	25845916	25845940	---
6924	chr20	+	30193945	30194285	NM_002165 // ID1
6925	chr20	+	30898953	30898980	NM_004798 // KIF3B
6926	chr20	+	31381345	31381369	NM_006892 // DNMT3B
6927	chr20	+	31595459	31595505	NM_025227 // BPIFB2
6928	chr20	+	32251689	32251720	NM_080825 // C20orf144
6929	chr20	+	32357914	32357938	NM_032819 // ZNF341
6930	chr20	+	32376687	32376713	NM_032819 // ZNF341
6931	chr20	+	33147012	33147051	NM_032514 // MAP1LC3A
6932	chr20	+	33297239	33297327	NM_021202 // TP53INP2
6933	chr20	+	34783254	34783278	NM_012156 // EPB41L1
6934	chr20	+	35169917	35169947	NM_006097 // MYL9
6935	chr20	+	35240425	35240449	NR_026562 // C20orf24
6936	chr20	+	37144967	37144991	NM_020336 // RALGAPB
6937	chr20	+	37214154	37214268	OTTHUMT00000079197 // ADIG
6938	chr20	+	37279326	37279361	OTTHUMT00000276801 // ARHGAP40
6939	chr20	+	37658210	37658510	ENST00000493450 // DHX35

6940	chr20	+	39801393	39801417	NM_002660 // PLCG1
6941	chr20	+	42252714	42252741	ENST00000467024 // IFT52
6942	chr20	+	43036049	43036073	NM_178849 // HNF4A
6943	chr20	+	43945550	43945574	NM_014276 // RBPJL
6944	chr20	+	45947366	45949126	NR_024594 // LOC100131496
6945	chr20	+	46431524	46431570	---
6946	chr20	+	47852018	47852042	ENST00000484427 // DDX27
6947	chr20	+	48411406	48411450	---
6948	chr20	+	49458314	49458367	NM_017843 // BCAS4
6949	chr20	+	52224897	52225047	OTTHUMT00000079761 // OTTHUMG00000032767
6950	chr20	+	53267126	53267150	NM_018431 // DOK5
6951	chr20	+	55027005	55027759	NM_001164116 // CASS4
6952	chr20	+	55206861	55206907	NM_003222 // TFAP2C
6953	chr20	+	55966713	55966737	NM_017495 // RBM38
6954	chr20	+	56139998	56140022	BX648510 // PCK1
6955	chr20	+	57253072	57253096	NR_037941 // STX16
6956	chr20	+	57472986	57473010	AK054862 // GNAS
6957	chr20	+	57594413	57594527	NM_030773 // TUBB1
6958	chr20	+	57597913	57597941	NM_030773 // TUBB1
6959	chr20	+	57899397	57899421	NM_000114 // EDN3
6960	chr20	+	58203709	58203763	AK295459 // PHACTR3
6961	chr20	+	60736530	60736591	NM_198935 // SS18L1
6962	chr20	+	61300360	61300384	NM_016354 // SLCO4A1
6963	chr20	+	61456838	61456862	OTTHUMT00000315860 // COL9A3
6964	chr20	+	61870838	61870867	NM_139317 // BIRC7
6965	chr20	+	61910278	61910302	NM_018209 // ARFGAP1
6966	chr20	+	61916043	61916067	BC127893 // ARFGAP1
6967	chr20	+	61918176	61918206	NR_036220 // MIR4326
6968	chr20	+	61953128	61953152	---
6969	chr20	+	61956717	61956741	AL390141 // COL20A1
6970	chr20	+	62153086	62153159	NM_024299 // PPDPF
6971	chr20	+	62290041	62290065	ENST00000488316 // RTEL1
6972	chr20	+	62376972	62376996	---
6973	chr20	+	62526480	62526509	NM_025219 // DNAJC5
6974	chr20	+	62699430	62699472	NM_003195 // TCEA2
6975	chr20	+	62701585	62701609	BC050623 // TCEA2
6976	chr20	-	644668	645079	NM_033129 // SCRT2
6977	chr20	-	3089066	3089662	NM_014948 // UBOX5
6978	chr20	-	3096048	3096072	NM_014948 // UBOX5
6979	chr20	-	5925526	5925550	NM_015939 // TRMT6
6980	chr20	-	5931124	5931148	NM_015939 // TRMT6

6981	chr20	-	6077609	6077633	NM_017671 // FERMT1
6982	chr20	-	10858984	10859012	---
6983	chr20	-	11799520	11799684	---
6984	chr20	-	13850812	13850836	NM_001271539 // SEL1L2
6985	chr20	-	16963502	16963554	---
6986	chr20	-	17602553	17602577	NM_001042576 // RRBP1
6987	chr20	-	17927955	17927979	AK296947 // SNX5
6988	chr20	-	18303209	18303234	---
6989	chr20	-	20018069	20018093	NM_016652 // CRNKL1
6990	chr20	-	20019000	20019028	NM_016652 // CRNKL1
6991	chr20	-	20033325	20033354	NM_016652 // CRNKL1
6992	chr20	-	21377696	21377971	NM_033176 // NKX2-4
6993	chr20	-	21607022	21607049	---
6994	chr20	-	22564928	22564959	NM_021784 // FOXA2
6995	chr20	-	23331983	23332123	---
6996	chr20	-	25026999	25027023	ENST00000376726 // ACSS1
6997	chr20	-	25123637	25123852	AK309387 // LOC284798
6998	chr20	-	25129842	25129866	OTTHUMT00000078389 // OTTHUMG00000032113
6999	chr20	-	25731276	25732271	---
7000	chr20	-	29521119	29521213	---
7001	chr20	-	31116583	31116607	---
7002	chr20	-	31172381	31172405	NM_001256798 // C20orf112
7003	chr20	-	31587749	31587774	ENST00000420875 // SUN5
7004	chr20	-	33880178	33880204	NM_178468 // FAM83C
7005	chr20	-	34189736	34189760	AY461812 // FER1L4
7006	chr20	-	34190640	34190664	AY461812 // FER1L4
7007	chr20	-	34214399	34214423	ENST00000473373 // CPNE1
7008	chr20	-	34215426	34215450	OTTHUMT00000078908 // CPNE1
7009	chr20	-	34241601	34242484	NM_006047 // RBM12
7010	chr20	-	35807627	35807651	NM_152503 // MROH8
7011	chr20	-	35885265	35885292	NM_021081 // GHRH
7012	chr20	-	36611868	36612003	NM_014657 // TTI1
7013	chr20	-	36869048	36869072	NM_001029864 // KIAA1755
7014	chr20	-	39314708	39316415	NM_005461 // MAFB
7015	chr20	-	40068728	40068752	NM_032221 // CHD6
7016	chr20	-	40247029	40247053	NM_032221 // CHD6
7017	chr20	-	43936942	43936967	NM_003833 // MATN4
7018	chr20	-	44577292	44577316	NM_022095 // ZNF335
7019	chr20	-	44991757	44991795	---
7020	chr20	-	45221143	45221167	NM_022829 // SLC13A3
7021	chr20	-	45978654	45978678	AK294511 // ZMYND8

7022	chr20	-	47869292	47869316	NM_021035 // ZNFX1
7023	chr20	-	48099053	48099079	NM_004975 // KCNB1
7024	chr20	-	49551473	49551647	NM_003859 // DPM1
7025	chr20	-	50400619	50400785	NM_020436 // SALL4
7026	chr20	-	50409490	50409566	OTTHUMT00000258920 // SALL4
7027	chr20	-	50414029	50414112	ENST00000483130 // SALL4
7028	chr20	-	51231292	51231333	---
7029	chr20	-	51823110	51823142	---
7030	chr20	-	52684973	52685013	NR_039913 // MIR4756
7031	chr20	-	53476228	53476314	---
7032	chr20	-	56195277	56195304	ENST00000538947 // ZBP1
7033	chr20	-	56884337	56884361	ENST00000475130 // PPP4R1L
7034	chr20	-	57392696	57392728	NR_029844 // MIR296
7035	chr20	-	58441402	58441426	NM_014258 // SYCP2
7036	chr20	-	60313341	60314109	---
7037	chr20	-	60888598	60888622	---
7038	chr20	-	62076591	62076615	NM_172107 // KCNQ2
7039	chr20	-	62376054	62376078	NM_025224 // ZBTB46
7040	chr20	-	62378287	62378311	NM_025224 // ZBTB46
7041	chr20	-	62595531	62595569	NM_020713 // ZNF512B
7042	chr21	+	14928726	14928810	---
7043	chr21	+	15599764	15600320	NM_144770 // RBM11
7044	chr21	+	17197353	17197377	NM_013396 // USP25
7045	chr21	+	17259228	17262194	---
7046	chr21	+	17266622	17267191	---
7047	chr21	+	29509401	29509891	AK093119 // LOC284825
7048	chr21	+	30415857	30415881	NM_006447 // USP16
7049	chr21	+	31988783	31988942	NM_181615 // KRTAP20-1
7050	chr21	+	32007597	32007633	NM_181616 // KRTAP20-2
7051	chr21	+	33865984	33866041	ENST00000496615 // EVA1C
7052	chr21	+	33891938	33892011	---
7053	chr21	+	34655474	34655536	NM_000628 // IL10RB
7054	chr21	+	34809198	34809222	NM_005534 // IFNGR2
7055	chr21	+	35122456	35122480	NM_003024 // ITSN1
7056	chr21	+	35122590	35122614	NM_003024 // ITSN1
7057	chr21	+	35467536	35467931	NM_006933 // SLC5A3
7058	chr21	+	37438873	37438916	---
7059	chr21	+	37626101	37626125	NM_005128 // DOPEY2
7060	chr21	+	40763860	40763884	AK299245 // WRB
7061	chr21	+	41033608	41034554	NM_006057 // B3GALT5
7062	chr21	+	43099381	43099665	NR_024367 // LINC00111
7063	chr21	+	43117409	43117472	---

7064	chr21	+	43491456	43491480	NM_001004416 // UMODL1
7065	chr21	+	43697005	43697029	NM_016818 // ABCG1
7066	chr21	+	44589742	44589831	X14789 // CRYAA
7067	chr21	+	45360088	45360154	---
7068	chr21	+	46058194	46058364	NM_181688 // KRTAP10-10
7069	chr21	+	46078014	46078044	NM_198697 // KRTAP12-3
7070	chr21	+	46117557	46117583	NM_198699 // KRTAP10-12
7071	chr21	+	46896326	46896350	NM_030582 // COL18A1
7072	chr21	+	46900689	46900713	NM_030582 // COL18A1
7073	chr21	+	47422270	47422294	NM_001848 // COL6A1
7074	chr21	+	47983778	47983802	NM_015151 // DIP2A
7075	chr21	+	48069731	48069755	ENST00000498151 // PRMT2
7076	chr21	-	11015348	11015513	---
7077	chr21	-	15868395	15868419	---
7078	chr21	-	27096799	27096930	NM_001003703 // ATP5J
7079	chr21	-	27317885	27317909	---
7080	chr21	-	30761749	30761810	---
7081	chr21	-	32090928	32091073	NM_001164435 // KRTAP21-3
7082	chr21	-	32127548	32127577	NM_181619 // KRTAP21-1
7083	chr21	-	34018074	34018098	NM_003895 // SYNJ1
7084	chr21	-	34143933	34143957	NM_016631 // PAXBP1
7085	chr21	-	35898968	35899021	NM_203418 // RCAN1
7086	chr21	-	38444981	38445005	NM_153681 // PIGP
7087	chr21	-	40110838	40111252	NR_027067 // LINC00114
7088	chr21	-	40360693	40361249	---
7089	chr21	-	40380099	40380154	---
7090	chr21	-	40400451	40400617	OTTHUMT00000141403 // OTTHUMG00000066033
7091	chr21	-	40452703	40452844	---
7092	chr21	-	42845317	42845422	NM_001135099 // TMPRSS2
7093	chr21	-	43186081	43186108	AK302592 // RIPK4
7094	chr21	-	43218658	43218682	NM_001040424 // PRDM15
7095	chr21	-	43243700	43243724	NM_022115 // PRDM15
7096	chr21	-	43342154	43342178	NM_015500 // C2CD2
7097	chr21	-	43720405	43720442	---
7098	chr21	-	43767615	43767734	NM_005423 // TFF2
7099	chr21	-	44384766	44384869	---
7100	chr21	-	44483255	44483279	ENST00000486098 // CBS
7101	chr21	-	44515806	44515832	NM_006758 // U2AF1
7102	chr21	-	44520630	44520655	BC032521 // U2AF1
7103	chr21	-	44522779	44523646	BC032521 // U2AF1
7104	chr21	-	44780375	44780455	---

7105	chr21	-	44895790	44895814	---
7106	chr21	-	45194088	45194197	NM_000100 // CSTB
7107	chr21	-	46761741	46761897	OTTHUMT00000206824 // LINC00316
7108	chr21	-	47256219	47256286	NR_038876 // LOC100129027
7109	chr21	-	47556798	47556822	NM_206965 // FTCD
7110	chr22	+	16277213	16278273	ENST00000422014 // LOC100508046
7111	chr22	+	17128568	17128592	NR_001591 // TPTEP1
7112	chr22	+	17592512	17593588	NM_014339 // IL17RA
7113	chr22	+	17809940	17810115	AF307449 // CECR9
7114	chr22	+	18978934	18979157	AB051434 // DGCR5
7115	chr22	+	19467715	19467739	NM_001178010 // CDC45
7116	chr22	+	19753628	19753809	ENST00000484336 // TBX1
7117	chr22	+	20117025	20117050	OTTHUMT00000318567 // ZDHHC8
7118	chr22	+	20328525	20328578	NR_038388 // LOC729444
7119	chr22	+	20378437	20378466	NM_001242313 // TMEM191B
7120	chr22	+	20695284	20695337	OTTHUMT00000319609 // OTTHUMG00000150686
7121	chr22	+	20922862	20922886	NM_001003891 // MED15
7122	chr22	+	20939252	20939276	NM_001003891 // MED15
7123	chr22	+	21057118	21057159	ENST00000442222 // TMEM191A
7124	chr22	+	21141185	21141311	NM_000185 // SERPIND1
7125	chr22	+	21319396	21319420	ENST00000399167 // AIFM3
7126	chr22	+	21327601	21327625	NM_144704 // AIFM3
7127	chr22	+	21372219	21372253	AK309079 // P2RX6
7128	chr22	+	21372309	21372335	NM_005446 // P2RX6
7129	chr22	+	21799694	21800716	NM_015094 // HIC2
7130	chr22	+	22569383	22569658	ENST00000390287 // IGLV10-54
7131	chr22	+	22661559	22661583	NR_027293 // LOC96610
7132	chr22	+	23114808	23115025	ENST00000390313 // IGLV3-12
7133	chr22	+	23241778	23241810	ENST00000390322 // IGLJ2
7134	chr22	+	23494652	23494700	NM_004914 // RAB36
7135	chr22	+	24560418	24560442	NM_001199281 // CABIN1
7136	chr22	+	24581988	24582053	NM_019601 // SUSD2
7137	chr22	+	24582642	24582741	AK126105 // SUSD2
7138	chr22	+	26222428	26222452	NM_032608 // MYO18B
7139	chr22	+	26231368	26231392	NM_032608 // MYO18B
7140	chr22	+	27304005	27304061	---
7141	chr22	+	31022480	31022504	NM_000355 // TCN2
7142	chr22	+	31731346	31731380	---
7143	chr22	+	31968943	31968967	ENST00000476010 // SFI1

7144	chr22	+	32003754	32003778	ENST00000491973 // SFI1
7145	chr22	+	32439320	32439394	NM_000343 // SLC5A1
7146	chr22	+	32479104	32479128	NM_000343 // SLC5A1
7147	chr22	+	32979289	32979319	---
7148	chr22	+	34140004	34140081	ENST00000445892 // LARGE-AS1
7149	chr22	+	34413487	34413512	OTTHUMT00000320580 // OTTHUMG00000150928
7150	chr22	+	35659081	35659126	NR_027780 // HMGXB4
7151	chr22	+	37678424	37678448	ENST00000248901 // CYTH4
7152	chr22	+	38030699	38030723	AK124370 // SH3BP1
7153	chr22	+	38266200	38266310	NM_016091 // EIF3L
7154	chr22	+	38352783	38352807	NM_021974 // POLR2F
7155	chr22	+	38363654	38363678	NM_021974 // POLR2F
7156	chr22	+	39417434	39417460	NM_152426 // APOBEC3D
7157	chr22	+	39473285	39473309	NM_021822 // APOBEC3G
7158	chr22	+	39828291	39828551	NR_040535 // LOC100506472
7159	chr22	+	39832502	39832566	NM_153497 // TAB1
7160	chr22	+	39868806	39868874	ENST00000429402 // MGAT3
7161	chr22	+	40069986	40070010	NM_021096 // CACNA1I
7162	chr22	+	40362022	40362155	NM_004810 // GRAP2
7163	chr22	+	40364104	40364155	NM_004810 // GRAP2
7164	chr22	+	41078400	41078713	NM_005297 // MCHR1
7165	chr22	+	41566468	41566492	NM_001429 // EP300
7166	chr22	+	41605880	41605904	NM_031488 // L3MBTL2
7167	chr22	+	42120042	42120066	NM_152513 // MEI1
7168	chr22	+	42141019	42141043	NM_152513 // MEI1
7169	chr22	+	42144304	42144328	AK128158 // MEI1
7170	chr22	+	43812855	43812969	AK316008 // MPPED1
7171	chr22	+	44464949	44464973	ENST00000404989 // PARVB
7172	chr22	+	44482855	44482879	ENST00000477795 // PARVB
7173	chr22	+	44965289	44965317	NR_028409 // LINC00207
7174	chr22	+	45960999	45961023	NM_006485 // FBLN1
7175	chr22	+	46451516	46451540	---
7176	chr22	+	49261422	49261737	---
7177	chr22	+	50295457	50295491	---
7178	chr22	+	50295592	50295616	---
7179	chr22	+	50295848	50295872	---
7180	chr22	+	50617516	50617552	NR_027691 // PANX2
7181	chr22	+	50635677	50635724	NM_025204 // TRABD
7182	chr22	+	50926124	50926169	NM_017584 // MIOX
7183	chr22	+	51025772	51025796	---
7184	chr22	+	51108238	51108301	---

7185	chr22	-	17445657	17445682	NM_001037814 // GAB4
7186	chr22	-	18661022	18661225	ENST00000415376 // LOC642633
7187	chr22	-	18682458	18682503	OTTHUMT00000316367 // OTTHUMG00000150103
7188	chr22	-	18908764	18908788	AB209472 // PRODH
7189	chr22	-	19044516	19044616	NM_005137 // DGCR2
7190	chr22	-	19442300	19442324	NM_005659 // UFD1L
7191	chr22	-	19799893	19799917	NM_053004 // GNB1L
7192	chr22	-	20383611	20383906	NR_003700 // PI4KAP2
7193	chr22	-	21663513	21663544	---
7194	chr22	-	21827288	21827680	NR_003700 // PI4KAP2
7195	chr22	-	21982518	21982622	NM_001017964 // YDJC
7196	chr22	-	22325393	22325417	AL833505 // TOP3B
7197	chr22	-	22336605	22336629	ENST00000434517 // TOP3B
7198	chr22	-	22899974	22899998	NM_006115 // PRAME
7199	chr22	-	23478238	23478429	OTTHUMT00000319070 // RTDR1
7200	chr22	-	23978125	23978240	CR627178 // GUSBP11
7201	chr22	-	24238023	24238095	NR_038911 // LOC284889
7202	chr22	-	24299741	24299893	NM_000854 // GSTT2
7203	chr22	-	24890740	24891040	NR_028484 // ADORA2A-AS1
7204	chr22	-	24951039	24951063	NM_031444 // GUCD1
7205	chr22	-	25755892	25755916	NM_182492 // LRP5L
7206	chr22	-	29950824	29950882	NM_003634 // NIPSNAP1
7207	chr22	-	30685453	30685483	NM_001037666 // GATSL3
7208	chr22	-	30921003	30921027	NM_001193336 // SEC14L6
7209	chr22	-	30921350	30921374	NM_001193336 // SEC14L6
7210	chr22	-	31058163	31058393	NM_152511 // DUSP18
7211	chr22	-	31501195	31501219	NM_080430 // SELM
7212	chr22	-	32555464	32555509	OTTHUMT00000315705 // OTTHUMG00000150003
7213	chr22	-	32590400	32590477	NM_001098527 // RFPL2
7214	chr22	-	32598359	32598437	NM_001098527 // RFPL2
7215	chr22	-	32628951	32628975	NM_014227 // SLC5A4
7216	chr22	-	32643407	32643431	NM_014227 // SLC5A4
7217	chr22	-	36205928	36205952	NM_001031695 // RBFOX2
7218	chr22	-	36698666	36698690	NM_002473 // MYH9
7219	chr22	-	36702568	36702592	NM_002473 // MYH9
7220	chr22	-	36723506	36723530	NM_002473 // MYH9
7221	chr22	-	36783894	36783918	NM_002473 // MYH9
7222	chr22	-	36841217	36841613	OTTHUMT00000319022 // OTTHUMG00000150597
7223	chr22	-	37162428	37162452	ENST00000495555 // IFT27

7224	chr22	-	37557872	37557969	---
7225	chr22	-	37640267	37640291	NM_002872 // RAC2
7226	chr22	-	37978464	37978622	ENST00000416480 // LGALS2
7227	chr22	-	38240313	38240426	ENST00000215941 // ANKRD54
7228	chr22	-	38428320	38429072	---
7229	chr22	-	38617588	38617612	NM_012264 // TMEM184B
7230	chr22	-	39388556	39388586	ENST00000513758 // APOBEC3B-AS1
7231	chr22	-	39631818	39631843	NM_002608 // PDGFB
7232	chr22	-	41632527	41632551	NM_138481 // CHADL
7233	chr22	-	42044110	42044193	---
7234	chr22	-	42341933	42341957	NM_024053 // CENPM
7235	chr22	-	42611363	42611422	NM_005650 // TCF20
7236	chr22	-	42764728	42764756	BC038245 // LOC100134361
7237	chr22	-	43091582	43091631	NM_017436 // A4GALT
7238	chr22	-	43117185	43117298	ENST00000465765 // A4GALT
7239	chr22	-	43464512	43464587	NM_012263 // TTLL1
7240	chr22	-	43485367	43485399	NM_012263 // TTLL1
7241	chr22	-	43739227	43739251	NM_173050 // SCUBE1
7242	chr22	-	45831793	45831915	---
7243	chr22	-	46642592	46642623	BC036462 // CDPF1
7244	chr22	-	47133996	47134020	NM_022766 // CERK
7245	chr22	-	48023190	48023317	NR_033377 // LINC00898
7246	chr22	-	49829892	49829991	ENST00000416411 // C22orf34
7247	chr22	-	50502494	50502553	NM_015166 // MLC1
7248	chr22	-	50692270	50692551	ENST00000496942 // MAPK12
7249	chr22	-	50699284	50699341	ENST00000497036 // MAPK12
7250	chr22	-	50739864	50739888	ENST00000432455 // PLXNB2
7251	chr22	-	50778089	50778113	---
7252	chr22	-	51221681	51221712	NM_001130921 // RABL2B
7253	chr3	+	65437	65473	OTTHUMT00000337363 // OTTHUMG00000154851
7254	chr3	+	2553072	2553096	ENST00000438282 // CNTN4
7255	chr3	+	9258614	9258663	AK302139 // SRGAP3-AS3
7256	chr3	+	9959519	9959543	---
7257	chr3	+	9959715	9959739	NM_153460 // IL17RC
7258	chr3	+	9975506	9975532	ENST00000397170 // CRELD1
7259	chr3	+	9989088	9989224	NR_046734 // PRRT3-AS1
7260	chr3	+	10974914	10974938	NM_014229 // SLC6A11
7261	chr3	+	13522595	13522736	OTTHUMT00000318590 // HDAC11
7262	chr3	+	14061211	14061239	ENST00000532924 // TPRXL
7263	chr3	+	14963967	14963991	NM_152536 // FGD5

7264	chr3	+	14974648	14974672	NM_152536 // FGD5
7265	chr3	+	15358168	15358220	---
7266	chr3	+	15915278	15915356	NR_030289 // MIR563
7267	chr3	+	17786865	17787127	XR_110041 // LOC100505786
7268	chr3	+	23315300	23315332	---
7269	chr3	+	28393067	28393092	ENST00000420223 // ZCWPW2
7270	chr3	+	32811297	32811321	---
7271	chr3	+	33427073	33427097	NM_012157 // FBXL2
7272	chr3	+	36534696	36534720	NM_003149 // STAC
7273	chr3	+	38044131	38044155	AB209574 // VILL
7274	chr3	+	38125655	38125679	NM_007335 // DLEC1
7275	chr3	+	38323792	38323817	ENST00000448498 // SLC22A14
7276	chr3	+	40524141	40524165	NM_001145082 // ZNF619
7277	chr3	+	41263743	41263767	ENST00000441708 // CTNNB1
7278	chr3	+	41265775	41265799	AK294778 // CTNNB1
7279	chr3	+	42265356	42265380	NM_001042646 // TRAK1
7280	chr3	+	44323494	44323522	NM_001145030 // TOPAZ1
7281	chr3	+	46599169	46599225	NR_073385 // LRRC2-AS1
7282	chr3	+	47030212	47030236	NM_015175 // NBEAL2
7283	chr3	+	47037096	47037120	NM_015175 // NBEAL2
7284	chr3	+	47450491	47450515	NM_015466 // PTPN23
7285	chr3	+	47451535	47451559	NM_015466 // PTPN23
7286	chr3	+	47891076	47891112	NR_031595 // MIR1226
7287	chr3	+	48481913	48481945	ENST00000479126 // TMA7
7288	chr3	+	48505145	48505169	NM_130384 // ATRIP
7289	chr3	+	49022757	49022781	NM_006321 // ARIH2
7290	chr3	+	49212515	49212567	NM_173546 // KLHDC8B
7291	chr3	+	49307588	49307671	---
7292	chr3	+	49514283	49514331	NM_001177642 // DAG1
7293	chr3	+	50232046	50232086	NM_144499 // GNAT1
7294	chr3	+	51395202	51395226	NM_004947 // DOCK3
7295	chr3	+	51705627	51705680	ENST00000415259 // TEX264
7296	chr3	+	51741146	51741172	NM_000839 // GRM2
7297	chr3	+	52325871	52325895	NM_145262 // GLYCTK
7298	chr3	+	52384014	52384038	NM_015512 // DNAH1
7299	chr3	+	52512331	52512355	ENST00000474188 // NISCH
7300	chr3	+	52574504	52574529	NM_001124767 // SMIM4
7301	chr3	+	52838225	52838249	ENST00000495622 // ITIH3
7302	chr3	+	52842611	52842635	NM_002217 // ITIH3
7303	chr3	+	57541992	57542105	NM_177966 // PDE12
7304	chr3	+	57970161	57970210	---
7305	chr3	+	58140609	58140633	NM_001164317 // FLNB

7306	chr3	+	58279345	58279447	NM_020676 // ABHD6
7307	chr3	+	58619867	58620155	---
7308	chr3	+	61548020	61548044	NM_002841 // PTPRG
7309	chr3	+	62153720	62153744	NM_002841 // PTPRG
7310	chr3	+	62188886	62188910	NM_002841 // PTPRG
7311	chr3	+	63104491	63104552	BC043407 // LINC00698
7312	chr3	+	63938123	63938147	NM_000333 // ATXN7
7313	chr3	+	68587907	68588001	NM_213609 // FAM19A1
7314	chr3	+	72201966	72202056	---
7315	chr3	+	73114392	73114439	OTTHUMT00000352326 // PPP4R2
7316	chr3	+	73111405	73111923	NM_018029 // EBLN2
7317	chr3	+	74665445	74665568	---
7318	chr3	+	98482176	98482200	ENST00000476833 // ST3GAL6
7319	chr3	+	99357427	99357479	ENST00000261037 // COL8A1
7320	chr3	+	99980166	99980190	ENST00000486274 // TBC1D23
7321	chr3	+	100368573	100368623	NM_032787 // GPR128
7322	chr3	+	100429816	100429878	ENST00000479672 // TFG
7323	chr3	+	100920685	100920729	---
7324	chr3	+	101292987	101293038	ENST00000265260 // PCNP
7325	chr3	+	101431339	101431907	NR_002941 // PDCL3P4
7326	chr3	+	101894529	101894572	ENST00000478083 // ZPLD1
7327	chr3	+	105238964	105238988	NM_001627 // ALCAM
7328	chr3	+	108828623	108828674	ENST00000480826 // MORC1-AS1
7329	chr3	+	110445870	110445968	---
7330	chr3	+	110852645	110852669	NM_015480 // PVRL3
7331	chr3	+	111799983	111800007	NM_001042575 // TMPRSS7
7332	chr3	+	112051968	112052037	NM_005944 // CD200
7333	chr3	+	112709779	112709803	ENST00000383678 // GTPBP8
7334	chr3	+	113005665	113005689	NM_033254 // BOC
7335	chr3	+	113136108	113136168	NR_046728 // WDR52-AS1
7336	chr3	+	113528216	113528270	NM_001690 // ATP6V1A
7337	chr3	+	115156730	115156799	---
7338	chr3	+	116442271	116442397	ENST00000477805 // TUSC7
7339	chr3	+	118922914	118923865	NM_006952 // UPK1B
7340	chr3	+	119328318	119328364	NM_015900 // PLA1A
7341	chr3	+	119528911	119528935	NM_003889 // NR1I2
7342	chr3	+	121310173	121310222	---
7343	chr3	+	124165088	124165112	NM_001024660 // KALRN
7344	chr3	+	125804213	125804295	---
7345	chr3	+	126006929	126006965	OTTHUMT00000370054 // OTTHUMG00000162679
7346	chr3	+	127317749	127317773	OTTHUMT00000356618 // MCM2

7347	chr3	+	127318243	127318303	NM_004526 // MCM2
7348	chr3	+	128780348	128780440	NM_000174 // GP9
7349	chr3	+	128780658	128780985	NM_000174 // GP9
7350	chr3	+	128792972	128793007	---
7351	chr3	+	129231387	129231411	AK057162 // IFT122
7352	chr3	+	129695566	129696022	NM_007117 // TRH
7353	chr3	+	129872274	129872391	---
7354	chr3	+	130345367	130345391	NM_001102608 // COL6A6
7355	chr3	+	130368334	130368358	NM_001102608 // COL6A6
7356	chr3	+	130613373	130613397	NM_014382 // ATP2C1
7357	chr3	+	130748572	130748596	NM_024800 // NEK11
7358	chr3	+	140685240	140685264	ENST00000512023 // SLC25A36
7359	chr3	+	141403970	141403994	---
7360	chr3	+	141457326	141457350	NR_037702 // RNF7
7361	chr3	+	142522950	142522974	NM_001251845 // TRPC1
7362	chr3	+	147878725	147878749	OTTHUMT00000355803 // OTTHUMG00000159500
7363	chr3	+	151094601	151094625	NM_053002 // MED12L
7364	chr3	+	152132839	152132863	NM_021038 // MBNL1
7365	chr3	+	153074926	153075027	OTTHUMT00000356566 // OTTHUMG00000159625
7366	chr3	+	153600146	153600198	OTTHUMT00000356697 // OTTHUMG00000159649
7367	chr3	+	153970914	153970972	NM_001251962 // ARHGEF26
7368	chr3	+	159744420	159744669	OTTHUMT00000352657 // OTTHUMG00000158954
7369	chr3	+	160740046	160740100	ENST00000497343 // PPM1L
7370	chr3	+	160945079	160945103	NM_015938 // NMD3
7371	chr3	+	160969961	160969985	ENST00000351193 // NMD3
7372	chr3	+	167119129	167119156	OTTHUMT00000350572 // OTTHUMG00000158284
7373	chr3	+	168427094	168427173	NR_021485 // EGFEM1P
7374	chr3	+	169781026	169781050	OTTHUMT00000352174 // GPR160
7375	chr3	+	178525086	178525110	ENST00000358316 // KCNMB2
7376	chr3	+	178174402	178174562	NR_046786 // KCNMB2-IT1
7377	chr3	+	180325485	180325509	NM_133462 // TTC14
7378	chr3	+	180650839	180650863	ENST00000461801 // FXR1
7379	chr3	+	182587040	182587064	NM_014616 // ATP11B
7380	chr3	+	183756846	183756870	NM_001145143 // HTR3D
7381	chr3	+	183861070	183861094	AB208821 // EIF2B5
7382	chr3	+	183994401	183994425	NM_001100120 // ECE2
7383	chr3	+	185697887	185698402	NR_033752 // LOC344887

7384	chr3	+	186383745	186383815	ENST00000232003 // HRG
7385	chr3	+	186648903	186648927	ENST00000430309 // ST6GAL1
7386	chr3	+	188838058	188838082	ENST00000479720 // LOC101060141
7387	chr3	+	190126200	190126276	NM_006580 // CLDN16
7388	chr3	+	193856073	193856418	ENST00000232424 // HES1
7389	chr3	+	195416219	195416246	---
7390	chr3	+	196159094	196159351	ENST00000598881 // UBXN7-AS1
7391	chr3	-	3102770	3102826	ENST00000442749 // CNTN4-AS1
7392	chr3	-	3213921	3213945	ENST00000498700 // CRBN
7393	chr3	-	8406218	8406333	---
7394	chr3	-	8794714	8794847	AY389507 // OXTR
7395	chr3	-	8809904	8810014	BC137443 // OXTR
7396	chr3	-	9101954	9101978	NM_014850 // SRGAP3
7397	chr3	-	9799268	9799299	NM_003656 // CAMK1
7398	chr3	-	9825836	9825896	NM_006354 // TADA3
7399	chr3	-	10342794	10342818	NR_024272 // SEC13
7400	chr3	-	10430043	10430067	NM_001001331 // ATP2B2
7401	chr3	-	11849579	11849603	AK126587 // TAMM41
7402	chr3	-	12200297	12200322	NM_003256 // TIMP4
7403	chr3	-	12940909	12940933	NM_001134382 // IQSEC1
7404	chr3	-	13361393	13361417	NM_024923 // NUP210
7405	chr3	-	13363151	13363175	NM_024923 // NUP210
7406	chr3	-	13905238	13905328	OTTHUMT00000340427 // WNT7A
7407	chr3	-	14193879	14193903	NM_004628 // XPC
7408	chr3	-	15137717	15137741	NM_022340 // ZFYVE20
7409	chr3	-	15563155	15563179	NM_005677 // COLQ
7410	chr3	-	16555008	16555115	NM_015150 // RFTN1
7411	chr3	-	24390068	24390103	ENST00000453729 // THRB
7412	chr3	-	25706380	25706420	NR_039644 // MIR4442
7413	chr3	-	27215957	27215981	BC045758 // NEK10
7414	chr3	-	27465899	27465923	ENST00000491211 // SLC4A7
7415	chr3	-	28378305	28378365	NM_022461 // AZI2
7416	chr3	-	32576028	32576136	NM_016141 // DYNC1LI1
7417	chr3	-	38050097	38050121	NM_001130964 // PLCD1
7418	chr3	-	38738782	38738806	ENST00000449082 // SCN10A
7419	chr3	-	38830464	38830488	NM_006514 // SCN10A
7420	chr3	-	42448666	42448709	NM_144634 // LYZL4
7421	chr3	-	42794128	42794152	NM_144719 // CCDC13
7422	chr3	-	45996839	45996863	NM_024513 // FYCO1
7423	chr3	-	46718307	46718331	AK126505 // ALS2CL
7424	chr3	-	46755738	46755950	NM_013270 // PRSS50

7425	chr3	-	46757062	46757185	NM_013270 // PRSS50
7426	chr3	-	47312890	47312914	NM_022342 // KIF9
7427	chr3	-	48559438	48559462	NM_004567 // PFKFB4
7428	chr3	-	48691412	48691436	NM_001407 // CELSR3
7429	chr3	-	48732303	48732327	NM_001190317 // IP6K2
7430	chr3	-	49021332	49021418	AF099153 // ARIH2
7431	chr3	-	49162728	49162752	NM_002292 // LAMB2
7432	chr3	-	49454384	49454469	NM_000481 // AMT
7433	chr3	-	49457693	49457717	NM_000481 // AMT
7434	chr3	-	49866699	49866813	ENST00000491060 // TRAIP
7435	chr3	-	49898297	49898325	ENST00000478149 // CAMKV
7436	chr3	-	49933998	49934022	NM_002447 // MST1R
7437	chr3	-	50325967	50325991	AK097765 // IFRD2
7438	chr3	-	50356408	50356464	NM_003773 // HYAL2
7439	chr3	-	51451427	51451451	NM_014703 // VPRBP
7440	chr3	-	51993929	51993953	NM_033008 // PCBP4
7441	chr3	-	52181008	52181032	NM_015426 // POC1A
7442	chr3	-	52330677	52330709	---
7443	chr3	-	52558905	52558929	ENST00000469616 // NT5DC2
7444	chr3	-	53904247	53904271	ENST00000488802 // ACTR8
7445	chr3	-	53915737	53915788	AK094507 // ACTR8
7446	chr3	-	56667955	56667979	NM_001112736 // FAM208A
7447	chr3	-	57522005	57522043	---
7448	chr3	-	58419173	58419197	ENST00000479945 // PDHB
7449	chr3	-	59643972	59644000	---
7450	chr3	-	62423827	62423851	NM_003716 // CADPS
7451	chr3	-	64000919	64000943	AL832109 // PSMD6
7452	chr3	-	65428499	65428523	NM_015520 // MAGI1
7453	chr3	-	69025446	69025746	NM_173654 // EOGT
7454	chr3	-	69054329	69054375	ENST00000295571 // EOGT
7455	chr3	-	72109917	72109943	OTTHUMT00000352208 // OTTHUMG00000158784
7456	chr3	-	74311769	74311793	NM_020872 // CNTN3
7457	chr3	-	74474037	74474061	NM_020872 // CNTN3
7458	chr3	-	84911918	84911942	NR_033860 // LINC00971
7459	chr3	-	86988480	86995225	NM_016206 // VGLL3
7460	chr3	-	98234516	98234540	NM_001040181 // CLDND1
7461	chr3	-	101374834	101374866	ENST00000471673 // ZBTB11
7462	chr3	-	110611249	110611428	---
7463	chr3	-	112251382	112251406	NM_022488 // ATG3
7464	chr3	-	112255325	112255446	NM_022488 // ATG3
7465	chr3	-	112256586	112256685	NM_022488 // ATG3

7466	chr3	-	112260688	112260721	NM_022488 // ATG3
7467	chr3	-	113850031	113850105	NM_000796 // DRD3
7468	chr3	-	113890840	113890866	NM_000796 // DRD3
7469	chr3	-	118951267	118951291	ENST00000487579 // B4GALT4
7470	chr3	-	119388122	119388477	ENST00000261070 // COX17
7471	chr3	-	119905549	119905573	NM_153002 // GPR156
7472	chr3	-	120130751	120130801	NM_007085 // FSTL1
7473	chr3	-	120134841	120134865	NM_007085 // FSTL1
7474	chr3	-	120360496	120360520	NM_000187 // HGD
7475	chr3	-	121228930	121228954	NM_199420 // POLQ
7476	chr3	-	121410417	121410441	NM_001256486 // GOLGB1
7477	chr3	-	122255022	122255095	NM_031458 // PARP9
7478	chr3	-	122459255	122459279	NM_024610 // HSPBAP1
7479	chr3	-	123047523	123047547	NM_183357 // ADCY5
7480	chr3	-	126220716	126220740	NM_001165974 // UROC1
7481	chr3	-	126283420	126283503	---
7482	chr3	-	128184143	128184279	NM_153330 // DNAJB8
7483	chr3	-	128204571	128205180	NM_001145661 // GATA2
7484	chr3	-	128211891	128211978	NM_032638 // GATA2
7485	chr3	-	128689133	128689157	ENST00000265068 // KIAA1257
7486	chr3	-	129688107	129688133	---
7487	chr3	-	130424405	130424429	NM_014602 // PIK3R4
7488	chr3	-	130745435	130745505	NM_014065 // ASTE1
7489	chr3	-	133547672	133547696	NM_016577 // RAB6B
7490	chr3	-	135915030	135915073	OTTHUMT00000357351 // MSL2
7491	chr3	-	138219034	138219058	NM_024491 // CEP70
7492	chr3	-	138363459	138363484	---
7493	chr3	-	138665640	138665966	NM_023067 // FOXL2
7494	chr3	-	139173630	139173655	NM_004164 // RBP2
7495	chr3	-	142119329	142119353	NM_019001 // XRN1
7496	chr3	-	145795198	145795222	BX537521 // PLOD2
7497	chr3	-	145939934	145939962	ENST00000498625 // PLSCR4
7498	chr3	-	146233722	146233783	NM_021105 // PLSCR1
7499	chr3	-	149102093	149102733	---
7500	chr3	-	149686153	149686179	NM_053024 // PFN2
7501	chr3	-	156158963	156159196	---
7502	chr3	-	156867659	156867683	NM_020307 // CCNL1
7503	chr3	-	156870832	156870856	NM_020307 // CCNL1
7504	chr3	-	160061499	160061523	ENST00000472555 // IFT80
7505	chr3	-	160093643	160093667	NM_020800 // IFT80
7506	chr3	-	162919334	162919387	NR_033945 // CT64
7507	chr3	-	164714530	164714554	NM_001041 // SI

7508	chr3	-	164735342	164735366	NM_001041 // SI
7509	chr3	-	164748501	164748525	NM_001041 // SI
7510	chr3	-	167319957	167319981	NM_178824 // WDR49
7511	chr3	-	171222068	171222140	---
7512	chr3	-	178789254	178789320	ENST00000414084 // ZMAT3
7513	chr3	-	182833698	182833722	---
7514	chr3	-	182933778	182933802	NM_015078 // MCF2L2
7515	chr3	-	184064401	184064425	NM_004366 // CLCN2
7516	chr3	-	184096101	184096153	---
7517	chr3	-	184483110	184483257	---
7518	chr3	-	185209477	185209526	NM_080652 // TMEM41A
7519	chr3	-	185270215	185270239	NM_139248 // LIPH
7520	chr3	-	185636161	185636210	NM_004593 // TRA2B
7521	chr3	-	185775219	185775243	NM_004454 // ETV5
7522	chr3	-	186838769	186838902	NM_052969 // RPL39L
7523	chr3	-	187439262	187439383	NM_001706 // BCL6
7524	chr3	-	190991181	190991263	ENST00000446788 // UTS2B
7525	chr3	-	193153501	193153525	NM_032279 // ATP13A4
7526	chr3	-	193207606	193207630	NM_032279 // ATP13A4
7527	chr3	-	193928403	193928464	---
7528	chr3	-	195309966	195310056	ENST00000453131 // APOD
7529	chr3	-	196242150	196242237	ENST00000397537 // C3orf43
7530	chr3	-	196359390	196359452	---
7531	chr4	+	526620	526644	AL137741 // PIGG
7532	chr4	+	654271	654295	NM_000283 // PDE6B
7533	chr4	+	1020040	1020064	NM_001004356 // FGFRL1
7534	chr4	+	1126123	1126221	---
7535	chr4	+	1549381	1549461	---
7536	chr4	+	1801084	1801233	NM_000142 // FGFR3
7537	chr4	+	2698018	2698042	---
7538	chr4	+	2734102	2734126	NR_046335 // FAM193A
7539	chr4	+	2928114	2928138	ENST00000503062 // ADD1
7540	chr4	+	3230348	3230372	NM_002111 // HTT
7541	chr4	+	4076360	4076396	---
7542	chr4	+	5527984	5528049	ENST00000195455 // C4orf6
7543	chr4	+	5758059	5758083	NM_153717 // EVC
7544	chr4	+	6303295	6303335	NM_006005 // WFS1
7545	chr4	+	7056074	7056711	NM_152293 // TADA2B
7546	chr4	+	7940962	7941597	BC031673 // LOC389199
7547	chr4	+	8242745	8242769	NM_018986 // SH3TC1
7548	chr4	+	8271891	8272004	NM_053044 // HTRA3
7549	chr4	+	8293105	8293218	NM_053044 // HTRA3

7550	chr4	+	8582432	8582681	NM_080819 // GPR78
7551	chr4	+	8589182	8589426	NM_080819 // GPR78
7552	chr4	+	8602697	8602804	ENST00000382480 // CPZ
7553	chr4	+	8604018	8605519	AK127844 // CPZ
7554	chr4	+	9783323	9783632	NM_000798 // DRD5
7555	chr4	+	11780208	11780232	---
7556	chr4	+	20469419	20469443	NM_004787 // SLIT2
7557	chr4	+	20535052	20535076	---
7558	chr4	+	25666582	25666689	ENST00000510033 // SLC34A2
7559	chr4	+	27022624	27022648	NM_001169117 // STIM2
7560	chr4	+	27219101	27219139	---
7561	chr4	+	28821229	28821278	NR_036237 // MIR4275
7562	chr4	+	29120073	29120263	---
7563	chr4	+	31144883	31146331	NM_032457 // PCDH7
7564	chr4	+	38117539	38117563	NM_015173 // TBC1D1
7565	chr4	+	37962670	37962694	ENST00000504686 // PTTG2
7566	chr4	+	38945211	38946010	NR_033290 // FAM114A1
7567	chr4	+	39257552	39257576	NM_025132 // WDR19
7568	chr4	+	40777136	40777160	ENST00000473399 // NSUN7
7569	chr4	+	41937188	41937251	NM_018126 // TMEM33
7570	chr4	+	43197900	43197925	OTTHUMT00000360573 // OTTHUMG00000160432
7571	chr4	+	47033681	47033747	NM_000812 // GABRB1
7572	chr4	+	49033000	49033164	ENST00000507372 // CWH43
7573	chr4	+	52911018	52911043	OTTHUMT00000361472 // OTTHUMG00000160622
7574	chr4	+	55140701	55140725	NM_006206 // PDGFRA
7575	chr4	+	57450716	57450769	NM_001256475 // THEGL
7576	chr4	+	59431619	59431713	---
7577	chr4	+	70866507	70866578	BX649104 // STATH
7578	chr4	+	71008895	71008923	NR_033311 // CSN1S2BP
7579	chr4	+	74369601	74369671	NM_001133 // AFM
7580	chr4	+	75311089	75311115	NM_001657 // AREG
7581	chr4	+	75480864	75480891	OTTHUMT00000362747 // AREGB
7582	chr4	+	76333108	76333215	---
7583	chr4	+	76481259	76481292	NR_046429 // C4orf26
7584	chr4	+	77138767	77138791	NM_001242936 // FAM47E
7585	chr4	+	77670213	77670237	NM_020859 // SHROOM3
7586	chr4	+	78531789	78531813	NM_006419 // CXCL13
7587	chr4	+	79447741	79447765	NM_025074 // FRAS1
7588	chr4	+	89299979	89300003	NM_017912 // HERC6

7589	chr4	+	100109842	100109866	ENST00000506160 // LOC100507053
7590	chr4	+	105412043	105412080	---
7591	chr4	+	105890451	105890493	OTTHUMT00000363583 // OTTHUMG00000161051
7592	chr4	+	106160003	106161766	NM_017628 // TET2
7593	chr4	+	106892319	106892343	NM_001184690 // NPNT
7594	chr4	+	110902043	110902067	NM_001963 // EGF
7595	chr4	+	111470694	111470718	NM_001977 // ENPEP
7596	chr4	+	113565961	113565985	NM_016648 // LARP7
7597	chr4	+	113578527	113578551	NR_049768 // LARP7
7598	chr4	+	113991281	113991305	---
7599	chr4	+	119154193	119154221	NM_004784 // NDST3
7600	chr4	+	120057688	120057756	NM_016599 // MYOZ2
7601	chr4	+	120610323	120610357	---
7602	chr4	+	129392020	129392083	---
7603	chr4	+	138586689	138586740	---
7604	chr4	+	138728860	138728899	OTTHUMT00000364611 // OTTHUMG00000161345
7605	chr4	+	141633329	141633437	---
7606	chr4	+	142155230	142155713	NM_014487 // ZNF330
7607	chr4	+	144434701	144434725	NM_003601 // SMARCA5
7608	chr4	+	146029178	146029202	NM_002940 // ABCE1
7609	chr4	+	147501288	147501350	---
7610	chr4	+	148538605	148538629	NM_018241 // TMEM184C
7611	chr4	+	150879440	150879663	OTTHUMT00000364771 // OTTHUMG00000161395
7612	chr4	+	152021598	152021628	OTTHUMT00000364963 // RPS3A
7613	chr4	+	152567768	152567792	NM_001109977 // FAM160A1
7614	chr4	+	154197074	154197098	NM_015271 // TRIM2
7615	chr4	+	154243881	154243905	NM_015271 // TRIM2
7616	chr4	+	154624300	154625235	NM_003264 // TLR2
7617	chr4	+	159627840	159627929	NM_004453 // ETFDH
7618	chr4	+	159757307	159757331	ENST00000504704 // FNIP2
7619	chr4	+	165708444	165708477	---
7620	chr4	+	166140804	166140869	OTTHUMT00000364446 // KLHL2
7621	chr4	+	166173732	166173764	---
7622	chr4	+	169825079	169825103	---
7623	chr4	+	172735801	172735825	NM_001034845 // GALNTL6
7624	chr4	+	174298366	174298393	NM_003864 // SAP30
7625	chr4	+	175839535	175839559	NM_014269 // ADAM29
7626	chr4	+	177063181	177063205	NM_170710 // WDR17

7627	chr4	+	184129245	184129269	NM_024949 // WWC2
7628	chr4	+	184587383	184587407	OTTHUMT00000361684 // TRAPPC11
7629	chr4	+	187093387	187093411	NM_015398 // FAM149A
7630	chr4	+	187192817	187192915	NM_000128 // F11
7631	chr4	+	188632925	188633109	---
7632	chr4	+	190580761	190580856	---
7633	chr4	+	190581100	190581281	---
7634	chr4	-	1242719	1242743	NM_001328 // CTBP1
7635	chr4	-	1986607	1986631	NM_005663 // NELFA
7636	chr4	-	1991546	1991570	NM_005663 // NELFA
7637	chr4	-	2043604	2043628	OTTHUMT00000347682 // WHSC2
7638	chr4	-	2260625	2260682	ENST00000510822 // MIR4800
7639	chr4	-	2307201	2307225	NM_001172659 // ZFYVE28
7640	chr4	-	2743387	2743574	NM_024309 // TNIP2
7641	chr4	-	3071816	3071893	NR_045414 // HTT-AS1
7642	chr4	-	3760569	3761730	ENST00000511928 // LOC100507150
7643	chr4	-	4228204	4228551	NM_177998 // OTOP1
7644	chr4	-	4285358	4285455	NM_017816 // LYAR
7645	chr4	-	5925012	5925044	NR_039608 // MIR378D1
7646	chr4	-	7061493	7062448	ENST00000264954 // GRPEL1
7647	chr4	-	7436641	7436674	NM_001085382 // PSAPL1
7648	chr4	-	7967893	7967917	NM_001130083 // ABLIM2
7649	chr4	-	9382936	9382963	---
7650	chr4	-	9682463	9682613	---
7651	chr4	-	11430401	11431041	ENST00000002596 // HS3ST1
7652	chr4	-	11742665	11742689	OTTHUMT00000358986 // OTTHUMG00000160041
7653	chr4	-	15019426	15019458	---
7654	chr4	-	16057035	16057059	AK310415 // PROM1
7655	chr4	-	17488530	17488615	NM_000320 // QDPR
7656	chr4	-	17690057	17690085	NM_015688 // FAM184B
7657	chr4	-	22414908	22414932	NM_145290 // GPR125
7658	chr4	-	39128328	39128422	---
7659	chr4	-	40058585	40058621	NR_027277 // LOC344967
7660	chr4	-	41256129	41256182	ENST00000510073 // UCHL1-AS1
7661	chr4	-	46366520	46366544	OTTHUMT00000360846 // GABRA2
7662	chr4	-	57268308	57268332	NM_002703 // PPAT
7663	chr4	-	68527419	68527443	BC031637 // UBA6
7664	chr4	-	68566851	68566875	NM_018227 // UBA6
7665	chr4	-	69817479	69817509	NM_024743 // UGT2A3

7666	chr4	-	70715177	70715230	NM_005420 // SULT1E1
7667	chr4	-	70999348	70999374	---
7668	chr4	-	74853773	74853797	NM_002704 // PPBP
7669	chr4	-	75675794	75675917	NM_001729 // BTC
7670	chr4	-	76925992	76926039	NM_002416 // CXCL9
7671	chr4	-	76957090	76957135	NM_005409 // CXCL11
7672	chr4	-	77303786	77303810	NM_001042784 // CCDC158
7673	chr4	-	82815748	82815772	---
7674	chr4	-	83811848	83811872	ENST00000513323 // SEC31A
7675	chr4	-	89012641	89012720	NM_004827 // ABCG2
7676	chr4	-	89042832	89042940	NM_004827 // ABCG2
7677	chr4	-	90032287	90032311	AK091881 // FAM13A
7678	chr4	-	96141220	96141270	NM_003728 // UNC5C
7679	chr4	-	101111487	101111637	NM_145244 // DDIT4L
7680	chr4	-	104037550	104037574	---
7681	chr4	-	105415981	105416054	NM_025212 // CXXC4
7682	chr4	-	106853787	106853851	---
7683	chr4	-	109086329	109086353	AK303143 // LEF1
7684	chr4	-	109734421	109734445	NR_045756 // COL25A1
7685	chr4	-	109862527	109862551	NM_198721 // COL25A1
7686	chr4	-	111541237	111541289	OTTHUMT00000411894 // PITX2
7687	chr4	-	122261619	122261745	NM_198179 // QRFPR
7688	chr4	-	122590852	122590876	NM_001154 // ANXA5
7689	chr4	-	122599618	122599642	NM_001154 // ANXA5
7690	chr4	-	124457534	124457592	---
7691	chr4	-	130648151	130648175	---
7692	chr4	-	134184083	134184113	---
7693	chr4	-	138970623	138970694	---
7694	chr4	-	140222475	140222504	ENST00000503453 // NDUFC1
7695	chr4	-	141598049	141598073	NM_015130 // TBC1D9
7696	chr4	-	144797932	144798002	NM_002102 // GYPE
7697	chr4	-	147866890	147866987	NM_031956 // TTC29
7698	chr4	-	152638255	152638279	ENST00000515490 // PET112
7699	chr4	-	153332492	153332516	NM_033632 // FBXW7
7700	chr4	-	159046860	159048190	NM_001031700 // FAM198B
7701	chr4	-	162841650	162841703	NM_020116 // FSTL5
7702	chr4	-	167932427	167932452	ENST00000515316 // SPOCK3
7703	chr4	-	169282428	169282452	ENST00000513103 // DDX60L
7704	chr4	-	176372388	176372576	---
7705	chr4	-	185691457	185691481	AK296826 // ACSL1
7706	chr4	-	186130480	186130546	ENST00000503223 // KIAA1430
7707	chr4	-	187345272	187345313	NR_033901 // LOC285441

7708	chrU	+	175230	175324	---
7709	chr5	+	171197	171221	NM_052909 // PLEKHG4B
7710	chr5	+	640621	640713	NM_018140 // CEP72
7711	chr5	+	1042714	1042907	---
7712	chr5	+	1043792	1043820	---
7713	chr5	+	1044555	1044659	---
7714	chr5	+	1047258	1047320	---
7715	chr5	+	1246066	1246133	NM_182632 // SLC6A18
7716	chr5	+	6750629	6750854	ENST00000505457 // PAPD7
7717	chr5	+	6766010	6766080	OTTHUMT00000365835 // OTTHUMG00000161703
7718	chr5	+	7829209	7829233	NM_020546 // ADCY2
7719	chr5	+	10249514	10250010	---
7720	chr5	+	14388027	14388051	ENST00000510757 // TRIO
7721	chr5	+	14477316	14477340	---
7722	chr5	+	16129288	16129403	---
7723	chr5	+	18844011	18844070	---
7724	chr5	+	27472475	27472622	NR_038848 // LOC643401
7725	chr5	+	31843904	31843928	ENST00000502824 // PDZD2
7726	chr5	+	32602586	32602610	NM_006713 // SUB1
7727	chr5	+	34716298	34716322	ENST00000515448 // RAI14
7728	chr5	+	35800182	35800206	NM_024867 // SPEF2
7729	chr5	+	35856177	35856201	ENST00000508941 // IL7R
7730	chr5	+	37064093	37064117	NM_015384 // NIPBL
7731	chr5	+	38932572	38932596	NM_003999 // OSMR
7732	chr5	+	41870137	41870284	ENST00000508458 // OXCT1-AS1
7733	chr5	+	41904478	41904548	ENST00000381647 // C5orf51
7734	chr5	+	43515959	43516066	---
7735	chr5	+	50124183	50124207	NM_001178055 // PARP8
7736	chr5	+	51182522	51182565	ENST00000516064 // RNA5SP182
7737	chr5	+	52979059	52979083	NM_002495 // NDUFS4
7738	chr5	+	56869862	56869915	OTTHUMT00000369240 // OTTHUMG00000162503
7739	chr5	+	58021848	58021905	NM_138453 // RAB3C
7740	chr5	+	61661106	61661130	NM_004520 // KIF2A
7741	chr5	+	63621082	63621214	NM_001113561 // RNF180
7742	chr5	+	72196747	72196771	ENST00000503084 // TNPO1
7743	chr5	+	72337118	72337142	NM_138782 // FCHO2
7744	chr5	+	74016273	74016297	NM_000521 // HEXB
7745	chr5	+	76079931	76079978	---
7746	chr5	+	76646927	76646951	NM_003719 // PDE8B
7747	chr5	+	79707482	79707506	NM_001105251 // ZFYVE16

7748	chr5	+	80388669	80388693	NM_006909 // RASGRF2
7749	chr5	+	80597908	80599652	AL512712 // ZCCHC9
7750	chr5	+	80604333	80604370	ENST00000505860 // ZCCHC9
7751	chr5	+	80608368	80608393	NM_032280 // ZCCHC9
7752	chr5	+	82999267	82999301	---
7753	chr5	+	87988646	87988676	ENST00000511000 // LOC100505949
7754	chr5	+	90049606	90049630	NM_032119 // GPR98
7755	chr5	+	90142252	90142276	---
7756	chr5	+	90445946	90445970	NM_032119 // GPR98
7757	chr5	+	90714538	90714585	NR_027435 // ARRDC3-AS1
7758	chr5	+	95583487	95583701	OTTHUMT00000370577 // OTTHUMG00000162824
7759	chr5	+	109219598	109219671	NR_033175 // LOC100289673
7760	chr5	+	111066096	111066121	ENST00000513221 // STARD4-AS1
7761	chr5	+	115152312	115152347	---
7762	chr5	+	115359185	115359209	---
7763	chr5	+	118407146	118407170	NM_005509 // DMXL1
7764	chr5	+	118812144	118812168	ENST00000505181 // HSD17B4
7765	chr5	+	122154594	122154618	NM_003100 // SNX2
7766	chr5	+	122343385	122343435	NM_014035 // SNX24
7767	chr5	+	124310988	124311026	---
7768	chr5	+	124316293	124317839	---
7769	chr5	+	128359343	128359398	NM_014031 // SLC27A6
7770	chr5	+	131755588	131755627	NR_045116 // C5orf56
7771	chr5	+	132409759	132409783	NM_002154 // HSPA4
7772	chr5	+	133481704	133481728	NM_001134851 // TCF7
7773	chr5	+	135382916	135382940	AB209598 // TGFBI
7774	chr5	+	135529053	135529124	XR_110573 // LOC100506219
7775	chr5	+	137804542	137804698	NM_001964 // EGR1
7776	chr5	+	138270504	138270528	NM_001903 // CTNNA1
7777	chr5	+	137959202	137959264	---
7778	chr5	+	139027560	139027584	ENST00000504944 // CXXC5
7779	chr5	+	140027440	140027482	NM_006083 // IK
7780	chr5	+	140034102	140034126	NM_006083 // IK
7781	chr5	+	140207859	140208544	NM_018909 // PCDHA6
7782	chr5	+	140221287	140223172	NM_018911 // PCDHA8
7783	chr5	+	141756773	141756932	---
7784	chr5	+	142348909	142348933	AK095220 // ARHGAP26
7785	chr5	+	142985194	142985259	---
7786	chr5	+	143853238	143853489	NM_020768 // KCTD16
7787	chr5	+	146658863	146658887	NM_001112724 // STK32A

7788	chr5	+	147803487	147803511	---
7789	chr5	+	148624539	148624563	NM_014945 // ABLIM3
7790	chr5	+	148725261	148725311	ENST00000507562 // GRPEL2
7791	chr5	+	149214885	149214909	NM_133263 // PPARGC1B
7792	chr5	+	154238934	154238963	ENST00000518782 // CNOT8
7793	chr5	+	157158235	157158445	ENST00000231198 // THG1L
7794	chr5	+	158697560	158697607	NM_145049 // UBLCP1
7795	chr5	+	159640744	159640772	NM_001040442 // FABP6
7796	chr5	+	161114488	161114522	OTTHUMT00000374414 // GABRA6
7797	chr5	+	167718700	167718724	ENST00000265293 // WWC1
7798	chr5	+	168445658	168445700	ENST00000504527 // LOC728095
7799	chr5	+	175467772	175467836	---
7800	chr5	+	176017657	176017681	NM_001171976 // CDHR2
7801	chr5	+	176719111	176719135	NM_172349 // NSD1
7802	chr5	+	178805724	178805837	OTTHUMT00000374445 // OTTHUMG00000163594
7803	chr5	+	179091330	179091412	---
7804	chr5	+	180619072	180619139	---
7805	chr5	+	180661538	180661671	NM_033549 // TRIM41
7806	chr5	+	180760776	180760900	BC118988 // LINC00266-1
7807	chr5	-	442997	443220	ENST00000408966 // C5orf55
7808	chr5	-	472223	472558	AK023178 // PP7080
7809	chr5	-	654145	654171	---
7810	chr5	-	654330	654449	---
7811	chr5	-	758875	758899	---
7812	chr5	-	1394452	1394660	NM_001044 // SLC6A3
7813	chr5	-	1576294	1576320	NR_003263 // SDHAP3
7814	chr5	-	9051995	9052019	NM_003966 // SEMA5A
7815	chr5	-	9197377	9197401	NM_003966 // SEMA5A
7816	chr5	-	11098735	11098759	NM_001332 // CTNND2
7817	chr5	-	13737362	13737386	NM_001369 // DNAH5
7818	chr5	-	13865934	13865958	NM_001369 // DNAH5
7819	chr5	-	16067380	16067558	ENST00000332432 // MARCH11
7820	chr5	-	16684005	16684029	NM_012334 // MYO10
7821	chr5	-	24491752	24491814	NM_006727 // CDH10
7822	chr5	-	24885397	24885540	OTTHUMT00000366295 // OTTHUMG00000161887
7823	chr5	-	26890018	26890042	NM_016279 // CDH9
7824	chr5	-	31094133	31094163	---
7825	chr5	-	31532242	31532266	NM_013235 // DROSHA
7826	chr5	-	32174378	32174456	ENST00000265070 // GOLPH3
7827	chr5	-	39124355	39124379	NM_001465 // FYB

7828	chr5	-	39211167	39211191	---
7829	chr5	-	39385481	39385505	ENST00000512525 // DAB2
7830	chr5	-	39417681	39417705	---
7831	chr5	-	40777404	40777428	ENST00000511248 // PRKAA1
7832	chr5	-	41000882	41000906	NM_173489 // MROH2B
7833	chr5	-	43039330	43039566	NM_001014279 // ANXA2R
7834	chr5	-	43527487	43527511	NM_006451 // PAIP1
7835	chr5	-	44776893	44777105	ENST00000503179 // LOC100506674
7836	chr5	-	50230298	50230333	OTTHUMT00000368771 // OTTHUMG00000162405
7837	chr5	-	54252179	54252350	OTTHUMT00000367807 // OTTHUMG00000162192
7838	chr5	-	54468444	54468474	NM_152623 // CDC20B
7839	chr5	-	59189561	59189585	NM_001104631 // PDE4D
7840	chr5	-	60983676	60983749	---
7841	chr5	-	63179373	63179401	---
7842	chr5	-	64748694	64748718	NM_197941 // ADAMTS6
7843	chr5	-	65000115	65000139	NM_019072 // SGTB
7844	chr5	-	67734938	67735083	---
7845	chr5	-	68616173	68616280	NM_176816 // CCDC125
7846	chr5	-	68660744	68660768	NM_003187 // TAF9
7847	chr5	-	74677870	74677894	NM_005713 // COL4A3BP
7848	chr5	-	77638727	77638751	OTTHUMT00000369106 // OTTHUMG00000162481
7849	chr5	-	77885943	77886015	ENST00000510949 // LHFPL2
7850	chr5	-	78281579	78281688	NM_000046 // ARSB
7851	chr5	-	79705950	79705995	---
7852	chr5	-	80689887	80689911	NM_130767 // ACOT12
7853	chr5	-	82146860	82146959	---
7854	chr5	-	86703931	86703987	NM_001239 // CCNH
7855	chr5	-	90675896	90675966	OTTHUMT00000370472 // ARRDC3
7856	chr5	-	95224588	95224612	NM_012081 // ELL2
7857	chr5	-	98204272	98204296	NM_001270 // CHD1
7858	chr5	-	100222107	100222263	NM_005668 // ST8SIA4
7859	chr5	-	107035638	107035882	---
7860	chr5	-	109733495	109733519	ENST00000507188 // TMEM232
7861	chr5	-	110382223	110382301	---
7862	chr5	-	111005173	111005316	AK307346 // NREP
7863	chr5	-	111595623	111595647	NM_022140 // EPB41L4A
7864	chr5	-	114856718	114858751	NM_020177 // FEM1C
7865	chr5	-	115149627	115149651	OTTHUMT00000371008 // CDO1

7866	chr5	-	121772388	121772412	NR_051996 // MGC32805
7867	chr5	-	122425776	122425801	---
7868	chr5	-	125890061	125890085	NM_001182 // ALDH7A1
7869	chr5	-	125897215	125897239	ENST00000497231 // ALDH7A1
7870	chr5	-	125911116	125911140	NM_001182 // ALDH7A1
7871	chr5	-	125930846	125930870	NM_001182 // ALDH7A1
7872	chr5	-	130500753	130500787	NR_024611 // HINT1
7873	chr5	-	131563927	131563951	ENST00000428841 // P4HA2
7874	chr5	-	131977909	131977964	---
7875	chr5	-	133530638	133533228	ENST00000481195 // PPP2CA
7876	chr5	-	133537835	133538083	ENST00000495833 // PPP2CA
7877	chr5	-	134466754	134466915	OTTHUMT00000371551 // OTTHUMG00000163061
7878	chr5	-	135527185	135528831	NR_024418 // LOC389332
7879	chr5	-	135561985	135562059	ENST00000509288 // TRPC7
7880	chr5	-	135732577	135732708	---
7881	chr5	-	136448124	136448148	NM_004598 // SPOCK1
7882	chr5	-	138463713	138463737	OTTHUMT00000373070 // SIL1
7883	chr5	-	138716329	138716372	ENST00000503919 // SLC23A1
7884	chr5	-	138717651	138717725	NM_005847 // SLC23A1
7885	chr5	-	138860514	138860538	AK095896 // TMEM173
7886	chr5	-	139624829	139625052	NM_002622 // PFDN1
7887	chr5	-	139714265	139714289	NM_001945 // HBEGF
7888	chr5	-	139715547	139715571	NM_001945 // HBEGF
7889	chr5	-	139930286	139930495	NM_001035235 // SRA1
7890	chr5	-	139941632	139941656	AK304824 // APBB3
7891	chr5	-	140683434	140683573	NM_031947 // SLC25A2
7892	chr5	-	141044883	141044907	NM_022481 // ARAP3
7893	chr5	-	141242295	141242549	NM_002587 // PCDH1
7894	chr5	-	141248163	141248347	NM_002587 // PCDH1
7895	chr5	-	141993702	141993726	NM_000800 // FGF1
7896	chr5	-	142783353	142783377	---
7897	chr5	-	144851951	144851975	---
7898	chr5	-	145969177	145969201	NM_001271948 // PPP2R2B
7899	chr5	-	146435612	146435636	NM_181674 // PPP2R2B
7900	chr5	-	148421130	148421154	NM_024577 // SH3TC2
7901	chr5	-	148928949	148928973	OTTHUMT00000373586 // CSNK1A1
7902	chr5	-	149500461	149500485	NM_002609 // PDGFRB
7903	chr5	-	150727097	150727121	NM_181776 // SLC36A2
7904	chr5	-	150914023	150914047	NM_001447 // FAT2
7905	chr5	-	151047163	151047191	ENST00000520687 // SPARC

7906	chr5	-	154271109	154271133	NM_015465 // GEMIN5
7907	chr5	-	156533438	156533500	ENST00000522902 // HAVCR2
7908	chr5	-	159631788	159631831	---
7909	chr5	-	159696500	159696524	ENST00000377503 // CCNJL
7910	chr5	-	160038898	160038922	---
7911	chr5	-	160076207	160076231	NM_025153 // ATP10B
7912	chr5	-	162886026	162886290	ENST00000519395 // NUDCD2
7913	chr5	-	166734962	166735005	---
7914	chr5	-	172660469	172660497	NM_001166175 // NKX2-5
7915	chr5	-	174877819	174877881	---
7916	chr5	-	175583914	175583938	NR_036494 // LOC643201
7917	chr5	-	175811046	175811131	NM_001256539 // NOP16
7918	chr5	-	176022840	176023342	NM_052899 // GPRIN1
7919	chr5	-	176023980	176024590	NM_052899 // GPRIN1
7920	chr5	-	176056984	176057033	ENST00000508006 // SNCB
7921	chr5	-	176729189	176729246	ENST00000478234 // RAB24
7922	chr5	-	176943839	176943863	AK310525 // DDX41
7923	chr5	-	176965993	176966017	NR_024019 // FAM193B
7924	chr5	-	176981262	176981286	NR_024019 // FAM193B
7925	chr5	-	177989684	177989708	---
7926	chr5	-	179228649	179228673	NM_014275 // MGAT4B
7927	chr5	-	179229033	179229057	NM_054013 // MGAT4B
7928	chr5	-	180277024	180277276	NM_152283 // ZFP62
7929	chr6	+	1610809	1610859	NM_001453 // FOXC1
7930	chr6	+	2994200	2994224	ENST00000426637 // NQO2
7931	chr6	+	3286980	3287270	AK096219 // LOC100422781
7932	chr6	+	4490922	4491087	---
7933	chr6	+	6759636	6759727	---
7934	chr6	+	7427116	7427146	---
7935	chr6	+	7879311	7879335	NM_001718 // BMP6
7936	chr6	+	13961725	13961791	NM_001165032 // RNF182
7937	chr6	+	15246551	15246575	NM_004973 // JARID2
7938	chr6	+	15452256	15452280	NM_004973 // JARID2
7939	chr6	+	17514122	17514183	NM_006366 // CAP2
7940	chr6	+	20321428	20321769	---
7941	chr6	+	21594653	21594678	NM_003107 // SOX4
7942	chr6	+	21595160	21595978	NM_003107 // SOX4
7943	chr6	+	24166515	24166602	---
7944	chr6	+	26124861	26124954	NM_003512 // HIST1H2AC
7945	chr6	+	26383442	26383466	NM_001197237 // BTN2A2
7946	chr6	+	26394636	26394660	NM_006995 // BTN2A2
7947	chr6	+	26988149	26988184	ENST00000459170 // TRNAI2

7948	chr6	+	27115415	27115457	NR_036096 // MIR3143
7949	chr6	+	28254909	28254944	NM_001184743 // PGBD1
7950	chr6	+	29096441	29096648	---
7951	chr6	+	30104148	30104314	ENST00000497688 // TRIM40
7952	chr6	+	30312971	30313003	NM_001199120 // RPP21
7953	chr6	+	30457563	30457763	NM_005516 // HLA-E
7954	chr6	+	30877744	30877827	NM_001517 // GTF2H4
7955	chr6	+	30920749	30920877	NM_080870 // DPCR1
7956	chr6	+	30951515	30951713	NM_001010909 // MUC21
7957	chr6	+	31631070	31631101	---
7958	chr6	+	31959622	31959646	NM_007293 // C4A
7959	chr6	+	31961622	31961646	ENST00000487749 // C4B
7960	chr6	+	31992360	31992384	NM_007293 // C4A
7961	chr6	+	31994360	31994384	ENST00000487749 // C4B
7962	chr6	+	32125665	32125689	NM_005155 // PPT2
7963	chr6	+	33048244	33048308	ENST00000474044 // HLA-DPB1
7964	chr6	+	33049819	33049898	AK301322 // HLA-DPB1
7965	chr6	+	33383052	33383081	NR_027692 // PHF1
7966	chr6	+	33410885	33410909	NM_006772 // SYNGAP1
7967	chr6	+	33415671	33415695	NM_006772 // SYNGAP1
7968	chr6	+	33418304	33418328	---
7969	chr6	+	35213073	35213097	NM_152753 // SCUBE3
7970	chr6	+	36926945	36927040	NM_153370 // PI16
7971	chr6	+	36976634	36976658	NM_173558 // FGD2
7972	chr6	+	37013007	37013033	ENST00000423336 // COX6A1P2
7973	chr6	+	37143049	37143143	NM_002648 // PIM1
7974	chr6	+	38626253	38626294	---
7975	chr6	+	38702354	38702378	NM_001206927 // DNAH8
7976	chr6	+	38941519	38941543	NM_001206927 // DNAH8
7977	chr6	+	39816490	39816514	BC078153 // DAAM2
7978	chr6	+	41303615	41303644	NM_004828 // NCR2
7979	chr6	+	42832544	42833133	NM_015349 // GLTSCR1L
7980	chr6	+	42851368	42851493	OTTHUMT00000314420 // RPL7L1
7981	chr6	+	42985653	42985682	NM_057161 // KLHDC3
7982	chr6	+	43100387	43100411	NM_001270398 // PTK7
7983	chr6	+	43154700	43154724	NM_015089 // CUL9
7984	chr6	+	43181454	43181478	NM_015089 // CUL9
7985	chr6	+	43623306	43623341	NM_152732 // RSPH9
7986	chr6	+	44012160	44012190	---
7987	chr6	+	46803067	46803091	NM_005588 // MEP1A
7988	chr6	+	47800316	47800372	ENST00000489301 // OPN5
7989	chr6	+	47824781	47825000	---

7990	chr6	+	52860659	52860745	NR_001445 // RN7SK
7991	chr6	+	56708801	56708831	---
7992	chr6	+	71104593	71104620	OTTHUMT00000041135 // OTTHUMG00000014989
7993	chr6	+	74072404	74072434	NM_001017361 // KHDC3L
7994	chr6	+	82981704	82981782	---
7995	chr6	+	84799709	84800529	NM_138409 // MRAP2
7996	chr6	+	94428233	94428345	AY314751 // TSG1
7997	chr6	+	102337709	102337733	NM_021956 // GRIK2
7998	chr6	+	105404925	105405109	NM_001004317 // LIN28B
7999	chr6	+	106534432	106534465	NM_001198 // PRDM1
8000	chr6	+	108497314	108497457	OTTHUMT00000316396 // NR2E1
8001	chr6	+	109662134	109662178	BC128119 // CCDC162P
8002	chr6	+	109763955	109764084	NM_003080 // SMPD2
8003	chr6	+	110301202	110301245	NM_005284 // GPR6
8004	chr6	+	111616770	111616906	---
8005	chr6	+	116575338	116575453	ENST00000540275 // DSE
8006	chr6	+	116905893	116905985	NM_015952 // RWDD1
8007	chr6	+	116951618	116951686	NM_001010892 // RSPH4A
8008	chr6	+	126667392	126667463	NM_001012507 // CENPW
8009	chr6	+	135581134	135581211	---
8010	chr6	+	138483076	138483100	NM_020340 // KIAA1244
8011	chr6	+	138649169	138649193	NM_020340 // KIAA1244
8012	chr6	+	142764627	142764651	NM_020455 // GPR126
8013	chr6	+	145142102	145142126	NM_007124 // UTRN
8014	chr6	+	147091720	147091744	ENST00000523560 // ADGB
8015	chr6	+	148835519	148835543	NM_015278 // SASH1
8016	chr6	+	148867239	148867263	NM_015278 // SASH1
8017	chr6	+	149718930	149719039	ENST00000484505 // TAB2
8018	chr6	+	150263215	150263241	NM_025217 // ULBP2
8019	chr6	+	150723062	150723086	NM_001164694 // IYD
8020	chr6	+	152701677	152701728	ENST00000412161 // SYNE1-AS1
8021	chr6	+	160199916	160199940	NM_005891 // ACAT2
8022	chr6	+	160564591	160564626	NM_003057 // SLC22A1
8023	chr6	+	160864673	160864697	NM_021977 // SLC22A3
8024	chr6	+	167313661	167315313	---
8025	chr6	+	167559902	167560055	ENST00000539001 // TCP10L2
8026	chr6	+	170345079	170345112	---
8027	chr6	-	4079150	4079178	NM_173563 // FAM217A
8028	chr6	-	4115997	4116071	NM_006117 // ECI2
8029	chr6	-	5999217	5999415	NM_016588 // NRN1
8030	chr6	-	10694729	10694806	ENST00000259983 // C6orf52

8031	chr6	-	13814248	13814599	NM_001031713 // MCUR1
8032	chr6	-	15524828	15524852	NM_032122 // DTNBP1
8033	chr6	-	17646356	17646380	NM_005124 // NUP153
8034	chr6	-	17950726	17951380	NM_001243423 // KIF13A
8035	chr6	-	19804916	19804942	AK092541 // LOC100506885
8036	chr6	-	22147299	22147401	NR_034143 // LOC729177
8037	chr6	-	24583838	24583862	NM_014809 // KIAA0319
8038	chr6	-	26250390	26250422	NM_021018 // HIST1H3F
8039	chr6	-	26365746	26365779	---
8040	chr6	-	27440767	27440814	NM_007149 // ZNF184
8041	chr6	-	28217524	28217548	NM_019110 // ZKSCAN4
8042	chr6	-	28303910	28303934	NM_030899 // ZSCAN31
8043	chr6	-	28473550	28473578	NM_182701 // GPX6
8044	chr6	-	30899813	30899843	NM_205854 // SFTA2
8045	chr6	-	30913818	30914136	ENST00000455908 // HCG21
8046	chr6	-	31508940	31508964	AK127767 // DDX39B
8047	chr6	-	31513831	31513855	ENST00000460751 // ATP6V1G2
8048	chr6	-	31614176	31614200	NM_004639 // BAG6
8049	chr6	-	31648030	31648070	NM_025262 // LY6G5C
8050	chr6	-	31680126	31680314	NR_003673 // LY6G6E
8051	chr6	-	31694843	31694867	NM_013974 // DDAH2
8052	chr6	-	31760170	31760194	NM_006295 // VARS
8053	chr6	-	32084278	32084311	NM_004381 // ATF6B
8054	chr6	-	32120691	32120732	NR_037169 // LOC100507547
8055	chr6	-	32138264	32138346	NM_006411 // AGPAT1
8056	chr6	-	32155075	32155099	NM_002586 // PBX2
8057	chr6	-	32155820	32155844	NM_002586 // PBX2
8058	chr6	-	32796749	32796799	ENST00000374897 // TAP2
8059	chr6	-	32810660	32810711	AK300962 // PSMB8
8060	chr6	-	33148463	33148487	NM_080680 // COL11A2
8061	chr6	-	33154341	33154365	NM_001163771 // COL11A2
8062	chr6	-	33264911	33264935	ENST00000495238 // RGL2
8063	chr6	-	33265199	33265223	ENST00000467836 // RGL2
8064	chr6	-	33291465	33291638	ENST00000480469 // DAXX
8065	chr6	-	34214296	34214394	ENST00000476320 // C6orf1
8066	chr6	-	35465866	35466020	NM_003322 // TULP1
8067	chr6	-	35911364	35911388	NM_052961 // SLC26A8
8068	chr6	-	36334452	36334518	NM_016135 // ETV7
8069	chr6	-	36515028	36515179	NM_007271 // STK38
8070	chr6	-	36710169	36710193	NM_020939 // CPNE5
8071	chr6	-	36711468	36711524	NM_020939 // CPNE5
8072	chr6	-	37616918	37616942	NM_153487 // MDGA1

8073	chr6	-	38900655	38900683	ENST00000453417 // LOC100131047
8074	chr6	-	38904133	38904168	NR_038401 // LOC100131047
8075	chr6	-	40243745	40243864	---
8076	chr6	-	41162239	41162438	NM_024807 // TREML2
8077	chr6	-	41177395	41177428	NR_027256 // TREML3P
8078	chr6	-	41653862	41653886	NM_007162 // TFEB
8079	chr6	-	41708654	41708679	NM_001166424 // PGC
8080	chr6	-	42237540	42237564	NM_033502 // TRERF1
8081	chr6	-	43023637	43023702	NM_015950 // MRPL2
8082	chr6	-	43422513	43422545	NM_023932 // DLK2
8083	chr6	-	44081445	44081567	NM_032111 // MRPL14
8084	chr6	-	47277158	47277190	NM_014452 // TNFRSF21
8085	chr6	-	49815942	49816003	NM_001131 // CRISP1
8086	chr6	-	49936422	49936541	NM_001037729 // DEFB113
8087	chr6	-	49986591	49986683	NM_001037497 // DEFB110
8088	chr6	-	52016176	52016202	---
8089	chr6	-	53659012	53659038	---
8090	chr6	-	70970377	70970401	NM_001851 // COL9A1
8091	chr6	-	71603868	71603963	NM_080742 // B3GAT2
8092	chr6	-	74133566	74133590	ENST00000370315 // MB21D1
8093	chr6	-	75901446	75901470	NM_004370 // COL12A1
8094	chr6	-	75947676	75947702	NM_001865 // COX7A2
8095	chr6	-	75950029	75950084	NM_001865 // COX7A2
8096	chr6	-	80631362	80631504	NM_022726 // ELOVL4
8097	chr6	-	89888562	89888749	NM_002042 // GABRR1
8098	chr6	-	90045023	90045114	NM_016021 // UBE2J1
8099	chr6	-	105624072	105624098	---
8100	chr6	-	107435334	107435461	NM_001080450 // BEND3
8101	chr6	-	107832590	107832625	---
8102	chr6	-	108543459	108543518	BC016863 // SNX3
8103	chr6	-	109767751	109767775	ENST00000465904 // MICAL1
8104	chr6	-	110421350	110421682	NM_003931 // WASF1
8105	chr6	-	111620509	111620533	NM_002912 // REV3L
8106	chr6	-	111698946	111698970	NM_002912 // REV3L
8107	chr6	-	112461048	112461072	NM_001105206 // LAMA4
8108	chr6	-	112522836	112522860	NM_001105206 // LAMA4
8109	chr6	-	113667222	113667294	---
8110	chr6	-	116289769	116289842	NM_002031 // FRK
8111	chr6	-	117086841	117086875	NM_001085480 // FAM162B
8112	chr6	-	117710940	117710964	NM_002944 // ROS1
8113	chr6	-	128239693	128239764	NM_001164687 // THEMIS

8114	chr6	-	132618295	132618403	NM_015529 // MOXD1
8115	chr6	-	133119554	133119579	NM_052831 // SLC18B1
8116	chr6	-	134081345	134081369	BC041459 // LOC100507308
8117	chr6	-	135715850	135715874	OTTHUMT00000392259 // AHI1
8118	chr6	-	136597022	136597046	NM_014739 // BCLAF1
8119	chr6	-	136682279	136682303	NM_001198608 // MAP7
8120	chr6	-	137017107	137017131	NM_005923 // MAP3K5
8121	chr6	-	137018434	137018458	NM_005923 // MAP3K5
8122	chr6	-	137518840	137518897	NM_000416 // IFNGR1
8123	chr6	-	138413318	138413345	NM_022121 // PERP
8124	chr6	-	138539549	138539628	NM_021635 // PBOV1
8125	chr6	-	139228653	139228677	NM_031922 // REPS1
8126	chr6	-	140415553	140415705	---
8127	chr6	-	143358174	143358681	NR_038987 // LOC100507489
8128	chr6	-	145946654	145946678	NM_005670 // EPM2A
8129	chr6	-	146266699	146266723	NM_001042683 // SHPRH
8130	chr6	-	149970070	149970094	ENST00000420200 // KATNA1
8131	chr6	-	150205289	150205559	NM_001243328 // RAET1E
8132	chr6	-	152599322	152599346	NM_182961 // SYNE1
8133	chr6	-	154799465	154799489	AK309680 // CNKSR3
8134	chr6	-	155620643	155620671	ENST00000489874 // TFB1M
8135	chr6	-	160113781	160113805	NM_000636 // SOD2
8136	chr6	-	167271642	167271666	---
8137	chr6	-	166876480	166876624	NR_046793 // RPS6KA2-IT1
8138	chr6	-	167386230	167386271	---
8139	chr6	-	167794507	167794553	OTTHUMT00000043138 // TCP10
8140	chr6	-	169322157	169322196	---
8141	chr6	-	169687160	169687298	OTTHUMT00000105437 // OTTHUMG00000045406
8142	chr6_apd_hap1	+	399877	400084	---
8143	chr6_apd_hap1	+	928299	928380	OTTHUMT00000309275 // MOG
8144	chr6_apd_hap1	+	1344383	1344549	---
8145	chr6_apd_hap1	+	2263154	2263352	ENST00000376296 // MUC21
8146	chr6_apd_hap1	+	3440404	3440428	ENST00000480383 // EGFL8
8147	chr6_apd_hap1	+	3453538	3453562	ENST00000480383 // EGFL8
8148	chr6_apd_hap1	+	4335051	4335115	---
8149	chr6_apd_hap1	+	4336626	4336705	---
8150	chr6_apd_hap1	-	1823282	1824449	---
8151	chr6_apd_hap1	-	2821321	2821394	---
8152	chr6_apd_hap1	-	3074920	3074944	---
8153	chr6_apd_hap1	-	3453005	3453087	---
8154	chr6_apd_hap1	-	3469831	3469902	---

8155	chr6_apd_hap1	-	4097664	4097715	---
8156	chr6_cox_hap2	+	615317	615524	---
8157	chr6_cox_hap2	+	1143574	1143655	---
8158	chr6_cox_hap2	+	1616282	1616448	---
8159	chr6_cox_hap2	+	1824981	1825013	---
8160	chr6_cox_hap2	+	1969627	1969827	ENST00000415649 // HLA-E
8161	chr6_cox_hap2	+	2363939	2363963	---
8162	chr6_cox_hap2	+	2368484	2368508	---
8163	chr6_cox_hap2	+	2373209	2373233	NM_013994 // DDR1
8164	chr6_cox_hap2	+	2389819	2389843	ENST00000469489 // VARS2
8165	chr6_cox_hap2	+	2394481	2394505	ENST00000469489 // VARS2
8166	chr6_cox_hap2	+	2608168	2608213	---
8167	chr6_cox_hap2	+	3200751	3200775	NM_138277 // C6orf25
8168	chr6_cox_hap2	+	3463011	3463035	OTTHUMT00000076368 // C4B
8169	chr6_cox_hap2	+	3465011	3465035	---
8170	chr6_cox_hap2	+	3596337	3596361	ENST00000480383 // EGFL8
8171	chr6_cox_hap2	+	3609478	3609502	ENST00000480383 // EGFL8
8172	chr6_cox_hap2	-	64753	65880	---
8173	chr6_cox_hap2	-	1331699	1333579	---
8174	chr6_cox_hap2	-	1714038	1714139	---
8175	chr6_cox_hap2	-	2083518	2083542	---
8176	chr6_cox_hap2	-	2411736	2411766	---
8177	chr6_cox_hap2	-	2425722	2426040	---
8178	chr6_cox_hap2	-	2594324	2594726	---
8179	chr6_cox_hap2	-	2627995	2628019	---
8180	chr6_cox_hap2	-	3018599	3018623	---
8181	chr6_cox_hap2	-	3023490	3023514	---
8182	chr6_cox_hap2	-	3123794	3123818	---
8183	chr6_cox_hap2	-	3157650	3157690	---
8184	chr6_cox_hap2	-	3180747	3180771	---
8185	chr6_cox_hap2	-	3204460	3204484	---
8186	chr6_cox_hap2	-	3269739	3269763	---
8187	chr6_cox_hap2	-	3608945	3609027	---
8188	chr6_cox_hap2	-	3625771	3625842	---
8189	chr6_cox_hap2	-	3639437	3639461	---
8190	chr6_cox_hap2	-	4241304	4241328	---
8191	chr6_cox_hap2	-	4255188	4255239	---
8192	chr6_cox_hap2	-	4592299	4592323	---
8193	chr6_cox_hap2	-	4598177	4598201	---
8194	chr6_cox_hap2	-	4708725	4708749	---
8195	chr6_cox_hap2	-	4709013	4709037	---
8196	chr6_cox_hap2	-	4735283	4735456	---

8197	chr6_dbb_hap3	+	399850	400057	---
8198	chr6_dbb_hap3	+	928126	928207	OTTHUMT00000309969 // MOG
8199	chr6_dbb_hap3	+	1397874	1398040	---
8200	chr6_dbb_hap3	+	1751203	1751403	ENST00000415649 // HLA-E
8201	chr6_dbb_hap3	+	2145943	2145967	---
8202	chr6_dbb_hap3	+	2150488	2150512	---
8203	chr6_dbb_hap3	+	2152945	2152969	ENST00000412329 // MIR4640
8204	chr6_dbb_hap3	+	2154196	2154220	NM_013994 // DDR1
8205	chr6_dbb_hap3	+	2155227	2155251	NM_013994 // DDR1
8206	chr6_dbb_hap3	+	2171856	2171880	ENST00000464084 // VARS2
8207	chr6_dbb_hap3	+	2245626	2245824	ENST00000376296 // MUC21
8208	chr6_dbb_hap3	+	2976704	2976728	NM_138277 // C6orf25
8209	chr6_dbb_hap3	+	3234377	3234401	ENST00000483467 // STK19
8210	chr6_dbb_hap3	+	3247204	3247228	---
8211	chr6_dbb_hap3	+	3271576	3271600	ENST00000449788 // C4B
8212	chr6_dbb_hap3	+	3273576	3273600	---
8213	chr6_dbb_hap3	+	4329583	4329647	---
8214	chr6_dbb_hap3	+	4331158	4331237	---
8215	chr6_dbb_hap3	-	1865103	1865127	---
8216	chr6_dbb_hap3	-	2410365	2410389	---
8217	chr6_dbb_hap3	-	2799409	2799434	---
8218	chr6_dbb_hap3	-	2794447	2794501	---
8219	chr6_dbb_hap3	-	2794513	2794542	---
8220	chr6_dbb_hap3	-	2899750	2899774	---
8221	chr6_dbb_hap3	-	2933611	2933651	---
8222	chr6_dbb_hap3	-	2956701	2956725	---
8223	chr6_dbb_hap3	-	2980412	2980493	---
8224	chr6_dbb_hap3	-	3045752	3045776	---
8225	chr6_dbb_hap3	-	4092038	4092089	---
8226	chr6_dbb_hap3	-	4429770	4429794	---
8227	chr6_dbb_hap3	-	4435648	4435672	---
8228	chr6_dbb_hap3	-	4546237	4546261	---
8229	chr6_dbb_hap3	-	4546525	4546549	---
8230	chr6_dbb_hap3	-	4572792	4572965	---
8231	chr6_mann_hap4	+	399842	400049	---
8232	chr6_mann_hap4	+	927733	927814	---
8233	chr6_mann_hap4	+	1452713	1452879	---
8234	chr6_mann_hap4	+	1805641	1805841	NM_005516 // HLA-E
8235	chr6_mann_hap4	+	2199926	2199950	---
8236	chr6_mann_hap4	+	2204471	2204495	---
8237	chr6_mann_hap4	+	2208159	2208183	NM_013994 // DDR1
8238	chr6_mann_hap4	+	2209190	2209214	NM_013994 // DDR1

8239	chr6_mann_hap4	+	2225823	2225906	ENST00000480149 // GTF2H4
8240	chr6_mann_hap4	+	2299601	2299799	ENST00000376296 // MUC21
8241	chr6_mann_hap4	+	2726587	2726611	NR_036523 // MICA
8242	chr6_mann_hap4	+	2816636	2816829	---
8243	chr6_mann_hap4	+	3034023	3034047	NM_138277 // C6orf25
8244	chr6_mann_hap4	+	3468491	3468515	ENST00000480383 // EGFL8
8245	chr6_mann_hap4	+	3481621	3481645	ENST00000480383 // EGFL8
8246	chr6_mann_hap4	+	4505790	4505854	---
8247	chr6_mann_hap4	+	4507365	4507444	---
8248	chr6_mann_hap4	-	1285268	1285477	---
8249	chr6_mann_hap4	-	2247894	2247924	---
8250	chr6_mann_hap4	-	2461593	2461617	---
8251	chr6_mann_hap4	-	2856727	2856752	---
8252	chr6_mann_hap4	-	2851831	2851860	---
8253	chr6_mann_hap4	-	2957065	2957089	---
8254	chr6_mann_hap4	-	2990921	2990961	---
8255	chr6_mann_hap4	-	3014020	3014044	---
8256	chr6_mann_hap4	-	3037733	3037814	---
8257	chr6_mann_hap4	-	3481088	3481170	---
8258	chr6_mann_hap4	-	3497914	3497985	---
8259	chr6_mann_hap4	-	4253944	4253994	---
8260	chr6_mann_hap4	-	4267856	4267907	---
8261	chr6_mann_hap4	-	4605779	4605803	---
8262	chr6_mann_hap4	-	4611656	4611680	---
8263	chr6_mcf_hap5	+	927966	928043	OTTHUMT00000312013 // MOG
8264	chr6_mcf_hap5	+	1486045	1486211	---
8265	chr6_mcf_hap5	+	1839427	1839627	NM_005516 // HLA-E
8266	chr6_mcf_hap5	+	2233798	2233823	---
8267	chr6_mcf_hap5	+	2259699	2259723	ENST00000469311 // VARS2
8268	chr6_mcf_hap5	+	2333461	2333659	ENST00000376296 // MUC21
8269	chr6_mcf_hap5	+	3070817	3070841	NM_138277 // C6orf25
8270	chr6_mcf_hap5	+	3372204	3372228	OTTHUMT00000310371 // C4A
8271	chr6_mcf_hap5	+	3374204	3374228	---
8272	chr6_mcf_hap5	+	3505492	3505516	ENST00000480383 // EGFL8
8273	chr6_mcf_hap5	+	3518626	3518650	ENST00000480383 // EGFL8
8274	chr6_mcf_hap5	+	4385105	4385169	---
8275	chr6_mcf_hap5	+	4386680	4386759	---
8276	chr6_mcf_hap5	-	1358635	1358672	---
8277	chr6_mcf_hap5	-	2281752	2281782	---
8278	chr6_mcf_hap5	-	2495171	2495195	---
8279	chr6_mcf_hap5	-	2893578	2893603	---
8280	chr6_mcf_hap5	-	2888616	2888670	---

8281	chr6_mcf_hap5	-	2888682	2888711	---
8282	chr6_mcf_hap5	-	2993849	2993873	---
8283	chr6_mcf_hap5	-	3027710	3027750	---
8284	chr6_mcf_hap5	-	3050810	3050834	---
8285	chr6_mcf_hap5	-	3074526	3074607	---
8286	chr6_mcf_hap5	-	3139867	3139891	---
8287	chr6_mcf_hap5	-	3518093	3518175	---
8288	chr6_mcf_hap5	-	3534899	3534988	---
8289	chr6_mcf_hap5	-	3548959	3548983	---
8290	chr6_mcf_hap5	-	4133663	4133687	---
8291	chr6_mcf_hap5	-	4147537	4147588	---
8292	chr6_mcf_hap5	-	4622228	4622252	---
8293	chr6_mcf_hap5	-	4628105	4628129	---
8294	chr6_mcf_hap5	-	4738655	4738679	---
8295	chr6_mcf_hap5	-	4738943	4738967	---
8296	chr6_mcf_hap5	-	4765207	4765380	---
8297	chr6_qbl_hap6	+	399844	400051	---
8298	chr6_qbl_hap6	+	928092	928173	OTTHUMT00000309969 // MOG
8299	chr6_qbl_hap6	+	1397095	1397261	---
8300	chr6_qbl_hap6	+	1750478	1750678	ENST00000415649 // HLA-E
8301	chr6_qbl_hap6	+	2144828	2144852	---
8302	chr6_qbl_hap6	+	2149373	2149397	---
8303	chr6_qbl_hap6	+	2153067	2153091	NM_013994 // DDR1
8304	chr6_qbl_hap6	+	2154098	2154122	NM_013994 // DDR1
8305	chr6_qbl_hap6	+	2170729	2170753	ENST00000469311 // VARS2
8306	chr6_qbl_hap6	+	2209680	2209713	---
8307	chr6_qbl_hap6	+	2247785	2247867	ENST00000376296 // MUC21
8308	chr6_qbl_hap6	+	3242586	3242610	ENST00000483467 // STK19
8309	chr6_qbl_hap6	+	3253413	3253437	---
8310	chr6_qbl_hap6	+	3255413	3255437	---
8311	chr6_qbl_hap6	+	3386680	3386704	ENST00000480383 // EGFL8
8312	chr6_qbl_hap6	+	3399817	3399841	ENST00000480383 // EGFL8
8313	chr6_qbl_hap6	+	4280701	4280765	---
8314	chr6_qbl_hap6	+	4282276	4282355	---
8315	chr6_qbl_hap6	-	1864373	1864397	---
8316	chr6_qbl_hap6	-	2192784	2192814	---
8317	chr6_qbl_hap6	-	2379967	2380004	---
8318	chr6_qbl_hap6	-	2409072	2409096	---
8319	chr6_qbl_hap6	-	2807506	2807531	---
8320	chr6_qbl_hap6	-	2802544	2802598	---
8321	chr6_qbl_hap6	-	2802610	2802639	---
8322	chr6_qbl_hap6	-	2907816	2907840	---

8323	chr6_qbl_hap6	-	2941674	2941714	---
8324	chr6_qbl_hap6	-	2988473	2988554	---
8325	chr6_qbl_hap6	-	3127562	3127632	---
8326	chr6_qbl_hap6	-	3399284	3399366	---
8327	chr6_qbl_hap6	-	3416110	3416181	---
8328	chr6_qbl_hap6	-	4028855	4028905	---
8329	chr6_qbl_hap6	-	4042767	4042818	---
8330	chr6_qbl_hap6	-	4380686	4380710	---
8331	chr6_qbl_hap6	-	4386563	4386587	---
8332	chr6_qbl_hap6	-	4497151	4497175	---
8333	chr6_qbl_hap6	-	4497439	4497463	---
8334	chr6_qbl_hap6	-	4523714	4523887	---
8335	chr6_ssto_hap7	+	437324	437531	---
8336	chr6_ssto_hap7	+	965329	965410	---
8337	chr6_ssto_hap7	+	1434608	1434774	---
8338	chr6_ssto_hap7	+	1642949	1642981	---
8339	chr6_ssto_hap7	+	1789853	1790053	ENST00000415649 // HLA-E
8340	chr6_ssto_hap7	+	3014131	3014163	OTTHUMT00000412423 // OTTHUMG00000171227
8341	chr6_ssto_hap7	+	3021951	3021975	NM_138277 // C6orf25
8342	chr6_ssto_hap7	+	3292332	3292356	OTTHUMT00000269131 // C4B_2
8343	chr6_ssto_hap7	+	3294332	3294356	---
8344	chr6_ssto_hap7	+	3325070	3325094	OTTHUMT00000269131 // C4B_2
8345	chr6_ssto_hap7	+	3327070	3327094	---
8346	chr6_ssto_hap7	+	3473391	3473415	ENST00000480383 // EGFL8
8347	chr6_ssto_hap7	+	3486525	3486549	ENST00000480383 // EGFL8
8348	chr6_ssto_hap7	+	4528748	4528812	---
8349	chr6_ssto_hap7	+	4530323	4530402	---
8350	chr6_ssto_hap7	+	4863298	4863327	NM_024165 // PHF1
8351	chr6_ssto_hap7	+	4891131	4891155	NM_006772 // SYNGAP1
8352	chr6_ssto_hap7	+	4895913	4895937	NM_006772 // SYNGAP1
8353	chr6_ssto_hap7	-	1532348	1532449	---
8354	chr6_ssto_hap7	-	1903744	1903768	---
8355	chr6_ssto_hap7	-	2004637	2004661	---
8356	chr6_ssto_hap7	-	2839745	2839769	---
8357	chr6_ssto_hap7	-	2844636	2844660	---
8358	chr6_ssto_hap7	-	2944981	2945005	---
8359	chr6_ssto_hap7	-	2978836	2978876	---
8360	chr6_ssto_hap7	-	3001947	3001971	---
8361	chr6_ssto_hap7	-	3025660	3025741	---
8362	chr6_ssto_hap7	-	3090982	3091006	---
8363	chr6_ssto_hap7	-	3485992	3486074	---

8364	chr6_ssto_hap7	-	3502819	3502890	---
8365	chr6_ssto_hap7	-	4241433	4241484	---
8366	chr6_ssto_hap7	-	4628629	4628653	---
8367	chr6_ssto_hap7	-	4634506	4634530	---
8368	chr7	+	881494	881518	ENST00000493681 // SUN1
8369	chr7	+	1660709	1660759	OTTHUMT00000322898 // OTTHUMG00000151498
8370	chr7	+	1786731	1787255	NM_001128636 // ELFN1
8371	chr7	+	2419790	2419814	ENST00000465670 // EIF3B
8372	chr7	+	3678677	3678701	NM_152744 // SDK1
8373	chr7	+	4201435	4201459	NM_152744 // SDK1
8374	chr7	+	4798951	4799147	NM_001037165 // FOXK1
8375	chr7	+	4799247	4799271	ENST00000496023 // FOXK1
8376	chr7	+	5563979	5564027	---
8377	chr7	+	6715751	6715775	---
8378	chr7	+	12255373	12255409	AK311651 // TMEM106B
8379	chr7	+	12270694	12270730	NM_018374 // TMEM106B
8380	chr7	+	16685768	16685797	NR_027624 // BZW2
8381	chr7	+	20739507	20739531	NM_001163941 // ABCB5
8382	chr7	+	23286442	23286466	NM_001005340 // GPNMB
8383	chr7	+	26400599	26400661	NR_037670 // SNX10
8384	chr7	+	26404713	26404761	NR_037670 // SNX10
8385	chr7	+	27832735	27832759	NM_006024 // TAX1BP1
8386	chr7	+	30671073	30671097	NM_002047 // GARS
8387	chr7	+	31009499	31009523	NM_000823 // GHRHR
8388	chr7	+	31356693	31356738	---
8389	chr7	+	31594045	31594069	AK095663 // CCDC129
8390	chr7	+	31736648	31736672	NM_006658 // PPP1R17
8391	chr7	+	32535206	32535230	NM_015060 // AVL9
8392	chr7	+	32772627	32772689	NR_030320 // MIR550A2
8393	chr7	+	38052976	38053168	---
8394	chr7	+	39172066	39172090	---
8395	chr7	+	39606490	39606514	---
8396	chr7	+	39991012	39991124	NM_003718 // CDK13
8397	chr7	+	43436292	43436316	ENST00000471043 // HECW1
8398	chr7	+	43158561	43158792	AK093262 // HECW1-IT1
8399	chr7	+	43846875	43846899	NM_000712 // BLVRA
8400	chr7	+	48075157	48075185	ENST00000348904 // C7orf57
8401	chr7	+	48139336	48139360	NM_003364 // UPP1
8402	chr7	+	48144348	48144810	AK096167 // UPP1
8403	chr7	+	48147869	48147934	NM_003364 // UPP1
8404	chr7	+	50606813	50606847	NR_033845 // LOC100129427

8405	chr7	+	54427627	54427688	---
8406	chr7	+	55210053	55210077	NM_005228 // EGFR
8407	chr7	+	56047741	56048524	AK125036 // GBAS
8408	chr7	+	66463856	66463880	NM_018264 // TYW1
8409	chr7	+	70242163	70242187	ENST00000439256 // AUTS2
8410	chr7	+	73101203	73101227	NM_001202560 // WBSCR22
8411	chr7	+	73458222	73458246	NM_000501 // ELN
8412	chr7	+	73731823	73731847	NM_003388 // CLIP2
8413	chr7	+	73938450	73938474	NM_016328 // GTF2IRD1
8414	chr7	+	74170484	74170508	---
8415	chr7	+	74433164	74433244	NM_001145063 // GATSL1
8416	chr7	+	76548405	76548494	---
8417	chr7	+	76634934	76634981	NR_023383 // DTX2P1-UPK3BP1-PMS2P11
8418	chr7	+	77299330	77299530	---
8419	chr7	+	89751381	89751405	NR_003551 // DPY19L2P4
8420	chr7	+	89976058	89976086	NM_001042717 // GTPBP10
8421	chr7	+	90237861	90237885	DQ655966 // CDK14
8422	chr7	+	91737953	91737977	AF091711 // AKAP9
8423	chr7	+	92077054	92077105	NM_021167 // GATAD1
8424	chr7	+	94292827	94292864	NM_015068 // PEG10
8425	chr7	+	94905932	94905992	---
8426	chr7	+	95166913	95167062	NM_016116 // ASB4
8427	chr7	+	95289677	95289713	---
8428	chr7	+	98513385	98513409	NM_001244580 // TRRAP
8429	chr7	+	98543387	98543411	NM_001244580 // TRRAP
8430	chr7	+	98579434	98579458	NM_001244580 // TRRAP
8431	chr7	+	99007758	99007782	NM_003910 // BUD31
8432	chr7	+	99017085	99017208	NM_003910 // BUD31
8433	chr7	+	99070530	99070563	NM_213603 // ZNF789
8434	chr7	+	99214572	99214608	NM_145115 // ZSCAN25
8435	chr7	+	99595399	99595449	---
8436	chr7	+	99662241	99662269	NM_145914 // ZSCAN21
8437	chr7	+	99703770	99703794	---
8438	chr7	+	99997640	99997669	NM_013439 // PILRA
8439	chr7	+	100028906	100028930	NM_019606 // MEPCE
8440	chr7	+	100451820	100451844	NM_020246 // SLC12A9
8441	chr7	+	101196629	101196655	NM_133457 // COL26A1
8442	chr7	+	102201564	102201622	NM_001031618 // SPDYE2
8443	chr7	+	102300654	102300712	NM_001031618 // SPDYE2
8444	chr7	+	103969137	103969170	NM_199000 // LHFPL3
8445	chr7	+	104702473	104702497	---

8446	chr7	+	106837380	106837510	AK074353 // HBP1
8447	chr7	+	107217406	107217488	AK127802 // DUS4L
8448	chr7	+	107338501	107338525	NM_000441 // SLC26A4
8449	chr7	+	108215113	108215260	NM_012328 // DNAJB9
8450	chr7	+	110568375	110568418	---
8451	chr7	+	112116994	112117018	NM_001550 // IFRD1
8452	chr7	+	115874593	115874673	NM_015641 // TES
8453	chr7	+	121674086	121674110	ENST00000468641 // PTPRZ1
8454	chr7	+	121947097	121947324	ENST00000424404 // FEZF1-AS1
8455	chr7	+	128169724	128170843	---
8456	chr7	+	128849146	128849170	NM_005631 // SMO
8457	chr7	+	129124391	129124496	---
8458	chr7	+	129917680	129917730	NM_001869 // CPA2
8459	chr7	+	129959166	129959221	---
8460	chr7	+	130538480	130538542	---
8461	chr7	+	133615198	133615222	ENST00000478265 // EXOC4
8462	chr7	+	134647642	134647666	ENST00000443197 // CALD1
8463	chr7	+	135357501	135357537	NM_001130929 // C7orf73
8464	chr7	+	136013769	136013828	OTTHUMT00000340910 // OTTHUMG00000155618
8465	chr7	+	137010179	137011674	---
8466	chr7	+	137641331	137641390	NM_001243523 // LOC100130880
8467	chr7	+	139025271	139025295	NR_073058 // C7orf55
8468	chr7	+	139133530	139133561	---
8469	chr7	+	139221051	139221090	NM_001080511 // CLEC2L
8470	chr7	+	142326571	142326604	AF043180 // TRBV19
8471	chr7	+	143806633	143806666	ENST00000408979 // OR2A2
8472	chr7	+	148904500	148904524	NM_003575 // ZNF282
8473	chr7	+	148990737	148990761	ENST00000418158 // ZNF783
8474	chr7	+	149564412	149564436	NM_001099220 // ZNF862
8475	chr7	+	149697974	149700096	---
8476	chr7	+	150690867	150690891	NM_000603 // NOS3
8477	chr7	+	150698662	150698686	NM_000603 // NOS3
8478	chr7	+	150748260	150748335	NM_004769 // ASIC3
8479	chr7	+	150935883	150935907	ENST00000035307 // CHPF2
8480	chr7	+	150946415	150946547	---
8481	chr7	+	151048344	151048368	ENST00000493588 // NUB1
8482	chr7	+	151597428	151597459	---
8483	chr7	+	151711852	151711876	NM_145292 // GALNTL5
8484	chr7	+	154561134	154561158	NM_130797 // DPP6
8485	chr7	+	154862717	154863346	NM_024012 // HTR5A
8486	chr7	+	155094348	155094372	ENST00000468307 // INSIG1

8487	chr7	+	156432989	156433014	ENST00000404282 // RNF32
8488	chr7	+	157161837	157161861	ENST00000468928 // DNAJB6
8489	chr7	+	157178990	157179014	NM_005494 // DNAJB6
8490	chr7	+	157259113	157259894	---
8491	chr7	+	158769629	158770316	---
8492	chr7	-	1040122	1040187	ENST00000357429 // C7orf50
8493	chr7	-	1192582	1192702	NM_182491 // ZFAND2A
8494	chr7	-	1511211	1511235	NM_001080453 // INTS1
8495	chr7	-	2946211	2946235	NM_032415 // CARD11
8496	chr7	-	3180669	3180697	ENST00000457522 // LOC392621
8497	chr7	-	5363879	5363903	NM_001080495 // TNRC18
8498	chr7	-	6566350	6566374	NM_001145118 // GRID2IP
8499	chr7	-	6838542	6838566	ENST00000316731 // CCZ1B
8500	chr7	-	14647080	14647104	NM_004080 // DGKB
8501	chr7	-	15239998	15240878	NM_001004320 // AGMO
8502	chr7	-	16415776	16415860	NM_001101426 // ISPD
8503	chr7	-	16502218	16502347	NM_015464 // SOSTDC1
8504	chr7	-	17497091	17497134	---
8505	chr7	-	17869642	17869666	NM_015132 // SNX13
8506	chr7	-	22861793	22861855	OTTHUMT00000326716 // TOMM7
8507	chr7	-	24758764	24758788	NM_004403 // DFNA5
8508	chr7	-	26897149	26897173	AK299317 // SKAP2
8509	chr7	-	27702458	27702612	NM_152740 // HIBADH
8510	chr7	-	29034982	29035006	ENST00000265394 // CPVL
8511	chr7	-	30536351	30536426	NM_024051 // GGCT
8512	chr7	-	31920385	31920409	NM_001191056 // PDE1C
8513	chr7	-	32907886	32908937	NM_015483 // KBTBD2
8514	chr7	-	38505095	38505119	NM_001635 // AMPH
8515	chr7	-	42957177	42957222	NM_002787 // PSMA2
8516	chr7	-	42957377	42957413	NM_002787 // PSMA2
8517	chr7	-	43247423	43247465	---
8518	chr7	-	44258996	44259020	NM_001220 // CAMK2B
8519	chr7	-	44323773	44323797	NM_001220 // CAMK2B
8520	chr7	-	44605784	44605808	OTTHUMT00000339410 // DDX56
8521	chr7	-	44613449	44613477	NM_019082 // DDX56
8522	chr7	-	45022748	45022834	NR_003697 // SNHG15
8523	chr7	-	45145057	45145081	NM_004749 // TBRG4
8524	chr7	-	45960799	45960850	NM_001013398 // IGFBP3
8525	chr7	-	47848841	47848865	ENST00000483616 // PKD1L1
8526	chr7	-	47869655	47869679	NM_138295 // PKD1L1
8527	chr7	-	47933553	47933577	NM_138295 // PKD1L1
8528	chr7	-	50560642	50560703	NM_001242890 // DDC

8529	chr7	-	50595840	50595912	NM_001082971 // DDC
8530	chr7	-	50772854	50772878	NM_001001550 // GRB10
8531	chr7	-	51111210	51111234	NM_015198 // COBL
8532	chr7	-	54825200	54825277	NM_014302 // SEC61G
8533	chr7	-	55755639	55755708	NR_027340 // FKBP9L
8534	chr7	-	55756617	55756672	NR_027342 // FKBP9L
8535	chr7	-	56154609	56154647	ENST00000467726 // PHKG1
8536	chr7	-	57245965	57246017	NR_030766 // GUSBP10
8537	chr7	-	62693636	62693660	---
8538	chr7	-	65957267	65957293	---
8539	chr7	-	66019180	66019575	---
8540	chr7	-	66452818	66453319	NM_016038 // SBDS
8541	chr7	-	71877287	71877322	---
8542	chr7	-	72430246	72430273	NM_198853 // TRIM74
8543	chr7	-	72990895	72990920	ENST00000426966 // TBL2
8544	chr7	-	73010773	73010797	NM_032951 // MLXIPL
8545	chr7	-	73097754	73097782	ENST00000395176 // DNAJC30
8546	chr7	-	75988202	75988337	NM_012479 // YWHAG
8547	chr7	-	77648030	77648054	NM_012301 // MAGI2
8548	chr7	-	81579711	81579735	NM_000722 // CACNA2D1
8549	chr7	-	82784567	82784591	NM_033026 // PCLO
8550	chr7	-	86520844	86520868	---
8551	chr7	-	86522266	86522290	NR_030672 // KIAA1324L
8552	chr7	-	87846476	87846502	NM_003130 // SRI
8553	chr7	-	90236334	90236399	---
8554	chr7	-	91747838	91747862	NM_000786 // CYP51A1
8555	chr7	-	91752513	91752576	NM_000786 // CYP51A1
8556	chr7	-	91758297	91758322	NM_000786 // CYP51A1
8557	chr7	-	91874780	91874804	NM_194456 // KRIT1
8558	chr7	-	92744108	92744206	NM_017654 // SAMD9
8559	chr7	-	93628971	93628996	ENST00000457139 // BET1
8560	chr7	-	95039156	95039180	ENST00000459842 // PON2
8561	chr7	-	95848983	95849068	NR_030322 // MIR591
8562	chr7	-	96135967	96136009	ENST00000466986 // SHFM1
8563	chr7	-	97860317	97860341	NM_015395 // TECPR1
8564	chr7	-	99011638	99011697	---
8565	chr7	-	99097865	99097947	ENST00000337673 // ZNF394
8566	chr7	-	99250240	99250264	NM_000777 // CYP3A5
8567	chr7	-	99270413	99270437	NR_033807 // CYP3A5
8568	chr7	-	99764803	99764829	NM_024637 // GAL3ST4
8569	chr7	-	99771496	99771520	NM_152742 // GPC2
8570	chr7	-	99933554	99933855	NR_003613 // PMS2P1

8571	chr7	-	100183560	100183584	NM_002319 // LRCH4
8572	chr7	-	100884411	100884454	ENST00000463406 // FIS1
8573	chr7	-	102097841	102098301	NM_017621 // ALKBH4
8574	chr7	-	102957629	102957653	AK126382 // DNAJC2
8575	chr7	-	103293179	103293203	NM_005045 // RELN
8576	chr7	-	105893943	105893967	---
8577	chr7	-	105925297	105925321	NM_005746 // NAMPT
8578	chr7	-	107602051	107602075	NM_002291 // LAMB1
8579	chr7	-	107626734	107626758	NM_002291 // LAMB1
8580	chr7	-	111381646	111381670	NM_014705 // DOCK4
8581	chr7	-	115878349	115878386	---
8582	chr7	-	115926677	115926706	AK097428 // LOC286009
8583	chr7	-	116584355	116584392	ENST00000410218 // RNA5SP239
8584	chr7	-	120480100	120480156	NM_012338 // TSPAN12
8585	chr7	-	121731860	121731884	NM_005763 // AASS
8586	chr7	-	121942874	121942938	NM_001024613 // FEZF1
8587	chr7	-	121944523	121944565	NM_001024613 // FEZF1
8588	chr7	-	121959938	121959962	NM_017954 // CADPS2
8589	chr7	-	123517895	123517951	---
8590	chr7	-	127224534	127224981	NM_024523 // GCC1
8591	chr7	-	127998829	127998853	NM_001174164 // PRRT4
8592	chr7	-	128517658	128517682	NM_001135914 // KCP
8593	chr7	-	130597742	130598009	NR_034120 // LOC646329
8594	chr7	-	132261211	132261605	NM_020911 // PLXNA4
8595	chr7	-	137080416	137080440	NM_004717 // DGKI
8596	chr7	-	137172406	137172430	NM_004717 // DGKI
8597	chr7	-	137590570	137590594	NM_194071 // CREB3L2
8598	chr7	-	138566233	138566292	NM_020910 // KIAA1549
8599	chr7	-	141437998	141438110	NR_015392 // WEE2-AS1
8600	chr7	-	143076345	143077187	ENST00000429630 // LOC100507507
8601	chr7	-	145378332	145378440	---
8602	chr7	-	150912018	150912042	NM_007189 // ABCF2
8603	chr7	-	151105659	151105972	ENST00000484630 // WDR86
8604	chr7	-	151839555	151839579	ENST00000485655 // KMT2C
8605	chr7	-	153109805	153109935	---
8606	chr7	-	154754085	154754109	NM_007349 // PAXIP1
8607	chr7	-	156540618	156540642	ENST00000461603 // LMBR1
8608	chr7	-	157532988	157533034	OTTHUMT00000329049 // OTTHUMG00000153023
8609	chr7	-	158909823	158909972	OTTHUMT00000322678 // VIPR2
8610	chrU	+	137967	138019	---

8611	chr8	+	7581889	7581996	NR_046351 // FAM90A10P
8612	chr8	+	7597184	7597291	---
8613	chr8	+	7612480	7612587	NR_046351 // FAM90A10P
8614	chr8	+	7620128	7620235	NR_046351 // FAM90A10P
8615	chr8	+	7682701	7682744	NM_152251 // DEFB106A
8616	chr8	+	7738945	7739001	NM_001081551 // DEFB103A
8617	chr8	+	10557984	10558035	ENST00000304519 // C8orf74
8618	chr8	+	10621856	10622145	BC043573 // PINX1
8619	chr8	+	15508353	15508377	ENST00000509177 // TUSC3
8620	chr8	+	15379412	15379443	---
8621	chr8	+	19796387	19796430	AK297164 // LPL
8622	chr8	+	21849383	21849407	NM_015024 // XPO7
8623	chr8	+	21927786	21927810	NM_001978 // DMTN
8624	chr8	+	21937691	21937715	NM_001978 // DMTN
8625	chr8	+	21951991	21952015	NM_022749 // FAM160B2
8626	chr8	+	21952199	21952223	AK126408 // FAM160B2
8627	chr8	+	22291904	22292006	---
8628	chr8	+	22462701	22462725	NM_021174 // KIAA1967
8629	chr8	+	22475809	22475833	ENST00000520536 // KIAA1967
8630	chr8	+	24339675	24339699	NM_003817 // ADAM7
8631	chr8	+	24358308	24358332	NM_003817 // ADAM7
8632	chr8	+	26240414	26240502	ENST00000380629 // BNIP3L
8633	chr8	+	27312003	27312027	ENST00000522245 // PTK2B
8634	chr8	+	30255452	30255476	---
8635	chr8	+	31030534	31030558	NM_000553 // WRN
8636	chr8	+	32585605	32585629	NM_004495 // NRG1
8637	chr8	+	33397586	33397617	---
8638	chr8	+	33613391	33613416	---
8639	chr8	+	33654020	33654091	---
8640	chr8	+	36694340	36694364	NM_001031836 // KCNU1
8641	chr8	+	37440295	37440471	---
8642	chr8	+	37695318	37695342	NM_032777 // GPR124
8643	chr8	+	38264885	38264909	NM_144652 // LETM2
8644	chr8	+	38818345	38818382	---
8645	chr8	+	39007351	39007375	NM_145004 // ADAM32
8646	chr8	+	40019092	40019208	---
8647	chr8	+	42178205	42178229	AB209090 // IKBKB
8648	chr8	+	42828482	42828506	NM_032410 // HOOK3
8649	chr8	+	42940669	42940713	NM_002027 // FNTA
8650	chr8	+	49551132	49551162	---
8651	chr8	+	50242949	50243104	---
8652	chr8	+	55370519	55370566	NM_022454 // SOX17

8653	chr8	+	55619017	55619041	AK316511 // RP1
8654	chr8	+	55682304	55682328	AK316511 // RP1
8655	chr8	+	58132742	58132810	NR_038235 // LOC100507651
8656	chr8	+	58658720	58658890	AK090741 // LOC286178
8657	chr8	+	59483289	59483377	ENST00000520228 // SDCBP
8658	chr8	+	59483494	59483523	NM_005625 // SDCBP
8659	chr8	+	59492423	59492447	ENST00000523441 // SDCBP
8660	chr8	+	63831013	63831053	NM_173688 // NKAIN3
8661	chr8	+	64085247	64085271	NM_001277813 // YTHDF3
8662	chr8	+	64086210	64086236	NM_001277815 // YTHDF3
8663	chr8	+	64369370	64369514	---
8664	chr8	+	66556936	66556976	NM_014637 // MTFR1
8665	chr8	+	67342619	67342865	NM_015169 // RRS1
8666	chr8	+	67425816	67425840	ENST00000305454 // C8orf46
8667	chr8	+	69009348	69009372	NM_024870 // PREX2
8668	chr8	+	70571415	70571439	NM_001128205 // SULF1
8669	chr8	+	71383395	71383885	---
8670	chr8	+	74888548	74888584	NM_017866 // TMEM70
8671	chr8	+	74903736	74903784	NM_015364 // LY96
8672	chr8	+	75764054	75765847	NM_015886 // PI15
8673	chr8	+	75929565	75929627	NM_031461 // CRISPLD1
8674	chr8	+	76034611	76034640	---
8675	chr8	+	77596075	77596169	---
8676	chr8	+	77690491	77690570	NM_024721 // ZFHX4
8677	chr8	+	82069857	82070024	OTTHUMT00000379358 // OTTHUMG00000164595
8678	chr8	+	85052425	85052510	OTTHUMT00000379412 // OTTHUMG00000164613
8679	chr8	+	86027680	86027704	NM_033402 // LRRCC1
8680	chr8	+	86351146	86351171	NM_005181 // CA3
8681	chr8	+	90933317	90933397	NM_001126111 // OSGIN2
8682	chr8	+	94827606	94827630	NM_153704 // TMEM67
8683	chr8	+	94930143	94930167	NM_001161779 // PDP1
8684	chr8	+	95690512	95690581	NM_017697 // ESRP1
8685	chr8	+	95751987	95752011	NM_181787 // DPY19L4
8686	chr8	+	95908018	95908042	OTTHUMT00000379939 // NDUFAF6
8687	chr8	+	96981663	96981719	---
8688	chr8	+	97541464	97541488	ENST00000519587 // SDC2
8689	chr8	+	98954063	98954087	NM_002380 // MATN2
8690	chr8	+	99028823	99028847	NM_002380 // MATN2
8691	chr8	+	102166260	102166286	---

8692	chr8	+	102381268	102381497	NR_002182 // NACAP1
8693	chr8	+	103541559	103541627	OTTHUMT00000380207 // OTTHUMG00000164777
8694	chr8	+	103545985	103546018	---
8695	chr8	+	107719412	107719436	AK096148 // OXR1
8696	chr8	+	114612552	114612615	OTTHUMT00000380837 // OTTHUMG00000164895
8697	chr8	+	118541080	118541143	ENST00000519879 // MED30
8698	chr8	+	120007702	120007812	ENST00000521788 // COLEC10
8699	chr8	+	121528277	121528301	NM_022045 // MTBP
8700	chr8	+	124194701	124195035	NM_032899 // FAM83A
8701	chr8	+	125559289	125559315	NM_005005 // NDUFB9
8702	chr8	+	125562087	125562112	NM_005005 // NDUFB9
8703	chr8	+	125562698	125562738	ENST00000517830 // NDUFB9
8704	chr8	+	126021217	126021295	NM_003129 // SQLE
8705	chr8	+	126021452	126021476	NM_003129 // SQLE
8706	chr8	+	126033065	126033089	NM_003129 // SQLE
8707	chr8	+	126034033	126034104	NM_003129 // SQLE
8708	chr8	+	126034436	126034460	NM_003129 // SQLE
8709	chr8	+	127530952	127531069	OTTHUMT00000381486 // OTTHUMG00000165033
8710	chr8	+	133883695	133883719	NM_003235 // TG
8711	chr8	+	134034239	134034263	NM_003235 // TG
8712	chr8	+	143279784	143279817	NR_024378 // LINC00051
8713	chr8	+	143599577	143599601	NM_001702 // BAI1
8714	chr8	+	143781951	143782028	NM_017527 // LY6K
8715	chr8	+	143783135	143783162	AK092545 // LY6K
8716	chr8	+	144354568	144354593	ENST00000519876 // GLI4
8717	chr8	+	144356941	144356967	NM_138465 // GLI4
8718	chr8	+	144375144	144375171	NM_030895 // ZNF696
8719	chr8	+	144494978	144495012	---
8720	chr8	+	144871098	144871122	---
8721	chr8	+	145134940	145135042	NM_019037 // EXOSC4
8722	chr8	+	145448798	145448823	---
8723	chr8	+	145599267	145599316	ENST00000525136 // ADCK5
8724	chr8	+	145726265	145726292	NM_032902 // PPP1R16A
8725	chr8	+	145745016	145745070	NM_001272036 // LRRC14
8726	chr8	+	145748893	145749016	NM_001272036 // LRRC14
8727	chr8	-	566534	566558	AK297476 // ERICH1
8728	chr8	-	1236633	1236773	---
8729	chr8	-	1921512	1921621	---
8730	chr8	-	2387152	2387261	---

8731	chr8	-	4851905	4851929	NM_033225 // CSMD1
8732	chr8	-	7287595	7287651	NM_001081551 // DEFB103A
8733	chr8	-	7343859	7343902	NM_152251 // DEFB106A
8734	chr8	-	9724458	9724511	---
8735	chr8	-	10356154	10356211	AK307207 // PRSS51
8736	chr8	-	11853731	11853760	NM_001033019 // DEFB134
8737	chr8	-	12583442	12583495	ENST00000527055 // LONRF1
8738	chr8	-	13462072	13462119	---
8739	chr8	-	17504659	17504683	---
8740	chr8	-	18782232	18782256	---
8741	chr8	-	21996173	21996197	NM_025232 // REEP4
8742	chr8	-	22402705	22402914	---
8743	chr8	-	22545938	22547427	NM_004430 // EGR3
8744	chr8	-	23082765	23082957	---
8745	chr8	-	23282704	23282728	---
8746	chr8	-	23590077	23590124	OTTHUMT00000376059 // OTTHUMG00000163869
8747	chr8	-	25718607	25718631	NM_022659 // EBF2
8748	chr8	-	25898133	25898172	NM_022659 // EBF2
8749	chr8	-	28196548	28196756	---
8750	chr8	-	29047896	29047920	ENST00000522846 // KIF13B
8751	chr8	-	36622595	36622641	---
8752	chr8	-	37706114	37706173	NM_018310 // BRF2
8753	chr8	-	38280311	38280335	---
8754	chr8	-	38286783	38286807	M63889 // FGFR1
8755	chr8	-	39267729	39267828	---
8756	chr8	-	40210474	40210614	---
8757	chr8	-	41526038	41526062	NM_020476 // ANK1
8758	chr8	-	42083188	42083223	---
8759	chr8	-	42234601	42234735	ENST00000220812 // DKK4
8760	chr8	-	42623502	42623526	NM_004198 // CHRNA6
8761	chr8	-	48650699	48651642	ENST00000408965 // CEBPD
8762	chr8	-	48717652	48717686	---
8763	chr8	-	49830281	49830894	NM_003068 // SNAI2
8764	chr8	-	52811560	52811600	NM_052937 // PCMTD1
8765	chr8	-	53159159	53159183	ENST00000518037 // ST18
8766	chr8	-	54934736	54934760	NM_006756 // TCEA1
8767	chr8	-	56656049	56656083	BC043417 // TMEM68
8768	chr8	-	58803160	58803362	---
8769	chr8	-	59498246	59498270	NM_003580 // NSMAF
8770	chr8	-	59506810	59506834	NM_003580 // NSMAF
8771	chr8	-	59574839	59574871	---

8772	chr8	-	62672057	62674131	---
8773	chr8	-	65143117	65143159	---
8774	chr8	-	69218753	69218833	NR_038877 // LOC286189
8775	chr8	-	71574030	71574090	NM_016027 // LACTB2
8776	chr8	-	75149242	75149270	NM_020647 // JPH1
8777	chr8	-	75262171	75262282	---
8778	chr8	-	76189223	76189270	---
8779	chr8	-	81083495	81083519	OTTHUMT00000379392 // TPD52
8780	chr8	-	88659151	88659205	---
8781	chr8	-	90629260	90629284	---
8782	chr8	-	92999176	92999200	NM_004349 // RUNX1T1
8783	chr8	-	93083566	93083590	ENST00000517792 // RUNX1T1
8784	chr8	-	94712335	94712393	NR_033858 // LINC00535
8785	chr8	-	95384564	95384588	NM_012415 // RAD54B
8786	chr8	-	95423445	95423469	NM_012415 // RAD54B
8787	chr8	-	95725944	95726039	---
8788	chr8	-	97172922	97172946	NM_001001557 // GDF6
8789	chr8	-	97243378	97243426	OTTHUMT00000379870 // UQCRB
8790	chr8	-	97246706	97246743	NM_001199975 // UQCRB
8791	chr8	-	101280837	101280904	ENST00000524233 // RNF19A
8792	chr8	-	101422966	101422999	OTTHUMT00000379858 // OTTHUMG00000164708
8793	chr8	-	101721985	101722009	---
8794	chr8	-	101964363	101964387	ENST00000418997 // YWHAZ
8795	chr8	-	102211424	102211448	NM_001042510 // ZNF706
8796	chr8	-	102758145	102758169	---
8797	chr8	-	102803285	102803309	NM_032041 // NCALD
8798	chr8	-	104258659	104258742	AK125733 // LOC100499183
8799	chr8	-	105331034	105331133	---
8800	chr8	-	105518486	105518956	ENST00000519675 // LRP12
8801	chr8	-	106924048	106924072	---
8802	chr8	-	109095782	109095840	NM_178565 // RSPO2
8803	chr8	-	109923255	109923334	---
8804	chr8	-	118725069	118725124	---
8805	chr8	-	120868125	120868172	ENST00000313655 // DSCC1
8806	chr8	-	120885377	120885550	---
8807	chr8	-	121455425	121455493	NM_014078 // MRPL13
8808	chr8	-	124232442	124232493	ENST00000276704 // C8orf76
8809	chr8	-	126062819	126062843	NM_014846 // KIAA0196
8810	chr8	-	130765082	130765128	---
8811	chr8	-	131016785	131016821	---
8812	chr8	-	133041320	133041344	NM_001080399 // OC90

8813	chr8	-	133053856	133053880	NM_001080399 // OC90
8814	chr8	-	134579435	134579459	---
8815	chr8	-	135614558	135614582	NM_020863 // ZFAT
8816	chr8	-	137909260	137909332	---
8817	chr8	-	143957384	143957602	ENST00000314111 // CYP11B1
8818	chr8	-	143992041	143993241	NM_000498 // CYP11B2
8819	chr8	-	144618470	144618494	NM_015117 // ZC3H3
8820	chr8	-	144812487	144812700	NM_198488 // FAM83H
8821	chr8	-	144891169	144891193	NM_182706 // SCRIB
8822	chr8	-	145690842	145690866	ENST00000403000 // CYHR1
8823	chr8	-	145769271	145769295	ENST00000528810 // ARHGAP39
8824	chr9	+	745539	745563	NM_015158 // KANK1
8825	chr9	+	1929409	1929560	---
8826	chr9	+	2047429	2047453	NM_003070 // SMARCA2
8827	chr9	+	2158521	2158545	AK300093 // SMARCA2
8828	chr9	+	4860927	4860996	NM_005772 // RCL1
8829	chr9	+	5090839	5090863	NM_004972 // JAK2
8830	chr9	+	5233657	5233863	NM_002195 // INSL4
8831	chr9	+	21967137	21967164	NR_024274 // C9orf53
8832	chr9	+	22097283	22097341	NR_003529 // CDKN2B-AS1
8833	chr9	+	22823356	22824144	NR_038977 // FLJ35282
8834	chr9	+	26786834	26786867	OTTHUMT00000378353 // OTTHUMG00000164347
8835	chr9	+	33604365	33604401	OTTHUMT00000001042 // OTTHUMG00000000405
8836	chr9	+	33618208	33618455	ENST00000379435 // TRBV20OR9-2
8837	chr9	+	33638041	33638081	ENST00000390389 // TRBV23OR9-2
8838	chr9	+	33831041	33831076	---
8839	chr9	+	35481842	35481866	NR_003581 // ATP8B5P
8840	chr9	+	35806410	35806434	NM_003995 // NPR2
8841	chr9	+	35835285	35835373	ENST00000464519 // TMEM8B
8842	chr9	+	35841717	35841741	NM_001042590 // TMEM8B
8843	chr9	+	36110000	36110024	NM_021111 // RECK
8844	chr9	+	36599432	36599456	NM_014791 // MELK
8845	chr9	+	36677338	36677388	NM_014791 // MELK
8846	chr9	+	37362852	37362972	---
8847	chr9	+	37489321	37489345	NM_022490 // POLR1E
8848	chr9	+	42037464	42037558	---
8849	chr9	+	42386747	42386775	NM_032250 // ANKRD20A1
8850	chr9	+	42378941	42379038	NR_046929 // RNU6-55P
8851	chr9	+	42714459	42714483	BC043420 // CBWD5
8852	chr9	+	45733736	45733811	BC148261 // FAM27E2

8853	chr9	+	67340645	67340676	---
8854	chr9	+	67864533	67864627	---
8855	chr9	+	67937393	67937490	NR_046929 // RNU6-55P
8856	chr9	+	69392612	69392709	NR_046929 // RNU6-55P
8857	chr9	+	70862600	70862624	NM_018491 // CBWD1
8858	chr9	+	70914426	70914450	NM_018491 // CBWD1
8859	chr9	+	71549833	71549857	NM_003558 // PIP5K1B
8860	chr9	+	71651087	71651113	AK308620 // FXN
8861	chr9	+	71861489	71861513	AK308564 // TJP2
8862	chr9	+	72402051	72402109	---
8863	chr9	+	72933540	72933564	NM_015110 // SMC5
8864	chr9	+	75783960	75784063	NM_000700 // ANXA1
8865	chr9	+	79034758	79034784	AK313343 // GCNT1
8866	chr9	+	79118878	79120929	NM_001097634 // GCNT1
8867	chr9	+	80866901	80866925	NM_001098802 // CEP78
8868	chr9	+	82191169	82191193	ENST00000461758 // TLE4
8869	chr9	+	82286224	82286248	AK057236 // TLE4
8870	chr9	+	82649228	82649802	OTTHUMT00000052799 // OTTHUMG00000020075
8871	chr9	+	86096182	86096252	---
8872	chr9	+	89612564	89612910	---
8873	chr9	+	90346108	90346325	NM_001912 // CTSL1
8874	chr9	+	90503477	90503518	NM_178828 // SPATA31E1
8875	chr9	+	91606732	91606757	OTTHUMT00000052978 // C9orf47
8876	chr9	+	92168491	92168609	---
8877	chr9	+	92220690	92220792	NM_006705 // GADD45G
8878	chr9	+	95557946	95558047	---
8879	chr9	+	95858461	95858486	NM_032310 // C9orf89
8880	chr9	+	98678086	98678110	NM_001010895 // ERCC6L2
8881	chr9	+	101767190	101767214	NM_001855 // COL15A1
8882	chr9	+	104032119	104032143	ENST00000463206 // LPPR1
8883	chr9	+	105052409	105052905	---
8884	chr9	+	110267407	110267450	---
8885	chr9	+	112542712	112542736	NM_007203 // PALM2-AKAP2
8886	chr9	+	114338834	114339016	NM_001007169 // ZNF483
8887	chr9	+	114409409	114409538	NR_037148 // DNAJC25
8888	chr9	+	115181157	115181235	NM_032303 // HSDL2
8889	chr9	+	115600801	115600957	NM_001012994 // SNX30
8890	chr9	+	116116520	116116612	NM_017688 // BSPRY
8891	chr9	+	117031372	117031396	---
8892	chr9	+	121502841	121502922	---
8893	chr9	+	124071216	124071240	ENST00000485767 // GSN

8894	chr9	+	125047871	125047895	AK298046 // MRRF
8895	chr9	+	125237973	125238095	AK123016 // OR1J2
8896	chr9	+	125563370	125563395	ENST00000277309 // OR1K1
8897	chr9	+	126118505	126118530	NM_173689 // CRB2
8898	chr9	+	127218985	127219009	NM_001161808 // GPR144
8899	chr9	+	130111232	130111256	NM_032293 // GARNL3
8900	chr9	+	130446921	130446945	ENST00000494254 // STXBP1
8901	chr9	+	130578431	130579241	---
8902	chr9	+	130868029	130868053	NM_052901 // SLC25A25
8903	chr9	+	131182991	131183015	NM_016174 // CERCAM
8904	chr9	+	131258362	131258386	NM_153435 // ODF2
8905	chr9	+	132020633	132020663	OTTHUMT00000054571 // OTTHUMG00000020777
8906	chr9	+	132842015	132842039	NM_001136557 // GPR107
8907	chr9	+	132862949	132862973	NM_001136557 // GPR107
8908	chr9	+	133278259	133278283	AL834139 // HMCN2
8909	chr9	+	133325255	133325306	---
8910	chr9	+	134026053	134026077	NM_005085 // NUP214
8911	chr9	+	134382759	134382783	NM_007171 // POMT1
8912	chr9	+	136307580	136307604	NM_139025 // ADAMTS13
8913	chr9	+	136523534	136523558	NM_000787 // DBH
8914	chr9	+	136894216	136894957	NR_015427 // LINC00094
8915	chr9	+	137271270	137271308	NR_039816 // MIR4669
8916	chr9	+	137533917	137533941	NM_000093 // COL5A1
8917	chr9	+	138374549	138374645	NM_014811 // PPP1R26
8918	chr9	+	138469508	138469553	NR_034016 // LOC100130954
8919	chr9	+	138507230	138507354	---
8920	chr9	+	138644270	138644294	BC144304 // KCNT1
8921	chr9	+	138651663	138651687	NM_020822 // KCNT1
8922	chr9	+	139564369	139564460	NR_045110 // EGFL7
8923	chr9	+	139726222	139726246	NM_024718 // RABL6
8924	chr9	+	139728492	139728516	NM_001173989 // RABL6
8925	chr9	+	139750710	139750734	BC144259 // MAMDC4
8926	chr9	+	139847122	139847160	ENST00000495410 // LCN12
8927	chr9	+	139864413	139864499	ENST00000371629 // C9orf141
8928	chr9	+	139886948	139886973	BC002613 // C9orf142
8929	chr9	+	139947234	139947265	---
8930	chr9	+	139995521	139995545	NM_016219 // MAN1B1
8931	chr9	+	140051441	140051465	NM_001185091 // GRIN1
8932	chr9	+	140062189	140062213	NM_021569 // GRIN1
8933	chr9	+	140138097	140138128	NM_006088 // TUBB4B
8934	chr9	+	140147174	140147348	NR_046339 // C9orf173

8935	chr9	+	140694982	140695006	ENST00000488242 // EHMT1
8936	chr9	-	16733	16873	NR_024077 // WASH2P
8937	chr9	-	17355	17477	NR_024077 // WASH2P
8938	chr9	-	4386440	4386528	---
8939	chr9	-	5132026	5132078	---
8940	chr9	-	6566371	6566415	---
8941	chr9	-	6748879	6748942	OTTHUMT00000051687 // SNRPEP2
8942	chr9	-	19057276	19057300	ENST00000380496 // HAUS6
8943	chr9	-	21015251	21015375	ENST00000488436 // PTPLAD2
8944	chr9	-	22204004	22204058	OTTHUMT00000051934 // OTTHUMG00000019692
8945	chr9	-	23765026	23765050	ENST00000380110 // ELAVL2
8946	chr9	-	30771145	30771197	---
8947	chr9	-	33510985	33511086	NR_003667 // SUGT1P1
8948	chr9	-	34257350	34257667	NM_194313 // KIF24
8949	chr9	-	34381446	34381470	ENST00000379126 // C9orf24
8950	chr9	-	34389941	34389980	---
8951	chr9	-	34662050	34662074	NM_006664 // CCL27
8952	chr9	-	34691156	34691187	NM_006274 // CCL19
8953	chr9	-	35093368	35093392	AK074064 // PIGO
8954	chr9	-	35100861	35100895	AK130546 // STOML2
8955	chr9	-	35698141	35698165	NM_006289 // TLN1
8956	chr9	-	35704338	35704362	NM_006289 // TLN1
8957	chr9	-	35704781	35704805	NM_006289 // TLN1
8958	chr9	-	35707218	35707242	NM_006289 // TLN1
8959	chr9	-	35740281	35740305	NM_020944 // GBA2
8960	chr9	-	35813522	35813546	NM_032593 // HINT2
8961	chr9	-	40740925	40740966	OTTHUMT00000143686 // OTTHUMG00000067148
8962	chr9	-	43108310	43108334	NM_032250 // ANKRD20A1
8963	chr9	-	43122808	43122905	---
8964	chr9	-	44107813	44107919	---
8965	chr9	-	46669492	46669586	---
8966	chr9	-	65782688	65782808	---
8967	chr9	-	68429074	68429122	NR_033907 // LOC642236
8968	chr9	-	69200147	69200184	NM_001085476 // FOXD4L6
8969	chr9	-	70432482	70432506	NM_018491 // CBWD1
8970	chr9	-	70484376	70484400	NM_018491 // CBWD1
8971	chr9	-	73000583	73002582	NM_001206 // KLF9
8972	chr9	-	75838733	75839103	---
8973	chr9	-	77567230	77567502	ENST00000376854 // C9orf40
8974	chr9	-	85630761	85630785	NM_152573 // RASEF

8975	chr9	-	86583699	86583723	NM_002140 // HNRNPK
8976	chr9	-	87655759	87655831	---
8977	chr9	-	88934532	88934556	NM_024617 // ZCCHC6
8978	chr9	-	91703547	91703806	OTTHUMT00000052984 // OTTHUMG00000020177
8979	chr9	-	93225979	93226064	NR_034157 // LOC340515
8980	chr9	-	94171401	94171591	NM_005384 // NFIL3
8981	chr9	-	95267829	95267880	NM_001393 // ECM2
8982	chr9	-	97082736	97082767	NM_017561 // NUTM2F
8983	chr9	-	99012036	99012061	NM_000197 // HSD17B3
8984	chr9	-	100675191	100675215	AK302701 // C9orf156
8985	chr9	-	100707054	100707100	NM_018437 // HEMGN
8986	chr9	-	106192068	106192174	OTTHUMT00000053468 // OTTHUMG00000020400
8987	chr9	-	107753967	107754014	OTTHUMT00000053496 // OTTHUMG00000020419
8988	chr9	-	109378159	109378263	---
8989	chr9	-	109737815	109738523	AK097706 // LOC340512
8990	chr9	-	110681168	110681257	---
8991	chr9	-	112144031	112144055	NM_002829 // PTPN3
8992	chr9	-	113275220	113275244	NM_153366 // SVEP1
8993	chr9	-	116064281	116064305	AK091940 // RNF183
8994	chr9	-	116085390	116085433	NM_001012361 // WDR31
8995	chr9	-	116163546	116163571	NM_000031 // ALAD
8996	chr9	-	117113260	117113284	NM_030767 // AKNA
8997	chr9	-	119495743	119495767	NM_014010 // ASTN2
8998	chr9	-	123222852	123222876	NM_018249 // CDK5RAP2
8999	chr9	-	123298724	123298748	NM_018249 // CDK5RAP2
9000	chr9	-	123631880	123631904	NM_001009936 // PHF19
9001	chr9	-	123964125	123964209	NM_016322 // RAB14
9002	chr9	-	124132438	124132462	NR_073037 // STOM
9003	chr9	-	124338354	124338440	---
9004	chr9	-	124922057	124922090	NM_014222 // NDUFA8
9005	chr9	-	127533374	127533398	NM_033334 // NR6A1
9006	chr9	-	127652714	127652738	NM_002077 // GOLGA1
9007	chr9	-	127920550	127920631	NM_001123355 // PPP6C
9008	chr9	-	128434633	128434657	NM_001006617 // MAPKAP1
9009	chr9	-	131483605	131483663	NM_032799 // ZDHHC12
9010	chr9	-	131516183	131516229	NM_006336 // ZER1
9011	chr9	-	131517709	131517733	NM_006336 // ZER1
9012	chr9	-	135702694	135702770	ENST00000477396 // AK8
9013	chr9	-	136280950	136280974	ENST00000445916 // REXO4

9014	chr9	-	136897021	136897225	NM_007371 // BRD3
9015	chr9	-	137741481	137741517	NR_039693 // MIR3689D1
9016	chr9	-	137742612	137742642	NR_039696 // MIR3689F
9017	chr9	-	138391717	138391753	NM_001048265 // C9orf116
9018	chr9	-	138397697	138398272	---
9019	chr9	-	138530964	138530991	NM_182974 // GLT6D1
9020	chr9	-	138585662	138586082	NM_001012415 // SOHLH1
9021	chr9	-	139304693	139304718	OTTHUMT00000055064 // SDCCAG3
9022	chr9	-	139326951	139327008	NM_019892 // INPP5E
9023	chr9	-	139369812	139369836	NM_014866 // SEC16A
9024	chr9	-	139567921	139568202	NM_006412 // AGPAT2
9025	chr9	-	139902381	139902405	NM_001606 // ABCA2
9026	chr9	-	139906737	139906761	NM_001606 // ABCA2
9027	chr9	-	139933114	139933340	---
9028	chr9	-	139959347	139959371	NM_178448 // SAPCD2
9029	chr9	-	140242610	140242634	NM_017820 // EXD3
9030	chr9	-	140260576	140260600	AK091390 // EXD3
9031	chr9	-	140332470	140332524	NM_001033113 // ENTPD8
9032	chrUn	+	102173	102197	---
9033	chrUn	+	114003	114078	---
9034	chrUn	-	88888	88969	---
9035	chrUn	+	183278	183359	---
9036	chrX	+	9929495	9929523	---
9037	chrX	+	11312925	11312950	NM_001142 // AMELX
9038	chrX	+	16672673	16672769	NM_004057 // S100G
9039	chrX	+	17737384	17737434	OTTHUMT00000055933 // NHS
9040	chrX	+	17767588	17767612	NM_001037540 // SCML1
9041	chrX	+	23802428	23802452	NR_027783 // SAT1
9042	chrX	+	24745988	24746012	NM_016937 // POLA1
9043	chrX	+	30261863	30261915	NM_002363 // MAGEB1
9044	chrX	+	35816909	35816938	ENST00000399985 // MAGEB16
9045	chrX	+	38530666	38530700	NM_004615 // TSPAN7
9046	chrX	+	40597445	40597889	ENST00000456333 // MED14-AS1
9047	chrX	+	41075408	41075432	NM_001039590 // USP9X
9048	chrX	+	42342218	42342276	---
9049	chrX	+	46405915	46406855	NR_015378 // ZNF674-AS1
9050	chrX	+	47089339	47089363	NM_006201 // CDK16
9051	chrX	+	47101869	47101893	NM_004651 // USP11
9052	chrX	+	47138533	47138627	---
9053	chrX	+	48242869	48242981	ENST00000376886 // SSX4B
9054	chrX	+	48435512	48435550	BX647914 // RBM3

9055	chrX	+	48687534	48688097	NM_181532 // ERAS
9056	chrX	+	49777856	49777942	NR_030397 // MIR660
9057	chrX	+	55246795	55246831	NM_130467 // PAGE5
9058	chrX	+	64618501	64618525	---
9059	chrX	+	64709088	64709147	NM_001010888 // ZC3H12B
9060	chrX	+	65486383	65486407	NM_138737 // HEPH
9061	chrX	+	68256908	68256934	---
9062	chrX	+	68836169	68836514	NM_001399 // EDA
9063	chrX	+	69255740	69257191	NM_001399 // EDA
9064	chrX	+	69489558	69489583	ENST00000477379 // ARR3
9065	chrX	+	70704761	70704785	AJ549247 // TAF1
9066	chrX	+	71908809	71908849	ENST00000595890 // PHKA1-AS1
9067	chrX	+	73218608	73218678	AK056172 // JPX
9068	chrX	+	73285795	73285837	XM_003120308 // LOC100506745
9069	chrX	+	74511233	74511260	ENST00000373373 // UPRT
9070	chrX	+	77380897	77380921	NM_000291 // PGK1
9071	chrX	+	83141604	83141682	NM_021118 // CYLC1
9072	chrX	+	84342715	84342739	NM_198450 // APOOL
9073	chrX	+	92953450	92953484	NM_001171110 // FAM133A
9074	chrX	+	99839922	99839946	NM_022144 // TNMD
9075	chrX	+	100479605	100479629	NM_001939 // DRP2
9076	chrX	+	101908602	101908626	NM_014710 // GPRASP1
9077	chrX	+	102585186	102585212	NM_152278 // TCEAL7
9078	chrX	+	105167205	105167229	NM_198465 // NRK
9079	chrX	+	105883803	105883947	NM_018015 // CXorf57
9080	chrX	+	106083317	106083341	NM_017752 // TBC1D8B
9081	chrX	+	107844640	107844664	NM_000495 // COL4A5
9082	chrX	+	109693817	109693842	NM_020769 // RGAG1
9083	chrX	+	113886019	113886096	NR_031733 // MIR1912
9084	chrX	+	113992699	113992724	OTTHUMT00000057958 // HTR2C-IT1
9085	chrX	+	114874034	114874058	OTTHUMT00000356233 // PLS3
9086	chrX	+	117900836	117900908	NM_001560 // IL13RA1
9087	chrX	+	117904530	117904616	AK123515 // IL13RA1
9088	chrX	+	118370354	118370620	NM_006667 // PGRMC1
9089	chrX	+	118533580	118533605	NM_145305 // SLC25A43
9090	chrX	+	119053827	119053856	ENST00000491105 // AKAP14
9091	chrX	+	128888469	128888493	NM_003399 // XPNPEP2
9092	chrX	+	129139249	129139273	NM_021946 // BCORL1
9093	chrX	+	130678975	130679024	ENST00000338616 // OR13H1
9094	chrX	+	133684020	133684057	ENST00000434384 // LINC00629
9095	chrX	+	134654686	134654729	NM_182540 // DDX26B

9096	chrX	+	134866229	134866296	NM_001007551 // CT45A5
9097	chrX	+	134883503	134883570	AK098689 // CT45A4
9098	chrX	+	135496442	135496466	NM_153834 // GPR112
9099	chrX	+	135582876	135582975	NM_001163280 // HTATSF1
9100	chrX	+	147011700	147011724	NM_002024 // FMR1
9101	chrX	+	147029975	147029999	ENST00000595272 // FMR1
9102	chrX	+	149657872	149657909	---
9103	chrX	+	150891100	150891209	NM_033085 // FATE1
9104	chrX	+	151923684	151923737	BC007228 // CSAG3
9105	chrX	+	152613152	152613176	ENST00000421401 // ZNF275
9106	chrX	+	153005554	153005654	NM_000033 // ABCD1
9107	chrX	+	153237784	153238300	ENST00000369982 // TMEM187
9108	chrX	+	153678305	153678366	ENST00000599055 // FAM50A
9109	chrX	-	307010	307034	---
9110	chrX	-	1613006	1613163	ENST00000460672 // P2RY8
9111	chrX	-	2420820	2420846	ENST00000441131 // DHRSX
9112	chrX	-	2877690	2877740	AK301004 // ARSE
9113	chrX	-	3450180	3450272	---
9114	chrX	-	3785023	3785065	---
9115	chrX	-	5979714	5979790	---
9116	chrX	-	8565166	8565190	NM_000216 // KAL1
9117	chrX	-	11445829	11445853	BC035785 // ARHGAP6
9118	chrX	-	12632128	12632308	---
9119	chrX	-	13060079	13060103	BX648919 // FAM9C
9120	chrX	-	13738556	13738580	AK098253 // TRAPPC2
9121	chrX	-	13956487	13956515	AK294314 // GPM6B
9122	chrX	-	19389470	19389494	NM_001001671 // MAP3K15
9123	chrX	-	19390961	19390985	ENST00000470101 // MAP3K15
9124	chrX	-	20185740	20185764	NM_004586 // RPS6KA3
9125	chrX	-	20967725	20967782	---
9126	chrX	-	24006067	24006840	NM_030624 // KLHL15
9127	chrX	-	32456439	32456463	NM_000109 // DMD
9128	chrX	-	47436838	47436873	NM_006950 // SYN1
9129	chrX	-	48755071	48755097	NM_001167947 // TIMM17B
9130	chrX	-	48830203	48830227	NM_020137 // GRIPAP1
9131	chrX	-	48900676	48900701	NM_006521 // TFE3
9132	chrX	-	48932336	48932360	NM_007075 // WDR45
9133	chrX	-	49012346	49012492	---
9134	chrX	-	49460548	49460572	NM_003785 // PAGE1
9135	chrX	-	49963343	49963392	NM_003886 // AKAP4
9136	chrX	-	52673296	52673321	NM_173358 // SSX7
9137	chrX	-	53572053	53572077	NM_031407 // HUWE1

9138	chrX	-	53583185	53583302	NR_029513 // MIR98
9139	chrX	-	54475321	54475345	NM_004463 // FGD1
9140	chrX	-	54482947	54482988	NM_004463 // FGD1
9141	chrX	-	55515374	55515421	NM_201286 // USP51
9142	chrX	-	64732661	64732685	NM_031206 // LAS1L
9143	chrX	-	69507126	69507170	NM_016484 // PDZD11
9144	chrX	-	72347734	72347919	NR_027291 // NAP1L6
9145	chrX	-	73803431	73809760	NM_016120 // RLIM
9146	chrX	-	77381493	77381717	---
9147	chrX	-	83362019	83362043	NM_014496 // RPS6KA6
9148	chrX	-	100169989	100170071	NM_212559 // XKRX
9149	chrX	-	100546238	100546286	NM_001168474 // TAF7L
9150	chrX	-	100764368	100764479	---
9151	chrX	-	100914268	100914361	BC052628 // ARMCX2
9152	chrX	-	102530241	102530267	NM_001012979 // TCEAL5
9153	chrX	-	102755726	102755750	NM_080879 // RAB40A
9154	chrX	-	102940627	102941005	ENST00000423833 // MORF4L2
9155	chrX	-	105281083	105281294	M14091 // SERPINA7
9156	chrX	-	106235599	106235623	EF125210 // MORC4
9157	chrX	-	107457406	107457430	NM_001847 // COL4A6
9158	chrX	-	110644319	110644343	NM_000555 // DCX
9159	chrX	-	111155818	111155939	NM_012471 // TRPC5
9160	chrX	-	118676607	118676631	---
9161	chrX	-	119759582	119759964	NM_152692 // C1GALT1C1
9162	chrX	-	119760066	119760777	NM_152692 // C1GALT1C1
9163	chrX	-	128788847	128788930	NM_017413 // APLN
9164	chrX	-	129003073	129003097	---
9165	chrX	-	129281852	129281882	ENST00000533719 // AIFM1
9166	chrX	-	129611109	129611217	---
9167	chrX	-	130407861	130407885	NM_001555 // IGSF1
9168	chrX	-	130408110	130408134	NM_001555 // IGSF1
9169	chrX	-	131762441	131762465	NM_001077188 // HS6ST2
9170	chrX	-	134936653	134936720	---
9171	chrX	-	135333537	135333561	NM_024597 // MAP7D3
9172	chrX	-	138790302	138790326	NM_001099855 // MCF2
9173	chrX	-	139805670	139805701	---
9174	chrX	-	139805916	139805949	---
9175	chrX	-	139806335	139806389	---
9176	chrX	-	146271223	146271305	---
9177	chrX	-	151560691	151560752	NR_029521 // MIR105-1
9178	chrX	-	151562884	151562945	NR_029522 // MIR105-2
9179	chrX	-	151881746	151881799	BC007228 // CSAG3

9180	chrX	-	153131340	153131364	ENST00000596146 // L1CAM
9181	chrX	-	153134603	153134627	---
9182	chrX	-	153214803	153214827	NM_005334 // HCFC1
9183	chrX	-	153278765	153278789	NM_001569 // IRAK1
9184	chrX	-	153305256	153305280	ENST00000597080 // MECP2
9185	chrX	-	153579290	153579314	NM_001456 // FLNA
9186	chrX	-	153594958	153594982	NM_001456 // FLNA
9187	chrX	-	153775227	153775339	ENST00000393562 // G6PD
9188	chrX	-	154255118	154255142	AK295164 // F8
9189	chrX	-	154493636	154493873	ENST00000369454 // RAB39B
9190	chrY	+	148072	148132	NM_018390 // PLCXD1
9191	chrY	+	545401	545530	NM_000451 // SHOX
9192	chrY	+	3447135	3447164	NM_139214 // TGIF2LY
9193	chrY	+	3904572	3904714	OTTHUMT00000088134 // OTTHUMG00000036214
9194	chrY	+	4924956	4924981	NM_032971 // PCDH11Y
9195	chrY	+	9304921	9305001	NM_003308 // TSPY1
9196	chrY	+	9531130	9531307	NR_001533 // TTTY8
9197	chrY	+	14465804	14465937	---
9198	chrY	-	6339073	6339250	NR_001533 // TTTY8
9199	chrY	-	6736346	6736370	NM_001143 // AMELY
9200	chrY	-	16389234	16389324	OTTHUMT00000088597 // OTTHUMG00000036405
9201	chrY	-	24050312	24050337	NM_001006118 // RBMY1E
9202	chr12	+	49521577	49521733	NM_006082 // TUBA1B
9203	chr17	+	20859598	20859622	ENST00000437829 // LOC339260
9204	chr17	+	40121999	40123252	AK296534 // CNP
9205	chr17	+	76352957	76353340	---
9206	chr22	+	38352783	38352807	NM_021974 // POLR2F
9207	chr22	+	38363654	38363678	NM_021974 // POLR2F
9208	chr22	-	25739871	25740899	---
9209	chr6	+	105850806	105850970	---
9210	chr7	+	105890793	105891343	---
9211	chr7	+	136938218	136938346	AK297725 // PTN
9212	chr9	-	93968499	93972420	AK091154 // FP2234
9213	---	---	---	---	---
9214	---	---	---	---	---
9215	chrU	+	7	94	---
9216	chrU	+	9	81	---
9217	chrU	+	24	57	---
9218	chrU	+	14	60	---
9219	chrU	+	17	47	---

9220	chrU	+	4	76	---
9221	chrU	+	4	77	---
9222	chrU	+	11	51	---
9223	chrU	+	6	75	---
9224	chrU	+	87	131	---
9225	chrU	+	1	43	---
9226	chrU	+	6	75	---
9227	chrU	+	343	479	---
9228	chrU	+	12	219	---
9229	chrU	+	1	481	---
9230	chrU	+	1	526	---
9231	chrU	+	31	301	---
9232	chrU	+	175	207	---
9233	chrU	+	40	228	---
9234	chrU	+	195	396	---
9235	chrU	+	40	501	---
9236	chrU	+	167	591	---
9237	chrU	+	2	344	---
9238	chrU	+	9	42	---
9239	chrU	+	1	864	---
9240	chrU	+	94	575	---
9241	chrU	+	38	373	---
9242	chrU	+	1	234	---
9243	chrU	+	108	232	---
9244	chrU	+	82	522	---
9245	chrU	+	204	1392	---
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9247	chrU	+	12	233	---
9248	chrU	+	68	331	---
9249	chrU	+	77	370	---
9250	chrU	+	45	136	---
9251	chrU	+	21	1790	---
9252	chrU	+	9	906	---
9253	chrU	+	319	689	---
9254	chrU	+	6	199	---
9255	chrU	+	3	1941	---
9256	chrU	+	1	852	---
9257	chrU	+	44	137	---
9258	chrU	+	53	813	---
9259	chrU	+	338	441	---
9260	chrU	+	35	351	---
9261	chrU	+	38	174	---

9262	chrU	+	31	339	---
9263	chrU	+	210	300	---
9264	chrU	+	1	392	---
9265	chrU	+	9	203	---
9266	chrU	+	23	208	---
9267	chrU	+	113	525	---
9268	chrU	+	1	97	---
9269	chrU	+	41	7459	---
9270	chrU	+	2	251	---
9271	chrU	+	13	50	---
9272	chrU	+	34	246	---
9273	chrU	+	8	219	---
9274	chrU	+	66	1891	---
9275	chrU	+	1	29	---
9276	chrU	+	44	412	---
9277	chrU	+	9	697	---
9278	chrU	+	44	572	---
9279	chrU	+	1	71	---
9280	chrU	+	7	195	---

WHAT IS CLAIMED IS:

1. A method for analyzing a biological sample, comprising:

(a) obtaining said biological sample from a subject;

(b) wherein when said subject is a female subject, assaying expression levels of two or more genes from **a female targeted set of genes** to generate an output comprising said expression levels from (b) indicative of said female subject's having or risk of having a condition comprising perfusion shortage or neoangiogenesis; and

(c) wherein when said subject is a male subject, assaying expression levels of two or more genes from **a male targeted set of genes** to generate an output comprising said expression levels from (c) indicative of said male subject's having or risk of having a condition comprising perfusion shortage or neoangiogenesis.

2. The method of claim 1, wherein said subject has or is at risk of having a condition comprising perfusion shortage.

3. The method of claim 1, wherein said female targeted set of genes comprises a plurality of genes listed in Tables 1, 3, and 5.

4. The method of claim 1, wherein said female targeted set of genes comprises a plurality of genes listed in Table 1.

5. The method of claim 1, wherein said female target set of genes comprises one or more, two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, twenty or more, thirty or more, forty or more, fifty or more, sixty or more, seventy or more, eighty or more, ninety or more, one hundred or more, two hundred or more, or three hundred or more of the genes selected from the group consisting of ZNF807, LOC100130331, LOC100130872, LINC01502, FAM66A, SRGAP3-AS3, MIR1185-1, MIR1266, MIR1261, MIR4262, MTRNR2L10, MIR3928, LOC100507065, LOC100507642, MIR1273F, MIR4519, MIR4799, MIR4747, PTPRU, LOC100996660, DNAL4, XXYLT1-AS2, LOC101927230, LOC101927377, LOC101927479, LOC101927503, LINC01186, LOC101927735, LOC101927880, LINC01486, LOC101928775, RHOXF1P1, LOC101929108, LOC101929330, LOC101929696, CEACAM5, LAMTOR5, CELP, SLC27A4, RCC1, STMN2, CAPN11, FDX1L, MIR155HG, CSMD2, PNMA5, HSPA12B, CLN5, LRRC38, COL3A1, ARHGEF19, PROKR2, COX6C, PTRH1, KRTAP13-1, ASB9, CRYGC, VTI1A, BEST3,

SLC22A31, ADIG, LINC01104, PYDC2, PRSS3P2, OTUD7A, DCC, RBM46, TCEANC, ADAMTS17, EFNA5, CELSR2, U2AF1L4, PIKFYVE, KCTD6, PTPLB, EMX1, OR9I1, JAZF1, LAMB4, FOXC2, NCOA6, MESDC2, FBXO28, DNMBP, U2SURP, ABCA6, CBX5, CBLC, KIF4A, C20orf166-AS1, NUDT8, NUP210P1, SMCO1, MAP7D2, ALX3, FAM133B, SUN2, HECTD1, WIPI2, SNORD53, GJA8, DHDH, GPR4, MRGPRG-AS1, LOC283731, LINC00304, ZNF763, IGHV1-58, LOC284933, RBMY1A3P, GPX5, MED4, C6orf15, GUCY1A2, GUCA2A, HUNK, TFAP2E, POTEA, LEUTX, OR2T3, IGFALS, C19orf45, FAM99A, IGFL3, OR2M1P, FAM90A25P, C8orf86, TMEM8C, PABPN1L, LIG4, FLJ26245, KRT16P2, PRSS57, LTBP3, MIR215, ARSF, MEF2C, IQSEC3, LOC441179, ZNRF2P1, MT1M, MTIF2, MYO7A, NDUFB9, ATP2B1, MIR422A, CEND1, LARS, UFM1, PDHA2, CES1P1, PLTP, LURAP1, MRPS21, MED1, PPP1R3C, RBM41, ASIC4, ZNF821, PPP1R9A, TRMU, UTP6, CCDC177, TBC1D24, GPR158, NYNRIN, BAI2, GBA3, PTPRO, RAC3, CDH26, RPLP0, BGN, FAM204A, PJA1, MT1IP, SHBG, LOC646513, SLA, SKOR2, SLC34A1, SNRPD1, SOX9, SP1, MIR532, TDG, TNNI3, DNLZ, LOC729739, C8A, VIPR2, USP7, DDX39B, ICE2, DCSTAMP, HIST1H4J, ZNF484, REG4, LRRIQ1, FAM126A, DOCK7, RNMT, ST3GAL5, GAL3ST3, SLC25A21, FATE1, UNC5A, TBX18, FIBP, DLGAP1, MGME1, SYCE1, HAND1, TNFRSF8, MAP4K4, GOSR1, SETDB1, SLC23A2, DOPEY2, and TBX5-AS1.

6. The method of claim 1, wherein said male targeted set of genes comprises a plurality of genes listed in Tables 2, 4, and 6.

7. The method of claim 1, wherein said male targeted set of genes comprises a plurality of genes listed in Table 2.

8. The method of claim 1, wherein said female target set of genes comprises one or more, two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, twenty or more, thirty or more, forty or more, fifty or more, sixty or more, seventy or more, eighty or more, ninety or more, one hundred or more, two hundred or more, or three hundred or more of the genes selected from the group consisting of SNORD115-37, SNORD115-24, SNORA11B, MIR876, COL4A2-AS2, LOC100130373, LOC100130548, LOC100131496, LINC00240, BCL2L11, MED16, ERVV-2, KRTAP21-3, LOC100289230, LOC100289283, MIR1275, MIR1912, MIR1302-7, MIR1231, MIR1238, MIR1179, MIR1908, MIR1237, MIR2116, CSN1S2BP, MIR3148,

MIR4280, MIR3116-1, MIR3129, MIR4275, MIR4326, MIR4254, LINC00673, MIR3926-2, MIR3678, MIR548Z, MIR3657, MIR3935, LOC100505478, LINC01364, C16orf95, LINC00837, MIR3529, MIR4475, MIR4492, MIR4784, MIR4732, MIR4684, MIR4773-2, MIR4429, MIR4442, LINC00507, LOC100996345, CYYR1-AS1, LOC100996635, CDK4, LOC101927053, PDZRN3-AS1, MEOX2-AS1, LINC01186, NA, GBAT2, LINC01214, LOC101928101, LOC101928118, NA, LOC101928195, LOC101928385, TCONS_00029157, LOC101928668, LINC01450, NA, LOC101928823, LOC101928919, LINC01262, LOC101929031, LOC101929159, LOC101929468, LOC101929497, ZNF267, CHERP, IFI44, FUT9, RFPL2, IFI44L, MAPRE2, SLC27A5, CHD1, RABL2B, FSTL1, MRPL3, GLB1L3, GPR182, CHRM5, SMIM12, LRRC37B, SMYD4, TBCB, KLHDC3, RPL39L, CLTB, PRSS30P, PCP2, FITM2, SNTN, TMEM68, OTUD6A, CRP, DYNLL2, CRYGD, NA, TMC8, CSTB, SLC35F3, CCDC140, WDSUB1, SH3D19, TEX28, FEZF1-AS1, ESCO2, ZNF645, CYP51A1, DAB1, ZCCHC12, DNMT3A, DRP2, EGR2, ABCA2, CDY2B, SENP5, EVI2B, ALCAM, ABCD1, F12, FAH, OR5A2, CCDC89, FABP5P3, FGF4, FGF14, DIP2A, ATP11B, NUP210, EXOC6B, ARC, SASH1, GRIP1, SEC61G, SCRIB, POLA2, GABARAPL1, DEFB108B, DEFB113, FTH1P3, CDRT15L2, HEATR9, ALS2CL, ASPM, OR2F1, GATA2, PLA2G2D, GCNT1, AGO1, OR7A5, OR1J2, SNORA70, GNAI3, BCL9L, OTOGL, SLC46A3, EWSAT1, LINC00927, C16orf54, MAMSTR, MCHR1, LOC284825, IGHD2-21, IGHD2-15, EOGT, C8orf31, IGLV10-54, IGLV3-12, SNX24, ARHGAP35, SCG3, PYCR2, SLC39A3, H3F3B, ANXA5, CXXC1, CDR2L, HNF4A, HNRNPK, SNORD56B, KRTAP20-1, KRTAP20-2, LOC339166, ZFP69, LOC340074, KIAA1875, OR2T8, PAQR9, IFNGR1, IGFBP1, KRTAP10-10, IL13RA1, KCNA3, KCNA5, TPTE2P6, LHFPL3, KCNJ10, LINC00162, KCNS3, KRTAP5-1, CC2D2B, RPRML, LRRC14B, OR52N2, LAMA4, LIPE, LINC00200, LINC00668, ZNF880, LOC400756, ASB18, LRRD1, LDLRAD2, LYN, MIR127, MIR210, MIR181A1, MIR9-1, MIR98, MIR99B, MIR17HG, MAFG, MAS1, MAX, MLF1, SUGT1P1, RPS26P11, MYO10, NDUFB9, NKX3-1, NOS1, NRGN, MIR375, DUOX2, RRP15, NMD3, KLHL5, RPL26L1, EGFL7, PCYT1A, CDC40, UFC1, ERGIC3, SF3B6, PFDN4, PIK3C2G, DDIT4, EGLN1, FAM20A, HEATR3, CEP72, THSD1, PSME2, MIR362, MIR494, MIR520C, MIR516B2, MIR502, MIR508, ERMN, RANBP10, SH3RF1, FBRSL1, RET, EXOC4, TGIF2, RPL3L, BCORL1, CCL5, SDCBP, RRAGC, XYLT2, ACOT6,

POPDC3, LINC00535, CCT6P1, TSG1, NA, BLVRA, NARFL, CSMD1, SGSH, NDST4, NA, EFTUD1P1, SIPA1, SLC5A4, PCP4L1, SLC9A2, LYNX1, MIR539, CAPN15, SPAG1, SPRR3, SQLE, SRI, SCARNA2, SCARNA16, TACR1, SNORD66, SNORD84, SNORD91A, SNORD97, MIR552, MIR563, MIR591, TCF19, TNP1, MIR660, SDHAP3, LOC729224, FAHD2CP, SEC14L6, MEIS1-AS3, WNT9A, SNORD113-3, SNORD114-3, SNORD114-9, SNORD114-18, SNORD114-27, SNORD114-30, MIR758, MIR668, ZNF134, PPDPF, OR5H2, CERS4, OGFOD2, LIN28A, NEK11, DCAKD, GPR157, EFHC2, CXXC4, PBX4, CPTP, NPRL3, OR2B2, AKAP17A, PCDH11Y, FAM103A1, TRAPPC9, HYAL3, CASP5, TTTY11, RAB34, NACAP1, SPOP, ZMYND12, LLPH, C22orf23, GTPBP3, SUV420H2, HAT1, SHANK3, KIAA1755, DENR, NPFF, MARCO, JRKL, PAGE1, PABPC4, SYNGAP1, SGPL1, BUD31, HIST1H3F, SYT8, MAP7, ZFAND2A, RGN, VAPB, RCSD1, SLIT2, NCR2, PAGE4, RNF7, MTFR1, CD59, and ATP2C2.

9. The method of claim 1, further comprising obtaining a range of control expression levels of said female targeted set of genes.

10. The method of claim 1 or 5, wherein said assaying comprises comparing said expression levels of (b) with said range of control expression levels of said female targeted set of genes.

11. The method of claim 1, further comprising obtaining a range of control expression levels of said male targeted set of genes.

12. The method of claim 1 or 7, wherein said assaying comprises comparing said expression levels of (c) with said range of control expression levels of said male targeted set of genes.

13. The method of either claim 5-8, wherein when said expression levels from either (b) or (c) are outside said range of control expression levels, said subject has said condition comprising perfusion shortage or neoangiogenesis is at risk for having said condition.

14. The method of any of claims 1-9, wherein said biological sample comprises isolated hematopoietic endothelial precursor cells (EPCs), fractions thereof, or secretions thereof.

15. The method of claim 14, wherein said hematopoietic endothelial precursor cells (EPCs) is Flk-1+.

16. The method of claim 14, wherein said hematopoietic endothelial precursor cells does not express a cell surface marker, Flk-1.

17. The method of either claims 15 or 16, wherein said hematopoietic endothelial precursor cells are positive for makers selected from Flt1, Flt4, VEGFR1, CXCR4, CD31, CD34, CD105, CD133, Sca-1, and c-Kit.

18. The method of any of claims 1-10, wherein said output from (b) and said output from (c) both have an accuracy greater than about 84%.

19. A method for analyzing a biological sample obtained from a subject, comprising:

(i) subjecting **a plurality of hematopoietic endothelial precursor cells (EPCs), fractions of said plurality of hematopoietic EPCs, secretions of said plurality of hematopoietic EPCs,** or any combination thereof isolated from said biological sample, to a gene expression analysis, wherein said gene expression analysis comprises assaying expression levels of two or more genes from a plurality of identified genes; and

(ii) generating an output comprising said gene expression levels, wherein said gene expression levels are indicative of said subject's having or risk of having a condition comprising perfusion shortage at least in part based on said expression levels.

20. The method of claim 19, wherein said plurality of hematopoietic EPCs comprises a cell surface marker of Flk-1/KDR.

21. The method of claim 15, wherein said plurality of hematopoietic EPCs does not comprise a cell surface marker of Flk-1/KDR.

22. The method of claim 21, wherein said plurality of hematopoietic EPCs are positive for makers selected from Flt1, Flt4, VEGFR1, CXCR4, CD31, CD34, CD105, CD133, Sca-1, and c-Kit.

23. A method of analyzing a biological sample obtained from a subject, comprising:

(i) subjecting a biological sample obtained from said subject to a gene expression analysis, wherein said gene expression analysis comprises assaying expression levels of two or more genes from a plurality of identified genes; and

(ii) generating an output comprising said gene expression levels indicative that said subject has or is at risk of having a condition comprising perfusion shortage **with an accuracy that is greater than 91%,** wherein when said assaying comprises a method selected from the group consisting of cDNA chip array analysis, quantitative (RT) PCR, microarray analysis,

multiplexing, Luminex analysis, nucleic acid sequencing, northern blot analysis, genomic high throughput sequencing, nanostring, massive parallel signature sequencing (MPSS),serial analysis of gene expression (SAGE), enzyme-linked immunosorbent assay (ELISA), protein sequencing, mass spectrometry (such as MALDI TOF, QTOF, or SELDI TOF), quantitative western blot analysis, and peptide barcoding.

24. The method of claim 19, wherein said biological sample comprises isolated hematopoietic endothelial precursor cells (EPCs), fractions, or secretions thereof.

25. The method of either claim 15 or claim 19, wherein said plurality of identified genes comprises a female targeted set of genes and a male targeted set of genes.

26. The method of claim 19, wherein said female targeted set of genes comprises a plurality of genes listed in Tables 1, 3, and 5.

27. The method of claim 19, wherein said male targeted set of genes comprises a plurality of genes listed in Tables 2, 4, and 6.

28. The method of either claim 22 or claim 23, further comprising obtaining a range of control expression levels of said female targeted set of genes or of said male targeted set of genes and comparing said gene expression levels from (i) of either claim 15 or claim 19 to said range of control expression levels.

29. The method of claim 24, wherein when said expression levels from (i) of either claim 15 or claim 19 are outside said range of control expression levels, said subject has perfusion shortage or is at risk for having said condition comprising perfusion shortage.

30. A method of analyzing a biological sample, comprising:

obtaining said biological sample from a subject that has or is at risk for having a condition comprising perfusion shortage, **wherein said perfusion shortage is at an early stage and has not caused any detectable tissue damage**;

assaying expression levels of two or more genes from a plurality of identified genes to generate an output comprising said expression levels indicative of said subject's having or is at risk of having said condition comprising perfusion shortage.

31. The method of any of claims 1-26, wherein said perfusion shortage is neoangiogenesis.

32. The method of any of claims 1-26, wherein said perfusion shortage is ischemic heart disease.

33. The method of any of claims 1-26, wherein when said subject is a female subject, further comprising assaying less than 60, 40, or 14 genes from said plurality of genes listed in Tables 1, 3, and 5.

34. The method of claim 29, further comprising assaying less than 14 genes from said plurality of genes listed in Tables 1, 3, and 5.

35. The method of any of claims 1-26, wherein when said subject is a male subject, further comprising assaying less than 40, 25, 15 genes from said plurality of genes listed in Tables 2, 4, and 6.

36. The method of claim 31, further comprising assaying less than 15 genes from said plurality of genes listed in Tables 2, 4, and 6.

37. The method of claim 26, wherein said output has an accuracy greater than about 99%.

38. The method of claim 26, wherein said output has an accuracy greater than about 98%.

39. The method of any of claims 1-34, wherein said output further comprises providing an assessment of a severity of said subject's perfusion shortage.

40. The method of any of claims 1-34, wherein said output further comprises providing a prognosis report of said subject's perfusion shortage.

41. The method of any of claims 1-34, wherein said output further comprises providing a response report of said subject upon, during, and/or after a medical intervention.

42. The method of any of claims 1-34, wherein said output further comprises providing a monitoring report of said subject before or after receiving said medical intervention.

43. The method of any of claims 1-38, further comprising providing a treatment to said subject, wherein said subject has or is at risk of having a condition comprising perfusion shortage, at least in part based on said output.

44. The method of claim 39, wherein said treatment comprises administering an anti- or pro-ischemic medical intervention, anti- or pro- neoangiogenesis medical intervention to the subject, invasive monitoring, advanced imaging, or any combinations thereof.

45. The method of claim 40, wherein said medical intervention comprises a pharmacotherapy, or surgical or percutaneous procedure.

46. The method of claim 41, wherein said surgical or percutaneous procedure comprises a bypass surgery or a percutaneous coronary procedure.

47. The method of claim 40, wherein said medical intervention comprises administering a pharmaceutical composition selected from the group consisting of beta-blockers, calcium channels antagonists, nitrates, aspirin, cholesterol-lowering compounds, angiotensin-converting enzyme (ACE) inhibitors, and ranolazine.

48. The method of any of claims 1-43, wherein said medical intervention targets one or more genes listed in Tables 1-6.

49. The method of claim 43, wherein said medical intervention further comprises modulating expression levels of one or more genes listed in Tables 1-6.

50. The method of either claim 36 or claim 37, at least based in part on response report, prognosis report, or both, further comprising ceasing said medical intervention.

51. The method of claim 38, at least based in part on monitoring report, further comprising employing advanced imaging comprising invasive angiography, advanced imaging, nuclear imaging, MSCT, MRI analysis, tissue biopsy, monitoring of mechanical ventilation, or a combination thereof.

52. The method of any of claims 1-47, wherein said subject does not have any symptom.

53. The method of any of claims 1-47, wherein said subject is at least diagnosed with one of ischemic cardiovascular disease, ischemic heart disease, coronary artery disease, cardiovascular congenital disease, stroke, transient ischemic attacks, microvascular disease, microvascular dementia, claudication intermittents, Burgers disease, Thromboangiitis obliterans, Buerger disease, lymphangiogenic disease, hypertrophic or dilating cardiomyopathy, heart failure, pulmonary and peripheral emboli, oncological disease (including solid tumors, and hematological and lymphogenic metastatic oncological disease), macro angiopathy, micro angiopathy, neo angiogenesis, diabetes mellitus, ophthalmic disease, nephrological disease, orthopedic disease, gynecological disease, Parkinson's disease, multiple sclerosis, inflammatory or auto-immune disease, erectile dysfunction, sports injury, Crohn's disease, colitis ulcerosa, pulmonary fibrosis, COPD, emphysema, and cystic fibrosis.

54. The method of any of claims 1-47, wherein said subject has at least one symptom of chest pain, chest discomfort, shortness of breath, limited exercise tolerance, ventricular or atrial arrhythmia, profuse sweating, aphasia, loss of motor or sensory function, and vision disturbance.

55. The method of any of claims 1-47, wherein said subject has at least one risk factor for having a condition comprising perfusion shortage, wherein said risk factor is selected from the group consisting of high blood pressure; glucose intolerance; family history of cardiovascular disease, hypercholesterolemia, or dyslipidemia ; aging; smoking; physical inactivity; obesity; previous cardiovascular disease; diagnosis of diabetes mellitus, kidney disease, peripheral artery disease, or metabolic syndrome; gender; high low density lipoprotein (LDL) level; high cholesterol level; and specific DNA polymorphism associated with higher cardiovascular risk.

56. The method of any of claims 1-51, wherein said hematopoietic EPCs are positive for makers selected from VEGFR2, CD309, Flt1, Flt4, KDR1, VEGFR1, CXCR4, CD31, CD34, CD105, CD133, Sca-1, and c-Kit.

57. The method of any of claims 1-51, said obtaining further comprises isolating said Flk1+ cells, fractions thereof, or secretions thereof from a biological sample of said subject.

58. The method of claim 53, wherein said biological sample is selected from the group consisting of blood or blood fractions, saliva, urine, stool, cerebrospinal fluid, semen, vaginal secretions, sputum, sweat, breast milk, synovial fluid, mucus, tears, bile, gastric fluid, interstitial fluid, transudate, exudate, and tissue biopsy.

59. The method of any of claims 1-54, assaying further comprises detecting nucleic acid expression levels, splice variant expression levels, peptide expression levels, or any combination thereof corresponding to said plurality of genes listed in Tables 1-6.

60. The method of claim 55, detecting said nucleic acid expression levels or splice variant expression levels or both expression levels comprising employing cDNA chip array analysis, quantitative (RT) PCR, microarray analysis, multiplexing, Luminex analysis, nucleic acid sequencing, northern blot analysis, genomic high throughput sequencing, nanostring, massive parallel signature sequencing (MPSS),and serial analysis of gene expression (SAGE), or any combination thereof.

61. The method of claim 55, detecting peptide expression levels comprises employing enzyme-linked immunosorbent assay (ELISA), protein sequencing, mass spectrometry (such as MALDI TOF, QTOF, or SELDI TOF), quantitative western blot analysis, and peptide barcoding, or any combination thereof.

62. The method of any of claims 1-57, further comprising transmitting said output onto an intranet or internet.

63. The method of any one of claims 1-62, further comprising at least one of:

identifying a previous episode of the condition in the subject when the expression levels of at least two genes from Tables 1-6 are outside of a range of control expression levels of said at least two genes from Tables 1-6;

diagnosing the subject as having the condition when the expression levels of at least two genes from Tables 1-6 are outside of a range of control expression levels of said at least two genes from Tables 1-6;

determining the subject to be at risk of the condition when the expression levels of at least two genes from Tables 1-6 are outside of a range of control expression levels of said at least two genes from Tables 1-6;

prognosticating an outcome in the subject based on a presence of, or degree to which the expression levels of at least two genes from Tables 1-6 are outside of a range of control expression levels of said at least two genes from Tables 1-6;

predicting a response of the subject to a medical intervention or measuring the response of said medical intervention based on a presence of, or degree to which the expression levels of at least two genes from Tables 1-6 are outside of a range of control expression levels of said at least two genes from Tables 1-6;

selecting a medical intervention for the subject or measuring the response of said intervention, (for example such as, by way of a surrogate marker) based on a presence of, or degree to which the expression levels of at least two genes from Tables 1-6 are outside of a range of control expression levels of said at least two genes from Tables 1-6;

selecting a dose and/or frequency of a medical intervention based on a presence of, or degree to which the expression levels of at least two genes from Tables 1-6 are outside of a range of control expression levels of said at least two genes from Tables 1-6;

validating a candidate medical intervention based on an effect of the candidate medical intervention on a presence of, or degree to which the expression levels of at least two genes from Tables 1-6 are outside of a range of control expression levels of said at least two genes from Tables 1-6;

measuring a response to a candidate medical intervention, wherein the measuring comprises the expression levels of at least two genes from Tables 1-6 are outside of a range of control expression levels of said at least two genes from Tables 1-6;

monitoring a subject's response to a medical intervention based on the expression levels of at least two genes from Tables 1-6; or

treating a subject with a nucleotide sequence listed in Tables 3 and 4 or a peptide sequence listed in Tables 3 and 4.

64. A kit comprising a plurality of probes that is configured to detect expression levels of two or more genes listed in Tables 1-6.

65. The kit of claim 60, wherein said plurality of probes is a nucleic acid probe configured to bind to a sequence of a gene listed in Tables 1-6.

66. The kit of claim 60, wherein said plurality of probes is an antibody configured to bind to a protein encoded by a gene listed in Tables 1-6.

67. A method of **profiling gene expression for determining one or more genes as signature for a perfusion shortage risk**, comprising:

(a) assaying gene expression in a cell from a subject with a perfusion shortage risk, and a control set;

(b) detecting a subset of genes expressed at an altered state in the cell of the subject compared to the control set;

(c) using a machine learning algorithm for analysis of a combination of genes expressed at an altered state to determine the sufficient number of such genes to identify a gene expression signature for a perfusion shortage risk;

(d) **rectifying a possible accuracy score** based on a follow-up monitoring period with the subject;

(e) generating an output of one or more genes that is a signature for a perfusion shortage risk, such that the signature has a predictive accuracy of a perfusion shortage risk that exceeds 66%.